GARNish

X Y Z

Zoom In

Zoom Out

Rotate

Sample List:

Cauline Leaf

First Node

Flower Stage 15 Carpels

Flower Stage 15 Petals

Flower Stage 15 Sepals

Flower Stage 15 Stamens

Flowers Stage 15 Pedicel

Leaf 1 + 2 combined

Leaf 10

Leaf 12

Absolute   Relative

2165.47

1894.79

1624.11

1353.43

1082.75

812.07

541.39

270.71

0

GCOS expression level
TGT value = 100 units
Background ≈ 20 units

ePlant - 3D Visualization

Welcome to the May 2011 issue of GARNish!

Technology always challenges the status quo, enabling some but often leaving others behind. The computer revolution of the 1980s and 1990s was more or less "geek" driven. How many megahertz do you have? How large is your memory? How big is your hard drive? In the last decade, however, we have at last seen the disappearance of this debate as the consumer market has replaced this business lead mentality. The key question now is: what does this technology do for me? Also, we have in our hands now smart phones that have abilities close to science fiction level stories of two decades ago. Most recently we have the emergence of devices such as the iPad as a new paradigm in device ability. Here the ultimate portability of computing technology produces new challenges in accessing data and software that cannot all be stored on a heavy device that is carried around. These devices will also open up amazing new opportunities in research and teaching. Here Arabidopsis researchers are leading the way and this issue of GARNish gives some flavour of this.

Our new technologies will require that we break the "I'll carry everything I need on my laptop" approach and move to a distributed or "cloud" system. For this to happen the user will have to see a gain in functionality and ease of use. One component of this will be the ability to upload data to cloud servers and carry out sophisticated analyses and storing the outputs either locally or in the cloud. Our new portable devices will allow us to access these data, tools and results anytime, anywhere. The article by Seun-jin Kim, from the iPlant Collaborative, describes the great potential of the cloud and how they are making it work for plant science. Geoff Fucile and Nicholas Provart describe their attempts to visualise plant research data from the large to microscopic scale. This approach is exciting as it makes data simple to access and is potentially perfect for the new tactile devices that are increasingly being used to access data.

What will be really amazing about theses new tools and devices will be their application to both research and education. By layering complexity behind simple to access tools teachers at all levels will be able to enthuse young scientists in the wonder of the knowledge that is available and allow them to see that they can contribute to research at many levels. The article by Harriet Truscott on the initiative for Science & Plants for Schools is inspiring in the positive responses amongst school children when science is delivered in a stimulating manner. There are huge opportunities and challenges to implement software that can aid teachers at all levels in this goal. DNA Subway from iPlant is an excellent example of how this can be done.

Contents

Many thanks to all who contributed to this issue, particularly Jim Beynon, Sean May, Tina Lee, Nicholas Provart, Geoff Fucile, Harriet Truscott, Jim Murray and Marc Knight.

Another technology that is making a step change is the Affymetrix array service form NASC. NASC will soon be offering a much-reduced cost service to the Arabidopsis community using the new Titan system.

The GARNet committee has had one of its periodic changes and we thank departing members Anna Amtmann, Claire Halpin, and Patrick Hussey for all their hard work and welcome Malcolm Bennet, Jim Murray and Smita Kurup as new members. Finally, the GARNet committee has played an active role in the establishment of the UK Plant Sciences Federation. We will continue to represent the views and aspirations of the Arabidopsis research community but I feel it is essential that we work together as a broader community of plant scientists to meet the future challenges that we all face. I encourage you all to follow its progress and sign up to the UK Plant Sci website (www.plantsci.org.uk) so that you can be kept up to date with developments.

Jim Beynon

SAPS Launches New Website

The Science and Plants for Schools (SAPS) team have just re-launched their website (www.saps.org.uk/) which now includes over two hundred resources ranging from activities for primary pupils to articles and lab protocols for post-16 students.

The new site links together teaching resources on key topics such as photosynthesis and osmosis, encouraging teachers to use both their old favourite resources and new ideas. Teaching materials are linked to current news stories and research studies, helping teachers to put the lessons into a wider scientific context.

So if you are already involved in plant science outreach with schools and young people or would like to get involved then take a look at the new SAPS website.

Scientists aim to improve photosynthesis to increase food and fuel production

The BBSRC in partnership with the US National Science Foundation (NSF) awarded funding totaling £6.11M/$10.3M to four transatlantic research teams to improve photosynthesis with a view of increasing the yield of important crops for food production or sustainable bioenergy. The projects include:

CAPP (Combining algal and plant photosynthesis) - University of Cambridge, John Innes Centre, Oxford Brookes University, Carnegie Institute of Washington. Total funding: £1.25M

EPP (Exploiting prokaryotic proteins to improve plant photosynthetic efficiency) - University of Illinois at Urbana-Champaign, Rothamsted Research, Cornell University, University of California, Berkeley. Total funding: £1.36M

MAGIC (Multi-level Approaches for Generating Increased CO2) - University of Glasgow, University of Cambridge, University of Warwick, Penn State University, University of California, Berkeley. Total funding: £1.6M

Plug and Play Photosynthesis for RuBisCO independent fuels - University of Glasgow, Arizona State University, University of Southampton, Imperial College London, Penn State University, Michigan State University, Emory University School of Medicine. Total funding: £1.9M

£7M for public wheat pre-breeding programme announced

In February this year the BBSRC announced a £7 million grant to a consortium of researchers to increase the diversity of traits available in wheat via a comprehensive pre-breeding programme – the first of its kind in the UK in over 20 years. This project will be important to ensure the sustainability of wheat production in the UK and beyond at a time when we are facing a growing global population and changing environment.

The main thrust of the research will be to understand the genetics behind factors affecting wheat yield such as drought tolerance, plant shape and size, and resistance to pests and diseases. With this knowledge, researchers will cross different strains of wheat to produce the germplasm required for breeding. They will also generate a database of genetic markers, which can be used for precision breeding. The new germplasm generated in this project will be exploited by breeders for crossing with their elite lines to develop new varieties for use by farmers. All the information generated in the programme will be stored in a central database, and seed stored centrally in the UK, both being freely available to both academics and breeders alike.

Members of the breeding industry have been consulted from the conception of the project to ensure that the germplasm developed is useful for commercial breeding programmes.

Warwick Crop Centre Director wins RHS Award

Dr Rosemary Collier, Director of Warwick Crop Centre, was awarded the Marsh Horticultural Research Award 2010. The award is sponsored by the Marsh Christian Trust in conjunction with the Royal Horticultural Society (RHS) and awarded annually to recognise individuals who have made an outstanding contribution or conducted long-term research into fruit or vegetable growing. Dr Collier won the award for 'An outstanding contribution to horticultural science through entomological research'.

BBSRC Bioscience for Growth

BBSRC hosted it 'Bioscience for Growth' event in London on the 24th March. This provided an opportunity for senior figures from business, industry, investment and policymaking to find out about how the UK 's leading universities are contributing to economic growth and social good. The event also marked the end of the BBSRC's 'Excellence with Impact' competition and 'BBSRC Innovator of the year' and provided a platform to award the winner's their prizes.

The excellence with impact award acknowledges university departments that are most active in embedding a culture that recognises the impor-

tance of economic and social impact alongside excellent research. The 2011 winners and runners up were Greatest culture change: - Winner - University of Aberystwyth IBERS, Runner up - University of Liverpool School of Biological Sciences Greatest delivery of impact : - Winner - University of Dundee College of Life Sciences, Runner up - Newcastle University Institute for Ageing and Health. Well done to all our plant science colleagues at these institutions.

UK Plant Sciences Federation

In 2010 representatives of the plant and crop research communities (MONOGRAM, UK-Brassica, ORE-GIN, UK-Solanaceae and GARNet), met to explore the possibilities of forming 'one voice for UK plant and crop science' to help build a stronger UK plant research base. Establishing a Federation of organizations/grouping involved in UK plant science research and education would provided considerable added value for the whole community by pooling knowledge and expertise, identifying new opportunities and assessing where added value could be achieved by working together. In an era of reduced funding it is also becoming increasingly importance to have a strong and clear voice amongst 'opinion-formers', within political and funding circles and the Federation could be one possible mechanism for achieving this.

On the 31st January this year representative of a variety of stakeholders from industry, research, education and learned societies met at NIAB to discuss the establishment of the Federation and agreed that a UK Plant Science Federation should be formed as a special interest group of the Society of Biology.

Once formed the Federation would aim to:

1. Increase the understanding and perceived importance of plant and crop science amongst government, funders, industry and society in general.

2. Formulate a coordinated strategy and vision for plant and crop science in the UK that can be utilised to inform policy.

3. Help to improve the general funding environment for UK plant and crop science research and education.

4. Create a forum for debate that is independent and inclusive.

5. Provide a focus and contact point for UK plant and crop science.

6. To educate and inspire the next generation of plant and crop scientists.

The Federation will be made of organisations/groupings representing UK Plant and Crop Science research and education. To date the following organisations have expressed interest in joining the Federation.

Association of Applied Biologists (AAB)

ADAS

Agricultural and Horticultural Development Board (AHDB)

Bayer

British Ecological Society (BES)

British Society of Plant Breeders (BSPB)

Biochemical Society (BiochemSoc)

Arabidopsis Research Community (GARNet)

Gatsby Plants

The Genetics Society

Kew Gardens

Knowledge Transfer Network (KTN)

Linnean Society

Cereal and Grasses Research Community (MONOGRAM)

National Farmers Union (NFU)

Oilseed Rape Genetic Improvement Network (OREGIN)

Society of Experimental Biology (SEB)

Science & Plants for Schools (SAPS)

Syngenta

Brassica Research Community (UK-BRC)

Solanacea Research Community (UK-SOL)

Unilever

Vegetable Genetic Improvement Network (VEGIN)

Wheat Genetic Improvement Network (WGIN)

An inaugural UK Plant Science Meeting to showcase the wealth of UK Plant Science is planned for spring 2012 and the Federation will be launched later in 2011. If you would like to learn more about the Federation or perhaps you manage an organisation that would like to join the Federation please e-mail ruth@plantsci.org.uk

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Gene Titan @ NASC

Cheaper & better Affy arrays from NASC

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This year NASC will have a service available using Arabidopsis Affymetrix arrays based on TAIR10 including QC, hybridisation and data return, all for only £250 each (+VAT).

This has been made possible using Affy's new high throughput platforms with peg arrays instead of cartridges (see photo).

The GeneTitan (www.affymetrix.com/genetitan) combines the hybridisation oven, fluidics processing and imaging devices into one machine (the one at NASC is red ☺), allowing hands-free, highly automated processing of 16, 24, or 96 arrays samples in parallel on plates. This dramatically saves costs and time allowing us to increase throughput at a cheaper price. We can then pass these savings onto you, so you can make your grants go further (e.g. more replicates).

NASC already offer human, rat and mouse arrays for £250 (all-in) per chip/hyb so the price point is already characterised and we are working with Affymetrix to make it possible for Arabidopsis this year. Since we process about 1,000 chips p/a this will help us hugely.

Each of the genes on a titan ST array are represented by more than 20 probes spread across the full length of the gene, providing a more complete and more accurate picture of gene expression than 3' based expression array designs. They are a perfect match (PM)-only design using Whole Transcript (WT) Sense Target Labelling and a 5um feature size.

Remember that the existing highly successful ATH1 array is from the original TIGR annotation (2000) with 22,500 probe sets representing 24,000 gene sequences. The 2010 TAIR10 release contains 27,416 protein-coding genes (33,602 genes in all, 41,671 gene models).

Please visit: http://affy.arabidopsis.info/plates.html, or email affy@arabidopsis.info and remember that we also offer Brachypodium, Brassica and Tobacco chips (and many more).

Zoe Phillips (nee Emmerson) at NASC showing off the new GeneTitan machinery and plate.

News from NASC

Some notable donations of stocks from UK labs this year to the NASC/ABRC collections – thanks to all of our donors for their generosity over the years: Two recombinant inbred collections from Maarten Koornneef: Cal (male) x Tac (female) - The complete set of 105 lines + 2 parental lines (N97472). Ler (female) x Eri-1 (male) - The complete set of 110 lines + 2 parental lines (N97359). For more see: http://arabidopsis.info/CollectionInfo?id=123 and 124.

Homozygous silencing mutants donated by Ian Furner at the Department of Genetics, University of Cambridge. This re-donated collection comprises SALK insertion homozygotes with inserts in genes thought to be involved in gene silencing. Some of the alleles have been independently made homozygous and studied in other labs while others are unique to this collection.   http://arabidopsis.info/CollectionInfo?id=121.

Ten lines bearing mutations in the COMATOSE gene donated by Freddie Theodoulou at the Rothamsted Research Institute. N784135(cts1 allele), N784136(cts1), N784137(cts1), N784138(cts1), N784139(cts1), N784140(cts1), N784141(cts3), N784142(cts4), N784143(cts5), N784144(cts6)

Pleased donate your seed stocks to NASC using the "donate stocks" link on the NASC homepage at http://arabidopsis.info/

iPlant for Beginners

What is iPlant?

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In 2008, the National Science Foundation, a federal agency of the United States created to promote "the progress of science," funded the iPlant Collaborative, whose mission is to develop cyberinfrastructure for plant science research to empower a new plant biology.

The iPlant Collaborative's staff, currently around 75 full and part-time plant and computer scientists, programmers, and educators, is based at the University of Arizona in Tucson, Texas Advanced Computing Center (TACC) at University of Texas at Austin, Cold Spring Harbor Laboratory in New York, and University of North Carolina, Wilmington. Including collaborators, the iPlant Collaborative community encompasses more than 300 American and international academic, government, and industry plant scientists, bioinformaticians, and researchers, post-doctoral students, and college science educators.

iPlant's projects

iPlant, as it is known, used a community-building process to identify both the biological 'Grand Challenges' that plant scientists seek to answer and the cyberinfrastructure resources required to solve them. Through a series of five Grand Challenge Workshops held at Biosphere 2 near Tucson, Arizona in 2008-2009, two initial Grand Challenge projects were identified: the iPlant Tree of Life (iPToL) project and the iPlant Genotype-to-Phenotype (iPG2P) project.

iPToL's Grand Challenge is to assemble an evolutionary tree of a half-million green plants that will yield new insights across the plant sciences, from comparative genomics and molecular evolution, to plant development, to the study of adaptation, speciation, community assembly, and ecosystem functioning.

iPG2P's challenge is to elucidate the relationship(s) between plant genotypes and the resultant phenotypes in non-constant environments, focusing on pipelining NextGen sequencing data into virtual genotype and molecular phenotype databases, data integration, statistically-based tools for inferring relationships, visual analysis tools, and modeling framework tools.

Initially, several working groups involving dozens of scientists from more than 40 U.S. and foreign institutions were formed to develop specific requirements and use cases for the cybertools and workflows needed to resolve the iPToL and iPG2P Grand Challenges. These scientific requirements informed iPlant of the needed cyberinfrastructure which includes high-performance computing (HPC), large data stores, cloud computing, and data and algorithm management resources.

Accessing iPlant

Access to iPlant's cyberinfrastructure may be obtained through a variety of means, depending on the needs of scientists and their research questions. One primary interface is iPlant's web-based interface called the "Discovery Environment (DE)." The DE is an extensible web-based platform on which software tools and cyberinfrastructure resources developed by iPlant and community members can be integrated and used to manage data, create analytical workflows, and ultimately, 'discovery'. Currently, the newest working demonstration tools include:

- Taxonomic Name Resolution Service – performs exact and fuzzy matching of plant taxonomic names against a database provided by the Missouri Botanical Garden and returns all names within a set variance.

- Tree Reconciliation – allows users to investigate protein families by retrieving gene families from a database containing reconciliations for over 2500 gene families in six species.
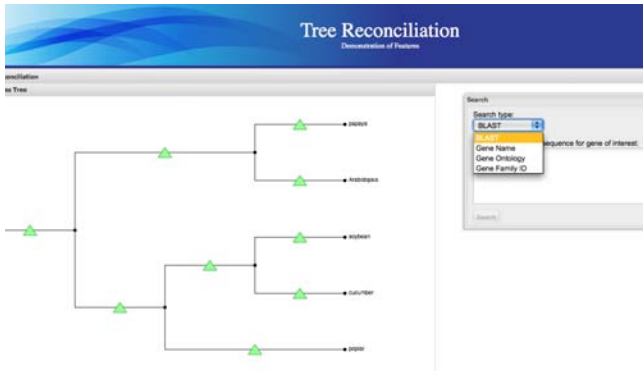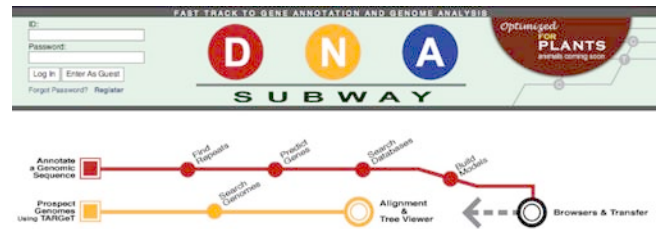

- Ancestral character estimation (for discrete and continuous traits) – allows estimation of continuous characters and discrete states, providing confidence measures and graphical plots.
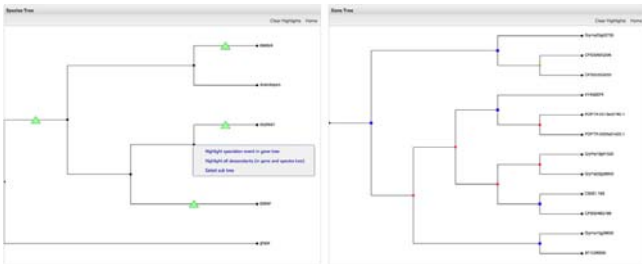
✳ Further information and resources

The complete list of services and analytical tools available in the iPlant DE can be found at www.iplantcollaborative.org/communities/how-iplant-can-advance-your-science To try the latest release of the DE, go to: http://preview.iplantcollaborative.org/de If you do not already have an iPlant user account, sign up: www.iplantcollaborative.org/forms/request-access. You can then begin to explore and use the iPlant DE to manage and analyze your data. For example you may upload your NextGen Sequencing data, pre-process them, and analyze them for transcript abundance or search for sequence variants/SNP using the transcriptomics tools within the DE. Alternatively, you could analyze a gene family history to look for gene duplication, loss, and lateral transfer, etc. using tools from the iPTOL project.

In addition to the DE, you can access iPlant's public cloud computing resource Atmosphere, 'ride' the DNA Subway (a gene annotation and genome analy-

sis workflow; hhtp://dnasubway.iplantcollaborative.org/, and 'congregate with your clade' at My-Plant.Org, iPlant's phylogenetically-based social networking and collaboration site (https://my-plant.org/). Whatever your interest, iPlant cyberinfrastructure, tools, and resources can help transform your research today and tomorrow.

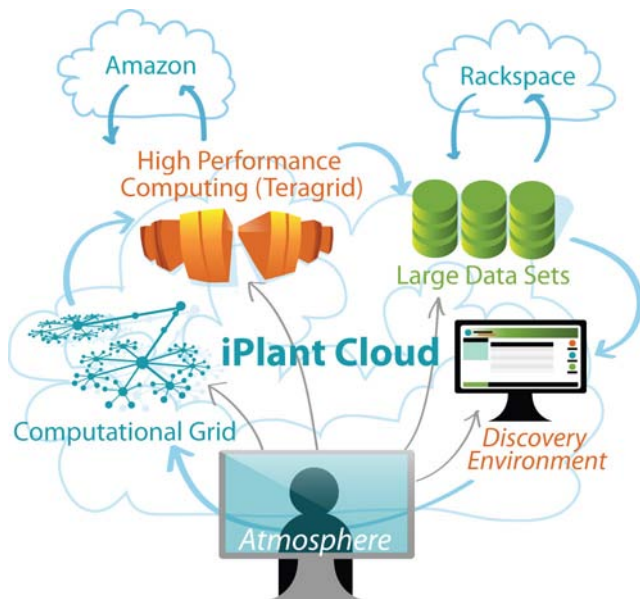For further information, visit the iPlant website: www.iplantcollaborative.org or contact Project Director Steve Goff, sgoff@iplantcollaborative.org

How cloud computing can empower a new plant biology

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What is Cloud Computing?

The world of computing is moving away from the on-site IT model, in which people continue to buy servers, software and administrating resources. Cloud computing is Internet-based computing, whereby shared servers provide resources, software and data to computers and other devices on demand, similar to an electricity grid. The Atmosphere Cloud service provided by the iPlant collaborative is an Internet-based computing resource and data gateway that handles many different bioinformatics tools and datasets of use to plant and computational scientists.

Infrastructure as a service

Cloud infrastructure services, also known as "Infrastructure as a Service (IaaS)", deliver computer infrastructure as a service. Rather than purchasing servers, software, data-center space or network equipment, clients can now outsource all these requirements to a Cloud service provider. Atmosphere provides a wide range of computing environments as a single service, allowing a user to establish computing resources, develop new algorithms, and provide tools to the community.

Supporting the primary mission of The iPlant Collaborative of enabling cyberinfrastructure for empowering new plant biology, Atmosphere strives to facilitate ease of access to diverse computational infrastructure. The target audience is not limited to plant biologists but also includes computational researchers from other disciplines.
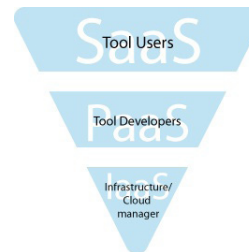
How is Atmosphere organised? The infrastructure/cloud manager group builds cloud infrastructure/hardware and operates Atmosphere. The tool developers group comprises users who develop bioinformatics tools and algorithms using Atmosphere's on-demand resources, which is a Linux-based virtual instance. Tool developers may substantiate various virtual machines with different stacks of programming libraries and tools through Atmosphere's web interface or APIs. They also create new algorithms or deploy software packages to share with biologists (i.e. tool users). Tool users, generally biologists who perform various analyses on their dataset, access Atmosphere's web-based user interface and launch applications developed by tool devlopers.

Atmosphere for researchers

The primary aim of Atmosphere is to accelerate the pace of scientific discovery by researchers. By providing them with easy and early access to their computational results without needing to repeatedly redo the underlying computational resources for each run, Atmosphere lowers the 'entry barrier' for researchers trying to adopt new tools and methodologies. Atmosphere allows users access and utilise tools that maybe too complex to install on their own machine and provides access to data intensive tools on a much more powerful system than would generally be available via its integrated access to grid and high performance computing. For example, plant biologists using Atmosphere can make snapshots (copies) of their active data sets, analyze them with new tools, and then discard or preserve virtual machine images and snapshots depending on the results, allowing them to exploit new technologies effectively as they become available.

Atmosphere for your existing projects (Application Programming Interface)

Utilizing the application programming interface (API) and Atmosphere's capabilities for creating self-service portals, iPlant aims to foster a vibrant marketplace which complements our Discover Environment effort, allowing consumers and providers of computational biology tools to work together in an effective, easy-to-use infrastructure which provides and promotes experimental and computational reproducibility.

How cloud computing can empower a new plant biology

Atmosphere as collaboration and research place between plant scientists and computer scientists
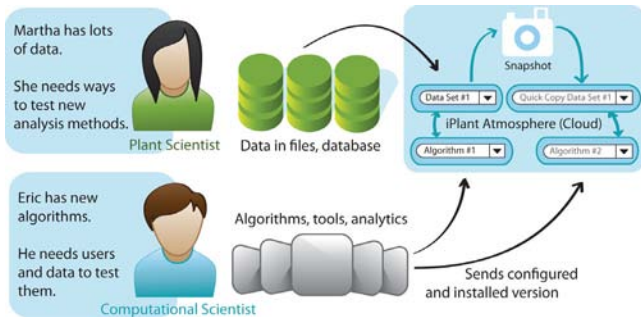
Plant scientist Martha has many datasets: some are files, others are in a database. She wants to try new analysis algorithms on her data.
Computational scientist Eric has made a new algorithm with multiple tools for plant scientists. Now, he needs a scientist to use his application with his or her own large datasets. Using Atmosphere, Martha can store her large datasets and run Eric's recently developed tools and algorithms in the same place. She can make quick copies of her data with snapshot technology and run multiple algorithms easily.

### Atmosphere with iPlant's existing services (e.g. Discovery Environment)
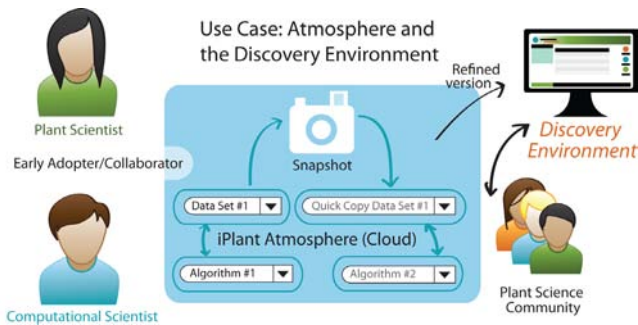
Plant Scientist Martha and Computer Scientist Eric work together with their data sets and their new tools in Atmosphere. They can develop and evaluate each others' data and tools. After finishing their work, they can define their dataset and tools for the plant science community at large. A refined version may then be adopted into the iPlant Discovery Environment (DE), within which the plant science community can run Martha and Eric's reference dataset and tools using the iPlant DE system.

NB Usage of Atmosphere is not limited to these two examples

Four Simple Steps for Using the Biotools Application Virtual Machine on Atmosphere

1 Log in to Atmosphere at https://atmo.iplantcollaborative.org using your iPlant login and password. You will be directed to the Applications screen. Choose the application titled "Atmosphere Biotools 1." Atmosphere will begin allocating the necessary computational and storage resources from the underlying hardware.
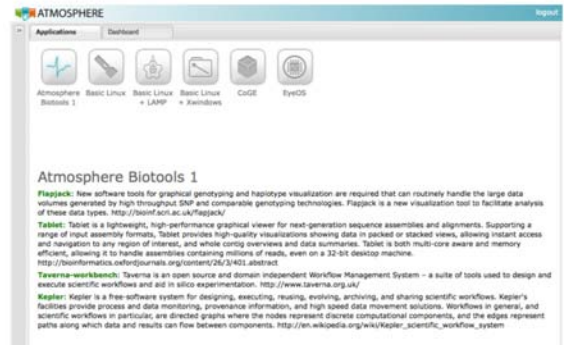
2 Once the application request has been successfully submitted, a pop-up box will notify you that it will be ready in 10-15 minutes. When it's ready, you will receive an email message with necessary details.
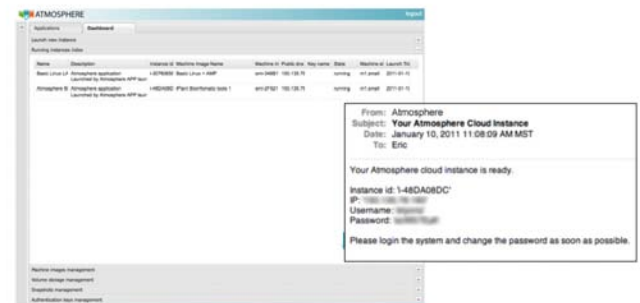
3 Using your browser, navigate to the url http://ip-address-of-application/vnc. If you receive a dialogue regarding an applet requesting access you should permit access.

4 Simply use the application on your virtual desktop.
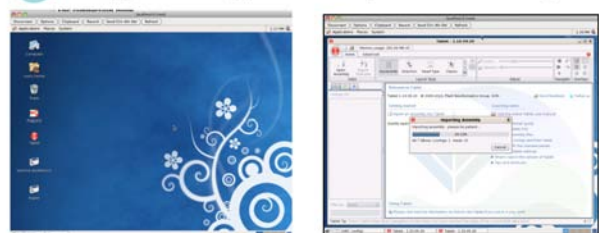
Seamless 3D visualization of kilometer- to nanometer-scale data sets from *Arabidopsis thaliana*

Geoff Fucile and Nicholas J. Provart
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Plant biologists increasingly rely on diverse and large data sets to help address their research questions. Although the various 'omics' platforms are now standard in modern laboratories, most plant biologists are not necessarily experts in any particular technology. Rather, they profit from integrative synthesis and visualization software for these complex data sets. ePlant is a prototypical web-based framework for the integration and 3D visualization of 'omics' data for model organisms applied to *Arabidopsis thaliana*.
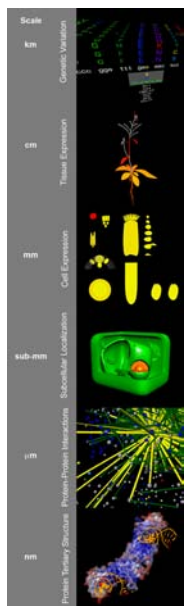
Currently, ePlant consists of the following data display modules in increasingly larger scales: a protein structure model explorer, a molecular interaction network explorer, a gene product subcellular localization explorer, a gene expression pattern explorer for cells and tissues, and a sequence conservation explorer. This form of semantic zooming, enabled by hyperinks between the modules, facilitates the integration of biological data from nanometer-scale molecular processes to genetic variation based on kilometer-scale geographic distributions. An ePlant query begins with entering an Arabidopsis Genome Initiative gene identifier (AGI ID) on the main query page and selecting one of the available modules to explore the properties associated with a query gene and its products – example outputs at each scale are shown in the accompanying figure. ePlant users can contemplate the relationships between these properties and their genes of interest towards a systems level understanding of model organism biology.

ePlant protein structure explorer

To take advantage of the ePlant framework we generated a proteome-scale protein structure prediction and annotation for Arabidopsis using the Phyre algorithm. We obtained predicted protein structure models with high levels of confidence for ~72% of the Arabidopsis proteome. We are currently working to improve this data set using the improved Phyre2 algorithm, which uses multiple independent structure predic-

tion templates to produce one multi-domain protein structure model. The ePlant protein structure model explorer implements a novel protein structure annotation scheme. Specifically, we integrate biological and protein structural data by mapping annotated domains and amino acids of curated functional importance from the Conserved Domain Database (http://www.ncbi.nlm.nih.gov/Structure/cdd/cdd.shtml) onto the 3D protein model. Curated sites mapped onto a structure are highlighted by selecting radio buttons. Multiple sequence alignments and text-based annotations associated with these curated sites are also displayed to provide context and validation of these site mappings. Mapping conserved sites of functional importance in their 3D context is more informative than lists or 2D schematics of conserved sites, as per the typical report during BLAST analysis at NCBI, as these often cluster spatially in 3D as sectors to define functional surfaces and other functionally important structures despite being distributed throughout the linear primary sequence. All of the Phyre predicted protein structure models for Arabidopsis are accessible for analysis and downloading. Useful functions for protein structure analysis such as molecular surfaces with scaled colour gradient displays or coloured mappings of hydrophobicity, polarity and charge states on ribbon diagrams have been precomputed to be easily accessed through radio buttons.

ePlant sequence explorer

The ePlant sequence explorer is a first attempt at the 3D display of primary sequence data. Nucleotide and protein sequences related to the query gene of interest are aligned across two axes in an interactive 3D environment. Paralogs and putative orthologs of the query gene are aligned on separate planes, with putative orthologous sequences being displayed on a plane that is orthogonal to the paralogs and splice variants of the query Arabidopsis gene. The ePlant sequence explorer also integrates publicly available single nucleotide polymorphism data. The interactive display indicates synonymous and non-synonymous polymorphic sites, the alternate amino acid encoded by non-synonymous polymorphisms, and the frequency and ecotypic distribution at each polymorphic site. Each of the one-letter amino acid sites in the ePlant structure explorer is rendered as a separate object to integrate additional biological data. The colour of the one-letter amino acid codes represents physico-chemical properties such as charge and solubility and the size of the letters are scaled to conservation scores in the alignment. This also allows the integration of primary sequence data with the cognate folded 3D protein structure by means of hyperlinks - each letter is clickable, allowing the user to see the location of the residue in the cognate structure in the ePlant protein structure model explorer – this is

GARNish

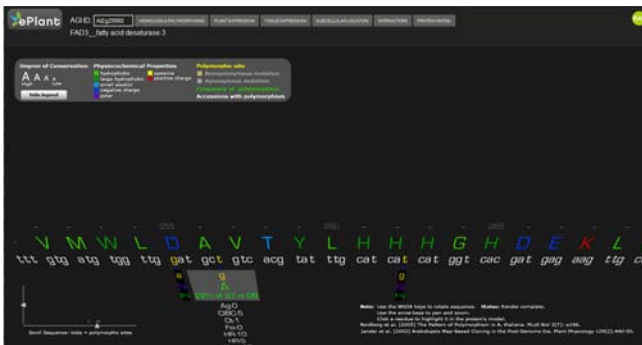## Vizualization software for 'omics' data

Figure of ePlant Homologs and Polymorphisms Viewer showing polymorphisms in a fatty acid desaturase, FAD3, based on Nordborg *et al.* (2005) data. Some accessions show non-synonymous changes at a couple of positions, several others have synonymous changes at position 256. The significance of the non-synonymous changes remains to be determined.

useful to investigate where sites which exhibit non-synoymous changes at the sequence polymorphism level map to in the protein's structure. Upon clicking a residue of interest, the user is prompted to select a protein structure related to his or her query sequence, which is rendered in the structure explorer module with the residue of interest labeled and highlighted in red. We are currently expanding the functionality of the ePlant sequence explorer through the display of metrics of selection acting on individual codons, and the integration of larger nucleotide polymorphism data sets, such as those being generated by the 1001 Genomes project.

ePlant gene expression pattern explorer

Figure of ePlant Expression Viewer at the plant level, illustrating the strong stem-specific expression of *IRX3*, a gene known to be involved in proper xylem formation.

The ePlant gene expression and localization explorers display interactive 3D models of gross anatomical, tissue level, and sub-cellular models of *Arabidopsis thaliana* to integrate molecular 'omics' data at physiological scales. ePlant permits easy access to ~3 million gene expression measurements, and documented subcellular localizations for ~7 thousand Arabidopsis proteins and predicted subcellular localizations for most of the remainder of the Arabidopsis proteome. These models can be freely rotated and signal values can be painted dynamically. An interactions viewer displays protein-protein interaction data from from the BAR's Arabidopsis Interaction Viewer's database of ~4,300 literature-documented and more than 70,000 predicted interactions. Subcellular localization data can also be included in this display to permit identification of protein interaction neighbours that are in the same sub-cellular compartment as one's gene product of interest.

Future developments and further reading

Future implementations of ePlant will incorporate Reactome pathways, coexpression neighbours, epigenetic modification information, and other data. We would also ideally like to render 3D representations of anatomy from direct measurements such as magnetic resonance imaging (MRI) and Z-stacks of confocal microscopic images. This has in principle been achieved by projects such as Cortona3D (web browser plug-in; http://www.cortona3d.com), which can render 3D objects reconstructed from MRI-based anatomical descriptions. The utility of mapping biological 'omics' data onto 3D anatomical reconstructions has been demonstrated in the mouse and human brains (http://www.brain-map.org).

Developing visualization software for biological data on the world wide web has several advantages. Software that functions entirely in the web browser avoids many compatibility issues and facilitates user-community development, and data can be efficiently shared via web-services and maintained between institutions across the globe which specialize in specific technologies. ePlant is accessed entirely through a web browser and therefore avoids the requirement for biologists to download, install, and configure data visualization and analysis software for their specific operating system and computing device. Additionally, web-based technologies benefit from the rapid advances in graphics handling. For example, HTML5 and WebGL will allow the development of interactive and hardware-accelerated 3D environments independently of plug-ins and compatible with any device that can run a modern web browser (Google's Body Browser offers a glimpse of a WebGL-enabled future, see http://bodybrowser.googlelabs.com/). However, long-term standards for displaying interactive 3D environments on the web have not been resolved. The current implementation of ePlant uses widely available technologies, such as Flash, towards testing the principles of the framework and soliciting feedback. We welcome feedback and look forward to developing ePlant into a more powerful and user-friendly framework for Arabidopsis systems biology.

ePlant is described in detail in a recent PLoS ONE publication by Geoff Fucile, David DiBiase, Hardeep Nahal, Garon La, Shokoufeh Khodabandeh, Yani Chen, Kante Easley, Dinesh Christendat, Lawrence Kelley, and Nicholas Provart. See http://dx.doi.org/10.1371/journal.pone.0015237. ePlant is available online without restriction at http://bar.utoronto.ca/eplant.

SAPS: Science & Plants for Schools

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In one corner of the classroom, a group of teenage boys from an inner-city London comprehensive are arguing intently. One stabs his finger at a photo on a laminated sheet. 'Are you blind?' he asks. "Can't you see it's Hibiscus, not Helianthus?" The boys turn back to the microscope, jostling each other, and stare down at the pollen grains on the slide. Under the guise of a murder mystery, the group is gaining an insight into plant science.

Their teacher is using resources from Science and Plants for Schools (SAPS), a project that for 20 years has helped teachers bring contemporary plant science to life, making teaching resources and lab protocols available via its website. Many of the pupils who first encountered SAPS resources in the 1990s, often in the form of rapid-cycling brassicas, went on to become plant scientists, teachers, and horticulturalists themselves.

Dan Jenkins, the SAPS project manager, was one of those students. Now he shares his enthusiasm with a new generation of young people.

"Plenty of biology teachers don't have a specialist background in plant science themselves," Dan explains, "and they can dread a student asking 'why are we learning about this?' If a teacher doesn't know about contemporary research into biofuels, for example, it makes it that much harder to explain to their students why it's valuable to learn about the plant cell wall. So a major part of our work is informing teachers about contemporary plant science, so they can pass the knowledge on to their students. For the teachers, it's hugely valuable – seventy science teachers came to a lecture we organised by a young researcher working on plant cells and biofuels."

Dan picks up an infra-red thermometer and shows me how it can measure the temperature of a leaf, part of a new SAPS practical introducing students to transpiration. By smearing the underside of a leaf with Vaseline, students block the stomata, and see the leaf temperature start to rise almost instantly. "This is a great example of how teachers and researchers can work together," he explains. "The resource was created by a teacher who'd been on the Gatsby Plants Summer School and seen a practical by a University lecturer. She took a complex idea and simplified it into something that really gets sixth formers thinking."

This model, introducing experienced teachers to new science and scientists, is one of the ways that the SAPS team plans to develop new teaching resources for the future. The SAPS team has plenty of other topics that they want to develop, including periodicity, tropisms, phytoremediation and selective breeding.

SAPS has a strategic role too, working with curriculum developers to ensure that the school biology includes plant science that is modern and relevant. This can range from small details to long-term discussions over which areas of plant science should be covered in the curriculum. "Awarding bodies aren't always abreast of the latest biology research," Dan says, "so we help them stay current, and then make sure there are the resources to help teach their qualifications."

Back in the classroom, as the pupils pack up their bags to leave, one girl has to be asked repeatedly to take her slide of pollen grains back to the teacher. "They're amazing," she says, still gazing down the microscope. "I never knew pollen was like this. It's fascinating." Perhaps a new plant scientist is in the making?

If you're interested in being involved in the work that SAPS does, take a look at www.saps.org.uk, or contact the team on saps@hermes.cam.ac.uk

ICAR 2011
International Conference on Arabidopsis Research

Madison

New!

1) 'Weed Stampede' 5K Fun Run- Free to all registered participants. Start Saturday morning off right with a run at the Lake!
2) Poster Sessions/Opening Reception/Banquet have Open Bars!
3) Community-organized workshops announced!
4) Childcare options posted

Keynote Speakers: Joanne Chory and Sophien Kamoun

Confirmed Invited Speakers

Julia Bailey-Serres
Dominique Bergmann
Siobhan Brady
Federica Brandizzi
Steve Briggs
Simon Chan
Xuemei Chen
George Coupland
Jeff Dangl
Joe Ecker
Jennifer Fletcher
Niko Geldner
Veronica Grieneisen

Mary Lou Guerinot
Rodrigo Gutierrez
Roger Hangarter
Stacey Harmer
Herman Hofte
Joe Kieber
Ljerka Kjunst
Ottoline Leyser
Xin Li
Yan Lu
Zach Lippman
Elliot Meyerowitz
Andrew Millar

Rebecca Mosher
Jose Pruneda-Paz
Przemek Prusinkiewicz
Sabrina Sabatini
Ben Scheres
Johanna Schmitt
Julian Schroeder
Paul Schulze-Lefert
Kazuo Shinozaki
Dolf Weijers
Cynthia Weinig
Ning Zheng

Scientific Sessions

Hormone Signaling • Biotic Interactions/Biotic Stress • Epigenetics/Small RNAs
Natural Variation/Quantitative Genetics/Evolution • Translational Plant Biology
Stem Cells • Systems Biology • Abiotic Stress Responses • Cell Biology
Biochemistry/Metabolism • Development 1: Organ and Cellular Polarity
Development 2: Cell Specification • Cell Walls and the Cuticle
Computational Biology • New Techniques • Light/Circadian Regulation

June 22-25, 2011
University of Wisconsin-Madison, USA

Poster Abstract Deadline: May 9, 2011

Online Registration Deadline: June 15, 2011 (on-site available)

Fee includes keynote lectures • all sessions • meals (optional low cost banquet)
poster session food/drinks • airport transportation • opening reception • abstract book
poster display • coffee breaks • conference bag • workshops • vendor show

NAASC
The North American
Arabidopsis Steering Committee

http://www.union.wisc.edu/arabidopsis/

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 breath 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 Cardiff and at Durham University.

Spotlight on the University of Cardiff

The School of Biosciences in Cardiff University is one of the largest biological sciences departments in the UK, with extensive facilities in both the historic Main Building of the University and in the adjacent large Biomedical Sciences building. Both are located overlooking beautiful Cathays Park within the historic sector close to the city centre. The School has around 100 academic staff, 150 graduate, and almost 2000 medical and bioscience undergraduate students reading Biological, Biomolecular or Biomedical Sciences, or pre-clinical Medicine/ Dentistry. This year a new business-focused Biotechnology 4 Year degree course is being launched led by Prof Jim Murray. In the 2010 Annual World University Ranking, Life Sciences at Cardiff University is in the top 100 worldwide and in the top 10 in the UK based on research strength and performance. The last few years have seen considerable investment in Plant Sciences with a particular focus on cell and developmental aspects. Appointment of three new staff members has been accompanied by extensive new laboratory, growing space, growth cabinets and equipment, as well as refurbished transgenic greenhouse provision on-site and at the Talybont facility situated about a mile away. The School is particularly keen to support prospective independent research fellows and informal enquiries are welcome. The School has been reorganised under its new Director, Prof Ole Petersen into four Research Divisions. Plant sciences are largely within the Division of Molecular Biosciences headed by Jim Murray, which focuses on model systems spanning from structural biology to developmental genetics, and also has a strong imaging theme around the physicist Paola Borri. Lynne Boddy is in the Organisms and Environment Division and the other two Divisions are Pathophysiology and Repair and Neurosciences.

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Plant cellular development; plant and molecular biotechnology

Jim Murray is Head of Division of Molecular Biosciences. Jim's research is focused on the cell division and cell differentiation in plants and in particular the role of cyclin D-type (CYCD) genes in integrating division processes in plant development and environmental responses. CYCD are the regulatory subunit of cyclin-dependent kinases that regulate the entry into the cell cycle and the decision of cells to divide. Mammals have three CYCD genes, and flies a single gene, but in Arabidopsis there are ten genes organised in six subfamilies that are conserved across all higher plants. This indicates their significance in plant development. Jim's work is partly focused on analysing the roles of CYCD and interacting cell cycle genes in development, using detailed analysis of mutants. This has uncovered important roles for different CYCD genes in (for example) responses to cytokinin during leaf development (CYCD3) and downstream of the *SCARECROW/ SHORTROOT* pathway in root ground tissue (CYCD6), as well as in lateral root density. The group has a wide range of experience in molecular, cell, developmental and systems biology and includes a computer scientist and an image processing engineer. Current funding from the ERA-NET in Systems Biology is focused on live shoot meristem imaging and cell division patterns in real-time in collaboration with Jan Traas (Lyon) and Christophe Godin (Montpellier). Further projects involve application of Bayesian network analysis to predicting and analysing regulatory networks in meristems, and the integration of environmental abiotic stress responses with growth and development.

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Acyl lipid metabolism and function

Prof John Harwood is Deputy Head of the School of Molecular Biosciences and his lab carries out research in several areas related to the metabolism and function of plant acyl lipids. He has elucidated several metabolic pathways for phosphoglyceride or sulpholipid synthesis and, in the latter case, catabolism. This has included the isolation and characterisation of key enzymes. John has applied the technique of flux control

Spotlight on the University of Cardiff

analysis to quantifying the regulation of oil synthesis in important crops. Recently, this has led to the successful production of oilseed rape lines with enhanced productivity. The lab has been responsible for elucidating the mechanism of action of three classes of herbicides – thiocarbamates, substituted pyridazinones and graminicides (aryloxyphenoxypropionates, cyclohexanediones). All of these act by inhibiting important reactions of fatty acid synthesis, namely elongation, desaturation and acetyl-CoA carboxylase, respectively. Finally John is interested in the effect of environmental stress on lipid metabolism. Most work has been on temperature, but also includes raised CO_2 and heavy metals and responses in algae and higher plants.

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Fungal community ecology, forest pathology

The fungal ecology group, led by Lynne Boddy, are world leaders in the study of wood-decaying basidiomycetes, the major agents of decomposition in forests. Interactions involving saprotrophic basidiomycetes form a large part of the group's research interests, including interactions with other wood decay fungi, pathogenic and mycorrhizal fungi, soil bacteria and invertebrates. The associated changes in fungal morphology, enzyme production and gene expression during interactions are of much interest to ecologists, conservationists and the natural products industry. Research is also being carried out into fungal mycelial architecture, using statistical mechanics approaches, in collaboration with Oxford University. These methods model mycelial networks, and changes in resource allocation, an area with wider implications for rail, road and other human network development. Conservation also plays a dominant role in the group's interests; research into the ecology of endangered woodland species, for example the rare oak polypore *Piptoporus quercinus*, can be used to generate better strategies for their protection. Central to this research is the use of various molecular techniques to study fungal diversity and distribution, including the detection of pioneer species present in functional sapwood and the identification of unculturable species. The responses of fungi to environmental disturbance are a further research area, with long-term survey data revealing that fungal fruiting seasons have almost doubled in length since the 1950s concurrent with climate change. Further work is investigating knock-on effects on other organisms and community development and

functioning. Lynne was also a prime mover behind the British Mycological Society's recent Silver Gilt and subsequent Gold Medals at the RHS Chelsea Show in the continuous learning section, and in putting together the "From Another Kingdom" exhibition which ran for 5 months at the Royal Botanic Garden Edinburgh (www.rbge.org.uk/), and is now at the National Botanic Garden of Wales (www.gardenofwales.org.uk/).


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Senescence mechanisms and cell cycle

Hilary's research focuses on the interactions between stress, senescence and cell death in plants. Although senescence is a programmed event forming the terminal phase in the development of both leaves and flowers, the onset of senescence is also modulated by stress. Overlapping patterns of gene expression between senescence and stress in both petals and leaves indicate crosstalk between these two pathways. Petal senescence in many species is coordinated by ethylene, however in others such as lilies it is not. A better understanding of the transcriptional changes elicited during normal developmental senescence and in response to stress treatments is helping to unravel the regulatory networks controlling petal senescence in ethylene sensitive and insensitive species. Reactive oxygen species (ROS) levels rise in leaves and petals both as a result of stress and senescence, but their role in either process is as yet not fully defined. Transcriptomic analysis of petal senescence in wallflowers (an ornamental species closely related to Arabidopsis) revealed up-regulation of a ROS-sensitive LEA protein SAG21/LEA5. This protein is up-regulated in Arabidopsis in response to a range of biotic and abiotic stresses, and perturbation of its expression in Arabidopsis affects growth, senescence and stress responses. Current work is aimed at understanding its role in senescence and stress responses. This research is in collaboration with Vicky Buchanan Wollaston (University of Warwick), Christine Foyer (University of Leeds), Freddie Theodoulou (Rothamsted Research) and Tony Stead (Royal Holloway, University of London).

Spotlight on the University of Cardiff
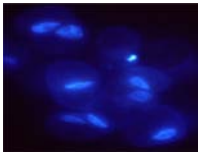
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Control of the plant cell cycle

The Francis group aims to examine how plant growth and development is altered when cell cycle gene expression is perturbed. Arabidopsis CDC25 encodes a homolog of yeast cell cycle regulator CDC25. It has a sole catalytic domain and devoid of the N-terminal regulatory region found in the human CDC25 and is capable of reducing the mitotic cell length of transformed fission yeast. It can show either phosphatase or arsenate reductase activity. Arabidopsis T DNA insertion lines for *Arath;CDC25* were hypersensitive to hydroxyurea (HU) but not zeocin, inducers of the DNA replication and DNA damage checkpoints. Plants over-expressing *Arath;CDC25* tolerate HU but not zeocin treatment. Hence, *Arath;CDC25* may have an involvement in the DNA replication but not DNA damage checkpoints. In contrast, over-expression of *Arath;WEE1* delays growth and morphogenesis both *in vivo* and *in vitro* compared with loss-of-function *wee1*. Arath;WEE1 protein also interacts with a 14-3-3 protein during the cell cycle. These observations suggest a role for *WEE1* at the interface between the cell cycle and development. For several years, tobacco and Arabidopsis transformed with *Schizosaccharomyces pombe* (Sp) *cdc25* have been used as tools to resolve cell cycle /developmental interfaces. *Spcdc25* expression induces small cell size phenotypes and is linked with endogenous cytokinin depletion, a pronounced rooting phenotype and precocious flowering. Current work involving microarrays and real time PCR is examining mechanisms whereby endogenous plant growth regulators maybe involved to bring about these phenotypes. In *Curcurbita pepo* root apical meristems, *in situ* hybridisation of A and B-type CDKs has also revealed links between cytokinins, cell division and CDKB whereas CDKA is a more general marker of mitotic competence. This research is in collaboration with HJ Rogers (Cardiff School of Biosciences), RJ Herbert (Univ of Worcester UK), H Lipavska (Charles Univ. Prague CZ), B Bitonti (Univ Calabria, Italy).

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Integrating cell division in plant embryogenesis

The post-fertilization development of the plant embryo remains a fascinating process. During this process the fertilised unicellular zygote develops into a multicellullar embryo imprinted with the plant's body plan, and progresses from a radially symmetric to a bilaterally symmetric structure. In Arabidopsis embryonic development follows a predictable sequence of cell divisions and this pattern is mainly under embryonic control. Superimposed on the proliferation of cells, new cell identities are adopted. During the last decades, asymmetric distribution of auxin has emerged as a major mechanism by which plants coordinate embryogenesis. At this point, we have only a fragmented knowledge about the mechanisms that coordinate cell proliferation in embryogenesis. Furthermore, the role of tissue compartmentalisation by cell division in this morphogenetic process is still not entirely clear. Walter's research focuses on the identification of core cell cycle regulators crucial for this process, more specifically on factors involved in the CYCD-RBR pathway, and the integration of those into developmental pathways involved in embryogenesis. Tissue specific activation of cell cycle factors and conditional knockouts address questions on the role of cell division in the different tissues during morphogenesis, and the interplay between cell division and the acquisition of different cell identities.

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Pollen proteomics to study pollen-pistil interactions

Sexual reproduction in flowering plants involves species-specific communication events between pollen and pistils. Very little is known about which pollen and pistil proteins play a role in the recognition between both partners during compatible pollen-pistil interactions in a single species. Moreover, nothing is known about the mechanisms by which male and female partners of different plant species discriminate between 'own' and 'foreign'. Pre-fertilization barriers are of central importance to the success of flowering plants and depend on recognition events between growing pollen tubes and different tissues of the female pistil. Although their genetic basis and molecular mechanisms are still largely unknown, these interactions should all depend on signalling through pollen tube membrane-associated processes. Membrane and membrane protein trafficking has been demonstrated to be important for the polarised growth of pollen tubes. However, the mechanism by which pollen tubes translate signals into growth responses, i.e., reorientation of pollen tube growth direction, is largely unknown. Barend's research focuses on

Spotlight on Durham University

the identification of novel pollen and pistil proteins that are involved in pollen pistil communication by applying an innovative strategy of organelle proteomics. Pollen tube organelles of interest, e.g., endosomes, will be isolated from pollinated *Nicotiana tabacum* and *Brassica napus* pistils at different stages of tube growth through the pistil. The protein content of these compartments, including the membrane protein fractions, will be subjected to mass spectrometry analysis. The function of putative receptor-like pollen membrane proteins and endocytosed pistil proteins will be established by cell biology, reverse genetics and gene silencing strategies.

Spotlight on Durham University

Durham University has a strong history and track record in Plant Science Research tracing its origins back to 1932 with the formation of the Botany Department. This Department, with that of Zoology and together with the Universities expansion into the Biomedical Sciences led to the formation of the School of Biological and Biomedical Sciences in the late 90's. In the 70's and 80's the media spotlight fell on the university, thanks to the TV series presented by Durham botanist and environmentalist David Bellamy OBE. His programmes attracted large audiences, won him a BAFTA Richard Dimbleby Award and established a tradition here for teaching plant science in an engaging and entertaining way. Durham continues to be a major international contributor to plant science teaching and research with current academic research strengths including plant cell biology, plant cell signalling, plant development and biochemistry with many of the major platform technologies housed on the Durham campus. Durham's newly created and very flexible research-led Biological Sciences undergraduate degree program delivers material pertaining to all these aspects of plant biology. In addition to our academic research and teaching, Durham has a strong applied research base. The Durham Centre for Crop Improvement Technology [DCCIT] has been newly established to build on these scientific strengths and tackle major problems in the area of food security and alleviating poverty. Strategic alliances have been formed with other parties, inside and outside the University; to enhance Durham's capabilities of tackling these problems by bringing together expertise from multiple disciplines. Major areas of DCCIT research are crop-protection, yield-improvement, stress-resistance and industrial plant-biotechnology.

DCCIT contributes a 3rd year undergraduate module, entitled "Crop for the Future" which covers contemporary research in this area, and provides an understanding of the challenges faced by the world.
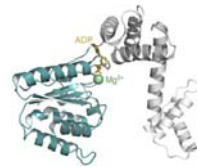
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Signalling biochemistry

The Cann laboratory's research in plant science is in the general area of signalling biochemistry. In particular, the laboratory is interested in the analysis of resistance (NB-LRR) protein function through a combination of *in vitro* biochemistry, *in vivo* functional analysis, and structural biology. Of recent interest is common themes in signalling biochemistry found between NLR family receptors that function in the immune system in plants and animals. The Cann laboratory is relatively new to plant science having historically worked on nucleotide based signalling systems in animals and microbes. The long-term goals of the laboratory are to uncover cross kingdom homologies in the signalling biochemistry of innate immunity and to exploit this for therapeutic benefit and crop protection.

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Protection of crops against invertebrates by exploitation of the molecular biology of hosts and herbivores

The main theme is to understand the molecular bases of plant interactions with invertebrate pests, both in terms of of how plants defend themselves against pests, and how pests are able to be successful herbivores despite the defences of plants. The work focuses on major agricultural pests in the UK and abroad, including caterpillars (Lepidoptera), beetles (Coleoptera), flies (Diptera), aphids and other sap-suckers (Hemiptera), and slugs (Mollusca). Within this theme several lines of research are being pursued: (i) Development of methods for crop protection against herbivores based on biotechnological solutions, including expression of foreign proteins in transgenic plants, and investigation of RNAi as a method of crop protection against invertebrates;

Spotlight on Durham University

(ii) Investigation of the molecular bases of adaptation by insects and molluscs which enable them to be successful herbivores, including investigation of the transcriptome in aphids and slugs, and functional studies of selected proteins using recombinant expression systems; (iii) Design, development and production of novel fusion proteins with oral toxicity towards pest insects and molluscs, based on fusions of protein and peptide toxins with plant lectins and other carrier proteins (with Fera, York). Although basic research in transcriptomics and functional characterisation of gene products is carried out, there is a strong theme of applied research, with fusion protein-based insecticides moving towards commercialisation.


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Gene regulation and plant development

Work in the Gilmartin lab is focused on identifying genes that regulate the development of different forms of flowers on plants of the same species using two distinct experimental systems, floral heteromorphy in *Primula vulgaris* and sex determination in dioecious *Silene latifolia*. *Primula vulgaris* plants produce either pin or thrum form flowers. Half the population produce pin flowers, with long styles and anthers mid way down the floral tube, the other half produces thrum flowers with short styles and anthers at the mouth of the tube. Fertilization is only possible following reciprocal crosses between the two forms of flower. Floral heteromorphy is orchestrated by a co-adapted linkage group of genes known as the S locus. Having identified several S locus-linked genes and generated a genetic map of the locus, current work is focused on isolation and characterization of the genes that coordinate heteromorphic flower development. *Silene dioica* plants produce either male or female flowers. Dioecy in this species is controlled by sex chromosomes, male plants have X and Y chromosome, females have two X chromosomes. The Y chromosome is dominant and suppresses carpel development and promotes stamen development in male flowers. In the absence of a Y chromosome, carpel development is not suppressed, and stamen development does not occur resulting in female flowers. On-going work is focused on characterizing a transposon-induced floral pigment mutant with the aim of identifying the transposon as a tool for mutagenesis to identify the Y chromosome genes that control of dioecy in this species.
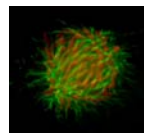
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Plant cytoskeleton

Patrick Hussey has been working on the plant cytoskeleton (actin and microtubules) for the last 25 years and his main interest has been the structure, function and regulation of the plant cytoskeleton in plant cell morphogenesis. The cytoskeleton is a key to many essential cellular functions and it is organised by a plethora of associated proteins that serve to anchor, crossbridge or otherwise regulate this fibrous network. These associated proteins are involved in competitive and/or cooperative interactions within cells to adjust the dynamics and organisation of the cytoskeleton, they are often stimulus responsive and are effectors of signalling cascades. Plant cells have to respond to different environmental cues in order to maximise energy production, to take up nutrients from the soil, to reproduce and to protect from pathogen invasion. In all these cases the cytoskeleton has to respond to signals and reorganise to generate organelle movement and cell expansion, polarise cell growth and thicken the cell wall. The major goal of Patrick Hussey's lab is to elucidate the plant signalling pathways that control cytoskeleton reorganisations that govern plant cell morphogenesis in plant cell differentiation, plant development and under biotic and abiotic stresses. Current project incorporate systems biology and mathematical modeling as well as utilising molecular and cell biology, genetics and biochemistry. A large focus in the lab is cell imaging and recent purchases include a Leica SP5 confocal laser scanning microscope (CLSM), a TIRF microscope and a Spinning Disk CLSM. Patrick has had extensive collaborations at the national and international level including Viktor Zarsky and Zdenek Opatrny (Prague, Czech Republic), Ian Moore (Oxford, UK), Peter Bozhkov (Umea, Sweden), Janice de Almeida Engler (Sophia Antipolis, France), Rui Malho (Lisbon Portugal), Haiyun Ren (Beijing, China), Martin Hulskamp (Koln, Germany), Peter Hepler (Amherst, USA), Laci Bogre (RHUL, UK), Seiji Sonobe (Himeji, Japan), Clive Lloyd (JIC Norwich, UK), Marie-Theres Hause (Vienna, Austria), Tijs Ketelaar (Wageningen, Holland), Diedrich Menzel (Bonn, Germany)., Laurie Smith (San Diego, USA). Grant funding from the BBSRC, HFSP, EU and industrial partners (Syngenta and Bayer) has supported his work.

Spotlight on Durham University
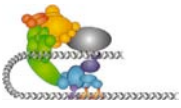
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#### Plant stress gene expression

When plants encounter unfavourable changes in their environment, they alter the expression of genes encoding proteins with protective functions. These enable them to withstand stress conditions such as frost, drought or attack by pathogenic organisms. Heather Knight's group are interested in the mechanisms whereby transcription of such genes is activated. Much of this work has involved the *sfr6* mutant of Arabidopsis, which shows a dramatic loss in cold-inducible gene expression and a consequent failure to acclimate to freezing temperatures. In addition to its inability to up-regulate cold genes, *sfr6* shows reduced expression of a umber of other stress-related gene regulons. The group is currently working on elucidating the role of SFR6 in gene transcription and identifying proteins with which it interacts. Heather Knight's group are also interested in identifying other proteins that contribute to freezing tolerance in plants.

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Calcium signalling

Marc's lab has been investigating signalling in plants, with a particular emphasis upon calcium. Marc's lab have investigated the calcium signalling responses to abiotic stress including cold, osmotic stress, heat stress and oxidative. The group demonstrated the sufficiency, necessity and specificity for calcium for the expression of specific genes in response to cold, oxidative stress and osmotic stress. Most recently they have taken a global approach by measuring calcium regulation of the whole Arabidopsis transcriptome, and identified key promoter elements and transcription factors which are responsible for calcium regulated stress gene expression in plants. Marc Knight's group are currently investigating the mechanisms of calcium-regulation of transcription factor activity.
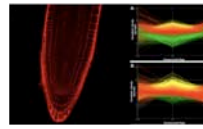
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http://www.dur.ac.uk/research/directory/staff/?mode=staff&id=29

Plant embryogenesis and root development

The Lindsey lab research programme is focused on the developmental genetics of plants, and in particular on molecular control mechanisms in embryogenesis and root development. The lab makes use of a range of techniques in functional genomics, and exploits the many advantages of *Arabidopsis thaliana* as a model experimental organism. The group has developed promoter trap insertional mutagenesis in a forward genetics approach to identify genes required for correct embryogenesis and root development. More recently, the lab has developed the use of laser-capture microdissection in combination with DNA microarray to identify transcription factors and signalling pathway components expressed in subdomains of developing embryos, and in roots in response to infection by plant-pathogenic nematodes. An integrating theme is that of polarity - in the establishment of the apical-basal axis of the embryo and of the root axis. This involves the genetic, cell biological and (with Junli Liu) mathematical modelling analysis of signalling pathways (auxin, ethylene, sterols) as coordinators of gene expression networks during embryo and root development. Keith is co-founder and co-Director, with Toni Slabas, of a spin-out company, Creative Gene Technology Ltd., which aims to exploit discoveries made in our basic research programmes, with a focus on biotechnological approaches to increase crop yield for sustainable food and energy production.
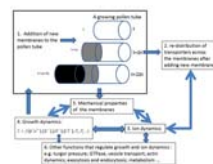
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Systems biology and mathematical modelling

Junli's research focuses on systems approaches to analyse, understand and predict the roles of complex interactions in biological systems. First, hormone signalling systems coordinate plant growth and development through a range of complex interactions. The activities of plant hormones, such as auxin, ethylene and cytokinin, depend on cellular context and exhibit interactions that can be either synergistic or antagonistic. An important question about understanding those interactions is how genes act on the crosstalk between hormones to regulate plant growth. Junli's research

Spotlight on Durham University

develops systems approaches that combine modelling and experimental data to study how hormonal crosstalk network and related genes form an integrative dynamic system to control and regulate plant development. Using these approaches the group is able to identify key regulatory points and context-dependent regulation in the entangled gene and hormone network in plants. Second, essential features of pollen tube growth are polarisation of ion fluxes, intracellular ion gradients, and oscillating dynamics. However, little is known about how these features are generated and how they are causally related. Junli's group aim to develop a Systems Tip Growth Model for a pollen tube to study how pollen tube development is regulated in an integrative manner by various components that include ions, vesicle transport, actin dynamics, exocytosis, endocytosis and metabolism. In addition, Junli is also developing systems approaches to link gene networks with biomass production via metabolic networks in plants.
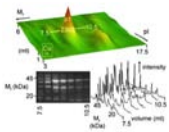
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Cell biology of metals

About a third of proteins and perhaps a half of enzymes require metals. Nigel Robinson leads a research group which is exploring how the correct metals locate to the correct proteins. The research group analyzes (and exploits) the contributions of gene products associated with the (i) perception-, (ii) acquisition or export-, (iii) intracellular distribution or storage-, of essential metals. With so much of biological catalysis needing metals this research has widespread implications in biology and broad applications in biotechnology, including within plant science.

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Protein degradation machinery in plant pathology

Plant diseases are major limiting factors of worldwide agriculture. Understanding the mechanisms by which pathogens invade plants and the means by which plant perceive the invasion is very important to developing novel control strategies in the future. The control of protein degradation through the ubiquitin-proteasome system (UPS) is a central modifier of signaling in animals and plants. An emerging paradigm in biology is the pathogen mediated targeting of the UPS to suppress host immunity but how pathogens achieve this is not known. Ari's group have identified regulatory factors of host UPS that could act as targets for defence suppression by plant pathogens. Using Arabidopsis, tobacco and tomato as model hosts Ari's lab employs a cross disciplinary approach including genetic, molecular and biochemical techniques to identify components that are specifically ubiquitinated by bacterial and fungal pathogens to undermine plant immunity. In recent years another class of ubiquitin-related polypeptide tags called small ubiquitin-like modifiers (SUMO) has emerged as a very influential regulator of stress signalling in plants and animals. Nearly all crops are highly susceptible to drought, heat stress and salinity. The work of Ari's group on post-translational modification of proteins has shown that specific signalling proteins are SUMOylated as part of plant survival strategy during drought, heat and high salinity. Ari's lab have developed experimental methods to specifically quantify and identify SUMOylated and Ubiquitinated proteins in plants. Understanding how protein modification is regulated will have huge implications for agriculture as this knowledge will be crucial for generating stress resistant crops.

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Lipid metabolism, proteomics, biofuels, eATP

Tony Slabas research activities are in the area's of 1. Lipid biosynthesis in Ricinus where they are elucidating the mechanism of storage lipid biosynthesis using a transcriptomic and proteomic approach, 2. The role of extracellular ATP in controlling cell death and pathogen responses in Arabidopsis and 3. Metabolic engineering of Cyanobacteria to make biofuels.

Spotlight on Durham University

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Organic synthesis and chemical biology

The Steel group has a broad spread of interests ranging from the development of new methods for organic synthesis through the design and synthesis of small molecule probes and modulators (inhibitors) of biological processes to applications in applied synthetic biology. In all of these a key goal is an understanding of how biological processes and the interactions between biological target and the small molecule are occurring at a molecular level. Much of this work is undertaken in collaboration. For example, within the Durham Centre for Crop Improvement Technologies they have collaborated with Patrick Hussey to generate fluorescent probes to study plant peroxisome dynamics and explore herbicides targeting plant cell wall biosynthesis. Similarly, in partnership with Robert Edwards they are studying the enzymes associated with herbicide detoxification and resistance with a specific goal to synthesise new herbicide synergists to understand and overcome multiple herbicide resistance in grass weeds.

SEB Society for Experimental Biology

Glasgow 2011

Annual Main Meeting July 1 - 4, 2011

CELL SESSIONS

Tip Growth in Plant Biology
Organized by: Kriss Vissenberg (University of Antwerp, Belgium) and Claire Grierson (Bristol University)
Confirmer Speakers: Prof. Dr. José Feijó (Instituto Gulbenkian Ciência and Univ. Lisboa, Fac. Ciências), Prof. Dr. Erik Nielsen (Univ. Michigan, USA), Dr. Vera Meyer (Leiden University)

Frontiers in Algal Biology
Organized by: John Love (University of Exeter)
Confirmed Speakers: Saul Purton (University College London)

Nuclear Envelope
Organized by: Martin Goldberg (Durham University)

Gas sensing and signalling in animal cells
Organized by: Martin Cann (Durham University)
Confirmed Speakers: Yosef Gruenbaum (Hebrew University of Jerusalem), Cormac Taylor (University College, Dublin) Nick Dale (University of Warwick) Mario de Bono (MRC Laboratory of Molecular Biology, Cambridge) Phillip Moore (Kings College, London)

PLANT SESSIONS

Regulation of resource allocation and growth
Organized by: Astrid Wingler (University College London) and Matthew Paul (Rothamsted Research)
Confirmed Speakers: Gerrit Beemster (Antwerp), David Jackson (Cold Spring Harbor), Hendrik Poorter (Utrecht/ Jülich), Paul Struik (Wageningen), Andy Fleming (University of Sheffield), Joost Keurentjes (Wageningen University), Céline Masclaux-Daubresse (INRA Versailles), Henriette Schluepmann (Utrecht University), Ronan Sulpice (MPI Golm), Cristobal Uauy (John Innes Centre), Carol Wagstaff (University of Reading), Achim Walter (ETH Zürich)

Pathways and fluxes: analysis of the plant metabolic network
Organized by: R. George Ratcliffe (University of Oxford) and Nicholas J Kruger (University of Oxford)
Confirmed Speakers: Stephanie Arrivault (MPI Golm), Andrew Hanson (University of Florida), Ron Milo (Weizmann Institute of Science), John Morgan (Purdue University), Jörg Schwender (Brookhaven National Laboratory), Yair Shachar-Hill (Michigan State University), Ralf Steuer (Humboldt University Berlin), Lee Sweetlove (University of Oxford), Guillaume Tcherkez (Université de Paris-Sud)

Plant Transcription: regulation and mechanism
Organized by: Heather Knight (Durham University) and Piers Hemsley (Durham University)
Confirmed Speakers: Professor Stefan Björklund (Umeå University), Ueli Grossniklaus (Institute of Plant Biology, Switzerland), Richard Meagher (Genetics Department, University of Georgia), John Brown (Plant Sciences Division, University of Dundee), Martin Huelskamp (Botanical Institute, University of Cologne), Nick Monk (School of Mathematical Sciences, Nottingham), Ari Sadanandom (Warwick HRI, University of Warwick), Jerzy Paszkowski (Department of Plant Biology, University of Geneva), Dao-Xiu Zhou (Institute of Plant Biology, CNRS Paris)

Integration of abiotic and biotic stress responses: from systems biology to field
Organized by: Katherine Denby (University of Warwick) , Christine Foyer (University of Leeds), Miriam Gifford (University of Warwick), Robert Hancock (SCRI)

EPA SESSIONS

Science Communication Training Day
Organised by: Jeremy Pritchard (Birmingham), Sarah Blackford (SEB), David Evans (Oxford-Brookes), Iain Barber (Leicester), Tijana Blanusa (Reading)

Media Workshop
Organised by: Jenny Sneddon (Liverpool John Moores)

Careers Workshop
Organised by: Sarah Blackford (SEB), and Peter Lumsden (University of Central Lancashire)

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2011 GARNet Meeting

Dynamic Biology

New Levels and New Dimensions of Regulation

University of Cambridge
6-7th September

Speakers

David Baulcombe
Malcolm Bennett
Mike Blatt
Vincent Colot
Caroline Dean
Katherine Denby
Wolf Frommer
Claire Grierson
Steve Jacobsen
Joerg Kudla
Elliot Meyerowitz
Richard Morris
Ortun Mittelsten-Scheid
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