

Europe: ECJ decision calls all mutagenesis "GMO" and subject to EU GMO regulation

Product based going discussions stem

Planted

Establishing a Community to Advance Plant Gene Editing in Europe

Australia: Revised regulation exclude editing applications

- Positive Decision**
- No formal decision**
- Restrictive Decision**

 Welcome to the December 2019 Issue of GARNish



Jill Harrison

University of Bristol

Member of GARNet Advisory Committee

Welcome to the December 2019 issue of GARNish, reporting on current news from the UK plant science community

As ever this issue highlights some recent conferences as well as highlighting forthcoming ICAR 2020 and 2021, Genetics society Arabidopsis and Monogram meetings. I would also like to highlight a recent Marchantia workshop hosted by Justin Goodrich and Laura Forrest at the Royal Botanic Garden Edinburgh and supported by The Genetics Society and Company of Biologists. It was great to hear about the advantages of the bryophyte life cycle in addressing reproductive transitions, and low genome complexity in addressing plant-microbe interactions and gene functions. It was also great to hear about BBSRC OpenPlant outcomes and roles for Botanic Gardens' research in basic plant science- we may narrowly escape a name change for Marchantia to Chlamydomonium!

A key theme emerging from recent GARNet committee meetings has been diversity of UK research and researchers. Although GARNet was founded to represent the interests of the Arabidopsis community, its remit is now broader, aiming to serve those interested in fundamental aspects of plant science in general. GARNet embraces the uses of newer model systems for basic research such as Marchantia in its Ethos, as well as seeking opportunities to make new links between academics and horticulturalists or

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Special thanks to: Jonathan Carruthers, Isabel Mendoza, Richard Wyatt, Laura Dixon, Vivek Raxwal, Mike Pound, Claire Domoney, Roxana Teodor, Jill Harrison, Vicky Spencer, Dennis Eriksson, the BBSRC grant holders and the faculty members at Leeds.

industrial partners.

In a new GARNet grant proposal that is currently under review we propose to explicitly promote training opportunities for researchers undertaking discovery-led research irrespective of organism of study. Therefore we will (hopefully) look forward to interacting with researchers in other communities both mentioned above and throughout this edition of GARNish.

The GARNet committee has recently discussed a UKRI Strategic Framework launched in autumn 2019 and established to promote a more inclusive research and innovation culture. GARNet also aims to strengthen opportunities for women and people of poorly represented ethnicities to improve the diversity of UK researchers, and is currently discussing possibilities for cross-institutional mentoring to address bias against

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
Committee member Jan 2017–Dec 2019

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

success in funding applications, particularly from minority ethnic applicants.

2020 will bring change for GARNet, as Dan Gibbs, Murray Grant, Steven Spoel and I roll off the committee [*Coordinators note: we thank each of these committee members for their input to GARNet activities*]. New appointments to the committee will be made subject to a successful outcome for GARNet's recent funding application.

As always, stay up to date with the advances of the community via @GARNetweets, our website (www.garnetcommunity.org.uk) and blog (<http://blog.garnetcommunity.org.uk/>).

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

UK Plant Sciences Federation Update



Jonathan Carruthers

Royal Society of Biology

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The UKPSF ran a session for biology undergraduates about plant science careers at the Royal Society of Biology's popular 'Bioscience Careers Day' event in October. Geraint Parry chaired the discussion, at which students learnt about career pathways from Richard Dale (Herbicide Molecular Sciences Team Leader, Syngenta), Rory Osborne (Postdoctoral Research Fellow, University of Birmingham), and Laura Crook (Research Technician and Weed Ecologist, Rothamsted Research). Increasing the visibility of career options in plant science is recommended in the UKPSF Growing the Future report, launched earlier this year (rsb.org.uk/growingthefuture).

We arranged nine summer placements in summer 2019 through our Plant Health Undergraduate Studentships (PHUGS) programme, now in its third year. These placements provide 10-week summer research projects for undergraduates, in line with priorities in plant health identified by Defra. PHUGS aims to address skills and capacity challenges in plant health science, provide training opportunities, generate plant health research outcomes and build networks of research groups, scientists and employers. This year, seven of the students attended and presented posters at the BSPP Presidential Meeting in September. PHUGS is run by the UKPSF, and was made possible by our sponsors: Defra, BSPP, N8 AgriFood and the David Colegrave Foundation. The scheme will return next year, and opportunities to host students will be advertised in February at rsb.org.uk/plant-studentships.

We are getting ready for the International Year of Plant Health, during which we will be hosting a workshop for early career professionals in plant health from across sectors. The workshop will be held on 20-22 October at Sand Hutton, York, in collaboration with Defra, Fera Science Ltd and the Animal and Plant Health Agency. It will be structured around grand challenges in plant health with the aim to provide opportunities to identify consensus actions and bring communities together to address current and future challenges.

Did you know the UKPSF creates a monthly round-up of policy news about plant science? You can subscribe to the newsletter and keep up to date with all our activities at rsb.org.uk/ukpsf.

The UKPSF is a special advisory committee of the Royal Society of Biology.

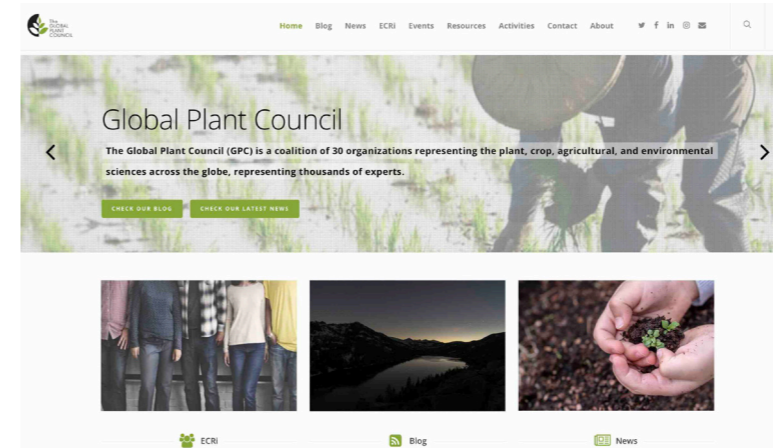
Global Plant Council Update

Isabel Mendoza
GPC Communications Officer
isabel@globalplantcouncil.org

The Global Plant Council (GPC) has continued working to promote plant science yet one big thing has changed since our last update. Our website was relaunched in early September with a new look and layout. Now, both blog and website are merged in one single site, and we have new events sections, easier to navigate.

<http://globalplantcouncil.org/>

Besides, GPC has continued its strategy of publishing plant science news daily, which are later distributed on our social channels (Twitter, Facebook, Instagram, and LinkedIn). According



The new GPC website: <http://globalplantcouncil.org/>

to our maths, we are now reaching 17.000 online plant science enthusiasts.

Additionally, the Early Career Researcher International Network (ECRI) is ongoing. The idea is to help early-career researchers with their job hunting, grant funding, dissemination and networking. As for now, the ECRI network is a set of activities:

- 1- The monthly #plantscijobs "twitterstorm". Each storm takes place every last Friday of the month, between 3-4 pm CEST, launched from our principal Twitter account.
- 2- We also manage a Facebook and a LinkedIn #plantscijobs devoted group, where we post daily opportunities related to plant science. Those posts are posted regularly, with the hashtags #plantscijobs, #plantsciprizes, #plantscinternships....
- 3- We have prepared a curated list of plant science jobs and grants resources provided by our members.
- 4- And we are gathering a collection of resources to help plant scientists disseminate their research more efficiently towards the general public.
- 5- We are planning hosting a workshop on science communication in parallel to our annual meeting. First workshop took place at the ICAR2019

conference held in June 2019 in Wuhan (China), and discussed how to promote "your" science to the media and general public. We are planning the next one to take place at Plant Biology Europe 2020 in Torino (Italy). Will keep you posted!

Please consider contacting our communications Officer Isabel Mendoza with suggestions on ECRI. Any offers of help in rolling out this network will be greatly appreciated

CONNECTED V4 Update

Richard Wyatt
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Heading into 2020 the CONNECTED Network has over 1,300 members: plant scientists and entomologists collaborating to find ways of tackling vector-borne plant diseases that devastate Sub-Saharan African food crops.

The past 12 months has been a focused whirlwind of activity, learning and collaboration.

CONNECTED organised three major training events, in Kenya, Nigeria and the UK. Working in collaboration with BecA-ILRI Hub, The International Institute of Tropical Agriculture, Newcastle University and The Natural Resources Institute they trained 54 early career researchers from 15 countries.

Feedback was extremely positive and, crucially, all delegates confirmed they're sharing new skills with others in their





home networks. Dissemination is taking place to over 1,000 colleagues across Sub-Saharan Africa. Other training opportunities included a Training Voucher scheme, funding training visits, each up to £3,000 in value. 18 awards went to members from 11 different countries.

CONNECTED has provided pump-prime funding for no fewer than 20 research projects, currently being undertaken in 13 countries. Short articles about them are available on the CONNECTED website.

The network ran a workshop at 'Ento 19', The Royal Entomological Society's major annual event. It also secured funded places for two members to attend the 2019 Grand Challenges Annual Meeting in Ethiopia, and provided two others with fully-funded places at a leading bioinformatics course in Uppsala, Sweden.

CONNECTED actively communicates opportunities and resources using its website, Twitter and Facebook channels. Five films were published in 2019, all are on the CONNECTED Vimeo page.

<https://vimeo.com/connectedvirusnetwork>

Two highlight research projects, two feature training courses, and there's a fun 90-second animated film.

<https://vimeo.com/368515777>

The CONNECTED Network relishes the chance to build on its work in 2020, not least as it's International Year of Plant Health (IYPH), a terrific opportunity to raise global awareness on how protecting plant health can help end hunger, reduce poverty, protect the environment, and boost economic development.

You can join the CONNECTED Network at www.connectedvirus.net/join

Visit Quantitative Plant

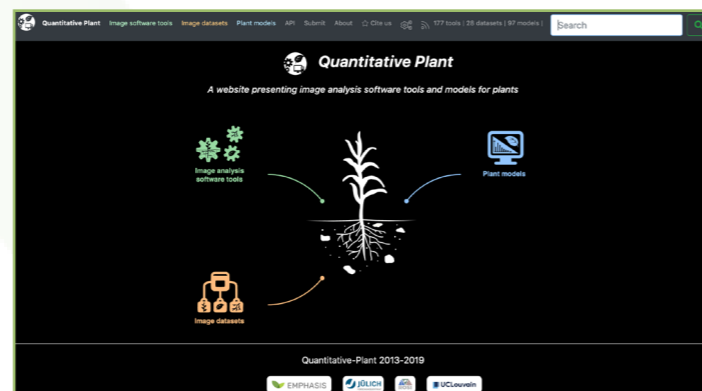
Please take some time to take a look at the resources at <http://quantitative-plant.org/>.

This is the new name for <https://www.plant-image-analysis.org> which is a resource founded and maintained by Guillaume Lobet who is an Assistant Professor at Forschungszentrum Jülich and the UCLouvain. The aim of this website is to help plant researchers to find the right tool or model for their research.

Quantitative Plant has extensive sections on:

1. Image Software Tool
2. Image datasets
3. Plant Models

This is truly a remarkable **community-facing resource** and is a must-go-to compendium for any plant scientist.



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/>

Twitter: #ICAR2020 @ICAR_2020

The annual flagship meeting for discovery-led plant science research with a focus on Arabidopsis will take place in Seattle in July 2020.

Detlef Weigel and Joanne Chory will provide the ICAR2020 Keynote talks.

The organisers have engaged with the community to ask for suggestions for concurrent sessions. The response has been remarkable with 88 different applications from across the globe. This clearly shows that given the opportunity, researchers want to take ownership of these large conferences so that they represent the needs of the community.



The organising committee has done a superb job of selecting an exciting and diverse set of plenary speakers. This meeting will truly represent all areas of the plant science community.

Registration for the meeting will open soon. This promises to be an outstanding event at a great location!

Genetics Society Arabidopsis Meeting

21st-22nd April 2020

University of Durham

After a 10 year Hiatus, the Genetics Society Arabidopsis Meeting is back with a two-day meeting on the 21st and 22nd of April, 2020 at the department of Biosciences at Durham University

Scientific sessions include:

- Development
- Abiotic Interactions
- Teaching Plant Biology
- Natural Variation
- Biotic Interactions
- Computational Biology



GenSoc Invited Speakers include:

Christian Hardtke (University of Lausanne)
 Veronica Grieneisen (Cardiff University)
 Steven Spoel (University of Edinburgh)
 Vardis Ntoukakis (University of Warwick)
 Mary Williams (ASPB & University of Glasgow)
 Henrik Jönsson (SLCU, Cambridge)
 Celia Knight (University of Leeds)
 Ian Henderson (University of Cambridge)
 Yoselin Benitez-Alfonso (University of Leeds)
 Uli Bechtold (University of Essex)
 Heather Knight (Durham University)
 Dan Gibbs (University of Birmingham)
 Sarah Robinson (SLCU, Cambridge).

Registration and Conference Fees:

Genetics Society Members: £45
 (Membership number required (see www.genetics.org.uk/membership to join)
 Non-members: £65

GARNet are delighted to support a pre-meeting workshop on the opportunities for translation of research from Arabidopsis to rice.

Contact Peter Etchells

peter.etchells@durham.ac.uk for more information

<http://www.genetics.org.uk/events/arabidopsis/>

 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 June 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](https://twitter.com/ICAR2021) @ICAR_2021



 Monogram 2020
 University of Dundee
 April 28th-30th 2020

<https://ics.hutton.ac.uk/monogram20/>

The Monogram Network consists of UK based researchers with an active interest in small grain cereal and grass (including the C4 energy grasses) research. Commercial scientists and plant breeders are active members and provide the link between Monogram science and commercial exploitation. Monogram includes both basic and more applied research and its members span disciplines including plant genetics, physiology, pathology, breeding, and bioinformatics. We also have extensive expertise in outreach activities and links with industry.

Monogram aims to promote coordination and information flow amongst the community and ensure its visibility at the national and international level, thereby strengthening UK

efforts in these species. Monogram is the focal point for integration of the UK grass and cereals community and represents it at the UK Plant Sciences Federation. We also hope to integrate more closely with the wider plant sciences community and provide a link to help lower the entry barriers for new researchers in the area.

Conference Themes

- > Development
- > Phenotyping
- > Recombination
- > Future Plant Sciences
- > Quality and Nutrition
- > Abiotic and Biotic Stresses
- > Genomic technologies for Crop Improvement
- > Below and Above Ground Processes
- > Rice and other Grasses

Monogram Early Career Excellence Awards

Nominations are invited for the 8th annual MonoGram Early Career Excellence Award (MECEA). These awards are aimed at PhD students and early career researchers. <https://ics.hutton.ac.uk/monogram20/>

GARNet are delighted to provide support to enable Early Career Researchers who work at the interface of model organisms and crops to attend the meeting.

Details of these £200 awards can be found here:

<http://blog.garnetcommunity.org.uk/garnet-grants-for-monogram2020/>

monogram20@hutton.ac.uk
[#monogram20](https://twitter.com/monogram20)

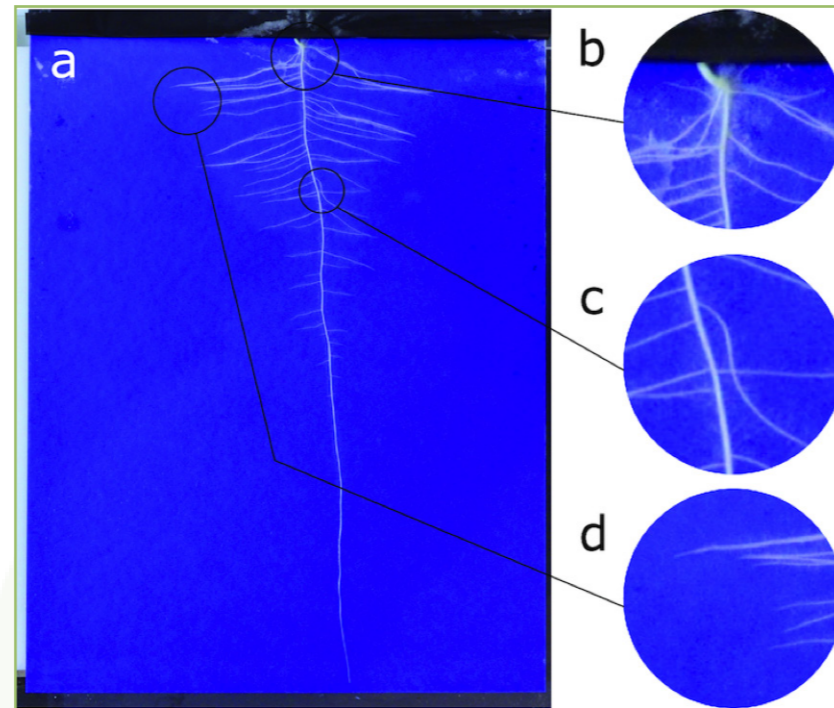


Introducing RootNav2.0

Plant Science research can involve making a lot of routine measurements that can demand significant researcher time, which might be better used setting up or planning additional experiments. Many plant scientists are therefore looking to use computer-aided automation to help with often-mundane phenotyping tasks.

One of the primary challenges with the development of automated systems for measuring plant roots is that they do not generally grow in straight lines! Plants grown vertically on paper or agar-plates will have roots that overlap and tangle whilst heterogeneous backgrounds and lighting mean that it can be challenging to obtain consistent images for subsequent downstream analysis.

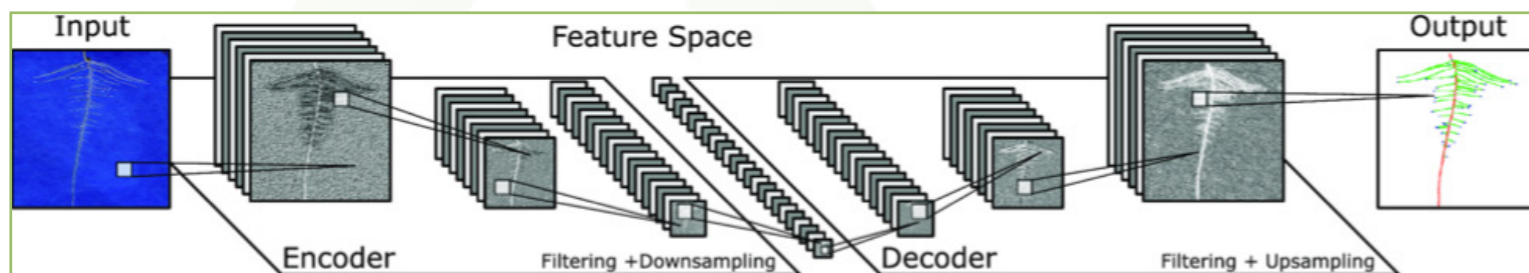
The recently published RootNav2.0 software tool uses modern deep-learning approaches to tackle many of these difficulties and can discriminate features within complex root architectures (Yasrab *et al*, 2019). In contrast to the previously developed and semi-automated RootNav1.0 system (<https://www.plant-image-analysis.org/software/rootnav>), RootNav2.0 is fully automated. The designers trained and subsequently tested the RootNav2.0 software using images of roots from Wheat, Arabidopsis and *Brassica napus*. This demonstrates that, following



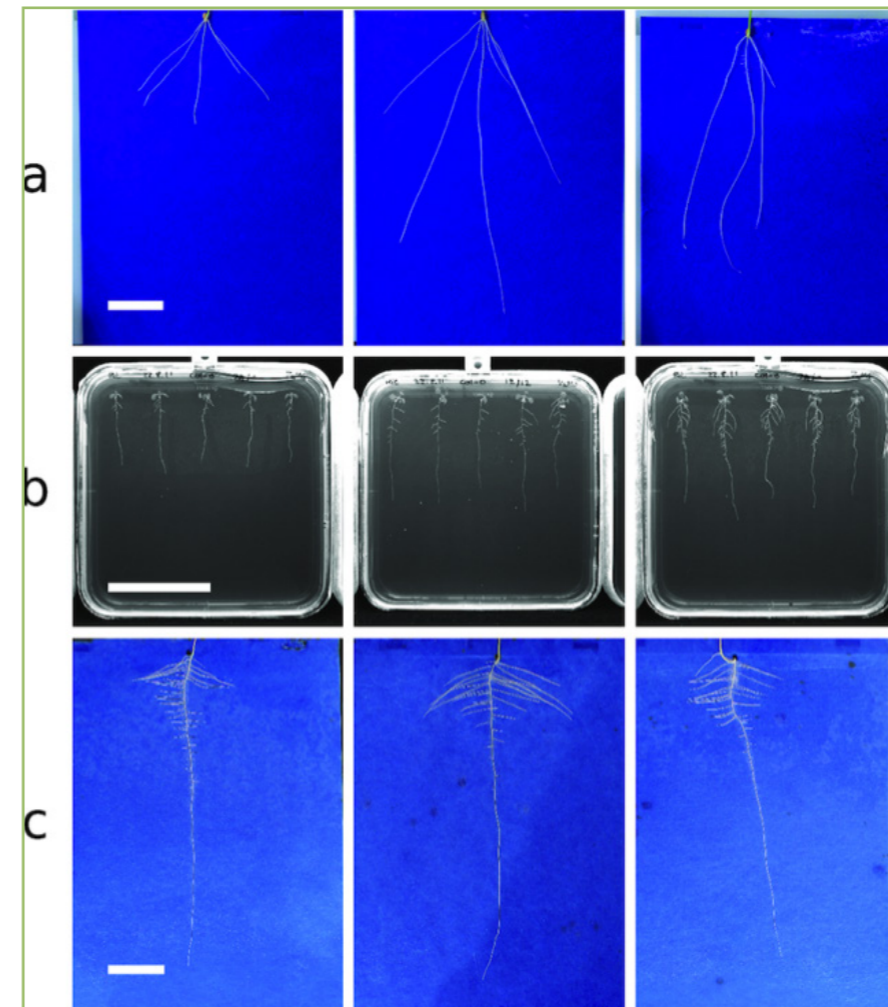
An example of the challenge root phenotyping presents for computer vision. a) A sample input image of a *Brassica napus* seedling grown on germination paper. This plant phenotype exhibits a single primary root and numerous lateral roots. b) Cluttered scenes make segmentation challenging. c) Complex occlusion and intersection makes extracting root topology difficult. d) Many small image features, such as root tips, occur in close proximity, making identification difficult. From <https://doi.org/10.1093/gigascience/giz123>

a short period of network training, the tool is applicable to many plant species.

RootNav 2.0 is driven by a deep network that segments images of root systems into classes: background, first-order roots, and second-order roots. Reliable segmentation of whole roots underpins all subsequent improvements and the network designers have achieved this goal whilst also reducing computer memory consumption.



A simplified example illustrating the major components of a CNN in an encoder-decoder configuration. The encoder performs a combination of filtering operations including convolutional filters, spatial downsampling, and normalization. These layers convert the original image into a high-dimensional feature space but with very low spatial resolution. The decoding network performs similar layer operations but replaces downsampling with upsampling to return the feature representation back into a spatially high-resolution image. From <https://doi.org/10.1093/gigascience/giz123>



Example images from each of the 3 datasets used during this work. (a) Wheat (*Triticum aestivum* L.). (b) Arabidopsis (*Arabidopsis thaliana*). (c) Rapeseed (*Brassica napus*). Scale bars are 50 mm long. From <https://doi.org/10.1093/gigascience/giz123>

The designers compared this automated system, which independently recognizes seeds, primary and secondary roots, with the semi-automated RootNav1.0 that requires an expert-user to initially identify these features. The tools compared very well and by learning from initial errors, the designers were able to improve the network learning capabilities of RootNav2.0.

The primary training dataset was comprised of 3,630 images of wheat roots and the designers then used 'transfer learning' to adapt the tool for learning and then analysis of smaller sets of first Arabidopsis and Brassica images. The challenges when moving from Wheat to Arabidopsis images include their different root structures, moving from

colour to BW images and the growth of five (not one) plants on a single plate. However after minor modifications the segmentation and path-finding algorithms were able to adapt to these images. The measurements of primary and secondary root lengths in Arabidopsis were favourably comparable with an expert using RootNav1.0, even though there were some challenges with over-counting of the number of roots on a plate.

A clear benefit of fully automated RootNav2.0 is that once images have been submitted the required human interaction time is zero. Therefore batch-processing of images could occur overnight, giving the user the delight of a morning dataset to investigate!

Finally it is worth noting that RootNav 2.0 doesn't measure root systems itself but rather outputs root architectures to RSML files. These can be analysed using the RootNav Viewer tool <https://github.com/robail-yasrab/RootNav-Viewer-2.0>

RootNav2.0 is free for all to use and the authors it has been tested across all commonly used operating systems. Full instructions and code can be obtained through GitHub <https://github.com/robail-yasrab/RootNav-2.0>.

If potential RootNav2.0 users have any questions then please contact Dr Mike Pound at the University of Nottingham michael.pound@nottingham.ac.uk

Introducing artMAP

Peter Javorka, Vivek K. Raxwal,
Jan Najvarek and Karel Riha

About artMAP

artMAP is an easy to use software developed for biologists with no bioinformatic expertise to analyze results of forward genetic screens in Arabidopsis. It identifies de novo mutations that associate with a desired genetic trait from deep sequencing data with a few clicks of mouse. The artMAP is available at github (<https://github.com/RihaLab/artMAP>) and its description is published in Plant Direct (<https://onlinelibrary.wiley.com/doi/full/10.1002/pld3.146>). artMAP is a result of collaboration between plant geneticists from Central European Institute of Technology at Masaryk University (Czech Republic) and the software developer company Artin (Czech Republic).

Why we develop it?

Forward genetic screen is an approach to identify and select individuals with desired phenotype from a mutagenized population and establish the relationship between phenotype of interest and its underlying genotype. The key advantage of forward genetic screen over gene knock out or other reverse genetic approaches is its ability to link biological functions to unknown genes in an unbiased manner. Furthermore, in contrast to knock-outs, forward genetic screens produce broad range of gene variants with different degree of gene functionality. For these reasons, forward genetic screens have been employed in many model organisms.

A genetic screen in Arabidopsis begins with the mutagenesis of seeds (M0), usually

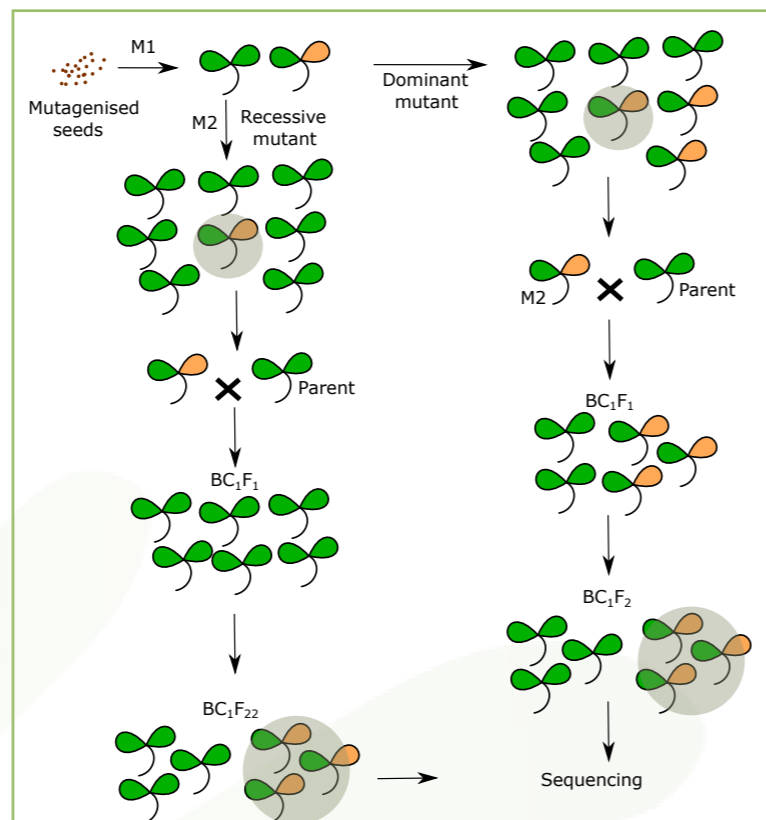


Figure 1: Schematic representation of forward genetic screen. Image credit: Javorka *et al* 2019 (<https://doi.org/10.1002/pld3.146>). License under CC- BY-NC-4.0

by ethyl methanesulfonate (EMS), followed by screening self-pollinated M1 or M2 plants for the phenotype of interest. Dominant mutations exhibit their phenotype in the M1 generation, whereas recessive mutations are scored in M2 (Figure 1).

For both dominant and recessive mutations, M2 plants are either crossed with another Arabidopsis ecotype or back-crossed to the parental strain to produce recombinant mapping populations. The pool of plants displaying the desired phenotype is sequenced, providing the location of the associated genomic region and a set of candidate mutations. This approach greatly reduces the time and resources required to identify the causal mutation and also circumvents the dependence on genetic markers. However, this approach requires extensive expertise in bioinformatics as well as computational infrastructure to analyze high throughput sequencing data. The artMAP provides

bioinformatics solution for data analysis of EMS based forward genetic screens in Arabidopsis. The artMAP: overnight data analysis solution for forward genetic screen

The artMAP pipeline consists of several open sources tools integrated into a docker container (<https://www.docker.com/>) to provide a graphical user interface and the ability to run on all the three computer platforms (Windows/Mac/Linux). The installation of the artMAP is easy and step by step guide is presented in the YouTube videos (https://www.youtube.com/channel/UCLuNTfubqt_Cs8VQ2Rn9UKg).

Usage of artMAP is simplified by its graphical user interphase where user provides basic information such as format of data, type of data, read length of the data and input/output file locations. The artMAP process the input file locally and store the output file in the user-defined folder. The artMAP also provides information about the undergoing process with processing bar.

artMAP displays the final results as a graph, where the frequency and position of each SNP are plotted along Arabidopsis chromosomes (Figure 2). These graphs can be zoomed in and can also be saved. Hovering the cursor over SNP reveals key information such as the location, frequency, affected gene, protein and DNA level changes, and the predicted the impact of the SNP. This visualization of the data facilitates a rapid assessment of the results and identification of the region associated with the phenotype.

The results are also provided as a tab-delimited file with information containing the location of each SNP (chromosome number and position), reference base, mutated base, coverage over the base (depth), frequency, gene identity, and effect on protein change if any. Based on the

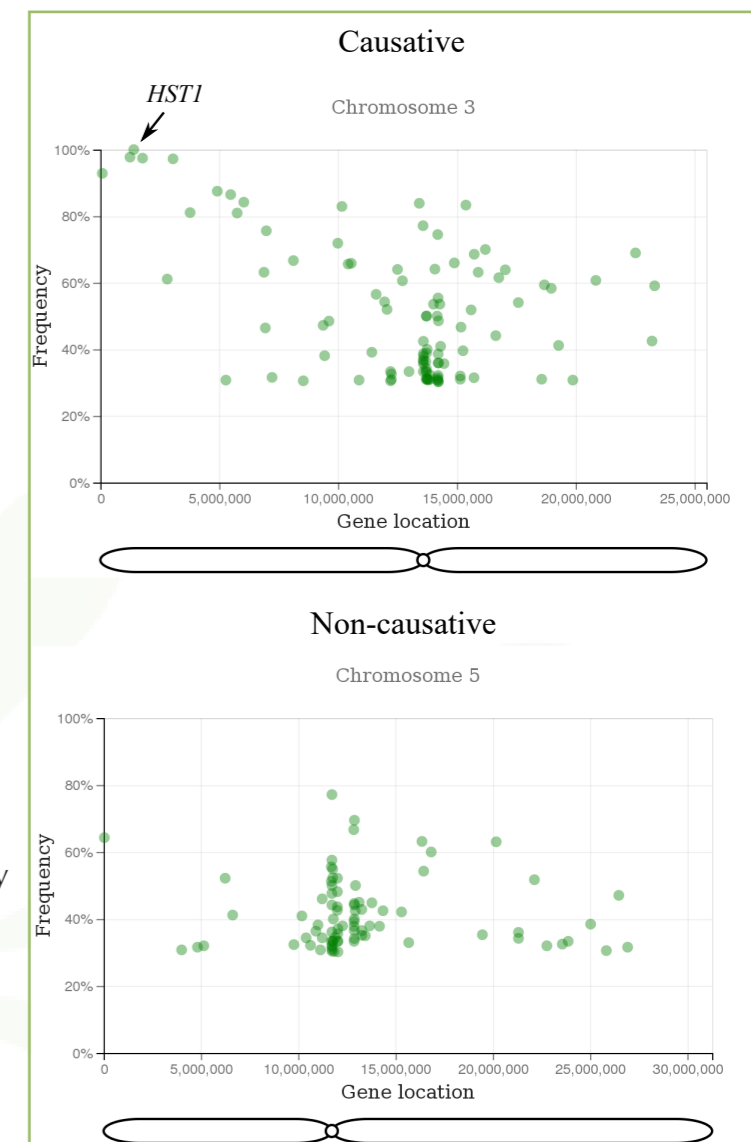


Figure 2: A representative figure of the example run showing the output of the artMAP analysis. Image credit: Javorka *et al* 2019 (<https://doi.org/10.1002/pld3.146>). License under CC- BY-NC-4.0

graph and tab-delimited file, a user can identify the putative candidate gene for further testing. In addition, artMAP produces the intermediary files for each stage of the pipeline, in case it is required.

In case of any queries please contact Vivek Raxwal (vivek.raxwal@ceitec.muni.cz) or Karel Riha (karel.riha@ceitec.muni.cz). The development of artMAP was supported by Ministry of Education, Youth and Sports of the Czech Republic, European Regional Development Fund-Project „REMAP“ (No. CZ.02.1.01/0.0/0.0/15_003/0000479) and by the Czech Science Foundation (16-18578S).



PCGIN Stakeholder Meeting:
November 14th 2019

Belton Woods Hotel, Grantham

Despite apocalyptic rain and imminent flooding it was a pleasure to travel to Grantham in Lincolnshire for the 2019 Stakeholder meeting of the Pulse Crop Genetic Improvement Network (PCGIN). The overall aim of the PCGIN network is to develop genetic resources in those pulse crops that are most relevant for UK industry and farming, namely Pea (*Pisum sativum*) and Faba Bean (*Vicia faba*).

PCGIN is one of four GINs that shared Defra investment of £5.5M for the period 2018-2023. The other GINs are VeGIN (leafy vegetables- <https://warwick.ac.uk/fac/sci/lifesci/research/vegin/>), WGIN (wheat- <http://www.wgin.org.uk/>) and OREGIN (oilseed rape- <http://oregin.info/>).

For non-experts it is important to note that the term “pulses” is limited to legume crops harvested solely as dry grains, which differentiates them from other legume vegetables that are harvested while still green (<https://pulses.org/what-are-pulses>). Therefore dry peas would be considered a pulse but not the green peas that are harvested earlier as vegetables. No doubt there

will be genetic components that make varieties more amenable for one use or another!

The PCGIN2019 meeting brought together a mixed selection of 70 stakeholders from academia, government and industry and was split into 3 broad sections. Firstly the academic GIN leaders Prof Claire Domoney (John Innes Centre), Dr Tom Wood (NIAB) and Prof Donal O’Sullivan (University of Reading) gave a progress report on the developing genetic resources in pea and faba bean. The second section provided an eye-opening industrial perspective on the UK pulses industry and in particular how the reality of ‘Plant Protein Power’ is stimulating the industry. Finally a set of short student talks was followed by updates from ‘pulse-facing’ community-resources.

Working toward linking traits to genes.

The PCGIN resource update highlighted the progress toward development of genetic maps in pea and faba bean, which will facilitate marker-assisted breeding in these species. Two cultivated pea mapping populations now have over 3500 SNP markers each and associated trait data has been collected for yield, plant height, seed parameters and disease resistance.

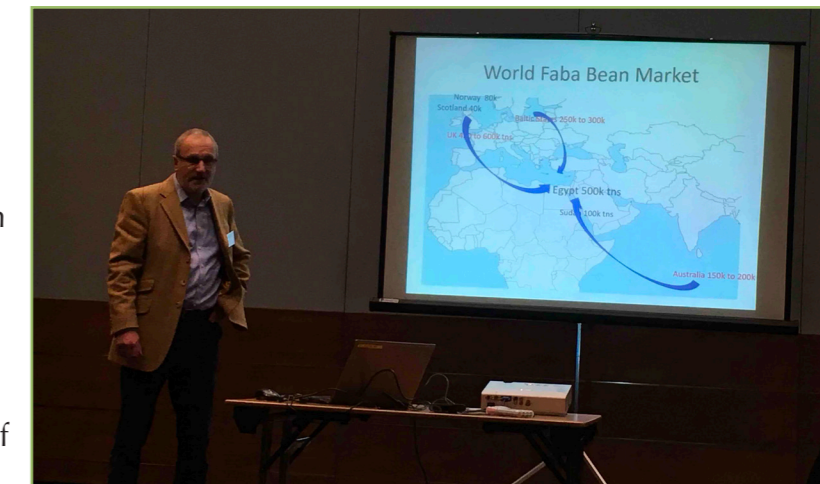
Existing pea germplasm has been successfully screened at NIAB for resistance to downy mildew, with the identification of 54 accessions that developed no disease symptoms. The available faba bean germplasm shows significant variation in the response to both downy mildew and chocolate spot (*Botrytis fabae*). The future interrogation of the genetic basis of these resistances will be extremely important in the future generation of cultivated disease resistance crops.

Researchers at the University of Reading have generated a high-density array in faba bean with over 28K SNPs that are well dispersed across its six chromosomes. In addition a novel germplasm population in the Hedin/2 reference line has been generated through EMS mutagenesis. The M2 plants will be screened in the spring of 2020 in Reading and they offer an open invitation for anyone interested in screening for their trait of interest to come along to help out!

The Future is Pulse(ing)

For those of us in attendance (...maybe it was just me) who hadn’t thought much about the current marketplace for peas and beans, the industry session was extremely informative. Growing environmental awareness, the embrace of veganism and consumer demand for plant protein should be a major boost for the UK pulse industry....

However Andy Bury from Frontier Agriculture suggested that UK farmers aren’t yet familiar enough with these crops to maximise outputs; with yields sitting at around 4.5tn/hect when there is potential for 7tn/hect. He also highlighted that farming faba bean is challenging as the crop is sensitive to hot weather and that insect predators are currently getting the upper



Andy Bury describing the global market for Faba Beans

hand in the UK. Clearly there will be opportunities to work toward the development of resistant crops!

The Healy group is a food ingredient company and as such is involved in many aspects of the UK pulse market. Paul Sheldrake provided a fascinating insight into the seemingly enormous potential of pea protein that is allergen and GMO-free (a problem with soybean). There is also a significant call for the development of varieties and processing techniques that enable the production of pea protein that has a ‘meaty’ texture ideal for the meat-free burger industry. In general Paul explained that the global availability and the wider flavor profile of peas was an important consideration as to why they are more popular than beans in the production of plant protein.

Nick Saltmarsh from Hodmedods (who sell dry pulses) and Chris Harrison from Novofarina (yellow pea powder) gave interesting insights into the challenges of bringing new products to the market. Nick described the challenging cycle wherein dried faba beans are not well-known by UK consumers so Hodmedods needed to engage with ‘celebrity chefs’ to create faba bean recipes. However consumer-facing media outlets were reluctant to use these recipes as dry faba beans could not be purchased in the shops.....thus

<https://www.jic.ac.uk/pulse-crop-genetic-improvement-network-pcgin/>





Barneys Faba Bean beer. Tasty!

preventing consumers learning about the product, completing the cycle! Hodmedods are making progress with this challenge and now some of the UK-grown faba beans are actually making it to UK consumers! <https://hodmedods.co.uk/>

Expanding Access to Pulse Germplasm

Pete Iannetta from the James Hutton Institute gave a brief progress update from the Horizon2020-funded 'TRUE: TRAnsition paths to sUstainable legume based systems in Europe' project. This is an extremely varied and wide-ranging project that heavily features pea and faba bean amongst the research of its partner organisations across 24 case studies. Dr Iannetta described (and provided samples of) the development of the Cool Beans IPA with Scottish beer maker Barneys, which is made from 40% faba beans. Your author can confirm these beans can make a tasty IPA! The TRUE project is coordinated from the JHI and is responsible for the informative website that

includes details about each partner, case study and ongoing output (<https://www.true-project.eu/>).

The final talk was from Noam Chayut who introduced the John Innes Centre Germplasm Resources Unit and the bespoke SeedStor interface. The unit manages the 3500+ JIC Pisum Collection and SeedStor provides detailed 'Passport' and 'Phenotype' information for each of these lines for interested users.

As someone new to this research-community it seemed many of the issues raised by industry might be a long way from the concerns of academic researchers. However it also appears that there would be significant opportunities for academic-industrial collaborations at many places along the production pipeline.

Both discovery-led and more applied research in this area will be enhanced by genetic information on traits, the use of the novel mutagenised faba bean population and development of the faba bean genome assembly as well as through use of recently available pea genomes (e.g Kreplak *et al* (2019) A reference genome for pea provides insight into legume genome evolution. Nature Genetics 51 <https://www.nature.com/articles/s41588-019-0480-1> and others produced within PCGIN).

The growing environmentally-driven consumer need for **locally grown, plant-derived protein** should provide opportunities for UK researchers to attempt to understand nitrogen-fixation, disease resistance and phenotypic determinants in UK pulse crops. Hopefully this is a research area that can make a greater move into the UKRI-funding space over the coming five years. I would encourage researchers to search-out these resources and make contact with the PCGIN leaders if they have any ideas!

OREGIN Stakeholder Meeting: November 26th 2019

Processor and Growers Research Organisations (PGRO)

Peterborough

OREGIN is the DEFRA-funded GIN that is focused on generating resources for the UK Oil Seed Rape (OSR) community. The Scientific Project manager is Professor Ian Bancroft at the University of York whilst the project website is held at the University of Hertfordshire.

<http://oregin.info/about-oregin>

This OREGIN stakeholder meeting very much focused on farmers and how the community can help in what is a challenging time for OSR growers. A general theme throughout the meeting was on the huge challenges that the community is facing from pathogens, particularly from Cabbage Stem Flea Beetle (CSFB). In particular the recent banning of neonicotinoid pesticides has made it extremely difficult to manage the spread of CSFB.

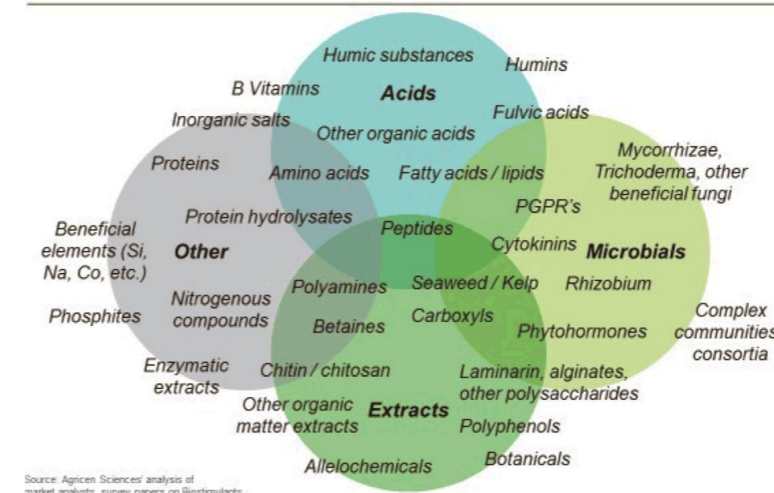
Stephen Beal from **BlueShed Consulting** provided a somewhat downbeat keynote talk in which he highlighted the limited current seed treatment options to tackle CSFB predation. Unfortunately the somewhat-bare cupboard has meant that UK OSR yields have decreased by 26% since 2012. Stephen suggested the future is with 'Biological' pesticides but the landscape for those products and their regulation is currently confusing.

Peter Berry from ADAS gave an overview of the AHDB Oilseed YEN, which is a national competition for farmers to report their best OSR yields. <https://yen.adas.co.uk/projects/oilseed-yen> He reported that recent weather conditions have accounted for 37% of yield variation with dry Decembers and Aprils conducive to higher productivity. This is potentially worrisome given the wetter conditions that we are expecting due to climate change.

Sacha White who is a Senior Entomologist at ADAS described a project that looked to develop an Integrated Pest Management plan to tackle CSFB infections. This involved the analysis of CSFB incidence from >1600 farm sites over 14 years. He showed that defoliation, through either grazing or mowing reduced the number of CSFB larvae but that this corresponded to a yield decrease. Late drilling of winter OSR (after Sept 21st) reduced CSFB larvae numbers yet had little effect on the leaf area lost to predation.

This project was challenging as, despite analysis of large datasets, no silver bullet emerged to be able to tackle the CSFB problem. Interestingly the ADAS study reported that no currently used OSR varieties exhibited any resistance to CSFB. This is area of interest to Jessica Hughes, who is a PhD student at the John Innes Centre. Across both greenhouse experiments

The Emerging Landscape of Products – Broad and (Potentially) Confusing



Source: Agriscience's analysis of market analysis, survey papers on Biostimulants



Jessica Hughes who works at the John Innes Centre discusses her PhD research

and field trials Jessica has tested 100 lines from the OREGIN OSR diversity set for CSFB resistance and found an excellent candidate that was both unpalatable to adult CSFB and also supported less larvae. This research is promising and she is currently working to identify candidate genes responsible for this resistance.

If Jessica can identify a causative locus then this might be an important candidate for future introduction into commercial varieties. This would be an excellent result for the OREGIN project and emphasise the strength of the Academic-Industry-Farming links that characterise this type of project.

Lenka Havlickova from York provided an update on the OSR genetic resources that have been developed both through the OREGIN and BBSRC-funded Renewable Industrial Products from Rapeseed (RIPR) projects. With multiple academic partners they have co-analysed the 285-line diversity panel with both Trait and Associative Transcriptomic data. Currently this strategy has identified 15 candidate genes for the 42

analysed traits.

Given future follow-on support these lines will be analysed to assess whether they are appropriate to be introduced into commercial lines. Furthermore Lenka reported on the resequencing of 600 RIPR lines that have been gamma irradiated. They are identifying both deleted regions as well as Inter-Homoeologue Polymorphisms throughout this collection, which will clearly add to the available genetic diversity available in OSR. The genetic resources generated by the RIPR and OREGIN projects can be accessed here: <https://yorkknowledgebase.hosted.york.ac.uk/resources.html>

The stakeholder meeting ended with a discussion about how the community can best tackle the current sector challenges.

Overall there was a real feeling that the connections between different stakeholder groups was increasing as this was the second year that there was an increased presence from industry stakeholders and farmers.



Lenka Havlickova from the University of York introduces UK Brassica Genetics Resources. Photo @defra_OREGIN

Introducing the SCI-Agrifood Group

I'd wager most GARNish readers will not be aware of the Society of Chemistry Industry (SCI) as, on the face of it, the name doesn't appear to be particularly relevant for plant scientists. However SCI is a surprisingly diverse society that has two main broad aims:

1. To promote links between chemistry related sciences and industry for the benefit of the public
2. Commercialisation of science via new products and processes = to foster Innovation

The activities of the society, which was founded in 1881, are driven by a series of technical and regional groups that bring together like-minded scientists from across academia, industry and other areas. Some of these Technical groups have a focus on chemical aspects of different areas of plant science, most clearly in the SCI-Horticulture and SCI-Agrisciences group.

<https://www.soci.org/interest-groups/technical-groups>

Other Technical groups that have a more peripheral interest to plant sciences include the 'Food', 'Lipids' and 'Environmental, Health and Safety' Groups. These groups obtain central funding to support the activities of a committee that organizes events and support competitions in relevant areas.

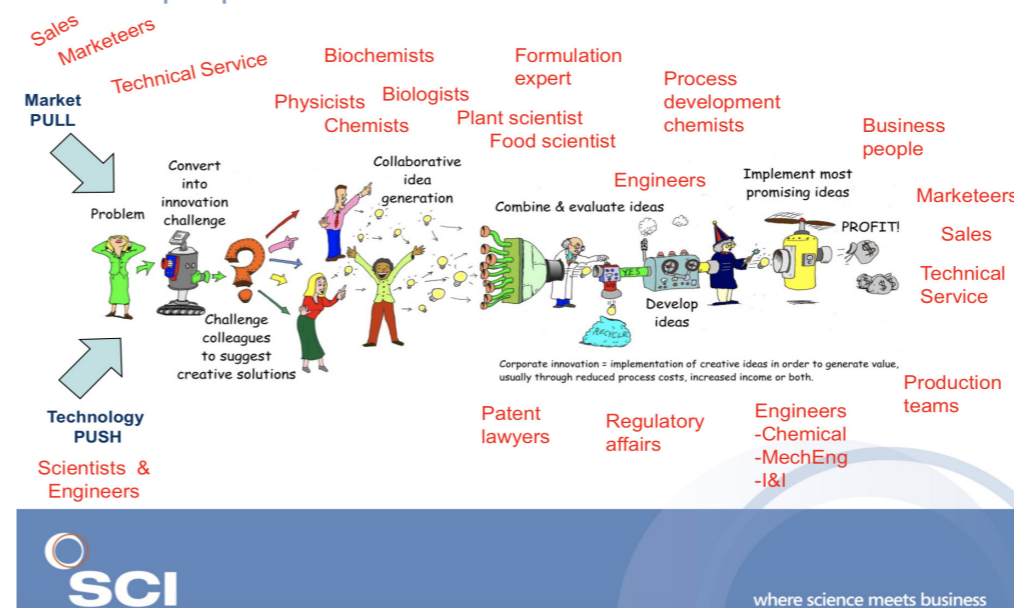
In October 2019 the Horticulture group hosted its David Millar Awards event at RHS-Wisley where PhD student award winners presented their research, which was very much in the discovery-led area of plant science and therefore of potentially great interest to the GARNet community. The winners receive £500 to support travel to present their research at an international conference. The 2019 award winners worked on modeling banana disease (Juniper Kiss from Exeter), the effect of climate change on dormancy in apple trees (Carlota Gonzalez Nogueur, NIAB-EMR) and the mechanisms of receptor kinase signaling in Arabidopsis (Jack Rhodes, The Sainsbury lab). These awards are administered by Sebastian Eves-van den Akker at Cambridge and GARNet will certainly advertise the 2020 awards.

Alison Foster (<https://thegardeningchemist.wordpress.com/>) is the chair of the SCI-

Horticulture committee and has a vision for this group to form further interactions with other plant science societies. There is little doubt that their focus on the chemistry of plant science will be an excellent complement to other peoples activities. Alison also authors a Plant of the Month blog-post that provides plenty of interesting insights into the chemistry of her selected plants.

<https://www.soci.org/interest-groups/technical-groups/horticulture-group/plant-of-the-month-2019>

SCI: The Innovation Process is complicated and needs lots of people – all of whom need to talk to each other!



✿ Introducing new projects funded through UKRI-BBSRC Responsive mode

✿ A Novel Set of SNARE Partners Facilitating Bacterial Pathogen Defence

Rucha Karnik,
University of Glasgow.

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Dr Rucha Karnik, is a Royal Society University Research Fellow and her lab is based within the Plant Science Group in the Institute of Membrane and Systems Biology at the University of Glasgow. Her research centres around understanding how plant growth and responses to the environment are influenced through the regulation of membrane traffic by endogenous hormones as well as various biotic and abiotic stress factors.

of efforts to mitigate challenges for achieving global food security in our future. Indeed, plants have evolved complex defence systems, however immunity comes at a cost to plant growth. Stomatal pores on the leaf surface exchange gas and water with the environment and are primary entry points for microbial pathogen. The initial defence against bacterial pathogen is stomatal closure, but pathogens commonly manipulate these defenses and force stomatal opening. At a cellular level, these plant-pathogen interactions include the commandeering ion transporters and their regulatory proteins to prevent stomata closure as well as secretion of defence-related molecules to the plant cell wall. Microbial pathogens also hijack cellular vesicle traffic for infection of their host plant. The so-called SNARE and SNARE regulatory proteins mediate secretory traffic at the plant plasma membrane. Assembly of SNARE protein complexes drives the final stages of membrane vesicle fusion and delivers the vesicle contents to the cell wall and space outside the cell. Following vesicle fusion, elements of this SNARE machinery are recycled.

Yet, the knowledge of molecular basis of these SNARE-mediated secretory processes during plant pathogenesis is sparse and virtually nothing is known of their coordination. This project will use multi-disciplinary approaches in plant cell biology, cell biology, proteomics and plant physiology to investigate how traffic of a novel set of SNARE partners involved in facilitating pathogen defence during pathogenesis. To highlight the value and importance of their research, the Karnik lab leads a multi-disciplinary outreach project. The team engages with public audiences through a variety of 'StomaToys' to educate concepts of stomatal defence in plants through play.

<https://www.gla.ac.uk/researchinstitutes/biology/publicengagement/stomataldefence/>

✿ Finding the Balance: Repression of Plant Gene Expression

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In all organisms, development and environmental adaptations are underpinned by precise regulation of gene expression, which is a balance between gene activation and repression. In this BBSRC-funded project, we set out to understand how a vitally important class of plant transcriptional co-repressors controls gene expression.

The TOPLESS (TPL)-family of transcriptional co-repressors regulates a myriad of essential processes in Arabidopsis and other plant species, including meristem maintenance, signalling of numerous hormones, lateral root development, branching, leaf growth, flowering time, flower development, germline development, circadian rhythm and immunity. Indeed, the central importance of TPL proteins is highlighted by the

striking phenotype of severe *tpl-1* mutants in which the embryonic shoot adopts root identity (Long *et al.* (2002) *Development* 129:2797) TPL proteins regulate this array of developmental processes through interaction with different families of transcription factors that control a wide range of target genes (Causier *et al.* (2012) *Plant Physiol* 158:423).

Mechanistically, TPL proteins link the DNA-recognition specificity, provided by transcription factors, to the enzymatic activity of chromatin remodelers such as histone deacetylases (HDACs). In other eukaryotes, HDACs form the catalytic component of well-characterised transcriptional co-repressor complexes, such as NuRD, CoREST and Sin3. However, despite the central importance TPL co-repressors play in development across the plant kingdom, we know surprisingly little about the regulatory complexes with which they associate.

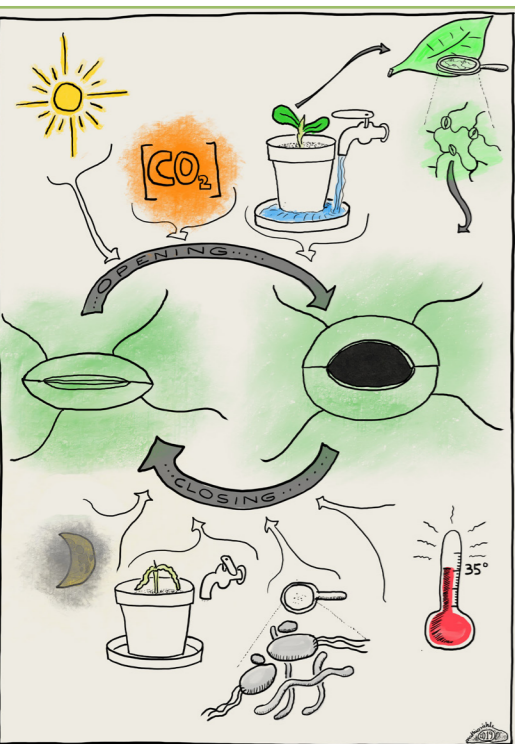
What we do know is that while plant genomes encode homologues of some NuRD, CoREST and Sin3 complex components (see Fig), many other essential components of these animal/fungal complexes are missing from plants. This

	Archetypal NuRD	Arabidopsis NuRD	Archetypal CoREST	Arabidopsis CoREST	Archetypal Sin3	Arabidopsis Sin3
Class I HDAC	Conserved	HDA6, HDA7, HDA9, HDA19	Conserved	HDA6, HDA7, HDA9, HDA19	Conserved	HDA6, HDA7, HDA9, HDA19
RbAp46, RbAp48	Conserved	MSI1-5	Conserved	MSI1-5	Conserved	MSI1-5
Mi-2 α , Mi-2 β (CHD3) (CHD4)	Conserved	PKL, PKR1, PKR2, CHR5	Conserved	FLD, LSD1-like1, LSD1-like2	Conserved	Sin3-like 1-6
MBD3	Conserved	e.g. MBD10	Conserved		Conserved	
p66 α , p66 β	Conserved		Conserved		Conserved	
MTA1, MTA2	Conserved		Conserved		Conserved	
			Conserved		Conserved	
			Conserved		Conserved	
			Conserved		Conserved	

Davies: Archetypal animal/fungal corepressor complexes compared to plant predictions. Some complex components are conserved across kingdoms, while others are either poorly conserved (dotted lines) or are completely absent in plants. Components with existing evidence for interactions with TPL-family proteins are marked by a red dot. Our aim is to uncover the nature of plant corepressor complexes, which we predict will have some similarities to, and distinct differences from, archetypal complexes described for animals and fungi.

Plant microbial pathogens destroy crop production worldwide, inflicting major agricultural and socio-economic losses.

Therefore, understanding mechanisms underlying plant defenses is at the centre



Karnik: A visual representation of the grant by Dr Mathis Riehle

shows that plant co-repressor complexes cannot exist in the same state as the archetypal animal/fungal complexes. In this project we will use a combination of proteomic and molecular genetic approaches to isolate and characterize the plant co-repressor complexes and unravel how they control gene expression. These findings should have far-reaching appeal, as we discover the extent to which co-repressor complexes evolved independently across the eukaryotes, and identify whether the composition and functionality of HDAC complexes reflects different regulatory needs in the different kingdoms.

Recently, the view that co-repressor complexes simply act to silence transcription was challenged by the finding that animal HDAC-containing complexes are present at transcriptionally active loci, and in some cases have been shown to be required for gene activation⁴. The emerging picture is that HDAC-containing complexes modulate the acetylation status of specific loci, targeted by the DNA-binding specificity of their recruiting transcription factors, giving them a critical role in both repression and activation of gene expression.

It is currently not known whether plant TPL/HDAC-containing complexes also associate with transcriptionally active and inactive gene targets. We will address this as part of this project, by examining whether plant co-repressor complexes modify histone acetylation to regulate gene expression both positively and negatively.

In the long term, discovering new plant transcriptional regulatory complexes and understanding how they control gene expression in multiple essential processes will open up new avenues to engineer gene expression in plants.

Divining Roots: uncovering how SUMO mediated responses control developmental plasticity

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Root branching is influenced by the soil environment to improve foraging efficiency. For example, lateral roots initiate and develop towards the availability of water employing a novel adaptive response termed hydropatterning. We recently identified the molecular mechanism regulating hydropatterning (Orosa *et al*, 2018, Science). In brief, this mechanism involves the SUMO-dependent post-translational modification of the lateral root regulator ARF7. SUMOylation of ARF7 is required to recruit the Aux/IAA repressor protein IAA3. Blocking ARF7 SUMOylation disrupts IAA3 recruitment and hydropatterning.

We conclude that this new form of auxin regulation controls root branching pattern in response to water availability. The new BBSRC proposal takes this research beyond ARF7 and addresses how SUMO-mediated environmental



Bennett and Sadanandom

responses control hydropatterning. By unravelling the SUMO mediated signal transduction pathway during hydropatterning we lay the foundations for understanding a major regulator of plant-environmental responses. The knowledge generated about the new signals, genes and their regulatory pathways will underpin on-going efforts to re-engineer root systems architecture and improve crop performance.

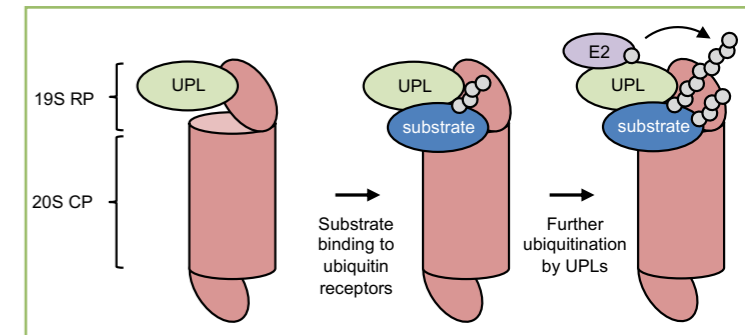
Cellular Functions of Proteasome-Associated Ubiquitin Ligase Activity

Michael Skelly & Steven Spoel
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Maintaining the optimal abundance and activities of cellular proteins, termed proteostasis, is critical for the survival of all organisms. The ubiquitin-proteasome system is essential for appropriate degradation of proteins that are short-lived or damaged. Substrates are labelled for proteasome-mediated degradation by repeated conjugation of ubiquitin, a small regulatory protein found in all eukaryotes. Proteotoxic stress caused by failure to degrade ubiquitin-marked substrates is associated with a wide range of developmental and immune defects in plants as well as humans. Thus, furthering our understanding of proteasome function in health and disease will impact diverse areas including biotechnology, agriculture and biomedicine.

Although detailed knowledge has been gathered on substrate ubiquitination and degradation, molecular events occurring upon arrival of the substrate at the proteasome remain poorly understood. We recently reported



Skelly and Spoel

that proteasome-associated HECT-type UPL ubiquitin ligases govern universal substrate polyubiquitination and are key determinants of phenotypic traits in Arabidopsis. This new BBSRC-funded project aims to build on this work and explore exciting new hypotheses for how UPL activities may allow proteasomes to do much more than simply break down substrates. Specific subunits of the proteasome contain ubiquitin receptors that efficiently recruit ubiquitinated substrates before commitment to degradation.

A major focus of our work aims to dissect the intriguing paradox of why substrates may then require further ubiquitination by UPLs even though they are already bound by the proteasome. We will investigate the association between UPLs and the proteasome and determine how these interactions shape global cellular ubiquitination, substrate degradation and proteasomal activity. We will also use a combination of genetic and proteomic experiments to catalogue the substrate repertoire of the proteasome-associated UPLs.

Ultimately, our goal is to reveal how proteasome-associated ubiquitin ligases may function as gatekeepers of the proteasome. This will allow for the design of novel strategies to improve proteasome function during disease.



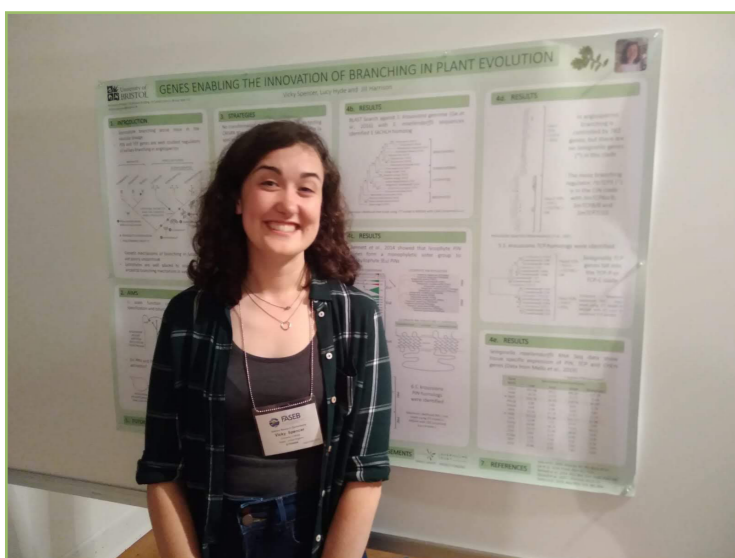
Meeting Report: FASEB The Mechanisms in Plant Development

St. Bonaventure University, New
York, July 28th to August 2nd 2019

Vicky Spencer
University of Bristol

This summer I was very fortunate to receive a travel grant from GARNet to attend the highly anticipated FASEB Mechanisms in Plant Development conference. Many prominent scientists regularly join this biennial event; this time held in the quiet town of Olean (New York) at Bonaventure University. Over 150 PIs, post docs and students attended from across the world, making it an exciting and diverse event. It was clear that the regular attendees have a lot of affection for this meeting, and there was a strong sense of support and community that was very welcoming.

I am a newly appointed postdoc at the University of Bristol, researching the genetic mechanisms of shoot branching evolution in vascular plants. This conference gave me a great opportunity to discuss the data that I have already collected and to elaborate my future project plans.



Vicky presenting her research

I was lucky to present a poster in one of the three evening poster and drink sessions. After three hours of presenting, I had a lot of useful advice and inspiration for future experiments, including technical help for protoplast extraction and transformation. Many tasks were added to my to-do list when I got back to Bristol!!

The conference had an exciting and busy schedule of talks from many renowned scientists. This was a great opportunity to learn about the recent advances in the plant development field, and its future directions. Many talks focused on the role of the CLV signalling pathway; including kernel row patterning by Paula McSteen, maize meristem organisation and ROS signalling by Andrea Gallavotti, and filament identity in *Physcomitrella patens* from our lab member, Zoe Nemeč Venza. I thoroughly enjoyed that there was a strong focus on evolution, with many examples of research in *Marchantia polymorpha*. In particular, I enjoyed talks about the role of CLE peptides in meristem specification by Yuki Hirakawa and ZHOUP1 function in cuticle and pegged rhizoid formation by Yen-Ting Lu.

Due to the alarming problems of plastic pollution and energy consumption, it is more critical than ever that biologists take responsibility for their environmental impact in the lab. Such issues were discussed in the Sustainability forum, which was a great way to raise awareness and share eco-friendly ideas between scientists. I think that this kind of event should become commonplace in scientific meetings, to encourage a sustained effort to reduce the environmental damage from our work. A single cell RNA-Seq workshop was also held, which was very timely and useful for the community as many attendees presented novel data from this new and exciting technique.

All meals and coffee breaks were held within the University campus, which was a great way to promote interactions between scientists at different stages of their careers. As well as thought-



provoking scientific discussion, it was very useful for me to discuss career development with both new and established PIs and postdocs. I also talked to PhD students about my experiences and hope I have encouraged others to stay in research after graduating and be excited about life after the PhD thesis!

Between the full schedule of talks and workshops, we went to 'enjoy' the local NY wine in the nearby winery, after a fun trip on an iconic yellow school bus. We also visited a local lake for paddle boarding, which (once stood on the board) was very relaxing after a busy morning. These events were great fun and a lovely way to catch up with old friends and meet new ones. Everybody was so welcoming and friendly, and it was clear that both the people and the quality of science are why researchers come back to this meeting throughout their careers.

As well as the generous travel funding from GARNet, thanks are due to Dr Jill Harrison and Dr Kenneth Birnbaum for organising such a great conference. I hope I have the opportunity to attend again in the future!

Jill Harrison from the University of Bristol (jill.harrison@bristol.ac.uk) is a member of the GARNet advisory committee and was co-lead organiser of the FASEB meeting. One priority of the meeting was to ensure equality across the board and she reports below that this was largely achieved albeit with some areas for improvement

'With one male and one female organizer and an almost equal ratio of 48% to 52% female and male invited speakers, respectively, this meeting represents an outstanding example for gender equality in science. Twenty-two abstracts were selected for short talks and presented by graduate students, postdoctoral fellows, and junior faculty. Again here, the numbers of female and male presenters was nearly equal (12 female, 10 male) and roughly reflective of the gender ratio of attendees in general (46% female and 54% male).

The overall race profile was 50% white to non-white; 22 % were asian, 10% were hispanic, 10% did not disclose, 2% were black or african american. Six of the invited speakers were asian and one was american indian, so there is room for improvement in this area in the future'.

Introducing COST Action I8111 PlantEd: Genome Editing in Plants

<https://plantgenomeediting.eu/>

Geraint Parry

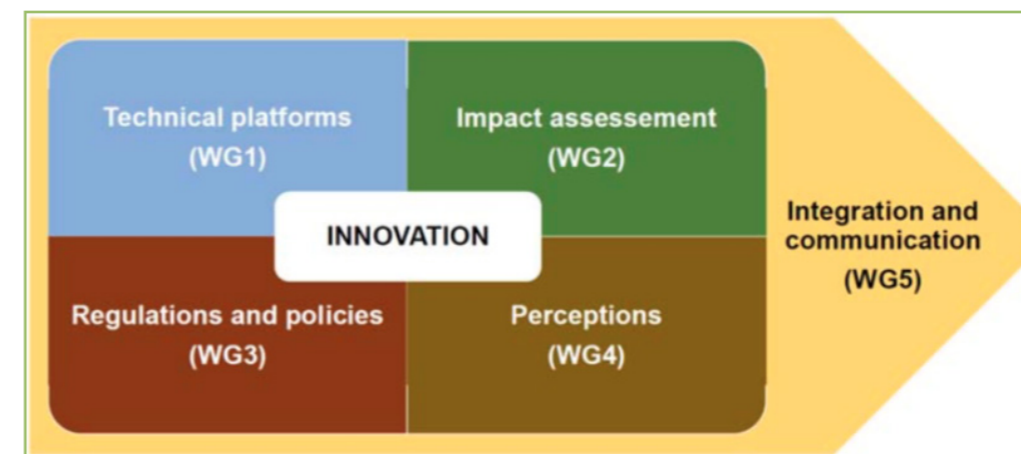
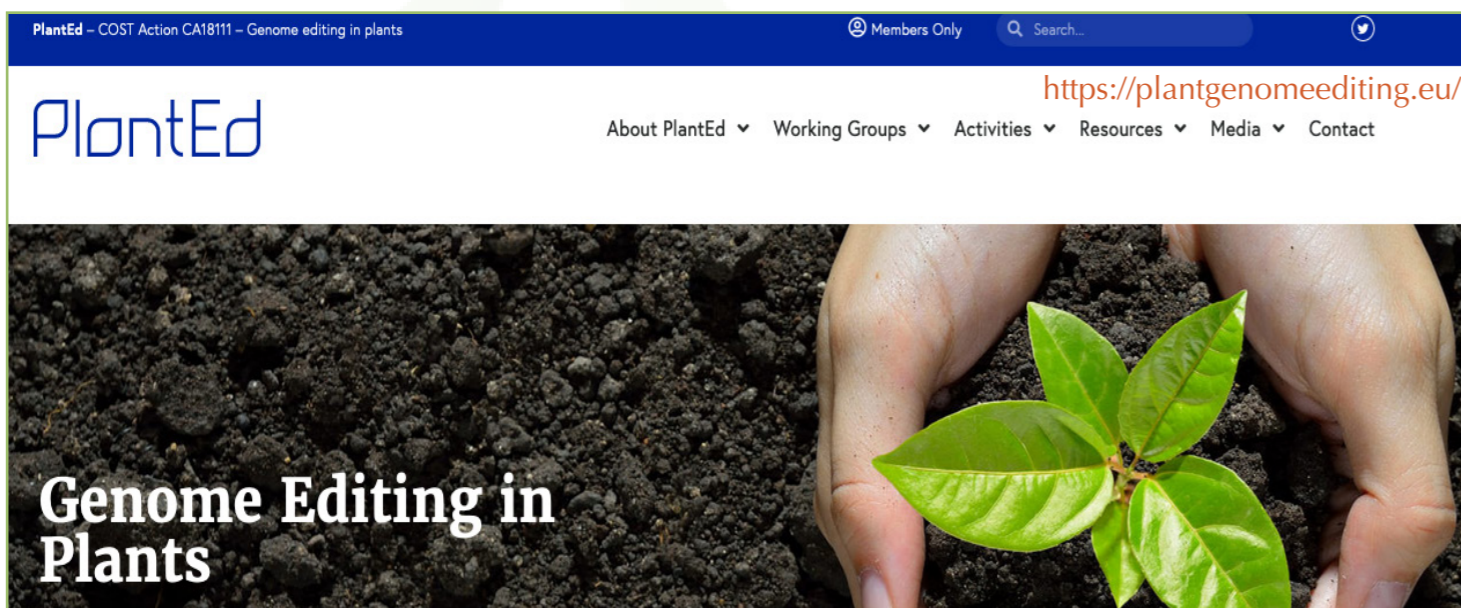
To the frustration of all EU Plant Scientists in the July 2018 the European Court of Justice (ECJ) judged that crops generated by newer forms of Breeding Technologies (NBTs), such as CRISPR-based genome editing, should be regulated in the same manner as crops created through conventional genetic transformation. This ruling prevents plant scientists across the EU using transformative gene editing technologies to generate novel crop varieties that are resistant to the effects of climate change and can help mitigate the catastrophic effects of global food insecurity.

As an effective riposte to the ECJ judgement, Dennis Eriksson at the Swedish University of Agricultural Sciences has brought together over 250 plant scientists and policy experts from academia, industry and supporting organisations to form **COST Action CA18111 PlantEd: Genome Editing in Plants**.

The main aims of the PlantEd are to assess the full innovation potential and impact of plant genome editing; to set the future direction of research priorities; to promote the link between research and innovation in a socially responsible manner; and to examine the synergistic interactions with closely related fields.

The mechanisms of action of PlantEd are the same as those shared across all COST Actions:

1. Organisation of Training Schools that provide (usually) Early Career Investigators (ECIs) with the opportunity to learn new skills relevant to PlantEd activities
2. Support Short Term Scientific Missions (STSMs). These are short (up to 6months) individual training opportunities for ECIs to travel to a different member country to develop new research skills.
3. Provide opportunities for Conference attendance. The COST Action will support the travel and attendance of researchers from member countries to an Annual meeting as well as Workgroup-specific organised events. PlantEd will also support attendance to external conferences for researchers from Inclusiveness Target Countries (ITC).



PlantEd Workgroups.

Applications will open soon for a Training School within the scope of Working Group 1: Technical platforms, which will take place in early 2020.

The activities of PlantEd are built around the activities of five Workgroups

WG1: Assess and validate the actual and potential capacities and output within existing technical platforms applying GE in plant research and breeding in both the public and private R+D sector research in Europe and beyond. Define and develop common research priorities and develop synergistic interactions with technical platforms related to sequencing technology and –omics technologies.

WG2: Map current and potential impact on plant research and breeding, in terms of 1) utility of this technology and novel opportunities for discovery, 2) utility as a facilitator for trait management in breeding, 3) identification and evaluation of the data requirements for rigorous socio-economic, environmental and health impacts.

WG3: Evaluate the approach to plant genome editing and the resulting products in the EU legislation as well as in other COST countries and also within international biosafety frameworks such as the CBD/Cartagena protocol. 2) Compare

regulatory approaches to GE in the EU with other countries that have already taken steps towards regulatory clarity in this area. 3) Monitor emerging patent landscape associated with the tools for genome editing and evaluate its relevance for plant breeding.

WG4: Collect and analyse surveys performed among

various stakeholder groups as well as the public in many European countries and beyond, in order to assess the perceived potential, risks, knowledge about, and attitudes toward the application of genome editing in plant breeding. Through outreach activities, the Action will also promote a widely improved understanding of genome editing and its use in plant research and breeding, taking advantage of the wide international coverage of the network of participants.

WG5: Integrate data provided in WG1-4 and develop a number of communication tools. This will build on a thorough communication plan and involvement of a sufficient number of active working members across the Action to reach out through Europe and beyond. This will also interact with local initiatives to reach all relevant stakeholders including the public, as well as widely facilitate access to accumulated knowledge and experience.

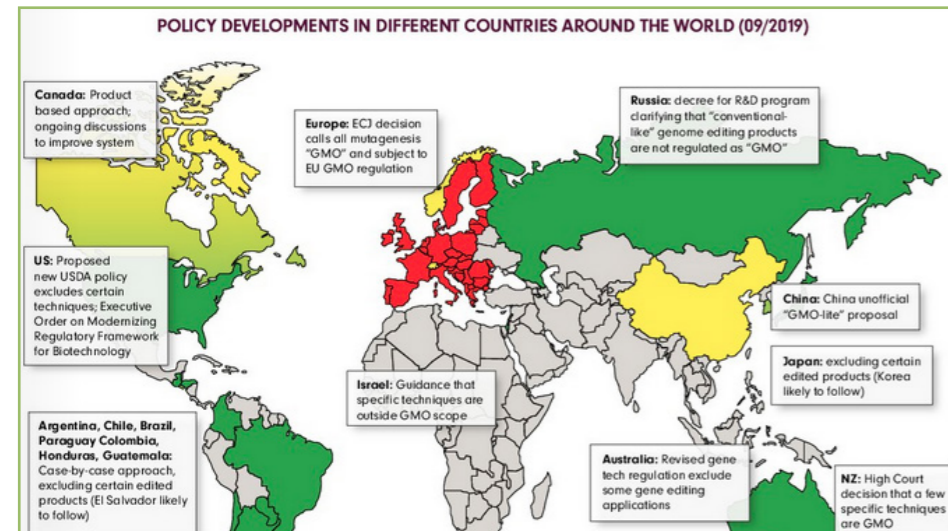
1st PlantEd Conference: Plant Genome Editing – State of the Art

<https://plantgenomeediting.eu/planted-is-organising-the-first-conference-in-serbia/>

The inaugural PlantEd conference took place in Novi Sad, Serbia in early November. This

GARNish

Introducing PlantEd



The WG1 session highlighted that CRISPR-based gene editing is allowing genome-manipulation in non-traditional model systems such as Tomato, Potato and Chicory (the CHIC project- <http://chicproject.eu/>). The excellent reach of this COST Action was highlighted across the WG2 session where PlantEd members from Spain, Serbia, Turkey, Armenia and Norway each discussed GE regulatory policies in their nations.

Petra Jorasch from EuroSeeds presents the sad situation for European researchers involved in gene editing technologies.

<https://www.european-seed.com/docs/books/volume-6/issue-4/?page=20>

brought together members of each WG to provide an overview of the current state of the genome editing field.

The meeting was opened with an introduction of Genome editing across the world, with speakers relaying the disappointing situation where the EU is lagging behind the rest of the world. This is undoubtedly having significant consequences for European Innovation in Plant Breeding.

The meeting ended with the promotion of two exciting initiatives that are supporting the update of

GE technologies. Firstly The Citizens Initiative (<https://www.growscientificprogress.org/>) is aiming to collect one million signatures from EU citizens who want to support this technology. Secondly, the GeneSprout Initiative (<https://www.genesproutinitiative.com/>) aims to be the voice of young plant scientists in future policy-making about NBTs across Europe.

PlantED will run until 2023 and there are plenty of opportunities to get involved with this activity.



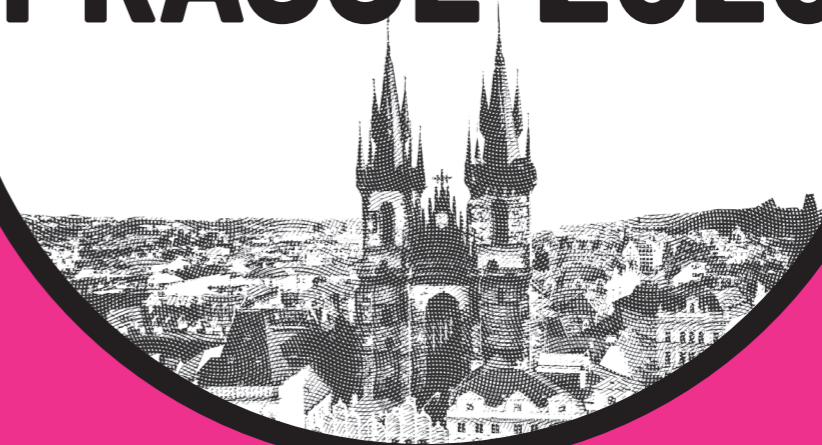
The PlantEd group in Serbia. Picture from @morontafelix

SOCIETY FOR EXPERIMENTAL BIOLOGY PRESENTS:

SEB PRAGUE 2020
7-10 JULY 2020
CLARION CONGRESS
HOTEL PRAGUE

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PRAGUE 2020



SESSION TOPICS WILL INCLUDE:

SCIENCE ACROSS BOUNDARIES – CELL, PLANT AND ANIMAL BIOLOGY

- CELL AND ANIMAL BIOLOGY: ENVIRONMENTAL FLUCTUATION**
- NEUROTRANSMITTERS TO PHEROMONES: THE RESPONSE OF PHYSIOLOGICAL AND BEHAVIOURAL SIGNALS TO ENVIRONMENTAL CHANGE
 - EPISODIC HYPOXIA: MAMMALIAN SPECIES WITH EXCEPTIONAL TOLERANCE AND HOW TO STUDY THEM
 - DO ENVIRONMENTAL CONTAMINANTS ALTER ENERGY BALANCE, HOW CAN WE FIND OUT AND HOW MUCH DOES IT MATTER?
 - THE PHYSIOLOGY BEHIND PHENOTYPIC PLASTICITY IN RAPIDLY CHANGING ENVIRONMENTS

- CELL, ANIMAL AND PLANT BIOLOGY: BIG DATA**
- AUSTRAL COMPARATIVE BIOCHEMISTRY AND PHYSIOLOGY

CELL BIOLOGY

- DYNAMIC ORGANIZATION OF THE NUCLEUS ACROSS KINGDOMS* NUCLEAR DYNAMICS SIG

ANIMAL BIOLOGY

- ECOIMMUNOLOGY**
- PARASITES, DISEASE AND HOST IMMUNITY: TOWARDS A MECHANISTIC UNDERSTANDING OF INFECTION-INDUCED PHENOTYPES
 - ECOIMMUNOLOGY IN A CHANGING WORLD: CHALLENGES AND PROGRESS

- ENVIRONMENTAL FLUCTUATION**
- AQUATIC ECTOTHERMS IN FLUCTUATING ENVIRONMENTS
 - PHYSIOLOGICAL AND ECOLOGICAL RESPONSES TO TEMPERATURE FLUCTUATION

- ENVIRONMENTAL FLUCTUATION AND BIODIVERSITY**
- NOT JUST DOWN THE HATCH: FOOD PROCESSING, TRANSPORT, AND ASSIMILATION IN JAWED VERTEBRATES

BIG DATA

- AUTOMATED ANIMAL TRACKING IN BEHAVIOURAL STUDIES
- PUTTING ANIMAL BIOLOGY IN ECOLOGICAL CONTEXT WITH ADVANCES IN ANIMAL TRACKING AND BIO-LOGGING

PLANT BIOLOGY

- CHALLENGES AND OPPORTUNITIES IN CANNABIS RESEARCH
- PLANT METABOLISM IN A CHANGING WORLD - CELEBRATING 70 YEARS OF THE JOURNAL OF EXPERIMENTAL BOTANY
- PLANT AND ALGAL CIRCADIAN CLOCKS
- RETROGRADE SIGNALLING AS A COMPONENT OF ENVIRONMENTAL SENSING
- PLANT PHENOTYPING
- LIFE AT THE INTERFACE - PLANT MEMBRANE-PROTEIN DYNAMICS AND INTERACTIONS DURING RESPONSES TO ENVIRONMENTAL CHANGE
- VOLATILES DO THE TALKING: INTERORGANISMIC INTERACTIONS ARE IN THE AIR

SEB+

BIG DATA

- WITHIN AND TRANS-GENERATIONAL PLASTIC RESPONSES AND ADAPTIVE EVOLUTION OF MARINE METAZOANS IN A CHANGING OCEAN: FROM MOLECULES TO BIOTIC COMMUNITIES
- OPEN ELECTRONICS IN EXPERIMENTAL BIOLOGY

SATELLITE MEETINGS

SEB+
WITHIN AND TRANS-GENERATIONAL PLASTIC RESPONSES AND ADAPTIVE EVOLUTION OF MARINE METAZOANS IN A CHANGING OCEAN: FROM MOLECULES TO BIOTIC COMMUNITIES

ANIMAL
THE SCIENCE OF ANIMAL SENTIENCE: REFINING EXPERIMENTAL BIOLOGY

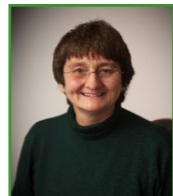


 Spotlight on:
University of Leeds

Kindly compiled by Laura Dixon

Department Twitter: @plantscileeds

- Alison Baker
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Membrane transport related processes
in plant cells

My group work on a range of membrane transport processes ranging from the transport of proteins into peroxisomes to the transport of phosphate into plant and algal cells. Catalase is a peroxisomal enzyme but its targeting signal is unusual. We are revisiting the targeting of catalase to peroxisomes trying to understand the role of conserved C terminal sequence in this process. We have previously explored the nature of the molecular recognition of peroxisome targeting signals by the import receptor PEX5 and developed an orthogonal targeting sequence-receptor pair that allows us to switch import specificity in vivo.

We are also interested in transport of metabolites into peroxisomes and have a long standing interest in the function of the peroxisomal ABC transporter COMATOSE a broad specificity transporter of substrates for beta oxidation which has an unusual substrate cleavage mechanism. We have recently uncoupled ATPase activity and acyl CoA thioesterase activity by mutagenesis.

We are interested in phosphate signalling and transport in orphan crops (foxtail millet) and have characterised the function of a family of phosphate transporters. We are also interested in using photosynthetic organisms (algae and duckweed) in nutrient recovery from waste water.

- Yoselin Benitez Alfonso
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Cell-to-cell communication, plasmodesmata cell walls, plant development and biomaterials. Dr Benitez-Alfonso's team takes a multidisciplinary approach to dissect the factors controlling communication between plant cells as a path for the design of strategies to modulate plant developmental responses to environmental cues. Her work focuses on the structural and physico-mechanical characterization of plasmodesmata cell walls combining cell biology, genetic, soft polymer physics and computational tools to expand and exploit knowledge on these intriguing structures. Plasmodesmata are microchannels connecting neighboring cells to facilitate the transport of small and large molecules including proteins and mRNAs.

Communication through these channels control several aspects of plant development and recent research in Benitez-Alfonso lab highlights their importance in lateral root development, the response to osmotic stress (Grison *et al.*, Plant Phys, 2019) and for the establishment of legume symbiosis with nitrogen-fixing soil borne bacteria (Gaudio-Pedraza *et al.*, Curr. Biol, 2018). Based on their structural features, recent models were applied to predict plasmodesmata transport capacity, i.e. permeability (Deinum *et al.*, 2019, eLife) while physical characterization of cell wall polymers enriched at plasmodesmata sites uncover the complexities of their regulatory function (Abou-Saleh *et al.*, Nat. Comm, 2018).

Current projects at Benitez-Alfonso lab takes advantage of these tools and approaches to discover novel roles for plasmodesmata in plant development and to identify targets for their exploitation in plant biotechnology and also as resources for the design of new biomaterials based on their unique cell wall composition.

- Tom Bennett
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My research is focussed on understanding how plants precisely coordinate their growth and development in space and time. Plant reproductive success requires the ability to constantly re-model root and shoot system architecture with respect to prevailing environmental conditions, in order to optimise resource capture and use. I am particularly interested in the ways in which plants can use environmental information to 'predict' future resource availability, and pro-actively alter their growth to avoid future resource limitations. These abilities require plants to systemically distribute information on environmental conditions and internal plant status, and for individual organs to appropriately respond to this information.

A small number of hormonal signals, including auxin, cytokinin and strigolactone are implicated in this informational exchange, both within root and shoot systems, and between them. Much of the work in my lab thus focuses on understanding these signals, their signalling pathways and their effects in a variety of development contexts. In particular, we study the hormonal control of 'reproductive architecture' in flowering plants (the arrangement of inflorescences, flowers, fruit and seed in space and time), and the hormonal control of shoot growth in response to the soil environment. I also have a very strong interest in the evolution of plant development, and another major project in the lab is looking at the evolution of strigolactones as signals in land plants, and how their role in development has changed through this process.

Although Arabidopsis remains the 'workhorse' of the lab, we study these processes in a diverse range of species including pea, barley, wheat, oilseed rape, with a view to translating the findings of our research to agricultural contexts

- Laura Carter
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The use of sustainable agricultural practices such as treated wastewater irrigation and organic soil amendments are inadvertently introducing emerging contaminants (e.g. veterinary antibiotics, human pharmaceuticals) to our agro-ecosystems. It is essential we are able to quantify the risks associated with introducing bioactive chemicals into soil-plant systems, given that these practices are set to increase in response to depleting freshwater supplies and a drive to move away from chemical based fertilisers.

My research explores the fate and impacts of land-applied emerging contaminants on soil and plant health. Investigations into the accumulation of emerging contaminants in soil-plant systems (including in-plant metabolism) will help us to understand potential impacts of these biologically potent chemicals on crop productivity and, ultimately, our ability to meet growing food demands. My research utilises a combination of laboratory and field scale investigations, to consider the risks of emerging contaminants in the environment with the ultimate aim of understanding the impacts of sustainable agricultural practices on crop health. Key to achieving this are cross-discipline collaborations with research expertise in the fields of agriculture, soil and plant health to utilise a variety of techniques and novel methods.

Laura Carter is a UKRI Future Leaders Fellow.



- Andrew Cuming
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The bryophytes are the most ancient group of extant land plants, diverging in the land plant lineage ca.450 million years ago. We use the model moss, *Physcomitrella patens* to investigate traits that were critical for the successful colonisation of land by plants.

Our principal focus is on the ability to resist dehydration: a factor of existential importance to the earliest land plants that lack the anatomical adaptations acquired by vascular plants. Lacking complex anatomical adaptations, many mosses exhibit a high level of desiccation tolerance, and in *P. patens* this is coordinated by abscisic acid (ABA). The ABA signal transduction pathway is conserved not only in all land plants, but the core components are also present in aquatic charophyte algae, whose origins predate the colonisation of land by ca. 250 million years.

We use cross-species complementation of gene targeted *Physcomitrella* mutants to determine the functional conservation of algal and angiosperm ABA signal transduction components, and have (i) identified novel components in algae and bryophytes that were lost from vascular plants, and (ii) have pinpointed the origins of ABA

perception through the characterisation of an algal receptor homologue that interacts with signal transduction components (PP2C phosphatases) in a ligand-independent manner.

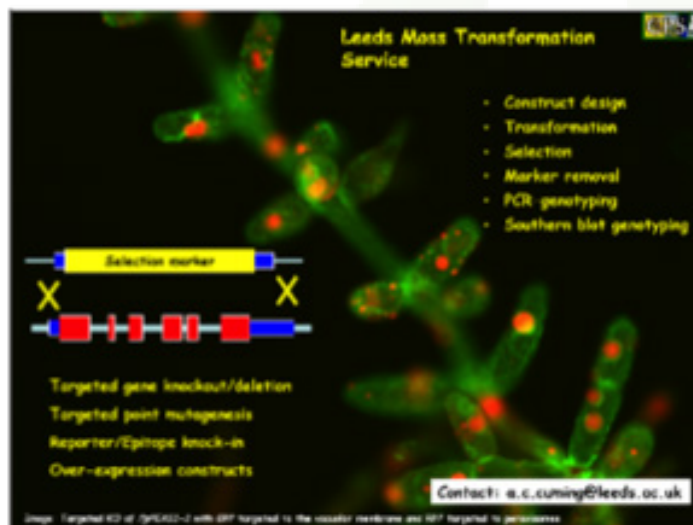
The moss *Physcomitrella* provides a powerful model system for “Evo-Devo” analysis of the evolution of plant gene functions, and we are keen to support Arabidopsis researchers to use *P. patens* in such investigations. We have provided a number of gene-targeted moss mutants to researchers in recent years on a semi-commercial basis (costs can be included in research grants), and we are happy to invite further requests to generate such lines in “your favourite genes” : please contact us for details!

- Brendan Davies
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The Davies group uses molecular genetic approaches to study plant development. We have three overlapping areas of interest: flowering, transcriptional repression and translational control. In flowering, we are interested in how flowering is initiated, how flowers are formed and how these processes are influenced by, and buffered from, environmental factors, especially temperature.

Through our work on flowering we became interested in an intriguing class of transcriptional corepressors, the TOPLESS (TPL) family. We are studying how TPL influences the expression of multiple target genes, affecting a huge variety of plant processes. We also have an interest in the ancestral functions of TPL and its central role in the evolution of land plants. Finally, through looking at alternative mechanisms to control gene expression, we identified several peptides that conditionally regulate the translation of associated open reading frames. We are using molecular and structural biology approaches to understand



Cuming: Leeds Moss Transformation Service

- Katie Field
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Katie is a BBSRC Translational Fellow and Professor of Plant-Soil Interactions who joined the Centre for Plant Sciences in 2015. She is Associate Director for Agriculture and Environment in the University of Leeds' Global Food and Environment Institute and leads the Soil, Plant, Environment Network across the university.

How do the biotic and abiotic environments interact to drive plant evolution and the development of the terrestrial biosphere?

This key question underpins the Field Lab's research into the physiology, ecology and evolution of atmosphere-plant-rhizosphere interactions in both natural and agro-ecosystems. Most of the research in the group focuses on the functional significance of symbioses between plants and diverse mycorrhizal fungi, in particular the carbon and nutrient fluxes between plants, root symbionts and the wider rhizosphere. The group has extensive experience in techniques in plant and soil physiology, including isotope tracing, physical and chemical properties of soil, and environmental metabolomics.

We apply these techniques to address important global challenges in agricultural and natural environments, aiming to shed new light on the role fungi may have played in the development of Earth's ecosystems and to enhance our understanding of the potential importance and exploitation of symbiotic soil fungi in sustainable agricultural systems. Ongoing projects are investigating the potential role of mycorrhizal fungi in sustainable agriculture, the influence of diverse mycorrhizal fungi on global climate throughout the Phanerozoic and the long-term fate and storage potential of soil organic carbon.

and engineer this novel form of gene regulation. Although we mainly work with Arabidopsis, we also use other systems, including moss, for comparative purposes.

- Laura Dixon
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Plants continuously respond to the environment. My group focuses on understanding the role of temperature signalling in controlling development and floral regulation in bread wheat (*Triticum aestivum*) and how this regulation influences the final yield potential.

An important temperature response in floral development is that of vernalization, or the requirement of a period of low temperatures before a winter habit plant can make the vegetative to floral transition. We know a number of genes in the vernalization pathway yet we do not fully understand how they interact or how the response proceeds in the field at a molecular level. We are combining genetics, molecular and developmental biology to identify and understand the processes controlling cereal vernalization in the field.

Beyond the defined vernalization response we are also investigating how a range of ambient temperatures regulate apex transition and development. The work is highly collaborative, with other academics and industry, and we focus on ensuring that the fundamental biological understanding we gain through our research has application with the wheat breeding and agricultural sector. Our research combines field-observed problems, molecular biology, genetics and then returning to the field to test our hypotheses.

Laura Dixon is a UKRI Future Leaders Fellow.

- Stefan Kepinski

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Stefan is Director of the Centre for Plant Sciences and leads the University of Leeds Future Crops initiative.

Stefan's research is focused on understanding the regulation of plant development by plant hormones, most commonly auxin with projects ranging from the earliest events of auxin receptor complex formation to the control of plant architecture.

Over recent years he has become deeply fascinated with how plants regulate the angle of growth of their lateral organs, partly because it is an interesting developmental biology question but also because it is a topic of tremendous agronomic importance—for the most part root and shoot branches grow at angles that are non-vertical, an important adaptation allowing plants to optimise the capture of resources above- and below-ground. Crucially, lateral branches are typically maintained at specific angles with respect to gravity rather than to whatever part of the plant they are attached to. In this case, these growth angles are known as gravitropic setpoint angles or GSAs and are intriguing because their maintenance requires that lateral root and shoot branches are able to effect tropic growth both with and against the gravity vector.

Stefan's lab is using genetics, cell biology and computational modelling to understand the mechanisms underlying GSA control. This work has also given rise to technologies to modify root growth angles that are currently under commercial development. While the majority of this research has been carried out in *Arabidopsis*, translational work now extends into wheat, maize, sorghum, and oilseed rape, with projects in the UK, Malawi and India.



- Paul Knox

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For many years, my laboratory has studied the occurrence, dynamics and functions of cell wall polysaccharides. Our research has been enabled by the generation of sets of oligosaccharide-directed monoclonal antibodies. Currently, many of our activities focus around the high molecular weight polysaccharides secreted by plant roots (New Phytologist (2018) 217:1128; Plant & Soil (2018) 428:57).

We are characterizing these exudate molecules in terms of their structures and functions. In cereals, they appear to be highly complex polysaccharide assemblies and to contain a range of structural features that are not generally present in cell wall polysaccharides. Key questions are the roles of the released polysaccharides in rhizospheres. One aspect we are studying is exudate polysaccharide roles in the maintenance of sheaths of soil attached along root bodies. These rhizosheaths have roles during periods of drought and result from combination of root hair entanglement and adhesive polysaccharides.



Knox: Visualising root exudates



To this end, we have identified that certain cell wall related polysaccharides such as xyloglucan and other glucans are potent aggregators of soil particles with significant soil-binding properties. Other questions concern how the polysaccharides are secreted from roots – in terms of the developmental zones and the cellular basis of how they get across cell walls to root peripheries. Additionally, they are likely to have important roles as substrates for soil microbes.

Our sets of glycan monoclonal antibodies are very useful to study and track released polysaccharides. These powerful molecular tools are used in rapid detection methods such as in the image, shown here, of the detection of released in solid media after removal of *Arabidopsis* seedlings.

- Peter Urwin

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The central focus of research in Plant Nematology Laboratory is the interaction between parasitic nematodes and their plant hosts. This knowledge is then used to develop new ways to control these important agricultural pests. The research activity of the group spans laboratory to field studies, and ranges from improving fundamental knowledge of plant nematology to using information gained, particularly from RCUK grants, to develop new agriculturally beneficial technologies.

The crop focus of the research in the U.K is potatoes, extending to rice, banana and cotton in India, Africa and China. The group has received research funding from companies in the UK (e.g. Syngenta, ATC, Biogemma), and worldwide (e.g. China Seeds, Limagrain, Nestle). Our biotechnology is donated freely for developing world use.



Urwin: Banana Field Trial

Work originating in the laboratory has led to numerous granted patents. The impact of the research has influenced government policy, and received attention on television, radio and in the international press.

- Marcelo Valadares Galdos

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Marcelo Galdos is a University Academic Fellow in Modelling Food Security and Climate Impacts, in a joint position at the University of Leeds and the Met Office. His research is focused on climate-smart agriculture using crop, soil and climate modelling from plot to landscape scale to simulate yields, soil organic matter, soil water, nutrients, and greenhouse gas fluxes in agricultural systems.

Marcelo evaluates the sustainability of food, fuel, fibre and feed production under different land use and climate scenarios, supporting stakeholders in the development and implementation of climate change mitigation and adaptation strategies. He is interested in



identifying and promoting crop and livestock production systems that preserve and restore natural resources, sustain agricultural livelihoods and provide ecosystem services.

- Chris West

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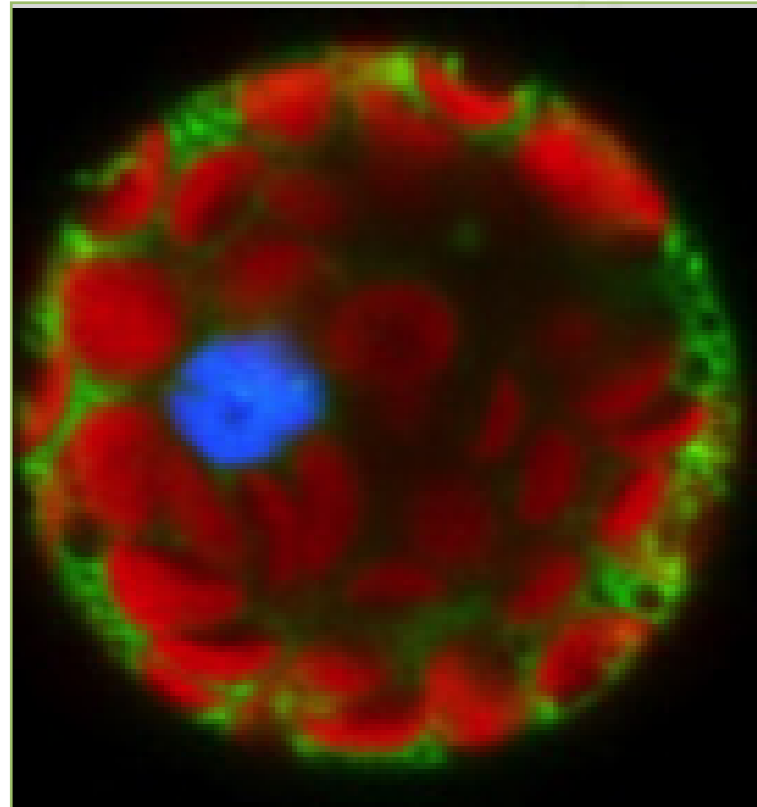
We are interested in the elucidating roles of DNA repair and recombination in plant growth and development and their potential to improve crop productivity and increase stress resistance.

Our research focuses on understanding DNA repair mechanisms in plants using model species such as Arabidopsis, barley and brassica. In particular, we have characterised the recombination pathways that repair chromosomal breaks, one of the most cytotoxic forms of DNA damage. Our interests also include characterisation of DNA damage responses, integrating genetic, biochemical and omic

approaches to understand the transcriptional and post-translational signalling pathways that regulate DNA repair, cell death and growth under stress.

Recent progress has identified important roles for recombination in the seed stages of the plant life cycle, with genome repair critical to rapid germination and successful seedling establishment. Our continued research is revealing the relationship between genome repair and seed vigour, including the mechanisms by which seed priming enhances germination vigour. We are currently investigating approaches to improve seed longevity and germination performance, and are evaluating novel molecular markers for seed quality.

Recombination pathways are also involved in transgene integration. Current projects are focussed on the mechanisms of transgene insertion at induced DNA breaks in the plant genome, and how these pathways can be manipulated to improve this technology. These approaches use CRISPR-Cas9 in combination with modified transgene constructs to influence integration patterns.



West: Reporter gene expression in a transgenic cell



Future Crops, at the University of Leeds, is using its world-leading fundamental plant science to generate real-world solutions for smarter, more efficient and sustainable agri-systems

<https://www.plants.leeds.ac.uk/futurecrops/index.php>

Impact of Chromatin Domains on Plant Phenotypes

SPECIAL ISSUE



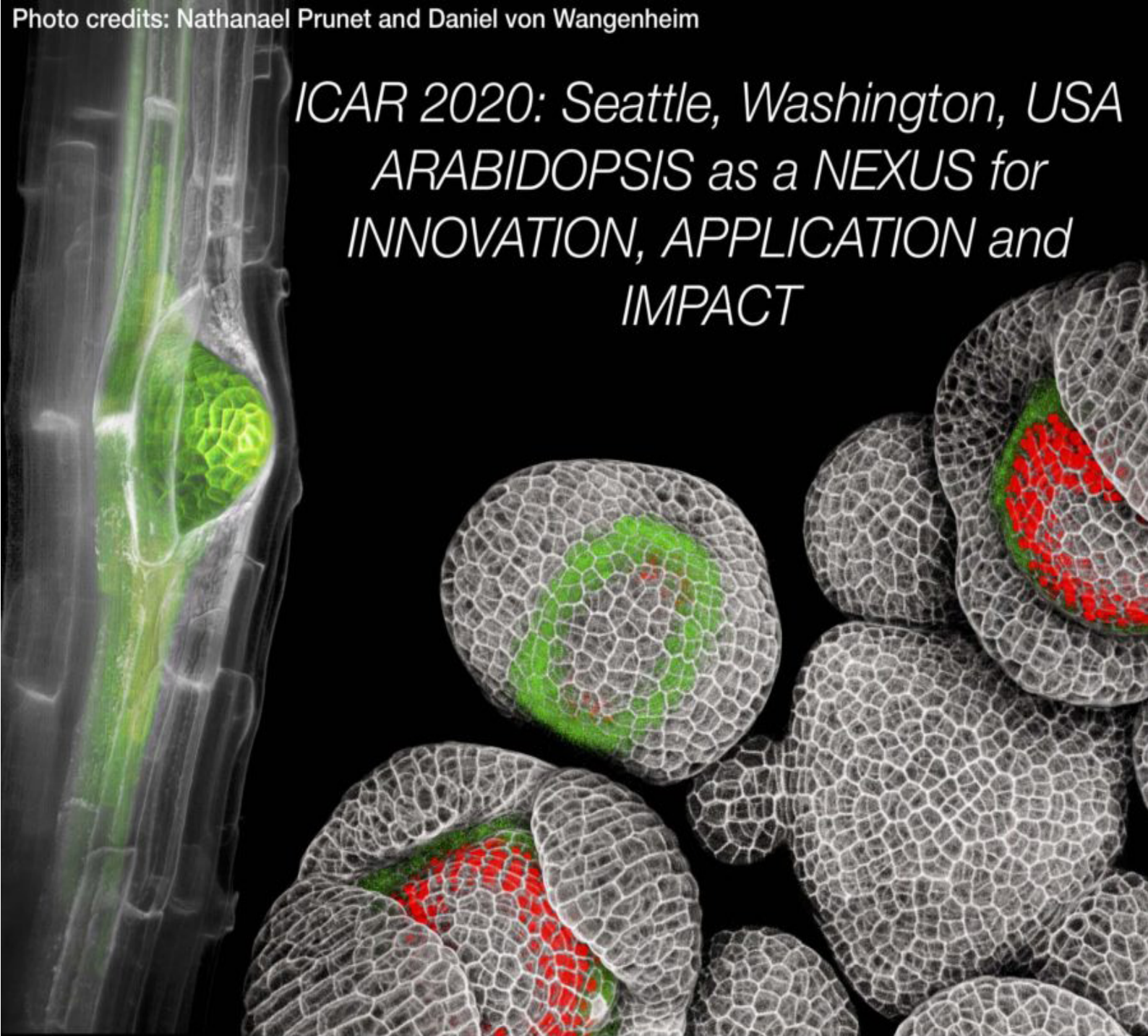
Image (INDEPTH logo) by Karin McClure

Edited by Monica Pradillo, Aline Probst, Geraint Parry, and Christophe Tatout

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ARABIDOPSIS as a NEXUS for
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