GARNish June 2013 Edition 19



GARNish Editorial and contents

Welcome to the June 2013 issue of GARNish

The past few months have seen a number of successful events on the outreach theme. The second annual meeting of the UK plant Sciences Federation (UKPSF) - of which GARNet is a member organization – with various satellite workshops (UK-PPN and Monogram) was held in Dundee with a wide range of talks illustrating the diversity of research and its potential applications to society (page 7). These ranged from the keynote address by David Baulcome on the general utility of model systems, such as Arabidopsis, informing us on basic molecular mechanisms - that have impact for beyond plant sciences - to the very specific, but nevertheless fascinating, talks on how bees get to grips with petals and the diversity of leaf shaped in tropical plants (just to mention two). The vital role of public outreach and education received attention, emphasising the need to train the next generation of scientists. This has to start with enthusing youngsters as they come through school, so that the cohort of students at University is open and receptive to the idea of plants is an exciting and rewarding area of research. With concern for the environment increasing amongst the younger generation, we should be pushing at an open door. It's just getting the message right, right?

Facilitating the exchange of information continues to be a key activity with articles on workshops and new resources (page 2-4) that promote the inchange of information from Arabidopsis to crops and other species. Bringing new technologies and developments to the attention of the Arabidopsis and wider plant research communities, GARNet has organised a number of meetings over the years that anticipate or help drive new developments in biology and promotes their uptake. The recent plant synthetic biology meeting at the University of Nottingham showcased the breadth of research opportunities opening up in this area (page 5). The announcement of two funding calls in this area may not have been completely coincidental, but illustrates the utility in having proactive organisation that enables us to take advantage of such opportunities as they arise.

The Spotlight in this edition falls on the Universi-

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Many thanks to all who contributed to this issue, especially John Doonan, David Salt, Frances Downey, Alex Webb, Eric Lyons, Emma Wallington, Rebecca Nesbit, and Mimi Tanimoto. Cover image credit: Daniela Peukert

ties of Aberdeen and Cambridge (pages 15 and 21), highlighting the world-class plant science research undertaken at these institutions, alongside a fascinating in-depth article on the topic of ionomics from David Salt (page 9).

As with any other dynamic organisation, little stays the same for long. This year, as of May 7, Ruth has increased her international presence with her appointment as the executive director of the Global Plant Council. Congratulations to Ruth, and I'm sure she will make a great a significant impact to this organisation. The Global Plant Council "aims to generate a critical mass and therefore a stronger voice for plant science in the global debate". At the helm of GARNet for nearly a decade, she clearly demonstrated the importance of coordination across the community and ensuring our opinions and interests are heard. I am sure that you will join me in wishing her every success in the future and thanking her for her unstintingly hard efforts on our behalf over the past years. However, it's not all doom and gloom as she will still be substantially involved in GARNet (40% of her time), and is handing over some responsibilities into the capable hands of Charis.

John Doonan

GARNet: www.garnetcommunity.org.uk Blog: http://blog.garnetcommunity.org.uk

You can follow Ruth and Charis on Twitter on @GARNetweets and @weedinggems.

GARNish Editorial

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University of Warwick GARNet PI

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Cyril Zipfel

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A Global Role for Dr Ruth Bastow

GARNet co-ordinator Ruth Bastow has recently been appointed Executive Director of the Global Plant Council. This position will take up 60% of her time, while the other 40% of her time will still be devoted to GARNet. The Global Plant Council is a coalition of plant and crop science societies from across the globe, aiming to bring plant scientists together to work toward solutions to global prob-

lems. A laudable cause – congratulations, Ruth!



GARNet: Have Your Say

Throughout its history, GARNet has focused on supporting basic plant science research by aiding researchers to exploit the rapidly developing resources available in order to make the best possible progress.

In the past we have provided access to genomic resources such as the transcriptomics service at NASC, facilitating the uptake of systems biology and more recently playing an essential role in ensuring that there will be a viable successor to TAIR after it ceases to be funded in August 2013. GARNet organises regular meetings and workshops to help bring you up to date with recent discoveries, or to provide training and support in new areas. GARNet also provides a communication hub for UK plant scientists. Internationally, GARNet ensures a UK presence on committees including the Multinational Arabidopsis Steering Committee (MASC) and the International Arabidopsis Informatics Consortium (IAIC).

We are currently evaluating the impact GARNet has had to date and assessing how we can help researchers make the best possible progress in the future. We would greatly appreciate a two minutes of your valuable time to complete a survey, found here: https://www.surveymonkey.com/s/L5V3PNK.



GARNish News and Views



Training the Trainers workshop

On 26-27 March, The Genome Analysis Centre (TGAC) hosted the first ELIXIR/GOBLET Training the Trainers workshop. ELIXIR and GOBLET are separate networks with shared interests in bioinformatics training. They will be





influencing bioinformatics and computational biology use and training over the next few years.

The ELIXIR project was FP7-funded in 2007 and aims to establish a sustainable European infrastructure for biological information. Sixteen countries are participating, each one a 'node' responsible for a different aspect of the project. ELIXIR-UK is based at the EBI in Cambridge, and is both the co-ordinating hub of the entire project and the training node.

The Global Organisation for Bioinformatics Learning, Education and Training (GOBLET) was established to support trainers and educators in bioinformatics and computational biology. Their aims include establishing guidelines and standards for training, gather funding, and forming a networking and support hub where resources can be shared internationally.

The purpose of the meeting at TGAC was to work out how ELIXIR and TGAC will interact, and what the bioinformatics training community needs from them. The discussions led to the conclusion that there are needs for credit for trainers and standardisation of training materials for easy sharing. You can see the minutes of the meeting on the GOBLET website.

If you do any bioinformatics training at all, I suggest you consider getting involved with GOB-LET. ELIXIR is due to receive its funding for the construction phase of the project in autumn.

UK Plant Sciences Federation Update

The past two months have been very busy for the UKPSF. As well as PlantSci 2013 (see page 7), we were the co-ordination hub for Fascination of Plants Day in the UK. The second international Fascination of Plants Day took place on Saturday 18 May 2013, and featured events around the world to celebrate the importance of plants in our lives and landscapes. At least 38 events involving more than 81 organisations ran in the UK - from hands-on activities and interactive exhibits, to guided walks, talks and debates.

Hubs of activities were around Bristol, Cambridge, London, Leicester, Oxford and Norwich. Bristol's events included a 'Leafy Murder Mystery' organised by the British Society for Plant Pathology (BSPP), in which participants will collect information on the viruses, bacteria and fungi causing plant diseases that damage our woodlands and crops. For more information about Fascination of Plants Day, go to: http://www.plantday12.eu/

New in Comparative Genomics Eric Lyons, Bio5 Institute, University of Arizona ericlyons@email.arizona.edu



CoGe (http://genomevolution.org) is a webbased comparative genomics system that provides access to 20,000 genomes from 15,000 organisms. Its web-based system contains over 30 tools for the analysis, comparison, and visualisation of genomic data from the scale of whole genomes to individual nucleotides. Extensive documentation and tutorials exist for how to use CoGe, and a recently published how-to article is available that walks through the comparative analysis of the genomics of Brassica rapa and Arabidopsis thaliana.

Recent develops to CoGe have focused on leveraging the iPlant Collaborative's cyberinfrastructure (http://www.iplantcollaborative.org/) to provide scalable computing resources of CoGe's on-the-fly analyses and creating a user-data management system that allows scientists to securely add their private genomes to CoGe and share them with collaborators. In addition, we are working on the EPIC-CoGe platform in order to provide integration of all Arabidopsis epigenetic data. This is a collaboration with EPIC (Epigenomics of Plants International Consortium) and



Dr. Brian Gregory, and is supported by the Gordon and Betty Moore Foundation.

Wheat Transformation Resource Emma Wallington, NIAB croptransformation@niab.com

The BBSRC Bioinformatics & Biological Resources fund has recently funded the NIAB Crop Transformation Team to provide a Community Resource in Wheat Transformation. This gives UK plant scientists free access, over a 5 year period, to the most efficient publically funded platform for wheat genetic modification.

Fifty novel genes will be tested in this project, selected with help from an external project advisory group comprised of researchers, industry members and stakeholders. We anticipate that half of the project capacity will be used by scientists working with model species such as *Arabidopsis thaliana* or *Brachypodium distachyon*, in order to find new sources of genes and to encourage and support the scientists to test them in wheat.



The team has implemented a new technology in the last few years to increase efficiency with a US spring wheat to over 30% (proportion of in-

oculated wheat seed embryos that produce a transformed plant). We have also successfully increased efficiency with a UK winter wheat, Glasgow. The funding allows us to extend the usefulness of this resource to UK and northern European wheat varieties - we will evaluate a further 50 varieties of winter and spring wheats in the project. This will increase the relevance of this technology for UK agriculture, and is crucial for disease resistance studies.

Applications must demonstrate a clear relevance to BBSRC food security targets and UK agriculture. Further information and an online application form are available on our website http://www.niab.com/transgenic. The current round of applications will close on 31st October 2013, for transformation into wheat during 2014. General enquiries can be emailed to croptransforma-

tion@niab.com.

Wheat seedling image by Flagstaff Fotos via Wikimedia Commons

iPlant Training Workshop at Daresbury Laboratory: September 2013

The iPlant Collaborative is a community of researchers, educators, and students working to develop cyberinfrastructure for plant science. Users are able to store and analyse their data, and use iPlant tools for genome assembly, CHiP and RNA Seq analysis, and much more. All the resources are free for users worldwide and all are web based.



Like every bioinformatics resource, some training is required to use iPlant effectively. Come and learn about how iPlant's major offerings – the Data Store, Discovery Environment, Foundation API, and Atmosphere – can radically enhancedyour scientific productivity at this four day workshop, held at the University of Warwick, in Coventry, on 17-20 September 2013.

The first day will be an introduction to iPlant and will feature a mixture of lectures and hands-on activities to introduce and familiarise users with iPlant's major offerings and services. This course will assume no prior experience with iPlant, and does not require any background in programming or advanced informatics.

During the following day and a half, delegates will recieve training in scientific application within iPlant. Three interactive tutorials will delve into the application of the iPlant cyberinfrastructure to perform RNAseq analysis, genome-wide association studies, and inference of genetic networks.

Advanced Topics in the iPlant Cyberinfrastructure will complete the workshop. It will follow a 'Bring Your Own Code or Data' model in which participants will schedule sessions with iPlant staff with the objective of using the iPlant infrastructure in their own analyses or extending the iPlant CI with scientific applications of their choosing. Participants will need to bring a dataset they wish to analyse, a workflow they wish to



incorporate within the infrastructure, or want to incorporate the iPlant API into their own bioinformatics applications. Registrants in this session will be contacted in advance to discuss specifics of what they wish to accomplish.

Introduction to Opportunties in Plant Synthetic Biology

The 2013 GARNet meeting was An Introduction to Opportunities in Plant Synthetic Biology, held on 21-22 May at the University of Nottingham. The timing of the meeting coincided almost to the week with the announcement of the BBSRC Centre for Synthetic Biology and ERA-SynBio funding calls, confirming the significance of synthetic biology not as an emerging field, but an opportunity that plant scientists cannot afford to miss.

The programme was diverse, reflecting the cross-cutting, outward-facing nature of synthetic biology. Experts in chemistry, microbiology, computer science, and plant science presented their research and gave their perspectives of synthetic biology. The delegates, a mixture of PhD students, post-docs, academics, and commercial scientists, were introduced to a number of tools and bioinformatics platforms for use in synthetic biology. Slides from the talks are online now.

The meeting served two purposes: to introduce the plant science community to synthetic biology, and to ascertain the status of plant synthetic biology in the UK. Breakout groups met twice in order to discuss the second objective, and concluded that as a flexible, innovative research community, UK plant science is ready to meet the synthetic biology challenge. There are some barriers to progress in plant synthetic biology however. These include specific technological problems, like efficiency in crop transformation, as well as issues with intellectual property and financial barriers to using some open access resources in practice.

A GARNet report on the status of UK plant synthetic biology, including a summary of the conclusions from the discussion sessions, will be published shortly. The Journal of Experimental Botany will be publishing several reviews by speakers from the meeting, as well as a meeting report.

Upcoming Funding deadlines

BBSRC Responsive mode: 25 September 2013

BBSRC Multidisciplinary Synthetic Biology Research Centres: 18 July 2013

ERASynBio 1st joint call for transnational research projects: 26 August 2013

ERA SynBio Twinning Programme: 15 July 2013

Marie Curie Actions: CIG,18 September 2013

NERC Independent Research Fellowships: 1 October 2013

Outreach Grants

- Biochemical Society: 30 September 2013
- British Ecological Society: 17 September 2013

Student travel grants

- Genetics Society: 1 August; 1 November
- Company of Biologists: 31 August
- Biochemical Society: 1 September, 1 November

Upcoming Plant Science Events in the UK

2-3 September 2013: Second International Workshop on Image Analysis Methods in the Plant Sciences, Nottingham

9-10 September 2013: Plant Environmental Physiology Group 2013 Symposium, Manchester

9-12 September 2013: CPIB Summer School: Mathematical Modelling for Biologists, Nottingham

11-13 September 2013: Regulation of Fertilization and Early Seed Development, Bath

17-20 September 2013: iPlant Training Workshop, Coventry

25 September 2013: International Advances in Plant Virology, Norwich

6 November 2013: Fruits and Roots: A Celebration and Forward Look, East Malling Research







Data mining with iPlant

17-20 September 2013 **University of Warwick**

Day 1: Introduction to iPlant (free)

A mixture of lectures and hands-on activities to introduce and familiarize users with iPlant's major offerings and services

Days 2 and 3: Interactive tutorials in the iPlant environment

How to perform RNAseg analysis, genome-wide association studies, and inference of genetic networks in iPlant

Days 3 and 4: Advanced Topics in the iPlant Cyberinfrastructure

Bring a dataset to analyse, a workflow to incorporate into iPlant, or learn how to incorporate the iPlant API into your own applications

For more information, contact charis@garnetcommunity.org.uk or go to http://www2.warwick.ac.uk/fac/sci/lifesci/news/iplant



GARNish Plant Science in a Changing World

UK PlantSci 2013: Plant Science in a Changing World

Charis Cook

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On 16-17 April, plant scientists from all over the country descended on Dundee for PlantSci 2013, the second annual conference organised by the UK Plant Sciences Federation. The theme of the conference was Plant Science in a Changing World, so it was fitting that plant breeders and educators joined representatives from fields as diverse as basic and applied research, molecular biology, and ecology. Many speakers made it clear that the challenge of sustainably providing for a burgeoning global population in a constantly changing physical environment requires all plant science stakeholders to work together.

The two keynote speakers gave thought-provoking lectures on the importance of plant science. David Baulcombe's talk was a rallying cry in defence of basic research and plant science. He kicked it off with a whistle-stop history of important scientific achievements, all by scientists carrying out basic research on plants: Robert Hooke, who identified and labelled 'cells' for the first time when studying woody plant biomass in 1665; 19th century monk Gregor Mendel, whose peas were the first genetic model system; Russian botanist Dmitri Iwanowsk, who in 1892 was the first scientist to identify and characterise a virus; and Barbara McClintock, who discovered transposable elements in maize. More recently even than McClintock's work, Argonaute proteins, tumour formation, and cellular totipotency were all identified first in plants.

The scientists involved in the discoveries listed above were carrying out what they presumably viewed as interesting work, simply because they wanted to know the answer – pure science, but all with far-reaching consequences. However at the time of their discoveries, their breakthroughs were not greeted with fanfare and celebrity. Agricultural, medical, nutritional, and technological advances that are close to market and/or easy to connect with real life are frequently promoted in the general media. Basic research on the other

hand, is circulated only in scientific journals and popular science publications. Yet if funders and commercial innovators ignore basic science, there will be nothing to base applied science on.

Baulcombe's take-home message was that basic excellent plant science research has to be celebrated in its own right rather than as a half-way point to a useful product in the future. Promoting and celebrating plant science will raise awareness of its importance to the taxpayers who fund science and to the policy makers who decide where funding will be focussed.

Charles Godfray, the first keynote speaker, and Baulcombe both discussed the complex interaction between science and politics. Baulcombe commented that, "When we do science, we are apolitical. But when we discuss the application of science, it is very political." He was referring to regulations surrounding agricultural technology and the lack of government involvement in bringing agri-tech developments to market; but Godfray could have said the same thing the previous day while discussing the impact of poverty on malnutrition (see the panel to the right for a more detailed overview of Godfray's talk). Both speakers emphasised that science alone is merely academic. If research, whether it is fundamental or applied, is to have any impact on the world, it must be supported by sensible regulations, evidence-based policy, and a sustainable infrastructure.

The rest of the talks showcased an appropriate mixture of excellence in UK plant science research, effective and sustainable applications of UK plant science, and inspirational examples of how delegates could get involved with plant science outreach. The broad spectrum of topics covered in the talks and the networking sessions during refreshment breaks, the wine reception, and the conference dinner provided a valuble opportunity for the plant science stakeholders to meet each other and begin working together.

You can read more about PlantSci 2013 in a meeting report in the July 2013 edition of New Phytologist (Cook et al., 2013; New Phytologist vol. 199).

Plant Science in a Changing World



Delegates wait for PlantSci 2013 to start in the Dalhousie Building at the University of Dundee.

No Single Answer: Perspective on Charles Godray's Keynote talk

Rebecca Nesbit

Society of Biology, Charles Darwin House Roger Street, London WC1N 2JU

UK PlantSci 2013 opened with a keynote talk from Professor Charles Godfray, who spoke very convincingly about the need for food production to become radically more sustainable. At the moment, our food production system is compromising our future capacity to grow food.

Professor Godfray, who is Director of the Oxford Martin Programme on the Future of Food at the University of Oxford, explained that we have to address the challenges of feeding 10 billion people in a new way.

Not only will we have more people to feed, but also they will be richer. They will expect more varied diets, which require more resources to produce. Population growth and changing diets were a focus of his talk and he believes that these are both important conversations to have.

The challenges become even greater as we experience a changing climate and increased competition for water and other natural resources.

Each night, around a billion people go to bed hungry, and a further billion lack essential nutrients. To meet the growing demand for food we need to increase crop yields, but we also need to ensure that food reaches the right people.

Most strikingly for me, Professor Godfray was keen to stress that feeding the hungry billion is not just about food production or food waste, but also about how we allow the poorest countries in the world to develop. Many organisations try to argue that one is enough, but he is convinced this is far too simplistic.

This article was adapted from a post orgininally published on the Society of Biology blog: http://societyofbiologyblog.org

GARNish Ionomics Hub

The ionomicsHUB (iHUB): A model for open access plant research in the 'cloud'

David E Salt

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The massive and continuing increase in our capacity to both sequence whole genomes and open source access to them now means that genotyping an organism is no longer a barrier to probing the molecular mechanistic basis of biological phenomena. The limiting factor is now our capacity to phenotype organisms in high-throughput to allow the efficient connection of genotype to phenotype.

To help overcome this barrier in the context of plant mineral nutrition research, a collaborative US National Science Foundation funded Arabidopsis thaliana ionomics project (0077378-DBI. 0419695-IOB) was initiated in 20111. The goal of this approach was to implement a high-throughput phenotyping platform with the capacity to quantify the elemental composition (aka ionome) of 1000s of A. thaliana genotypes in a precise2 and sustained manner; using the platform for both forward and reverse genetics to uncover the genes and gene networks that control the A. thaliana ionome. Since its initiation over 175.000 A. thaliana samples (primarily leaves but also seed) from over 13 000 unique genotypes have been analyzed for multiple elements including Li, B, Na, Mg, P, S, K, Ca, Mn, Fe, and Cd using inductively couple plasma mass spectrometry (ICP-MS) within a formalised analytical workflow.3

To support this high-throughput platform we have developed an information management system that utilises systems engineering approaches to integrate work flow control, data storage and analysis, and web-based access.⁴ This system models the physical work flow in the laboratory and divides it into stages, based on activity, information needs and data generated. In this way it can provide both work flow support and capture the contextual information (e.g. genotype, tissue-type, soil-type, light intensity, fertilization) called metadata necessary to reproduce the experiment and interpret the data. All metadata and

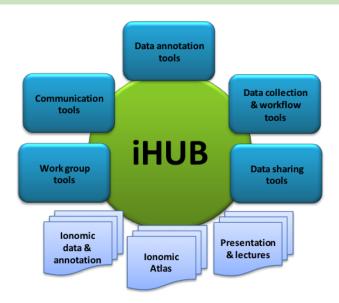


Figure 1 On-line iHUB tools and resources at www.ionomicshub.org

ICP-MS analytical data are associated in the database. The system is designed to not only be an ionomic workflow and data storage system but also to serve as an on-demand search engine to allow rapid retrieval of data and its associated metadata.

However, to truly enable the plant research community to efficiently probe gene function on a genomic and comparative genomic scale it is critical to design systems that take advantage of both large-scale datasets and web-enabled communication tools. It was with this goal in mind that during 2007, and in collaboration with the Purdue Cyber Center, we launched the ionomicsHUB (iHUB) (Fig 1 & 2) accessed at www.ionomicshub.org and currently funded by the US National Science Foundation (DBI-0953433).

iHUB overview

The iHUB is an open access, collaborative work-space designed to maximise both community access to ionomic resources, and knowledge extraction from these resources. Specifically, the iHUB delivers tools to allow the easy access, sharing and annotation of publically available ionomic data, as well as tools such as the lonomics Atlas to enable new ways to mine such data. Future ideas are also in development with the planned release of a tool to facilitate the collection of ionomic data from distributed laboratories. The iHUB is founded on the ionomics

GARNish Ionomics Hub

database developed for *A. thaliana*, which currently contains ionomic data on knockout alleles of 2,821 genes, natural accessions including the 360 HapMap population⁵, the 80 re-sequenced Eurasian regional set,⁶ the MAGIC population,⁷ and several diallelic RIL populations,⁸ and multiple EMS and FN mutants. In addition, the iHUB also provides access to ionomic data from the 11,942 strains of *Saccharomyces cerevisiae* full genome knockout, and over expression collections⁹ and prototypes for rice, soybean, maize and Brassica.

The User Experience

Anonymous users require no password and have full access to the ionomic data for searches (Fig 3) on gene, line name and experiment (tray) as well as a phenotype search. Once retrieved data can be viewed graphically (Fig 3), in table format or downloaded as a CSV file or as a combined PDF report. Anonymous users can also download 'flat' data files using the Data Exchange utility. This utility contains various types of information including R-scripts from published ionomic analyses and a full data dump of the A. thaliana database as a CSV file. Anonymous users also have full access to the Ionomic Atlas. 10 The Atlas contains multiple data sets relating to the A. thaliana HapMap population. These currently include leaf ionomic data, SNPs associated with leaf ionomic traits derived from GWA analysis,5 and soil and climate information extracted from the European Soils Database¹¹ for the home location of each of the accessions. Tools are provided to filter the set of accessions using the climate, soil and ionomic data, identify correlations between data sets, and display filtered accessions on a Google Map interface. Data can also be viewed graphically and downloaded as a CSV file. Each accession is also linked back to the main ionomics database providing simple access to the full set of ionomic data on all accessions included in the Atlas.

User registration at the iHUB is done through the simple one step online Sign Up procedure. Registered users have access to added functionality, including advanced search tools and the ability to create, annotate and share Datasets with other registered users within a flexible workgroup infrastructure. Datasets are created by grouping existing experiments together around concepts

of interest. Such groupings may reveal new ionomic relationships, for example between genes and physiological processes. These new observations and conclusions can be added to the Dataset as an annotation and shared with other users. A fixed copy of the Dataset is held permanently in the database and can be either public or viewable based on workgroup permissions. Datasets can also be published from within the iHUB. Publication creates a DOI (digital object identifier) for the Dataset providing a unique identifier that allows the Dataset to be cited in a publication and retrieved as an electronic document.

Innovation and Progress

Our hope is that the iHUB will lower the barrier for entry into the field of ionomics, allowing a diverse set of researchers from developed and developing nations to participate in advancing the field at the academic staff, postdoctoral, graduate, and undergraduate levels. Since Aug 2007, the iHUB has been accessed by 10,496 unique visitors from 1,426 cities in 100 different countries, including both developed and developing nations. The iHUB is now allowing laboratories without the capacity to perform ionomic analysis to access ionomic data on many 1000s of A. thaliana lines to directly test gene function, perform QTL analyses and identify potentially interesting mutants for further study. We hope that the iHUB will also provide a model for other datadriven community HUB's committed to helping to



Figure 2 iHUB homepage



Figure 3 Search tools and graphical output for A. thaliana ionomic data

democratise science by using the power of the internet to crowd source data analysis and hypothesis generation.

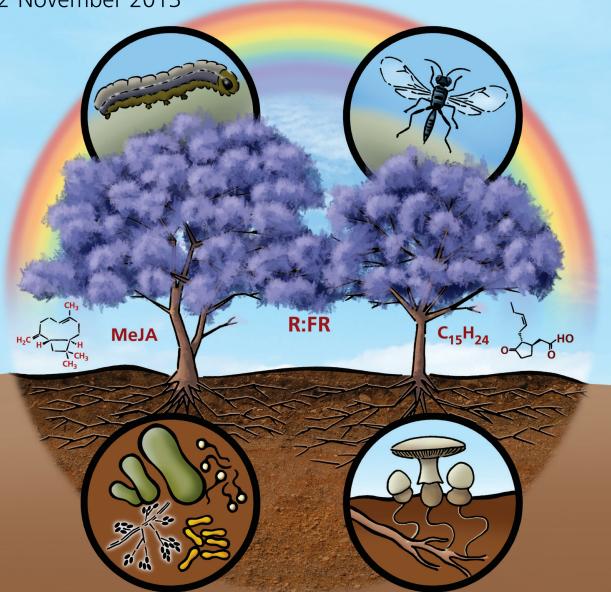
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Plant interactions with other organisms: Molecules, ecology and evolution

Universidad Católica, Puerto Madero Campus, Buenos Aires, Argentina 20–22 November 2013



Confirmed speakers

Marcelo Aizen Universidad Nacional del Comahue, Argentina Amy Austin University of Buenos Aires and IFEVA, Argentina Ian Baldwin Max Planck Institute for Chemical Ecology, Germany Carlos Ballaré University of Buenos Aires and IFEVA, Argentina Richard Bardgett University of Manchester, UK Joy Bergelson University of Chicago, USA Elizabeth Borer University of Minnesota, USA Ray Callaway University of Montana, USA Marcel Dicke Wageningen University, the Netherlands Edward Farmer University of Lausanne, Switzerland Martin Heil CINVESTAV, Mexico Richard Karban University of California-Davis, USA

Toby Kiers Vrije Universiteit, Amsterdam, the Netherlands Anna-Liisa Laine University of Helsinki, Finland Steven Lindow University of California-Berkeley, USA Richard Lindroth University of Wisconsin-Madison, USA Ariel Novoplansky Ben-Gurion University of the Negev, Israel Ralph Panstruga RWTH Aarchen University, Germany Ronald Pierik Utrecht University, the Netherlands Corné Pieterse Utrecht University, the Netherlands Natalia Requena Karlsruhe Institute of Technology, Germany Gary Stacey University of Missouri-Columbia, USA Ted Turlings University of Neuchâtel, Switzerland

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University, Lancaster, LA1 4YE, UK.

The New Phytologist Trust is a non-profit making organisation dedicated to the promotion of plant science.

Complete details and registration at

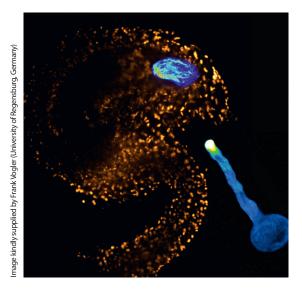
www.newphytologist.org





A Biochemical Society Focused Meeting

Regulation of fertilization and early seed development



Organizers: James Doughty Thomas Dresselhaus

Overview:

The meeting will bring together labs at the cutting edge of plant reproduction research and will focus on the processes that regulate successful gamete delivery to

the embryo sac and the complexity of post-fertilization regulation of early seed development.

Topics:

- * Pollen tube growth and self-incompatibility
- * Cell-cell communication in gamete delivery
- * Fertilization mechanisms
- * Role of small regulatory RNAs
- * Cell specification and embryonic pattern formation
- * Regulation of seed size
- * Epigenetics and imprinting



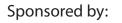
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GARNish Inspiring Across Generations

Plant Science Panel

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"I think I know what genes are, and that any protein they code for can be tested to see if it is dangerous or not. Am I right about this, if not what precautions have been taken when doing GM research?"

This is just one of over 200+ questions to be put to Sense About Science's Plant Science Panel over the last five months. Since the launch in December 2012 there have been over 8,000 hits on the plant science panel webpages, and we have run four live online Q&As. You can see information on the Panel and past Q&As on the Sense About Science website: http://www.senseabout-science.org/pages/plant-science-expert-panel.html



The strength of the Plant Science Panel lies in the willingness of the scientists on it to answer the public's direct questions, whenever they ask them and whatever they may be. We call it public-led, expert-fed. The questions are not filtered or edited; they go to the scientists as they arrive to us.

So, when rumours about viruses in GM food were flying around the internet, Huw Jones from Rothamsted Research answered people's questions. When a question came in asking for clarity on the numbers surrounding predicted ash tree mortality from ash dieback disease, the Forestry Commission's Joan Webber answered it.

The plant science panel does not just respond to questions from individuals. Often when a plant science-related topic comes up repeatedly in the media, we recieve lots of questions on it. In those instances, we organise a live online Q&A. Bringing together a group of scientists to answer questions online over the course of an hour creates a real sense of occasion and excitement. The Q&As are particularly good for areas where

there is no clear answer, as they allow each side to make their argument and lay out their evidence.

Following our Q&A on insecticides and bees, Guy Barter, Chief Horticultural Advisor of the Royal Horticultural Society, said, "I thought the Q&A was very balanced, with both sides of the debate being aired. It was really interesting to hear clear explanations of why the scientific evidence in support of a ban of neonicotinoids isn't unequivocal."

The online Q&As have now become a long term resource that can be used again and again, and as more questions are answered, the resource grows. The Bees and Insecticides Q&A has been reprinted in full in the June edition of the journal *Outlooks on Pest Management*. Following the EU decision to partially ban neonicotinoids, we were able to direct people to the Q&A when they asked us about the scientific evidence behind this decision.

What has perhaps surprised us most about the plant science panel is the effect it has had on the scientists involved. Professor Ottoline Leyser, plant science panel member and Director of the Sainsbury Laboratory in Cambridge, said, "I have very much enjoyed finding out about the kinds of question in plant science that people find interesting".

We always need more scientists to join in. If you are interested, there are three things you can do:

- Volunteer to be a member of the Panel;
- Promote the Plant Science Panel to friends and colleagues who do not have any plant science expertise. They can send questions via our online form, Twitter to @senseaboutsci using #plantsci, or email plantsci@senseaboutscience.org;
- Encourage your institute or organisation to become an official partner and support this work further. They can contact plantsci@senseabout-science.org.

The Plant Science Panel is supported by the Genetics Society, the UK Plant Sciences Federation, Society for General Microbiology, Rothamsted Research, Society of Biology, BBSRC, John Innes Centre, Society for Experimental Biology, the Biochemical Society and the James Hutton Institute.

Spotlight on the University of Aberdeen

There are over 350 plant research groups in the UK, in 42 institutions scattered from Aberdeen to Exeter. Many of these groups are international leaders in their field. To promote the breadth of plant science throughout the UK, and increase awareness of the different types of research being undertaken, GARNet is focusing on geographical areas and institutions across the UK. In this issue we continue our tour around the country highlighting the outstanding research being undertaken at the University of Aberdeen and the University of Cambridge.

Spotlight on the University of Aberdeen



Plant researchers at the University of Aberdeen are surrounded by rich and diverse habitats ranging from coastal dune systems, rich river valleys, moorland, mountains and farmland, providing both inspiration and the opportunity for excellent field work. Being situated within the Cruickshank Botanic Gardens (http://www.abdn. ac.uk/botanic-garden/) in historic Old Aberdeen further connects plant research in Aberdeen to its long history in Botany, Plant Ecology and Soil Science. The placement of the new Centre for Genome-Enabled Biology and Medicine within the gardens emphasises the willingness to build on this strong tradition by incorporate new approaches and ideas. The University of Aberdeen also sits within a larger community of plant researchers in North Eastern Scotland with the University of Aberdeen, the James Hutton Institute and the University of Dundee coming together to form the Crop Research Alliance for Food Security Scotland bringing a combined expertise in crop science, soil science, environmental modelling and human nutrition to address crop research within the global food security challenge. Most plant researchers in Aberdeen are based in the School of Biological Sciences with strong representation in both the Biological Interactions in Soils, and Ecology themes. The group addresses significant questions in plant research across scales from the molecular to the global, spanning molecular genetics to community ecology, with details of each of the groups interests described below.



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Plant-soil interactions; soil biogeochemistry; microbial pathways to greenhouse gas production

Professor Liz Baggs is an internationally renowned expert on the use of stable isotope techniques to investigate microbial sources of greenhouse gas emissions from soils, particularly N₂O and CH₄. She has developed ¹⁵N and ¹³C techniques to quantify N2O and N2 emissions and CH, oxidation rates, and to distinguish between different microbial sources in situ. These source investigations link to characterisation of plant trait, microbial functional diversity and metabolically active populations in soils. Recent research (BBSRC) is examining the role of plant traits in regulating soil N and C cycles, and the potential to use plants to manipulate trade-offs between soil C storage and greenhouse gas (GHG) emissions. Approaches range from application to soil of individual and composite rhizodeposit compounds through artificial roots, to plant-soil cores to distinguish microbial utilisation of plant carbon and soil organic matter carbon in driving heterotrophic GHG production and reduction, to isotope pulse chasing in situ.

Liz is a Fellow of the Society of Biology, a member of NERC's Science and Innovation Strategy Board and Peer Review College, President Elect of the British Society of Soil Science, and has previously served as a core member of BBSRC Committee B and as a member of the steering committee for the UK Life Sciences Mass Spectrometry Facility. She is a Section Editor for *Plant and Soil*, a member of the Editorial Board for *Soil Biology and Biochemistry*, and a member of the Editorial Advisory Board for *Global Change Biology*. She currently collaborates on two standard BBSRC grants, a BBSRC India Partnering Award, a NERC standard grant, a NERC small grant, and supervises six PhD students.

Spotlight on the University of Aberdeen



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Plant community ecology and conservation biology

David Burslem's research addresses the origin and maintenance of plant diversity, with a current focus on the ecology and conservation biology of tropical trees, and restoration of environments degraded by human activities. He is a participant in the Center for Tropical Forest Science network, which co-ordinates the collection and distribution of spatially-explicit data on the distribution of woody plants on a total of 48 large-scale (16 – 50 ha) forest dynamics plots in 23 countries (www.ctfs.si.edu/). Research in David's group investigates the mechanisms of community assembly on these plots, using experimental, molecular and statistical tools to determine how interactions between competing tree species and their symbionts regulate tree species distributions, relative abundance and diversity. He combines these community studies at point locations with research on the phylogenetics and biogeography of selected plant taxa. These targeted studies are designed to understand the origins and evolutionary history of tropical diversity and are generally conducted collaborative with plant taxonomists in major herbaria (Kew, Edinburgh, Singapore). Current research in his group focuses on Dipterocarpaceae, Myrtaceae (Syzygium), Malvaceae (Pterospermum) and Zingiberaceae (Amomum). Finally, research in David Burslem's group then assembles and analyse data-sets of localities for rare and endangered tropical tree species and models their distributions across environmental gradients and in response to landuse and climatic change. These models are superimposed on maps of current land-use in order to derive conservation assessments that contribute to priority-setting for plant conservation by national governments and statutory authorities.



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Modelling Miscanthus plant growth traits to assist in a breeding genotype suitable for different environments

Miscanthus is a giant C4 grass of East Asian origin that has attracted research funding to improve its suitability as a bio-energy feedstock. Its native habitat spans a wide range of climates from the sub-arctic of the Kabarovsk Krais of Russia the tropical oceanic Islands of the Pacific and so its various genotypes provide a rich variety of physical and genetic traits for selective breeding. Currently a sterile genotype Miscanthus x giganteus has been used for commercial trials for producing biomass feedstock. It is well adapted to temperate climates, but it's high yield is sensitive to drought and frost stress and it has to be in-vitro propagated. There is a need to extend the geographic and climatic range over which Miscanthus can be grown and to improve its yield and fuel quality.

The Hastings' group research models are being used to assist in the breeding process. The first use is assist in the collection of germplasm for breeding purposes by identifying germplasm collection sites is Asia with similar bio-climatic conditions to the areas that the target clones will be grown in Europe and North America. The second is to parameterise the model for different clones in terms of their growth stages such as seed germination, emergence from the rhizome, leaf expansion, photosynthesis rate, flowering time and rate etc, so that a given clone's performance can be predicted for different environmental and climatic conditions. Obviously early emergence and late flowering are the traits of interest to produce the most biomass. Late flowing is of interest to avoid natural propagation of an invasive species and seed germination is of importance to improve the economics of the establishment of plantations. Aberdeen is currently contributing to two projects to improve Miscanthus namely the GIANT-LINK and OPTIMISC projects in collaboration with Aberystwyth University.

Spotlight on the University of Aberdeen



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Plant-microbial interactions

The plant community is a key factor to take into account when analysing microbial communities in their natural environment, as various types of interactions (including symbiosis or parasitism) have been well described. Global microbial diversity, and especially that in terrestrial environments, is extremely important and the vast majority of microbes are uncultivated. Dr Cécile Gubry-Rangin aims to unravel the unknown function of an under-explored and uncultivated but abundant archaeal group, Group 1.1c, using pine plants. Group 1.1c archaea are frequently the most abundant prokaryotes in acidic soils and represent more than 30% of all cells in boreal forest soils. Additionally, specific associations between these archaea and pine mycorrhizas are found in boreal forests, but their basis is unknown.

Based on the sampling of 10 Scottish pine forests, non-sterile soil microcosms will be set up in the laboratory in presence or absence of pine plants (and of associated mycorrhizae). The abundance, functional activity and diversity of the Group 1.1c archaea will be characterised in order to analyse the influence of pine and mycorrhizas on their growth and selection. This approach will increase understanding of the ecological and functional roles of abundant Group 1.1c archaea in soils. Given the phylogenetic relatedness of this group to archaeal ammonia oxidizers, this project will decipher the potential involvement of Group 1.1c archaea in ammonia oxidation and N_oO production, as they may be key-players in terrestrial and atmospheric pollution, impacting on fertiliser loss and climate change.



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Soil physics with a specialisation on interactions with biological processes including plant roots

Much of Professor Paul Hallett's research examines the manipulation of soil physical properties by plants. He focusses on different scales and times, including the onset of seed germination, the formation of the rhizosphere, root anchorage and the reinforcement of soil by plant roots, all with a goal to understand the manipulation of soil physical conditions by plants to enhance productivity or improve the environment. His research also examines physical limitations to root growth, particularly related to soil management practices, and the selection of phenotypic traits to overcome associated stresses of soil compaction, waterlogging or drought. Techniques developed in his lab include microscale measurements of rhizosphere hydrological properties, mechanical tests to quantify the impact of root exudates on soil structure formation and biomechanical tests of plant roots to assess physical defences to root herbivory, tissue structure impacts and root-soil mechanical reinforcement. The approaches are adopted from a range of disciplines, in close collaboration with plant scientists, ecologists, microbiologists, engineers and modellers.



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Plant ecology

Research in the Johnson group is focused on understanding how plants interact with other organisms and the consequences of these interactions for biogeochemical cycling and biodiversity. In particular, a key focus is on plant-mycorrhizal fungal symbioses, and current research is testing i) how intra- and interspecific diversity of ectomycorrhizal fungi affects ecosystem functioning, ii) the role of bryophytes in regulating carbon and mineral nutrient transfer between trees and

Spotlight on the University of Aberdeen

ectomycorrhizal fungi, iii) the importance of common mycorrhizal mycelial networks in regulating how plants, insect herbivores and their parasites interact, and iv) how the diversity of plant functional traits in species rich grassland regulates greenhouse gas emissions and carbon turnover. Much of this work involves application of stable and radioisotopes, and manipulation of plant and mycorrhizal fungal diversity both in the field and the laboratory.



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Uptake and accumulation of elements in plants

Gareth's research interest is in the accumulation and distribution of elements in plants and their impact on human health and food security, with a focus on the potentially toxic elements arsenic and cadmium and beneficial minerals zinc and iron. Current work has been exploring both the genetic regulation and the environmental conditions that lead to the accumulation of these elements in plants, in particular the edible portions of plants. The main focus of the work has been on rice, as this is the dietary staple for 50% of the world's population. This has been done by screening populations of rice across diverse field conditions, integrating elemental concentrations with genetic mapping, and employing techniques such as transcriptomics, with the aim of identifying genes and the mechanisms responsible for the accumulation of elements in plants. In addition, work is also being performed to understand the cycling of metals in the environment.



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Genetic variation in rice at the breeding, physiological and molecular level

The Price group research focus is the genetics of rice, related to reduced water use including root growth, nematode and Striga resistance, interactions with mycorrhiza and uptake of nutrients including grain arsenic. Overall, research aims to provide options to grow rice with less water input. This is achieved principally through exploiting natural allelic variation via the genetic mapping of relevant traits using diallelic crosses and association mapping. Relevant genetic resources (mapping and association populations) are supplemented with transcriptomics and genome sequencing data to allow candidate genes to be hypothesised and tested. High throughput phenotyping, controlled environment experiments and field screens are employed to identify quantitative trait loci (QTLs) and candidate genes underlying them while experimental biology is used to test gene-based hypothesise on near isogenic lines, mutants and RNAi lines. Genes under investigation include MAX1 orthologue for Striga, nematode and mycorrhizal interactions, aquaporins for drought and root hydraulic conductance and auxin transporters for root growth. A major thrust of the work has been assessment of grain element composition with an emphasis on grain arsenic, with a view to reduce dietary exposure to the class 1 carcinogen. A new area of research is the use of high throughput genotyping (SNP arrays or next generation sequencing) to produce populations of local material for the investigation of natural variation in water userelated traits.

Spotlight on the University of Aberdeen



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The influence of plant diversity on ammonia oxidiser communities

Plants are believed to influence the diversity and community composition of soil microbial communities through a number of mechanisms, including root exudate composition. Their influences on the 'total' microbial communities in their environment are often difficult to detect and understand, due to the complex nature and multiple functional reduncancies of the microbiome. This project, which is being carried out by Dr Cécile Thion, in collaboration with Dr Franciska de Vries and Professor Richard Bardgett (University of Manchester), therefore focuses on the effects of plant community composition on a specific functional group, the ammonia oxidisers, comprising both bacterial and archaeal taxa that perform the first step in nitrification of soil ammonia to nitrate. This process is of economic importance, leading to significant losses of commercially applied ammonia-based fertiliser, and environmental concern, through pollution of groundwater by leached nitrate and atmospheric pollution by nitrous oxide.

Different responses are predicted by our previous work, which has provided evidence that the source of ammonia determines the relative contributions of archaeal and bacterial ammonia oxidisers to soil nitrification. The source of ammonia, in turn, will be modulated by the nature of organic material input as plant root exudates. Mesocosms are therefore being established to determine the influence of different plant communities and plant traits on archaeal and bacterial ammonia oxidiser communities and also to determine the resistant and resilience of ammonia oxidisers to drought and subsequent wetting. In addition, more specific hypotheses will be tested in better-controlled microcosm experiments to determine mechanisms involved in resilience, resistance and recovery from drought stress using molecular techniques, in particular transcriptional analysis.



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Plant-soil interactions

The performance of cultivated and wild plants can be influenced decisively by belowground processes such as nutrient and water supply and their interactions with vegetation. Yet, such interactions remain poorly characterised and quantified. Often using stable isotope approaches as investigative tools, David Robinson and his colleagues discovered how localised root proliferation and transient up-regulation of ion transport contribute to N capture by competing plants. Novel approaches that allow competition for soil N sources to be quantified directly allowed Robinson and collaborators at the James Hutton institute to show how the coupling between N capture and productivity is highly dynamic and context-dependent. Competing plants capture and use N differently from their isolated counterparts depending on species, climate and resource availability. That explains why it is always hard to predict competitive outcomes in mixed vegetation or between crops and weeds. Plants are involved in remarkably subtle interactions between elevated atmospheric CO2 concentration, water supply and denitrification at small spatial scales. If applicable to landscape scales, this suggests a mechanism for a previously unsuspected plant-induced amplification of the enhanced greenhouse effect. Theoretical, as well as experimental, approaches have been a continual feature of the group's work. Allometric scaling models have revealed a potentially huge under-estimation in global root biomass, which has implications for characterizing the size and dynamics of the terrestrial carbon sink and of soil carbon stores. Current analyses are focusing on how allometric constraints interact with local environmental conditions to influence the allocation of gross primary production in the world's forests.

Spotlight on the University of Aberdeen



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Functional and ecological genomics of mineral nutrient and trace element homeostasis in plants

Professor David E Salt's long term research interest is to understand the function of the genes and gene networks that regulate the mineral nutrient and trace element of plants (aka ionome), along with the evolutionary forces that shape this regulation. Salt has developed a novel functional genomics approach to study the ionome, combining high-throughput elemental analysis with bioinformatics, genetics and genomics in both laboratory and field-based studies. Using this approach he has published papers describing work using both induced and natural variation in Arabidopsis thaliana that provide molecular mechanistic insights into the regulation of the plant ionome. Salt's research has also started to reveal the molecular basis of plant adaptation to the environment, with a recently published article describing evidence that selection is acting on the Na-transporter HKT1 to adapt local populations of A. thaliana to coastal environments. Salt has also successfully used genome-wide association (GWA) mapping in A. thaliana to identify genes involved in regulating natural variation in the leaf ionome, including the accumulation of sodium and cadmium. Translating this fundamental work into crops, Salt has been screening large populations of rice and applying genetics coupled with next generation sequencing for the identification of genes that control the mineral nutrient and trace element content of rice grain. Further, to encourage a diverse group of researchers to participate in ionomics, Salt has developed a unique online web-based community portal called the ionomicsHUB (www.ionomicshub.org). The ionomicsHUB focuses on both workflow control for high-throughput data collection and also delivery of ionomic data to the community.



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woodin

Effects of drivers of change on native plant species, vegetation communities and ecosystem process in the British uplands and the Arctic

Sarah Woodin is involved in projects investigating the ecological impacts of climate change, herbivory, land management practices and atmospheric nitrogen deposition, often in interaction with each other, in the British uplands and the high Arctic. The processes studied range from the ecophysiology of individual species, through vegetation processes and inter-trophic interactions to ecosystem nutrient and carbon dynamics. A common theme is the functional importance, and sensitivity, of bryophytes within the ecosystem. Much of her research in Scotland is conservation based, undertaken in collaboration with Scottish Natural Heritage, and seeks to provide a scientific basis for conservation policy and management.

Spotlight on the University of Cambridge

Spotlight on the University of Cambridge



The Department of Plant Sciences, University of Cambridge encompasses research built on a strong foundation of basic botany in which we address the fundamental concepts and mechanisms of plant life. We cover all levels of organisation from molecules to cells to organisms to populations and landscapes, and we are interested in timescales from the very short duration of molecular reactions through to evolutionary transitions. Around 250 people work in the Department contributing to research, teaching and impact activities. The research facilities are excellent, with a large Plant Growth Facility housed in the Botanic Gardens. Also housed at the Botanic Gardens is the magnificent Sainsbury Laboratory, and we are fortunate to have some of the group leaders of the Sainsbury Laboratory as members also of our Department. The Department contributes to teaching in a wide range of Undergraduate courses, including a final year specialisation in Plant Sciences that usually attracts around 30 finalists. We have a thriving graduate population of around 60 - 70 students, mostly working towards a PhD. Our research is translated into key areas of economic benefit and global relevance and we engage with industry and the general public to ensure the continuing relevance of our work. These activities are supported by the Cam-Plants initiative (www.cambplants.group.cam. ac.uk) that provides an umbrella for activities across the University of Cambridge, partnership in business support achieved through EU-funded activities, which focus on supporting regional business (e.g. InCrops Enterprise Hub; www. incropsproject.co.uk/partners) and NIAB Innovation Farm (www.innovationfarm.co.uk), and public outreach.

Image credit: Dijana Maric



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RNA Silencing and Disease Resistance

The group researches various types of disease resistance in plants, with a particular interest in one of them, RNA silencing, which has significance beyond infection. RNA silencing controls the level of gene expression at various stages of the plant life cycle. Some of these effects are epigenetic, in that they persist through cell division or even from one plant generation to the next. The approach involves cell and molecular biology but the aim is always to understand plants at the whole organism or population level. The research currently focuses on artificial evolution of disease resistance, understanding hybrid plants, epigenetic modification of crops and RNA silencing in model organisms including Arabidopsis thaliana, tomato and Chlamydomonas reinhardtii.



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Virology & Molecular Plant Pathology

The group is interested in the interactions of plants with pathogens and pests, why some plants actively resist their attackers, and how some pathogens manipulate the resistance responses of plants. Topics of interest include: (1) Do viruses manipulate plant-aphid interactions to facilitate insect-mediated transmission? (2) Does virus infection affect interactions with other organisms in the environment including beneficial ones? and (3) How do signaling pathways mediated by salicylic acid, jasmonic acid and inositol phosphates work together to maintain resistance to pathogens and how are they sometimes subverted by pathogens, in particular viruses?

Spotlight on the University of Cambridge



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Forest Ecology and Conservation

Human population growth and resource consumption are placing enormous pressures on natural ecosystems. The group is interested in how and why the world's forests are changing, and using the research to inform conservation policy. Forest ecosystems provide habitat for the majority of the earth's biodiversity and are the source of numerous ecosystem services, ranging from the provision of timber to regulation of carbon sequestration and storage. A clear understanding of forest dynamics is therefore necessary if these resources are to be managed and protected effectively, especially in the face of global change. Describing and quantifying processes such as mortality, regeneration and species interactions, and how they change over time and across the landscape, is key if an attempt to predict and mitigate the impacts of drivers such as climate change and land use change is to be made. Several different approaches and methods are combined to the study of forest dynamics. LiDAR remote sensing and hyperspectral technology is being used alongside field studies to disentangle different aspects of forest dynamics, ranging in scope from individual trees to entire regions. In parallel, these datasets are being used to develop new, more accurate and comprehensive predictive models of forest dynamics. Taking oak forests of southern Iberia as a model system, airborne LiDAR is being employed to look at forest structure and plant diversity relationships. The same remote sensing technology is one of a number of approaches being adopted to study how forest biodiversity affects ecosystem function, through participation in the FunDivEurope consortium.



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Theoretical and computational epidemiology

Mathematical analysis and computer simulations are used to understand the spread and control of plant and tree diseases. The theoretical work attempts to isolate the ways in which factors including host growth, host topography, pathogen dispersal, asymptomatic infection and biological control affect the pattern of spread. The group has also been involved in developing large-scale, spatially-explicit, stochastic, simulation models that can be fitted to data on the realworld spread of pathogens of current regulatory concern. Examples include sudden oak death, Chalara ash dieback, Dutch elm disease, citrus canker and huanglongbing. This type of model can be used to predict the risk of disease in a given region and/or to quantify the likely effect of any proposed control strategy, together with its inherent risk of failure.



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Transport

The group investigates the roles of transport proteins in adaptation, nutrition and growth. The research focuses particularly on roots and how they sense, then respond to changes in environmental conditions, including the presence of other plants. For these studies, concentration is on the plasma membrane and studying the calcium channel proteins that can generate specific calcium signals governing adaptation and growth regulation. This research has identified extracellular nucleotides as novel plant cell regulators. How extracellular nucleotides are perceived at the plasma membrane and how this relates to known effects on cell viability, growth, immune and stress responses is being explored. The role of calcium transporters at the plasma membrane in controlling cell wall formation and re-modelling is also being investigated.

Spotlight on the University of Cambridge



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Epidemiology and Modelling

The group focuses on developing and testing a theoretical framework to understand the mechanisms that control invasion, persistence, scaling and variability of epidemics within changing agricultural and natural landscapes. The models are used to predict the spread of disease and to identify and optimise economically and ecologically sustainable strategies for disease management, encompassing genetical, chemical, biological and cultural methods. The research involves a synthesis of epidemiological theory, population and evolutionary genetics, landscape ecology and economic modelling. The models are tested using data from laboratory microcosms and extensive field and regional data-sets.



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Evolution and Development

The group is interested in the evolution and development of floral traits that are important in attracting animal pollinators. Knowledge of how plants build traits that attract particular animals will aid understanding of the diversification of the flowering plants. The group particularly focuses on petal characters such as colour, texture and insect-mimicking spots. Molecular genetic, systematic and developmental techniques are used to address these problems. A bee behavioural facility is incorporated to explore pollinator responses. Understanding plant-pollinator interactions in this integrated way provides tools to contribute to the design of strategies to protect biodiversity of plants and animals. It also allows engagement with plant breeders to optimise pollinator attraction and ensure crop security.



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Physiological Ecology

Plant molecular, physiological and environmental processes which regulate productivity and CO₂ sequestration are being investigated by the Griffiths group. The aim is to improve the operating efficiency of the primary carboxylase, Rubisco, and match water availability to use. Stable isotope methods are used to evaluate the origins and regulation of diverse photosynthetic carbon concentrating mechanisms (CCM). These include the C4 pathway and Crassulacean Acid Metabolism, as well as the biophysical CCM in algae and hornworts, with particular focus on the molecular determinants of the chloroplast pyrenoid. The research translates via fieldwork into food security and biomass crop productivity, as well as natural community diversity.



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Plant Growth Substances: sensitivity vs signal strength

The group aims to discover how changes in plant development are controlled. Sometimes a shift in the level of active hormone is responsible, sometimes an alteration in the ability of the tissue to respond, more often a combination of both. The role of inositol hexakisphosphate in development, and the regulation of dormancy by changes in the sensitivity of tissues to cytokinins are currently being investigated. This has led to the discovery that the insensitivity to cytokinins associated with potato tuber dormancy is caused by the accumulation of a cytokinin- sequestering protein. The level of expression of this protein is directly related to the duration of dormancy. Current projects include investigating the roles of cyokinins in potato tuber dormancy and using cytokinin sequestering proteins to improve resistance to pre-harvest sprouting in cereal crops.

Spotlight on the University of Cambridge



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Evolution of Plant Body Plans

Branching patterns, the arrangement of leaves around the stem and leaf shape are fundamental aspects of plant architectural diversification that impact strongly on plant productivity. Surprisingly, the earliest shoot systems that share an evolutionary history with flowering plants comprise just a small leafless stem. The research of the Harrison group aims to understand how this was modified in evolution to generate the variety of plant forms that abound today. This is being achieved by investigating mechanisms for bifurcation, identifying universal regulators of leaf initiation patterns and shape and also identifying novel regulators of stem cell function.



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Synthetic Biology and Reprogramming of Plant Systems

Synthetic Biology is an emerging field that employs engineering principles to construct new genetic systems. The approach is based on the use of well characterised and reusable DNA components, and numerical models for the design of biological circuits. Synthetic biology shows great potential for the engineering of multicellular systems, and plants are the obvious first target for this type of approach. Plants possess indeterminate and modular body plans, have a wide spectrum of biosynthetic activities, can be genetically manipulated, and are widely used in crop systems for production of biomass, food, polymers, drugs and fuels. Programmes underway include reprogramming simple cellular systems using close packed microbial cell populations as a testbed for genetic circuits and software models that can shape patterns of cell growth and capturing morphogenesis through visualisation and computer models, including studies of Marchantia polymorpha as a simple model for plant morphogenesis.



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Genetic and epigenetic inheritance in plants

The group is interested in understanding plant sexual reproduction and the processes that generate variation between generations. Focus is on the meiotic cell division where gametes are generated with half the number of chromosomes. During meiosis parental chromosomes are reshuffled to produce new combinations of genetic variation. This has a profound effect on patterns of natural genetic variation and is a vital tool in agriculture and crop breeding. Patterns of recombination are non-random along plant chromosomes, and the group is defining the mechanisms that control these patterns, for example testing whether epigenetic organisation of the genome contributes to recombination control. Consistent with this associations have been found between chromatin and recombination at both whole chromosome and hotspot scales. It has also been found that recombination is also itself modulated by sequence differences, in addition to shaping patterns of genetic polymorphism. Genetics and genomics are being used to understand the mechanisms acting during plant heredity, how they influence species evolution and how they can be applied during crop improvement.



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Molecular Physiology

The group works on the genetic basis of traits that underlie components of crop productivity. In the long term this may allow productivity to be improved. Currently the focus is on understanding how the efficient C4 photosynthetic pathway works, and in addition, the generation

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of increased genetic variation in domesticated rice, and screening for increased tolerance to stresses. C4 photosynthesis is associated with increased productivity and despite its complexity is currently documented in at least 62 lineages of angiosperms. The research approach is interdisciplinary, including the use of molecular and physiological techniques through to bioinformatics. The group has strong links with the International Rice Research Institute (IRRI).



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Developmental Biology

The group investigates how plants adapt their body plan to suit the environmental conditions in which they are growing. A network of hormones move over long distances in the plant and regulate the activity of buds at the base of each leaf. The three main hormones involved are auxin, cytokinin and strigolactone and they interact in multiple ways to control branching. For example, auxin is made in actively growing shoot tips. It is transported down the plant in the stem and inhibits the activation of dormant buds. Removal of the growing shoot tip removes the auxin source, allowing these buds to activate. This is the basis for pruning of roses and coppicing in trees. Current projects include the investigation of hormone signaling and the control of shoot branching and linking molecular to whole plant level events with computational modelling.



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Cereal Symbiosis

The mutually beneficial arbuscular mycorrhizal (AM) symbiosis is the most widespread association between roots of terrestrial plants and fungi

of the *Glomeromycota*. The association receives increasing scientific attention because of the nutritional benefit it confers to plants, its ubiquitous occurrence among contemporary plant species and, as a result of its evolutionary antiquity, an ancestral relationship to other plant interactions. The group's research focuses on molecular mechanisms underlying the formation and functioning of AM symbioses in rice and maize. It aims at developing knowledge to optimise the incorporation of the AM-symbiosis into sustainable yet modern agricultural practices.



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Plant Metabolism

Research in the group addresses several aspects of the metabolism of plants, algae and bacteria, in particular vitamin and cofactor biosynthesis, using a wide range of techniques from biochemistry through molecular biology to genomics, coupled with mathematical modeling approaches. The knowledge gained from these studies is being used to explore the potential for metabolic engineering of high value products in plants and algae, and other biotechnological uses of algae, such as for biodiesel production. Sequence information from algal genome projects is used to identify potential genes encoding biosynthetic enzymes, and these are then verified by characterizing the recombinant proteins. At the same time, by studying regulation of these genes, several genetic elements responsive to vitamins have been identified, which are now being developed as molecular tools to allow efficient and rational manipulation of transgene expression in algae and higher plants. In parallel, symbiotic interactions between algae and bacteria, where the algae supply fixed carbon in exchange for vitamins, are being investigated to establish the physiological and molecular basis of this mutualism. This has led to the concept of Synthetic Ecology, which aims to establish robust algal cocultures to facilitate large-scale algal cultivation.

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Tropical Ecology

Research in tropical forests addresses aspects of biodiversity and global change. The group's most recent work on diversity was done in the Blue Mountains of Jamaica, where it was shown that 170 year old secondary forest is almost as diverse as fragments of the remaining natural forest; this is important because it shows that secondary forest can be a significant reservoir of biodiversity. The group's studies of global change are done in Lowland Forest in Panama where litter inputs to large forest plots have been experimentally increased and decreased. This demonstrated that increased inputs of organic matter, as dead leaves, resulted in increased soil organic matter, thereby immobilizing some of the extra carbon dioxide in the atmosphere, but it has also increased the decomposition of older soil organic carbon. The production of carbon dioxide from old soil organic matter is potentially a huge source of increased carbon dioxide in the atmosphere and therefore very relevant to climate change.

Knowledge from these monographic works provides a basis to understand patterns of evolution, distributions and essential oil variation.



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Circadian Signal Transduction

The group studies the interaction between the circadian clock and cellular signalling, with particular focus on calcium-based stress signalling networks. The goal is to identify how the circadian clock provides benefits to plants to maximise their growth and productivity. Molecular genetic, transcriptomic, imaging and physiological techniques are used to understand circadian mechanisms and signalling pathways. In collaboration with Dr Jorge Gonçalves in the Department of Engineering new approaches for systems biology are being developed. Collaboration with Bayer Cropscience has the goal of converting the biological discoveries in to real world solutions for crop improvement.

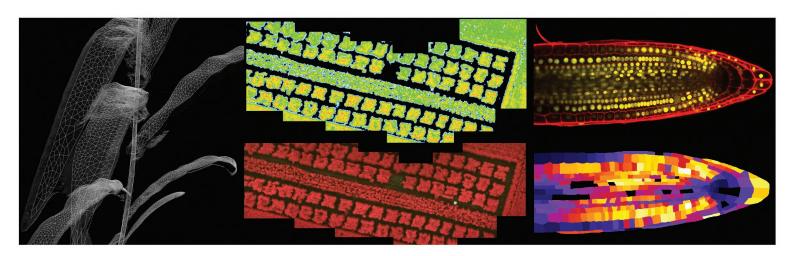


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Curator and Deputy Director of Cambridge University Botanic Garden

Curating and developing a plant collection of over 8000 species enjoyed by over 200,000 visitors a year raises constant questions of what to grow both now and in the future. Gardens are dynamic and with innovative displays and plantings the gardens reflect current issues in Plant Sciences that are attractive to a wide audience and sustainable, particularly in the light of likely climate change. The group's research is in plant systematics and conservation. Research interests in plant systematics focus on the *Lamiaceae* and the aromatic genera *Lavandula* and *Rosmarinus*, including their horticultural taxonomy.

Image Analysis Methods in the Plant Sciences Second International Workshop



2-3 September 2013 University of Nottingham, Jubilee campus, UK

Topics include:

- plant science-based image analysis techniques from laboratory to field environments and subcellular to whole plant scales, including:
 - 3D reconstruction
 - Image segmentation
 - Modelling motion
 - Modelling growth
 - Shape analysis & classification
 - Colour analysis
- User interaction and software tools for plant scientists
- The image analysis-biology pipeline (Imaging and *-omics)
- Novel and emerging plant imaging techniques
- Biological challenges for plant image analysis

Keynote speaker: Jason Swedlow (University of Dundee)

Organisers:

Tony Pridmore (University of Nottingham) Andy French (University of Nottingham) Hannah Dee (Aberystwyth University)

Contact:

Susie Lydon, CPIB Outreach Officer susannah.lydon@nottingham.ac.uk

Deadline (for abstracts & registration): Friday 26th July



