

# GARNish

June 2012 Edition 17

GARNet



 Welcome to the June 2012 issue

**GARNish Editorial - Embedding new technologies and promoting dialogue**

Jim Murray - GARNet Chair

I have taken on the responsibility as Chair of GARNet from the start of 2012. I'd like to thank my predecessor in this role, Alex Webb, who with his determination and energy will be a hard act to follow, although I am sure Ruth will help steer me in the right direction! The first part of this year has seen a highly successful inaugural meeting of the UK Plant Sciences Federation, which represents a very important development in raising the profile of the subject and its importance, and we have a report on this. It's particularly gratifying to report the award of the President's Medal of the Society of Biology to Ruth for her contribution in bringing the UKPSF to reality (News), as well as the election of Andrew Millar to the Royal Society and the E.K. Stakman Award to Jonathan Jones. Beyond the normal signposting of the content - and we have articles about the PhytoPath Pathogen Resource and the all-important Arabidopsis Information Portal that will replace and build on TAIR, and the new Phenomics Facility at Aberystwyth, amongst others - I would like to use this Editorial to set out the priorities and challenges for GARNet over the next couple of years, and the initial progress towards these.

The Committee sees major challenges for the Arabidopsis community in particular in adapting to new technologies, as well as changes in the emphasis and priorities of funding. As a result we set three main priorities at the GARNet committee meeting in February.

These are:

- i) Embedding technologies in the community, particularly Next Generation Sequencing (NGS) and phenomics, but also including proteomics, imaging and interactomics.
- ii) Act as a conduit between the BBSRC and the Arabidopsis community to help the Arabidopsis community to understand where it sits in relation to the surrounding plant science landscape and assist BBSRC fulfil its remit.
- iii) Promote interactions across UK Plant Science communities.

**Embedding new technologies:** The first of these was really brought to the fore by the challenges that NGS poses. The technology is advancing extremely rapidly, and, whilst some members of the Arabidopsis community have been at the forefront of its use, many others may have had more restricted experience. It is clear that this technology will transform much of the work with Arabidopsis and it is vital for the community to be well posi-

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Many thanks to all who contributed to this issue, particularly John Doonan, Aurora Levesly, Paul Kersey and Jim Murray.

tioned to make the best use of it. The situation has also been made perhaps less straightforward by evolving policies at BBSRC around the role of The Genome Analysis Centre (TGAC) and funding for NGS within research grants. GARNet has been involved in discussing the issues and the grant guidelines of BBSRC have now been clarified. We also supported a workshop held by TGAC in Norwich before the UKPSF meeting. We are organising a one day meeting later this year (in late November) in Liverpool on the applications of NGS in Arabidopsis research, which will both showcase successes and explore new opportunities.

This one day workshop format focused on new technologies or specific areas will be the model for GARNet-sponsored meetings in the future, as the longer meetings are felt to be largely replaced by the UKPSF, and we hope to organise two further workshops in 2013.

**Relationship with BBSRC:** It is clearly critical for the Arabidopsis community to have a clear route of communication with BBSRC to understand the motivations and priorities of our major funder, and hopefully to help shape and influence future policies. To help develop these interactions, Jim Beynon, Ruth and myself requested a meeting at BBSRC in April for which BBSRC kindly made available a number of relevant staff. This meeting was helpful in understanding BBSRC policy direction with respect to Arabidopsis research, as well as funding opportunities. My take was that BBSRC has no specific agenda on Arabidopsis research, and certainly no intention to curtail research on model systems that meets the right standard for responsive mode grants. At the same time, there are significant further funding opportunities through the new priorities of BBSRC, but these in turn require new thinking from the community. Whilst we are fairly familiar with the Food Security agenda, BBSRC highlighted that there are opportu-

nities within Industrial Biotechnology and Bioenergy (IBB) that are not currently being taken up fully by plant scientists in general. Since IBB will receive an additional £10M of funding by 2015, equivalent to around 50-70 active grants, this represents the only area of significant increase in BBSRC expenditure and there are clearly opportunities here for the community. As a result we invited Colin Miles to explain more about the BBSRC interests in this area at our May Committee meeting. We also plan to invite a BBSRC representative to our September committee to outline the opportunities that exist in the area of Synthetic Biology.

During our recent meeting Colin Miles outlined that the BBSRC definition of IBB is broad, covering the use of biological resources for producing and processing materials, chemicals and energy, including plants, algae, marine life, fungi and micro-organisms. In bioenergy there are plant-related aspects in feedstocks (these include algae, crop residues, food and municipal waste, animal wastes and perennial biomass), as well as the growth and composition of the feedstock together with metabolism, harvesting and processing any associated added-value co-products (bio-refinery approach). New approaches to producing high value chemicals from plants including the translation of knowledge from model plants to industrially-relevant plants is included, as is support for the development and application of approaches such as genomics, systems and synthetic biology. There are clearly challenges for the Arabidopsis community in adapting to this area, but the opportunities are also significant and it is important that we show that as a community we are able to rise to these.

I am also a member of the Bioscience for Industry Strategy Panel, and I would like to highlight to the community the funding routes of Industrial Partnership Awards (requiring 10% cash contribution from an industrial partner), which provides an uplift to the ranking order of your application, and Stand Alone LINK, in which the industrial partner puts in 50% contribution in cash or kind and for which the success rate is very high.

**Promoting interactions:** The support from GARNet members for the establishment of the UKPSF has been very significant in developing and shaping this new voice for plant science. Jim Beynon and Ruth Bastow are both on the Executive Committee of UKPSF, giving Arabidopsis a strong and clear voice. Our intention is to be fully engaged with UKPSF as an integrating platform for plant science.

Finally, good luck and good science to all!

Jim Murray

## The GARNet Committee

### **Malcolm Bennett**

University of Nottingham  
Term on committee Jan 2010 - Dec 2012

### **Jim Beynon**

University of Warwick  
GARNet PI

### **Juliet Coates**

University of Birmingham  
Term on committee Jan 2010 - Dec 2012

### **John Doonan**

University of Aberystwyth  
Term on committee Jan 2012 - Dec 2014

### **Anthony Hall**

University of Liverpool  
Term on committee Jan 2012 - Dec 2014

### **Smita Kurup**

Rothamsted Research  
Term on committee Jan 2010 - Dec 2012

### **Sabina Leonelli**

University of Exeter  
Ex-Officio Member

### **Sean May**

NASC  
Ex-Officio Member

### **Ian Moore**

University of Oxford  
Term on committee Jan 2010 - Dec 2012

### **Jim Murray**

University of Cardiff  
GARNet Chair Jan 2011 - Dec 2013

### **Heather Knight**

Durham University  
Term on committee Jan 2012 - Dec 2014

### **Nick Smirnoff**

University of Exeter  
Term on committee Jan 2010 - Dec 2012

### **Cyril Zipfel**

The Sainsbury Laboratory Norwich  
Term on committee Jan 2012 - Dec 2014

### Professor Andrew Millar FRS accepted as new Royal Society Fellow

On the 19<sup>th</sup> April 2012, Professor Andrew Millar was elected as a fellow of the Royal Society, in recognition of his important work in establishing the circadian clock of *Arabidopsis thaliana* as a model to study dynamic biological regulation. Along with colleagues he also developed reporter gene imaging of living plants to identify the first plant clock genes, and integrated disparate molecular results in the first mathematical models of the plant clock mechanism. The models revealed general operating principles, such as the flexible regulation of complex feedback circuits. His work on the alga *Ostreococcus tauri* identified a non-transcriptional circadian clock that is shared across the eukaryotes, overturning the central paradigm of circadian biology. Professor Andrew Millar acknowledges the important work of his lab and associates in the development of his research contributing to this honour.



for UKPSF, Ruth has created 'one voice for UK Plant and Crop Science', bringing together representatives from research communities, learned societies, educational networks and industry.

The first annual UKPSF conference (UK PlantSci 2012) was fully subscribed, representing the enthusiasm among the community for a network which brings plant scientists together. Professor Sir John Beddington, the Government's chief scientific advisor, delivered the conference opening address and the programme covered world-class science. Ruth's support was vital in ensuring that UK PlantSci 2012 was a success.

Ruth's support is on-going and the benefits of her work continue to be felt. She was instrumental in securing financial support for the creation of the post of UKPSF Executive Officer, that was filled in early June by Mimi Tanimoto.

The President's Medal was presented by Professor Dame Nancy Rothwell FSB, President of the Society of Biology since October 2009. Dr Mark Downs, Chief Executive of the Society of Biology, says: "Ruth has been instrumental in the foundation of UKPSF, which will be of huge value to the plant science community. We were very pleased to recognise her achievements with the President's Medal."

### Dr Ruth Bastow awarded the Society of Biology President's Medal

The Society of Biology President's Medal was awarded to Dr Ruth Bastow at its 2012 Annual General Meeting. The Medal is awarded annually to individuals who have made an outstanding contribution to the life sciences over the previous year. Ruth received the Medal for her leadership, drive, community knowledge and administrative support, which allowed the UK Plant Science Federation (UKPSF) to be founded.



Ruth says: "I am very honoured to be awarded the Society of Biology President's medal. A great number of people have been involved in establishing the UKPSF and I feel privileged that my input has been recognised in this way."

"The UKPSF provides a unique structure to bring together all those involved in plant science research and education, from the lab to field and beyond. Only by coming together to share knowledge and expertise can we hope to further plant biology and help to provide solutions to current problems."

Ruth's efforts were crucial to the establishment of the UKPSF, a Special Interest Group of the Society of Biology. She worked tirelessly behind the scenes to bring people on board and secure funding. Through her work

### Professor Jonathan Jones recipient of the E.C. Stakman Award

Professor Jonathan Jones of The Sainsbury Laboratory on the Norwich Research Park in the UK has been selected as the recipient of the 2012 E.C. Stakman Award, for his outstanding achievements in the field of plant pathology.

Professor Jones has made numerous and sustained contributions to the science of plant pathology. His group was among the first to isolate and characterize a plant disease resistance gene. By cloning the *Cf-9* gene in 1994, he was the first to demonstrate that resistance induced in plants towards pathogens is based on specific classes of innate immune receptors. His work preceded the 1996 discovery of innate immune receptors in animal systems, which was recognized by the 2011 Nobel Prize in Medicine and Physiology. In essence, Professor Jones' discovery that an R gene codes for a receptor-like protein was a validation of the concept of gene-for-gene and elicitor-receptor interactions that originated from the work of E.C. Stakman, Harold Flor, and other pioneers of plant pathology.

The E.C. Stakman Award is presented by the Department of Plant Pathology at the University of Minnesota to individuals of any country and nationality for outstanding achievements in plant pathology.

### ✿ £6.8M Phenomics Centre Opens

On Monday 14<sup>th</sup> May 2012, the new National Plant Phenomics Centre, which features the most advanced research greenhouse in the UK, was formally opened at Aberystwyth University's Institute of Biological, Environmental and Rural Sciences.

The new centre is a Biotechnology and Biological Sciences Research Council (BBSRC) supported national facility and has been developed at a cost of £6.8M.

The research conducted at this new national centre will help to develop new plant and crop varieties to help tackle the global challenges of climate change, food security and replacing oil based products.

Located on the University's Gogerddan campus, the centre was opened by BBSRC Chairman, Professor Sir Tom Blundell and is one of two significant capital investment developments that were opened on the same day. The other being the new teaching and researcher facilities on the University's Penglais campus. The new Penglais facility represents an investment of £5.6M and houses the Bioinformatics and Spatial Modelling laboratories as well as offering a hub for undergraduate and postgraduate teaching. Together the developments represent the culmination of a four year £25M capital investment programme made possible by financial support from the BBSRC, the Welsh Government and the European Union.

#### The National Plant Phenomics Centre

The centre, which features a state of the art greenhouse, the only one of its kind in the UK and one of only seven in the world, will enable researchers to study individual plants in a way that has never before been possible in the UK.

With the capacity to house up to 850 individually potted plants on a series of conveyor belts measuring over 300 meters long, scientists will be able to apply different feeding and watering regimes to individual plants as they study the influence of individual genes.

Ten computer controlled cameras using fluorescence, infra-red and near infra-red, laser and root imaging technology combine to provide 3D images of the plants and monitor their growth on a daily basis.

This level of detail, which cannot be achieved using current research methods, will enable researchers to speed up the process of identifying potentially beneficial genes.

The beneficial genes will be used for the development of new plant varieties to tackle the global challenges of climate change and food security and to replace oil based products.

### ✿ PBL and Alnylam sign RNAi licensing agreement

Plant Bioscience Limited (PBL), the UK technology management company, part owned by BBSRC, have entered into a licensing agreement with Alnylam Pharmaceuticals, Inc. PBL has granted Alnylam a world-wide, non-exclusive license to the Baulcombe patent (U.S. Patent No. 8,097,710) to enable the development of RNA interference (RNAi) therapeutics.



PBL's Managing Director Dr Jan Chojecki stated, "We are very pleased to enter into this agreement with Alnylam, a global leader in the development of novel human therapeutics based on RNA interference. We are excited to have Alnylam as a partner, which has an impressive pipeline of RNAi drug candidates in clinical development.

"This agreement further endorses the strength of our patent estate in the RNAi field and we look forward to working with other partners through our non-exclusive licensing strategy in agricultural, research, diagnostic and therapeutic commercial applications. This is an excellent example of how UK scientific research contributes inventions that have many beneficial applications across the life sciences. We are pleased to be able to make non-exclusive licences available on reasonable commercial terms to assist our partners in delivering benefits to patients in areas of unmet medical need."

Professor Sir David Baulcombe and Dr Andrew Hamilton's research at The Sainsbury Laboratory in Norwich, which was funded in part by BBSRC, resulted in a ground-breaking paper that was published in *Science* in 1999 (A species of small antisense RNA in posttranscriptional gene silencing in plants, 286, pp. 950-952). The paper provided the first identification of short RNA molecules as the active agents of silencing, also known as RNAi. Their pioneering work has led to a number of patents describing methods for detecting and inducing silencing in plants and mammals.

## UK Plant Sci 2012 Conference April 18-19<sup>th</sup> 2012

Laura Dixon  
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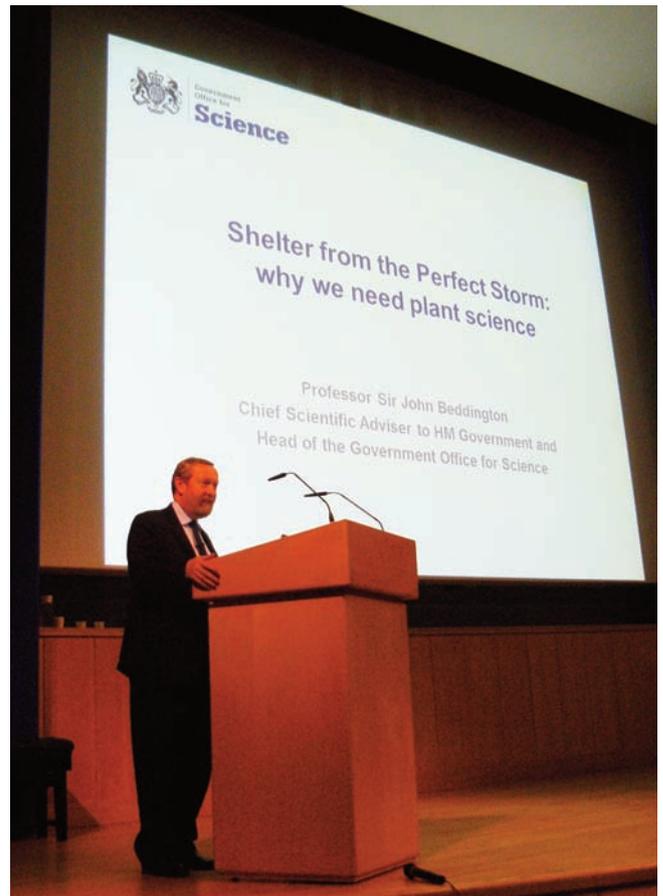
The inaugural UK Plant Sciences Conference of the UK Plant Science Federation (<http://www.plantsci.org.uk/>) was hosted at the John Innes Centre with the aim of bringing together all aspects of the plant science community. This was certainly achieved with the delegate list ranging from crop breeders to molecular biologists and including teachers, business professionals and innovators in plant science. The JIC provided an inspirational place to meet and the delicious food at the conference dinner at Delia Smith's Restaurant meant even the most ardent Ipswich Town supporter could overlook its location!



### The Perfect Storm

On behalf of the UK Plant Science Federation (UKPSF) the meeting was opened by Jim Beynon, Warwick University (UKPSF Chair), who highlighted the need for the development of applied plant science but not at the expense of fundamental research, a theme which was carried through the meeting. He also outlined the role and importance of plant science in society and the requirement for inspiring future generations of plant scientists. Dale Sanders, JIC Director, welcomed delegates to the JIC and introduced the plenary speaker Sir John Beddington, HM Government Chief Scientific Advisor.

In his talk Sir John Beddington outlined what he described as the 'perfect storm' facing humanity. This perfect storm could form due to the needs of an increasing human population, its urbanisation and prosperity combined with the impacts of climate change. He highlighted one of the roles plant scientists have to play in avoiding this storm; through the development of agricultural crops, reiterating the links between food price/av-



ailability and civil unrest. He went on to say that following the correct safety checks regarding health and environmental concerns relating to genetically modified crops must be a consideration if we are to feed the world's growing population.

How to create global food security for a growing population and balance this with the environment and natural resources was addressed many times throughout the meeting both explicitly - with the modification of crops which would be able to fix more carbon (Julian Hibberd, University of Cambridge) or nitrogen (Giles Oldroyd, JIC) - and more subtly through addressing how to inspire the next generation of plant scientists (Gatsby summer school, SAPS and ASPB).

### Diversity in Plant Science

The meeting comprised six sessions and two workshops through which the diversity across the plant science sector was really emphasised. This diversity firstly related to the different aspects of plant science from plant hunting in the Andes, to crop breeding, fundamental research, teaching and application into industry, as well as the number of different species being researched. Across the World, 80% of calorific intake is from the big six plant species: wheat, rice, maize, potatoes, sorghum and cassava. From these already inten-

sively farmed crops major yield and quality improvements need to be made if they are to keep pace with the increasing population. A number of the talks described strategies which are being implemented to achieve this using conventional breeding and genetic modification. Other talks identified the potential of other plant species relating to crops (broccoli and tomato), bioenergy (*Miscanthus* and alga) and medicinal and health functions (*Artemisia annua* and *Stevia rebaudiana*). For *Artemisia annua*, which produces the anti-malarial compound artemisinin, substantial increases in plant yield for the drug were reported and this reiterated biopharming as the best way to synthesise this compound.

The conference was not only a platform for new innovations in research but also business applications and the development of new technologies, notably the seawater greenhouse technology. This is a system that bypasses the need for fresh water by using sea water vapour in its greenhouses



(<http://www.seawatergreenhouse.com/>). Such a variety of topics and innovations really demonstrated how much plant science takes place in the UK. Ian Graham, York University, spoke about the increase in the speed of DNA sequencing, which makes this an optimum time to be developing applications in different plant species, as whole genome sequencing becomes a viable option within research projects.

The diversity and quality of plant science in the UK could also be seen in the variety of topics covered by the posters. Before the conference dinner the workshops covered two of the key challenges facing the development of plant science research. The first workshop highlighted the importance of intellectual property and its commercialisation, using examples from broccoli research and biopharming from the BBSRC's innovator of the year, George Lomonosoff. The second workshop covered grants available to support research groups and business to work together.

### Looking Forward

The popularity and support for this conference, not only from the plant science community but also industry and sponsors shows that the UK Plant Science Federation has a very important role to play in plant science research. As Sandy Knapp (Natural History Museum) remarked in her concluding comments, the meeting not

only identified the big challenges facing plant science, but also acted as a platform to enable scientists to tackle these challenges and exchange new ideas. The inaugural meeting was clearly a success and minds were quickly turned to next year's meeting, with requests for topics to be covered and any suggestion for improvements which could be made. If you have any ideas please contact ([ruth@plantsci.org.uk](mailto:ruth@plantsci.org.uk)).



## New Pathogen Resource Launched

Paul Kersey<sup>1</sup>, Helder Pedro<sup>1</sup>, Uma Maheswari<sup>1</sup>, Kim Hammond-Kosack<sup>2</sup>, Martin Urban<sup>2</sup>, Mansoor Saqj<sup>2</sup>, Jacek Grzebyta<sup>2</sup>.

<sup>1</sup> EBI

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<http://phytopathdb.org>

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The number of completely sequenced plant pathogens is rapidly growing, representing the combination of improved, lower cost technologies for genome sequencing with increasing global concerns about food security. PhytoPath (<http://phytopathdb.org>) is a new bioinformatics resource that integrates genome scale data from important plant pathogenic species with literature-curated information about the phenotypes of host infection. A collaborative UK-based project between the European Bioinformatics Institute (EBI) located south of Cambridge and Rothamsted Research (RRes) located just north of London, PhytoPath is bringing together the power of the Ensembl software platform for genome analysis and display with the Pathogen-Host Interactions (PHI-base) database (<http://phi-base.org>), which stores information about the role of particular genes in pathogenesis directly curated from the peer reviewed literature. PhytoPath was launched in January 2012 and already contains the genomes of 12 fungal and 4 oomycete phytopathogens. The resource provides researchers access to complete genome assemblies, gene models, supporting alignments, DNA and protein sequence alignments (between pathogens themselves, and with other fungal species), inferred evolutionary histories, and genomic polymorphism data. Agriculturally important species already in the resource include *Magnaporthe oryzae* (rice blast), *Mycosphaerella graminicola* (septoria tritici blotch of wheat), *Gibberella zeae* (fusarium head blight), *Puccinia graminis f sp tritici* (wheat stem rust) and *Phytophthora infestans* (late blight of potato), with *Blumeria graminis f sp hordei* (barley powdery mildew) scheduled for inclusion in the next release.

The website additionally supports mechanisms that allow users to visualise private high-throughput data (e.g. alignments, variant calls etc.) in the context of the

reference annotation simply by putting an appropriate file on a local FTP site. Meanwhile, a query-optimised-data warehouse provides access to a set of efficient data mining tools. Both the browser and the warehouse have already been enhanced to incorporate information from PHI-base, allowing users to identify genes with particular roles in pathogenesis in their genomic contexts. Future developments will further enrich this interface, and provide stronger links between the genomes of phytopathogens and those of their hosts (which are also available in the Ensembl interface), with a particular emphasis on the relationship between pathogen effector proteins and their host targets. In parallel, a major effort has been undertaken to curate the outstanding literature, and over 100 new articles have been curated into PHI-base in less than 3 months. But to ensure that the database remains up-to-date and accurate, the best solution is to actively engage the community to curate their own papers, as they are published. PHI-base already has a large number of international experts who contribute to the database. To expand these activities, a new public, web-based curation interface is in development, which will reduce the overhead and increase the complexity of submitting data to the resource. Kim Hammond-Kosack, PI at RRes, says, 'PHI-base is a unique resource, and our new submission tool will allow us to keep pace with the growing scale of experimental research in this area.'

Paul Kersey, EBI PI, says, "We're really keen to engage with the research community and assist them in connecting and submitting their data, to ensure we cover all the most important phytopathogens and to integrate the most important data sets. Please get in touch with us for more information about how we can support you."

A workshop will be held at EBI in the autumn (see the website for details) for those interested in receiving advanced training in the use of the resource, the data it holds and the interactive and programmatic interfaces that can be used to access it.

PhytoPath is funded by the United Kingdom Biotechnology and Biological Sciences Research Council.

The screenshot shows the PhytoPath website homepage. At the top is a navigation bar with links for Home, New Pathogens, Taxonomy, Contact, and About. Below this is a 'Welcome to PhytoPath' section with a brief description of the resource. The main content area is divided into two columns: 'Last added genomes' and 'This release'. The 'Last added genomes' section features a link to *Phytophthora infestans* with a small image of a potato and a description of its impact. The 'This release' section provides details about the current release of the resource, including the date and the types of data available.



# Aboveground–belowground interactions: technologies and new approaches

Joint meeting of the British Ecological Society, the Biochemical Society and the Society for Experimental Biology

Charles Darwin House, London, UK  
8–10 October 2012

For a full programme please visit:  
[www.jointbessebbs.org/2012](http://www.jointbessebbs.org/2012)

Abstract submission deadline: 13 August 2012  
Earlybird registration deadline: 10 September 2012

Please note that spaces are limited, and delegates are advised to register as early as possible to secure their attendance

Apply for a travel grant online:  
[www.jointbessebbs.org/2012/Grants.aspx](http://www.jointbessebbs.org/2012/Grants.aspx)

Slots for both oral and poster presentations are available:  
[www.jointbessebbs.org/2012/Abstracts.aspx](http://www.jointbessebbs.org/2012/Abstracts.aspx)

## Scientific background

This collaborative event aims to identify the specific skills that biochemists, molecular biologists, physiologists and ecologists can bring to cross-disciplinary research in the area of aboveground–belowground interactions. The conference will introduce examples where cross-discipline and across-scale research has successfully examined the mechanistic basis of multi-trophic interactions, and will aim to identify the potential for applying such approaches to aboveground–belowground systems, which are traditionally more intractable. The following three key questions will be addressed:

- What are the major challenges in aboveground–belowground research?
- What tools and approaches can be adopted from different disciplines to address these challenges?
- How can high-throughput tools aid integration across disciplines and scales to facilitate a unified approach to studies of aboveground–belowground systems?

The conference will be of particular interest to technology users and developers who are interested in applying their skills to address research questions at the whole organism and ecosystem scales, as well as to aboveground–belowground researchers aiming to exploit new technologies in their research. A key focus of the event will be to assist postgraduate and early career researchers in their field of study.

## Programme Committee

Alison Bennett (The James Hutton Institute, UK)  
Alison Karley (The James Hutton Institute, UK)  
Scott Johnson (The James Hutton Institute, UK;  
University of Western Sydney, Australia)  
Tim Daniell (The James Hutton Institute, UK)

## Sponsors

Biochemical Society  
British Ecological Society  
Society for Experimental Biology

## Speakers

Garret Suen (University of Wisconsin-Madison, USA)  
Ian Toth (The James Hutton Institute, UK)  
Marcel Dicke (Wageningen University, The Netherlands)  
Mirka Macel (University of Tuebingen, Germany)  
Nicole van Dam (Radboud University of Nijmegen,  
The Netherlands)  
Philippe Schmitt-Kopplin (Helmholtz Zentrum München,  
Germany)  
Richard Bardgett (Lancaster University, UK)  
Ted Turlings (University of Neuchatel, Switzerland)  
Thure Hauser (University of Copenhagen, Denmark)



## The Future of Arabidopsis Informatics

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Over the past two years a great number of discussions have taken place over the future of Arabidopsis informatics. Currently The Arabidopsis Informatics Resource (TAIR) provides access to the Arabidopsis gold standard genome and associated annotations as well as dealing with important tasks such as nomenclature, AGI codes and map positions. However, TAIR's current funding from the National Science Foundation will cease in August 2013. Faced with this funding deficit and the ever increasing level of data and new data types the challenge for the community is how to move from a single primary database surrounded by, yet often not connected to, numerous smaller Arabidopsis databases to a consortium of linked databases. To achieve this goal the International Arabidopsis Informatics Consortium (IAIC) was established in May 2010 to help the community build a distributed system of data, tools and resources accessed via single point – the Arabidopsis Information Portal (AIP)(1).

In December 2011 the IAIC hosted a design workshop to define the main characteristics of the AIP. Around 40 participants with backgrounds in plant research, informatics, cyberinfrastructure and computer science came together to 'dream up' potential designs for the AIP. The workshop attendees highlighted a wide range of needs and requirements that included:

- a) Web based user interface
- b) Visualisation tools – to clearly and easily display data
- c) Customizable interface – the user can choose and define datasets that are displayed and analysed
- d) Access to well curated datasets
- e) Support for *in silico* experiments and predictions
- f) Extensibility for future needs

All workshop delegates agreed that the underlying architecture for the AIP needed to be open, robust, dynamic and reliable.



Activities at the Design Workshop - Image kindly supplied by Joanna Friesner

### Functionality and Framework

One of the main functions of the AIP will be to integrate distributed databases containing genomic, transcriptomic, proteomic, metabolomic, functional, phenotypic and many other diverse data types. The AIP will therefore need to develop mechanisms to connect all these data on a common platform, and allow users to carry out seamless queries across a range of datasets.

To achieve this it is envisioned that the AIP will be built upon a set of platform services that allow access to low-level compute, data visualization and instrumentation resources (2). This framework would provide the AIP with its basic functionality including key utilities such as data management, data execution, data curation, data discovery/search, user authorization and registry of modules.

### Core Components and Modules

It has been proposed that the AIP will serve as a hub linking together the numerous databases, tools and resources. To ensure the AIP provides a set of critical functions to the community it must include the following set of core components;

- a) Gold Standard Genome and Annotation
- b) Curation of Functional Data
- c) Stock Centre Databases

In addition to these core components there are also a number of non-core modules, which would provide additional data, tools and resources for the community and extend the functionality of the AIP. These modules could build upon existing infrastructure, consolidation and investigator tier databases as well as including new resources that are created as new methods and technologies become available. The design of the AIP should provide core functions whilst remaining flexible enough to encourage constant innovation from multiple contributors.

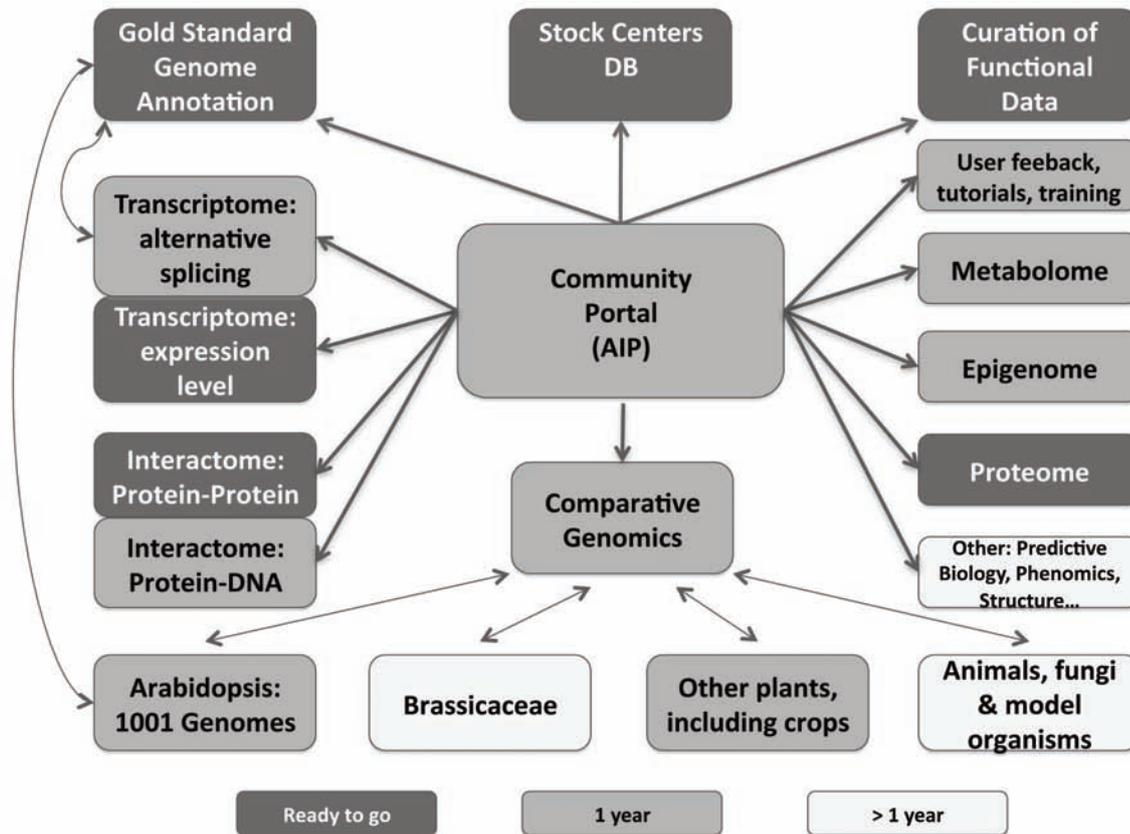
 **AIP Arabidopsis Information Portal v1.0 – Modules**


Figure 1 – Components of the AIP. The AIP will be built on a modular structure of databases tools and resources accessed via a single point. The modules listed are provided as examples of what is possible rather than an exhaustive list (Figure kindly provided by Nicholas Provart).

### Next Steps

Since the design workshop in December 2011, participants have begun discussions to build teams to develop the AIP and it is hoped that applications for funding will begin this summer. As the work to build the AIP begins it is essential that the data currently curated and maintained by TAIR is available to the community. To achieve this it has been proposed that the TAIR website will be moved to the iPlant Collaborative project during the development phase of the AIP and before the end of the TAIR funding period. This will provide users with a fully functional version of TAIR with updates being carried out by the TAIR team until August 2013.

### Management

An inaugural scientific advisory board (SAB) was appointed in February 2012 following nominations and suggestions from the community. The SAB consists of

the following members: Gloria Coruzzi (New York University, USA), Kazuki Saito (RIKEN, Japan), Magnus Nordborg (GMI, Austria), Mark Estelle (UC San Diego, USA), Mark Forster (Syngenta, UK), Paul Kersey (EBI, UK), and Xuemei Chen (UC Riverside, USA). The SAB membership covers a wide range of expertise including long standing Arabidopsis community members, plant biology researchers and computational scientists.

The SAB will actively oversee the IAIC and its activities and will be of critical importance to ensure the IAIC's long-term success.

### References

1. **International Arabidopsis Informatics Consortium**. (2010). An international bioinformatics infrastructure to underpin the Arabidopsis community. *Plant Cell* 22, 2530-2536.
2. **International Arabidopsis Informatics Consortium** (2012). Taking the next step: Building an Arabidopsis Information Portal. *Plant Cell*. Manuscript in press.

## The Gatsby Plant Science Summer School: Inspiring the Next Generation of Plant Science Researchers

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Plant science is crucial to addressing many of the global challenges facing us in the 21st Century. We are in need of new crops, drugs and alternative energy sources, yet plant science is one of the least popular science subjects at school and plant science degree courses struggle to attract applicants.

### How can we encourage university students to study plants?

A paper just published in *The Plant Cell* shows that a single intervention at the start of undergraduate study can have a clear and lasting effect on student attitudes towards plant science and can lead to changes in student practice. Attendance at a week-long, intensive plant science summer school in the first year of undergraduate study changed student attitudes towards plant science, with 92% finding plant science interesting after attendance, compared with 53% before - a view which persisted to graduation. Around 90% stated that the school had made them more positive about plant science. Attendance resulted in nearly a third of students changing modules or final year project to include more plant science and increased the numbers of graduates selecting plant-based PhDs. 44% of summer school alumni progressing to PhD chose plant-related projects, compared with 12% national figures, and 75% of those choosing plant-based PhDs reported that their choice had been positively influenced by the summer school. If this trend continues, we anticipate that the school will contribute around 10 students each year to the pool of plant science PhD researchers. As a comparison, the BBSRC national statistics indicate that an average of



Computer modelling of flower development is used in the developmental genetics practical to gain an insight into the relationship between maths, plant structure and development.

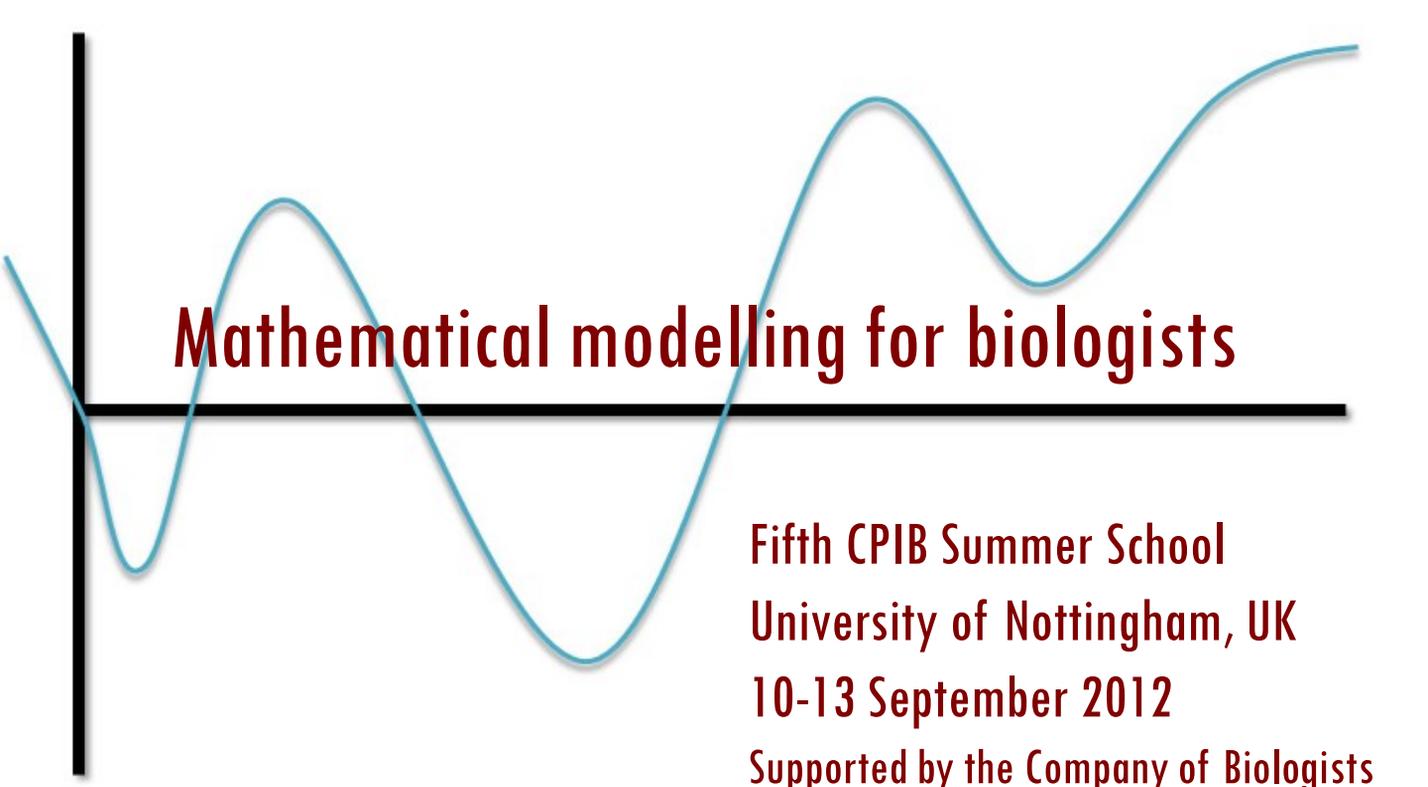
63 new BBSRC plant science PhDs are funded annually in the UK. The evidence, from this 5 year study, shows that the Gatsby Plant Science Summer School has appreciably increased the pool of high-quality plant science related PhD applicants in the UK; has had a positive lasting effect on attitudes towards plant science amongst students entering disparate career paths and has had a positive impact on students' career aspirations (Levesley *et al.*, *the Plant Cell* April 2012, doi: <http://dx.doi.org/10.1105/tpc.111.094326>).

### About the Summer School

Funded by the Gatsby Charitable Foundation, the summer school introduces the excitement and potential of plant science to 80 first-year undergraduates selected from 25 research-intensive UK universities. Initiated in 2005 and run by the University of Leeds, the annual week-long residential school takes place in a relaxed, rural setting. Through practicals and talks from international research leaders, students discover how plant science can help tackle global challenges such as food security, energy needs and climate change. The lecture programme is broad and topical and includes a mix of curiosity-driven and applied research talks. The school has gained an international reputation and attracts high calibre speakers; in 2011, Dr Robert Zeigler, Director of the International Rice Research Institute (IRRI), spoke on the importance of rice to world food security. All lectures are available online via the Plant Science TREE (Tool for Research-Engaged Education <http://www.gatsbyplants.leeds.ac.uk/TREE>).

Tutorials and a Q&A session with the speaker follow the lectures; facilitated by academics from UK universities and research organizations. Students report that these help them build confidence to learn through questioning. Practical classes, run by national experts in their field, introduce students to the excitement of enquiry and to techniques used in current plant science research not normally available to undergraduate students. The careers session gives students the chance to meet and talk to a number of professionals with plant science connections and students value the opportunity to speak with plant scientists during the week. A short video in which students deliver their feedback personally can be seen at: <http://www.gatsbyplants.leeds.ac.uk/SS>

Our findings highlight the importance of exposing students to inspirational ideas from enthusiastic experts and suggest that if plant science is introduced in a sufficiently prominent and engaging way from the first year of an undergraduate programme, then it is possible to change attitudes to plant science among undergraduates and to inspire the 'next generation' of plant science researchers, as well as inspiring future graduates entering disparate careers with a raised awareness of the importance of plant science to society.



# Mathematical modelling for biologists

**Fifth CPIB Summer School**  
**University of Nottingham, UK**  
**10-13 September 2012**  
**Supported by the Company of Biologists**

## Target audience

Open to all - PhD students and postdoctoral researchers with a biological background are particularly encouraged to attend.

## Aims

- To introduce modelling and quantitative approaches to biologists
- To explain where models come from, and how to investigate the behaviour of those models
- To introduce differential equation models, parameter estimation and sensitivity, randomness and spatial models
- To show how to create, simulate and analyse models using appropriate software

## Course structure

Four days integrating lectures and supervised computer-based exercises using biological examples, allowing participants to try out modelling techniques in a friendly, supportive environment.

## Tutors

- Dr Nick Monk (University of Nottingham, UK)
- Dr Markus Owen (University of Nottingham, UK)

## Programme overview

Day 1: Data, Networks and Models

Day 2: Multi-variable models

Day 3: Parameter estimation & sensitivity; Stochastic models

Day 4: Multicellular modelling

## Feedback from previous Summer Schools

"Excellent course, has been very useful and stimulated ideas for applying modelling to our research"

"I feel I could communicate better with mathematicians now ... I wouldn't have known where to start before this course!"

## Fee

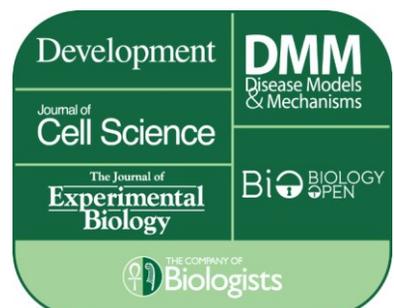
Registration is £100 and covers all tuition, 3 nights' accommodation in Halls of Residence and all meals.

## Deadline and applying:

Places are limited to 40. We will review applications as they come in and offer places, until all places are full. For further info on selection criteria and to apply visit:

<http://www.cpiib.ac.uk/events/cpiib-summer-school>

Contact: [susie@cpiib.ac.uk](mailto:susie@cpiib.ac.uk)



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 Aberystwyth University.

### Spotlight on the Aberystwyth University



The Institute of Biological, Environmental and Rural Sciences (IBERS) is the largest department of Aberystwyth University, with about 300 research, teaching and support staff, and conducts research at scales ranging from the molecular through to the landscape. The main activities directly or indirectly concern land use, but also include the aquatic environment, reflecting the University's location on the west coast of Wales. The core aim of the Institute is to support activities that minimise the negative environmental impact of human activity by delivering international quality science, by translating this science into applications that are being commercialized through spin out companies and partnerships with commercial organizations, and by engaging with consumer groups and policy makers. The research is organized into 3 themes, Genome Diversity, Environmental Impact and Animal & Microbial Sciences, spanning from primary biomass producers to converters and their respective commensals and parasites. The Genetic Diversity theme maintains IBERS' longstanding and unbroken reputation in public-good plant breeding while the Animal & Microbial Sciences theme contains research groups studying the herbivores that utilize those plants. The Environmental Impact theme includes internationally leading programs in biofuels and novel crops. Recent investments have been targeted at novel phenotyping and DNA sequencing technologies coupled with associated bioinformatics and high performance computing. These are grounded in programmes aimed at improving the rural economy both locally and internationally and promote interactions with academics elsewhere in the University, especially in Computation Sciences, as well as further afield and with companies both locally and nationally. In this synopsis of IBERS' activities we have restricted ourselves to plant specific projects.

For further details see: <http://www.aber.ac.uk/en/ibers/>

IBERS has a strong commitment to training, with about 1200 undergraduates, 50 MSc students and more than 60 PhD students. IBERS is unique within the university in offering vocational foundation degrees, as well as a wide portfolio of pure and applied biological and rural science honours degrees. Aberystwyth University has been consistently ranked as one of the top places to study in the UK. This reputation is built on the professional and friendly nature of the teaching staff and the relaxed ambiance of the town itself does much to contribute to student experience.

As well as under and post-graduate training, the department welcomes visitors from across the world and has active links with international plant breeding organizations and a wide range of overseas Universities. Visiting researchers are very welcome and fellowship applications are encouraged.

### Environmental Impact Theme

The Environmental Impact Theme, headed by Iain Donnison, is one of three cross-cutting research and teaching groupings in IBERS. The theme comprises five research groups: Energy Crop Biology, Energy Crop Breeding & Modelling, Ecology, Abiotic Stress & Nutrient Use, and Bioconversion & Biorefining. The aims of the theme are: 1) to provide practical solutions for the mitigation of climate change including the development of high yielding dedicated energy crops adapted to current and future environments and conversion technologies; 2) to understand ecosystems and the consequences of land use change; and 3) to understand the impacts of environmental change on plants including developing a mechanistic understanding of plant stress tolerance focusing on signalling mechanisms. The Environmental Impact Theme is therefore engaged in research, which is tackling major global challenges including food, water and energy securities, and climate change. Staff are also involved in teaching, research, and working with industry, to ensure that the research is translated into products and processes, to deliver environmental, economic, and wider societal benefits.



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### Bioenergy and biorefining

Iain's research spans the bioenergy pipeline from feedstock biology through to conversion to end products and the environmental sustainability of land use change. The primary focus is on temperate and tropical grasses as feedstocks and their optimisation and utilisation for energy and other products. The research is therefore

## Spotlight on Aberystwyth University

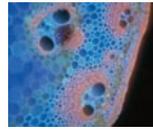
focused on tackling the global challenges of energy security and climate change. This includes developing *Miscanthus* genetic resources for the dissection of performance and quality traits in the BBSRC funded institute strategic programme on Energy Grasses & Biorefining. In the BBSRC Sustainable Bioenergy Centre (BSBEC) grant on perennial bioenergy crops, Iain and colleagues are working with Rothamsted Research, Imperial College and Cambridge University on the determination of crop growth parameters for process modelling. This involves the detailed measurement of multiple *Miscanthus* and willow genotypes in comparable trials in Aberystwyth and Harpenden. Information from this work is being used to help define energy crop ideotypes. In the EU Life+ project PROGRASS, Iain is working with collaborators in Germany and Estonia on using bioenergy as a land management tool in upland grasslands to provide a broad range of ecosystem services including biodiversity. In the NERC funded Carbo-BioCrop and Energy Technologies Institute funded ELUM projects, Iain and colleagues are working on soil C and GHG fluxes during land use change with a number of collaborators including CEH, Rothamsted research, Forest Research and Universities of Aberdeen, Southampton and Edinburgh. In the Welsh Government funded BEACON Biorefining Centre the group are working at lab and pilot scales, with collaborators at Bangor and Swansea Universities to process and convert a broad range of feedstocks into a range of higher value chemicals and products.



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### Cell wall biochemistry

Gordon's research focuses on how the composition of the cell wall affects the conversion of grass biomass crops to heat, power, chemicals and liquid with particular focus on *Miscanthus*. This work underpins energy grass breeding, the discovery and functional assessment of energy grass cell wall genes and the establishment of cell wall QTLs in *Miscanthus* mapping families. His work relies on classic and advanced analytical and gravimetric procedures to measure the concentrations of lignin, structural carbohydrates and cell wall bound hydroxycinnamic acids. Gordon's research makes particular use of vibrational spectrometry (mid and near infrared spectrometry) to allow the prediction and analysis of compositional parameters by chemometric methodologies. Furthermore, Raman microscopy is being used to image chemical composition in sectioned samples at the resolution of the cell.



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### Cell wall biology in energy grasses

Maurice's research focuses on increasing our understanding of the dynamic changes in cell wall composition and architecture during growth and development of grasses, and how these changes are regulated. The sugar components contained in cell wall polysaccharides can be used for the production of liquid biofuels as well as for biorefining to produce a range of bio-materials. However, a major bottleneck in making these processes efficient is that plant cell walls have evolved to resist microbial and enzymatic deconstruction - a factor collectively known as "biomass recalcitrance". A better understanding of the organization, abundance and molecular underpinnings of cell wall components is required before we can rationally breed and design commercially viable bioenergy crops. Using a differential expression profiling approach between elongating and non-elongating maize internodes Maurice's lab has previously identified candidate genes involved in cell wall biogenesis. One of the current research projects is to functionally characterize several transcription factors identified as potential cell wall regulators. Maize and *Brachypodium* plants in which these regulatory elements are over-expressed are currently being analyzed. Other research projects include the analysis of the cell wall polysaccharides (glycome) of a diverse set of *Miscanthus* genotypes with the aim to establish how different glycome characteristics link to the saccharification of the cell wall biomass. Apart from representing a source of energy, plant cell walls are important in defence responses to biotic and abiotic stresses. For instance, the plant cell wall plays an important role in conferring drought tolerance as this involves restructuring of the cell wall to allow growth in water limiting conditions. Maurice's lab is involved in a project which correlates changes in cell wall chemistry and gene expression with drought tolerance by exploiting variation in the model grass *Brachypodium distachyon*.

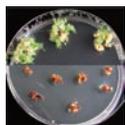
## Spotlight on Aberystwyth University



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### Miscanthus breeding

John Clifton-Brown was recruited to lead the Miscanthus breeding programme in August 2004. His background up to then was in plant ecophysiology (incorporating agronomy and quantification of greenhouse gas fluxes). Since 2004, he has led numerous germplasm collection trips in Asia, which have resulted in one of the largest Miscanthus collections outside of Asia. He combines ecophysiological approaches to phenotyping with traditional and state of the art breeding tools. A recently awarded LINK funding combines the efforts of the public and private breeding programmes into one large integrated programme for the next four years.



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### In vitro culture and genetic manipulation of grasses and cereals

Sue focuses on the development of genetic manipulation and other applications of *in vitro* culture to species of *Lolium*, *Festuca*, *Agrostis*, *Poa*, *Brachypodium*, *Miscanthus*, *Avena* and maize. Manipulated genes include those involved in cell wall composition and lignification, polysaccharide accumulation, protein decomposition, senescence and apomixis as well as the continuous evaluation of new marker genes and promoters. Other techniques available include *in vitro* virus elimination, plant storage and micro-propagation, the production of cell cultures and protoplasts, polyploidisation and the recovery of di-haploid plants through anther culture.



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### Energy Crop Biology

Research in the Farrar lab focuses on understanding the processes that regulate energy crop growth and development in order to replace fossil fuel usage, seques-

ter atmospheric carbon, and ultimately contribute to climate change mitigation.

### Biomass yield and carbon reduction potential

Increasing biomass & energy yield per hectare increases land use efficiency, allowing more bioenergy to be generated for any given area. This increases the potential to replace fossil fuel usage as well as increasing stocks of soil carbon. Understanding of the genetic control of biomass performance traits is required in order to accelerate breeding efforts. Trait phenotyping of diverse genotypes identifies individuals and traits for targeted breeding and the data required for predictive modelling. A combination of genetic mapping, transcriptomics and association studies are being deployed to develop trait-associated markers for use within the breeding programme at IBERS.

### Bacterial endophytes in Miscanthus

Endophytes are microorganisms capable of establishing within a plant without causing disease. They are considered to be endemic within Gramineous plants and are frequently linked to plant benefits such as nitrogen fixation and salinity tolerance as well as pathogen suppression. The majority of bacterial endophytes are recalcitrant to culture, and so the most reliable way to characterise endophytes is to employ a molecular approach using the 16S rRNA gene to identify the bacteria present in a plant tissue. Our aims are to determine 1) the diversity of endophytes within *Miscanthus* plants, and 2) whether an endophyte population confers any advantage to the *Miscanthus* host.



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### Carbohydrate metabolism and plants as feedstocks for biorefining

Dr. Gallagher's research area is concerned with improving plant feedstocks and optimising conversion to a range of products including bulk chemicals and biofuels. The main focus is on understanding the genetic components that affect saccharification and fermentation quality and makes use of the institute's extensive germplasm collections of grasses, including *Miscanthus*, to investigate how changes in chemical composition resulting from feedstock breeding programmes affect down-stream applications. An area of particular interest is in understanding/dissecting the 'high sugar' trait in forage grasses which is important for both animal feed and biorefining. This involves understanding the

## Spotlight on Aberystwyth University

genetic control of fructan metabolism. QTL and underlying genes for this trait have been identified. Dr Gallagher heads the Bioconversion and Biorefining Group, working on the breakdown of complex carbohydrates and the production of both fine and bulk chemicals through the use of recombinant enzymes and through genetic manipulation of fermenting micro-organisms. Projects within the group include: Transcriptome analysis to determine the genetic basis of the high sugar trait in ryegrass; Determining regulatory networks controlling yield and conversion efficiencies in biorefining feedstocks; Conversion of high sugar grasses to alcohol based transport fuel; Succinic esters from renewable feedstocks; Biomass processing for high-value products including bioactives; Carbohydrates for the production of novel biosurfactants and polymers as part of a ryegrass biorefinery; Metagenomic libraries from extreme environments for novel biorefining enzymes and Metabolic engineering of microbes for lactate and succinate production.



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### The design of forage grasses to combat climate change, for crop sustainability, and for environmental service

In combination more than 500 fescue (*Festuca*) species are adapted to temperate grasslands world-wide. Generally these are more persistent, stress-tolerant, water and nutrient-use efficient, and have more extensive root systems than closely-related ryegrass (*Lolium*) species, the forage considered ideal for livestock agriculture. Many fescue species hybridise naturally with ryegrass and genotype combinations have been designed that are fertile and exchange genes at very high frequency. The outcome is *Festulolium*, which shares complementary characters of both, providing forage grass that is productive, resilient to climate change, and sustainable. Through interspecific genome interactions, grass genotypes may be constructed that enhance trait expression beyond the potential of the parent. The outcomes include large, fast-growing, extensive, and strong root systems capable of plant-soil interactions for improved soil hydrology and C sequestration.

Fescue species provide important insights into the evolution of adaptations to diverse stresses. They are members of the Pooideae which includes many other major agricultural crops each having evolved from a common ancestor retaining extensive genome synteny. Understanding thereby gained in trait genetics in the *Lolium*-

*Festuca* complex may benefit many other crop species with access to less extensive genome variation.

Alternative breeding approaches are being developed for *Festulolium*, either combining and stabilising entire genomes through amphiploidy, or through a targeted gene introgression approach involving transfers of novel gene variants from fescue into ryegrass. Research combines discovery science for genotypes essential for a predictable phenotype, through to the translation of this into crop improvement programmes and knowledge transfer for commercial development.



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### Energy crop biology

Elaine's enthusiasm for plant biology is rooted (pardon the pun) in a passion for sustainable living and a desire to contribute to it. For her BSc dissertation at Aberystwyth Elaine studied the genetic dialogue between the model legume *Lotus japonicus* and its rhizobial symbiont, *Mesorhizobium loti*, and was able to continue this research focus into her PhD. Within the Energy Crop Biology group Elaine has worked on a BBSRC responsive-mode grant investigating the impact of flowering time on quality aspects of *Miscanthus* biomass, and researched the role of photoperiod and temperature on flowering time control in *Miscanthus*. The first high-resolution genetic map for *Miscanthus* has just been published as a result of this project which has been carried out in collaboration with Ceres Inc. The group are now in the process of mapping qualitative trait loci for flowering time using this map. Elaine's research areas have now expanded into BEACON (<http://beaconwales.org/en/team/view/elaine-jensen>), in which she is exploring the contribution that *Miscanthus* can make in providing alternatives for products currently derived from fossil fuels. Elaine will also be assessing variation in the chemical composition of *Miscanthus* and aims to map chemical and structural traits that are an important source of high value products.

## Spotlight on Aberystwyth University



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### Plant and community responses to environmental changes

Dylan's research focuses on global change biology investigating plants and communities, understanding trophic interactions including decomposition, plant-soil interactions, and herbivore-plant interactions in response to environmental changes (N deposition, elevated CO<sub>2</sub>, enhanced UV-B and variations in temperature/drought). Stress responses are quantified at the plant and landscape level based on metabolite, physiological and morphological characteristics.

At the ecosystem level the group also quantify carbon sequestration with an emphasis on how plants, communities and soil system will assimilate future elevated atmospheric CO<sub>2</sub>. This research is based around experiments spanning over two decades in the Swedish sub-arctic and runs alongside complementary experiments investigating the long-term impacts of UV-B radiation on terrestrial systems. Research output from this work is directly fed through to UNEP assessments on ozone depletion impacts.



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### Green chemistry

Society is demanding more and novel "green" chemicals from sustainable sources to be exploited in a range of biotechnological, agricultural and clinical contexts. Identification of commercially important chemicals in crops can help to increase value in a biorefining process.

Ifat leads a team of chemists that play a key role in the BEACON programme, which develops products and processes to turn non-food crops into high value chemicals and commercial products including cosmetics, pharmaceuticals, food and health products. This involves scaling up processes for the recovery and purification of bioactive and secondary compounds from biorefining systems. This will maximise outputs from sustainable feedstock inputs to increase cost effectiveness and, through the identification of novel compounds, add value. Compounds of particular interest include phenols, waxes and carbohydrates.

Another key objective of the research is to use synthetic chemistry to develop new products from renewable sources. This involves identifying mechanisms to enhance their recovery and transformation into other industrially useful molecules. This will reduce the reliance on crude oil as a chemical feedstock.

Ifat's interests extend to the analysis of cell wall composition, an important trait in bioenergy crops. Part of his research involves analysis of the intact plant cell wall, focusing on diferulates, which are involved in cross-linking and influence a range of properties including digestibility. Recently, he has been involved in synthesis of BSA-linked cell wall diferulates for antibody imaging studies.

UK Collaboration - Professor Michael D. Threadgill (Head of Medicinal Chemistry, Department of Pharmacy and Pharmacology, University of Bath) - Identification of secondary metabolites from plant feedstocks.

International Collaboration - Professor John Ralph (Department of Biochemistry, Enzyme Institute, University of Wisconsin, Madison) - Cell wall analysis of bioenergy crops.



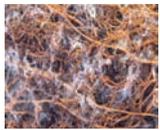
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### Sustainable improvements in energy crop yield and crop quality and the application of genomics and phenomics studies to improving energy crops

Resource capture and utilisation is a focus of Paul's research into yield improvement in energy crops at Aberystwyth. For example to improve light capture; canopy duration, canopy structure and photosynthetic activity are being studied in natural and mapping populations to identify correlations with yield and the underlying genetic determinants of yield. Variations in root structure and leaf traits are being studied to optimise water use efficiency and drought tolerance. Sustainable energy crop production requires that crops are grown with minimal inputs such as fertiliser and variation in senescence is being used to optimise nutrient flux within the Miscanthus crop. Senescence impacts on many plant processes, for example senescence determines leaf area duration which affects light capture and drought tolerance. The research has shown that senescence in Miscanthus affects crop quality and thermochemical conversion. The impact of different environmental factors is being related to trait develop-

## Spotlight on Aberystwyth University

ent toward establishing a bioenergy crop ideotype and to inform choices in the *Miscanthus* breeding programme at IBERS. Seed propagation is a high impact trait; currently mostly rhizome propagation is used in establishing *Miscanthus* crops which is expensive and slow. Useful variation in seed germination has been identified and is being developed in an industrial partnership. Research is also developing novel phenotyping methodologies such as laser scanning of field crops and utilising phenomics analysis to provide improved high-throughput quantification of traits of interest.



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#### Soil processes and ecology, including interactions with plant litter/roots

Several projects are currently underway which relate to plant-soil interactions. The effects of plant litters of varying quality on earthworms and earthworm mediated processes are being investigated. This work includes investigations on elevated CO<sub>2</sub> impacts on litter quality and belowground responses to this and other climate change factors. In a related study, the interacting effects of elevated CO<sub>2</sub> and UV-B radiation on rooting characteristics, rhizosphere processes and resulting nutrient acquisition have been investigated. Another research project, relating to carbon sequestration in soils disturbed by mining activities, is focussed on the impact of different vegetation systems on the potential for carbon accumulation and the stability of these carbon stocks when the ecosystems are perturbed. Further work will be undertaken on the effects of bioenergy crops and novel grasses on soil carbon stocks and the dynamics of these stocks.



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#### Statistical genomics

Dr. Slavov is interested in both fundamental and applied population genetics and genomics. His basic research is aimed at gaining greater understanding of the forces and processes that shape patterns of genetic variation within and among populations. More specifically, he has

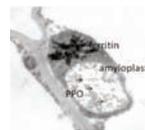
worked on 1) assessing the population genetic structure of forest tree species in the context of their life history characteristics, 2) developing molecular markers and analytical methods of direct quantification and modelling of pollen-mediated gene flow, and more recently 3) elucidating the molecular underpinnings of phenotypic traits using association mapping and characterising genomewide patterns of nucleotide diversity, recombination, and linkage disequilibrium. At the same time, all major research projects Dr. Slavov has been involved in have had a strong emphasis on technology transfer and serving the needs of breeding and conservation programmes.



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#### Ecological genetics and environmental impacts of agriculture

John Warren is a plant ecologist; with research interests in the origin and maintenance of diversity and enhancement of conservation value, particularly within agricultural ecosystems. Approaches used include the modelling of theoretical / evolutionary aspects of botanical diversity to field based studies of the importance of management for vegetation dynamics. Particular interests lie within ecological genetics, gene-flow and the interactions between breeding systems and niche.



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#### Legumes and symbiotic interactions

Judith's research primarily relates to understanding genetic interactions and physiological processes occurring between legumes and their symbionts. Currently these studies focus on the beneficial symbiotic rhizobium bacteria. Rhizobium fixes atmospheric nitrogen in the root nodules of legumes, such as clovers, and is a key component of low input farming systems. Her research centres on the role of polyphenol oxidase (PPO) in red clover during nodule development and in photosynthesis. PPO is found in most species but its function remains unclear. A combination of a range of unique pla-

## Spotlight on Aberystwyth University

nts including mutants and genetic transformants with altered PPO expression and phenotype and molecular, biochemical and microscopic approaches offer powerful tools in elucidating the physiological role of PPO.



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### Feedstocks for the bio-economy

Ana Winters is a senior research scientist with knowledge and experience in a wide range of fields covering plant molecular biology and biochemistry concerned with forage for ruminants and more recently with feedstocks for biofuels and biorefining. She has carried out studies on gene expression and identification of genes associated with carbohydrate accumulation in forage grasses. She has published extensively on the role of polyphenol oxidase (PPO) activity in ruminant nutrition. Her current research is focussed on postharvest stabilisation of biomass and bioconversion to biofuels and other high value biofuels. Other areas of interest include the effects of naturally occurring sugar analogues on carbohydrate hydrolytic enzyme activity and the application of natural products for protein stabilisation.



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### Drought tolerance and nutrient use efficiency

The focus of Dr Yadav's research is to apply molecular markers in traits dissection and breeding leading to development of improved cultivars providing sustainable production and benefits to environments (including increased adaptations to, and mitigations of, climate change). In particular, he has strong research interests in the areas of drought tolerance and nutrient use efficiency and has extensively used genetic maps, markers and genomics technologies in dissecting complex traits contributing to crops yield under drought and nutrient deficient stress conditions. In collaboration with scientists at ICRISAT, his work has resulted in the identification, validation and breeding of a major QTL contributing to yield of pearl millet under terminal drought stress conditions. He is currently leading an interdisciplinary team

of researchers from IBERS, ICRISAT, India and Ghana for fine mapping and characterization of this important QTL and develop gene-based markers for its efficient selection and breeding into the wider gene pool of pearl millet adapted to agro-climatic conditions of India and Sub Saharan Africa.

### Genome Diversity Theme

This theme is concerned with how the variety of forms of plants and animals is controlled. Research interests range from fundamental curiosity to practical outcomes. This theme is organised into five research groups:

The Aquatic, Behavioural and Evolutionary Biology Group undertakes multidisciplinary studies of ecology and evolution in wild species.  
<http://www.aber.ac.uk/en/ibers/research/research-groups/abeb-new/>

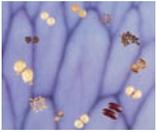
The Plant Genome and Chromosome Biology Group undertakes research into the biology of grasses, cereals and legumes principally by applying genomic, cytogenetic and bioinformatic analyses for the generation and analysis of novel crop plant phenotypes.  
<http://www.aber.ac.uk/en/ibers/research/research-groups/plant-genome-and-chromosome-biology/>

The Legume Biology Group seeks to exploit the close phylogenetic relationship of our target species for comparative genetics and genomics in order to understand the biology of UK legume crops.  
[http://www.aber.ac.uk/en/ibers/research/research-groups/legume\\_biology/](http://www.aber.ac.uk/en/ibers/research/research-groups/legume_biology/)  
<http://users.aber.ac.uk/noe2/lgp/index.htm>

The Breeding Methodologies Group is developing molecular and statistical approaches to the analysis of plant populations especially in alliance with our breeding programmes.  
<http://www.aber.ac.uk/en/ibers/research/gdgb/breeding-methodologies/>

The Public Good Plant Breeding Group applies our science to support multifunctional land-use and mitigate negative environmental impact of agricultural systems.  
<http://www.aber.ac.uk/en/ibers/research/research-groups/public-good-plant-breeding/>

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### Pea genetics and genomics

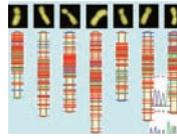
Noel's research is into the organisation of the pea genome, including the pattern of genomic diversity in the genus, the organisation of repetitive DNA in this 5Gbp genome and the relationship of its genetic map to sequenced genomes of close relatives. This programme has built the tools and resources for the isolation and characterisation of pea genes identified by their mutant phenotype.



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### Developing partnerships for international agricultural development

IBERS is developing a strong focus on partnerships for agricultural development particularly in Sub-Saharan Africa (SSA) but also Brazil, India and other countries. This is based on maximising the impact of our skills, resources and expertise in the context of sustainable consortia with partners who can bring their own capabilities to deliver to a range of stakeholders. IBERS has significant strengths in plant breeding, animal science (and the linking of these to develop more efficient grassland systems and ruminant production) and bioenergy and biorefining. The group are already deploying these strengths in the context of agricultural development e.g. pearl millet improvement for India and SSA. However a more strategic approach is developing strong alliances with key partners such as Africa Harvest and the Kenyan Agricultural Research Institute (KARI). This has led to the development of plans for a pasture breeding programme for Kenya to include both dairy production and semi-arid areas and BBSRC funding for a workshop to be held in Kenya focusing on the future of sorghum as a major crop for Eastern and southern Africa. Research, staff exchange, capacity building and training are all key elements and there are strong synergies with the developing postgraduate portfolio including the new MSc in Food and Water Security.



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### Genetics and genomics of perennial ryegrass (*Lolium perenne*), forage legumes (*Trifolium spp.*) and oats (*Avena sativa*).

Perennial ryegrass is the most important forage grass within the UK and is a major component of many amenity grass mixtures. The ryegrass research at IBERS focuses on developing an understanding of the genetics and genomics of ryegrass with a view to determining biological mechanisms which underpin key traits. This involves defining a reference genome ryegrass assembly using a combination of next-generation sequencing and physical mapping; analysis of biparental and association genetics mapping populations for comparative genetics and to dissect the genetic control of key traits; working closely with ryegrass breeders to implement genomic selection protocols for relevant breeding lines; investigating factors that influence meiotic recombination and self-incompatibility; and exploiting *Lolium/Festuca* introgression populations to broaden the germplasm resources for ryegrass and to gain a greater understanding of processes associated with wide hybridisation.

In addition to ryegrasses and related species, parallel research programmes focus on hexaploid cereal oats and the forage legumes white clover and red clover, the latter two of which are grown as companion crops to ryegrasses in mixed swards. As with ryegrass, the major research focus in these crops is on developing genetic and genomic platforms for understanding the control of key traits and delivering improved germplasm tools and resources to plant breeders. Additionally, as both oats and white clover are polyploids, there is also an interest in exploiting diploid models to further our understanding of both the genome structures and the biological consequences of polyploidy in crop plants.

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### Plant interactions in grass/legume mixtures

Rosemary's research focuses on species dynamics, biomass production, forage nutritive properties and the ecosystem services provided by multispecies grass/legume mixtures. Rosemary plays an active role in the EU FP7 project 'Multisward' ([www.multisward.eu](http://www.multisward.eu)), including involvement in a multi-site experiment seeking to establish whether complex mixtures can capitalise on species diversity effects to give productive grazing pastures (picture shows grazed plots in IBERS).



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### Plant bionformatics

Narcis' research interests relate to a number of areas within Bioinformatics and more relevant in Structural Bioinformatics. He has a long-standing interest in protein structure prediction and structure-to-function relationship, the study of biomolecular interactions, modelling of protein complexes in genome-wide interactomes, modulation of protein-protein interactions and structure-based protein design. Narcis is also researching in computational modelling and design of peptides for the modulation of protein interactions as potential therapeutic agents or diagnostic tools. In the area of Plant Bioinformatics, he is developing bioinformatics-based approaches to complement, guide, and improve plant-breeding programmes and also bioinformatics-driven approaches to understand the underlying biological mechanisms linked to the response to abiotic stresses. Narcis is also interested in the modelling of genetic variation, e.g. SNPs, and the assessment of functional impact at protein level.

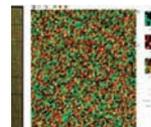


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### Fungal ecology and plant-microbe interactions

Gareth Griffith heads the Fungal Ecology group whose main interests include in the study of both beneficial and pathogenic plant-microbe interactions. We are particularly interested in grassland ecosystems with projects ranging from the nutritional biology of *Hygrocybe* spp. and other fungi of conservation concern to the taxonomy and physiology of dark septate endophyte fungi. It is evident that this latter group of ascomycetous mycorrhizal fungi play an important role in plant nutrition and their significance has yet to be fully appreciated. Other more applied projects in the lab relate to the ecology of anaerobic rumen fungi and the role of leaf epiphytes in the aerobic spoilage of silage.

The Griffith group has research links with Universities in Brazil and India focusing on 1) witches' broom disease of cacao, or 2) the role of anaerobic fungi in feed digestion by herbivores respectively.



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### The development and application of next-generation sequencing and high-throughput genotyping to plant breeding

Matt Hegarty is a research lecturer in quantitative genetics and heads the Translational Genomics facility attached to the National Plant Phenomics Centre. His remit is to drive the development and use of high-throughput, high density marker technologies to help underpin key scientific research at IBERS. His personal research interests involve the use of these marker systems to try and identify causative polymorphisms underpinning key agricultural and adaptive traits in plants. RAD sequencing (RADseq) is one such technology which he and his group have been working to establish at IBERS. RADseq is a genotyping-by-sequencing approach which generates high coverage of short sequence contigs adjacent to restriction sites, providing a snapshot of diversity across the genome. Because coverage of each contig is high, multiple individuals (up to 96) can be pooled within a single Illumina lane using unique barcoded adaptors. The read mappings can

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then be screened for SNPs or other polymorphisms, enabling genotyping. His team have also used RNAseq analysis to identify SNPs within expressed transcripts, for use in development of custom genotyping assays, such as a custom Illumina Infinium microarray assay for ~4000 SNP markers in *Lolium perenne*.



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### Pea genetics and genomics

Julie's primary interest is in understanding the genetic mechanisms regulating leaf formation. Plants can develop different shapes and sizes of leaf and even specialised organs eg. tendrils or motor organs, depending on their habitat, but most leaves are large, porous surfaces extended into the environment to catch light and exchange gases. Leaf shape affects photosynthesis and transpiration, so it has an impact on the energy efficiency and water economy of crop plants. Leaf shape also contributes to the formation of a microclimate within a crop and this influences disease progression. Leaves can have important roles in physically supporting the plant, for example, semi-leafless genotypes of pea are cultivated in the UK to improve yield instability due to lodging (crop collapse due to wind and rain).



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### Physiological and genetic basis of agronomic traits

Catherine's research is concerned with understanding the physiological and genetic basis of important agronomic traits including yield, nitrogen use efficiency and quality traits in oats and drought tolerance in tropical cereals using genomic techniques. This involves both the development of molecular markers and their use in marker assisted selection in the IBERS oat breeding programme. Wild diploid relatives of cultivated oats are being utilised as a model system, as a source of novel alleles and to understand domestication. Current PhD projects include analysis of the genetic and environmental factors influencing grain quality of oats. Catherine is a project leader of a BBSRC-DEFRA funded Sustainable Arable LINK project entitled "Harnessing

new technologies for sustainable oat production and utilisation" and involved in a Technology Strategy Board project, "Generation of oat varieties with enhanced resistance to crown rust and mildew". Catherine has a keen interest in the development of robust high throughput phenotyping methodologies and their use with plant breeding programmes.



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### Bioinformatics and computational modelling

Lin had over 10 years of research activities in engineering computation, simulation and modeling, and high performance computing experience prior to joining the IGER/IBERS, Aberystwyth University. She has been one of the members of the Biomathematics team and has been a key member of several bioinformatics projects funded by the EU, BBSRC and Defra in temperate forage grasses (*Lolium*) and  $C_4$  energy crop *Miscanthus*. Her recent research activities have been focused on:

Development of bioinformatics solutions platforms to the integration, analysis and visualisation of sequence, high-throughput genotyping and phenotyping datasets for the exploiting of multi-dimension information to underpin gene and allele discovery, comparative genomics and their use in marker-assist selection for breeding programme.

Development of novel decision-making tools for plant breeding.

Application of computational modelling approaches to associate and predict the relationship between phenotype x genotype x environment and the application of novel models for genomics selection.

Currently, Lin is involved in several projects at IBERS on the area of bioinformatics and computational modelling:-

BBSRC Institute Strategic Programme Grant (ISPG) 'Energy Grass and Bio-refinery: WP5 - Integrative bioinformatics platform, data integration and modelling'.

DEFRA Link: Genetic Improvement of the Biomass Crop *Miscanthus* (GIANT).

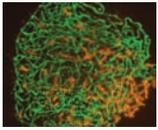
BBSRC ISPG "Crop Genetics, Genomic and Germplasm ": WP4 'Bioinformatics and genomic and phenomic platform development'.

BBSRC Sustainable Bioenergy Centre: BSBEC-BioMASS.

BBSRC *Lolium Perenne* Physical Mapping.

BBSRC CASE PhD studentship project "Computational Modelling of the Relationships between *Miscanthus* Genotype, Environment and Phenotype".

## Spotlight on Aberystwyth University



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## Chromosome genetics

Glyn Jenkins is a molecular cytogeneticist specialising in the genetic control and proteomics of meiosis and recombination in members of the Poaceae, including wheat, barley, ryegrasses, rye and *Brachypodium distachyon*. His particular focus is on forward and reverse genetic approaches to manipulate recombination in cereals and grasses, with the aim of releasing new genetic variation for the optimisation of breeding programmes. He is also engaged in a collaborative program to exploit *B. distachyon* as a model system to understand chromosome and genome evolution, and epigenetic effects on gene expression. He is interested too in the sequence organisation, expression, meiotic behaviour and nuclear disposition of supernumerary B chromosomes, and their potential for use as artificial chromosome vectors in plants.



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## Genetics and genome evolution of oats and relatives

Oats are temperate cereals with very large genomes. They are likely to have been domesticated independently at least four times, and they are typically a crop for poor land with minimal inputs. They have close relatives which are highly invasive or noxious weeds (*A. barbata* and *A. fatua*) but the relationship between these and the cultivated species is still unclear, with continuing uncertainty about the timing and location of domestication events, and the phylogeny of the hexaploid crops. Other genera in the Aveneae tribe also show complex phylogenies and it is likely that introgression and hybridisation have played significant roles in creating the genomes of *Avena* and relatives. Research into these fundamental processes of grass and cereal evolution is being carried out alongside conventional marker development and dissection of agronomic traits in oats. An area of particular interest is the use of mobile elements to detect ancestral hybridisation events during both polyploid and homoploid formation, with *Brachypodium* providing an unexpected model system. Resources being developed include diversity panels, NAM

TILLING populations, and genome sequencing of model diploid *Avena* species.



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## Grass genetics, breeding and commercial variety production

Alan leads the grass breeding programmes at IBERS which concentrate on breeding perennial, Italian and hybrid ryegrasses for agricultural use and perennial ryegrass, in the main, for amenity use. For agriculture, IBERS programmes place a strong emphasis on novel herbage quality and reduced nutrient inputs and aim to combine these traits with significant improvements in total and seasonal yields, disease resistance, stress tolerance, persistence and seed production. The main amenity breeding targets are: shoot density, wear tolerance, leaf fineness, persistence, tolerance of close mowing, slow vertical growth, colour, and disease resistance. The programmes also make increasing use of genetic and genomic approaches coupled with improvements in field phenotyping techniques. The ability and success of the grass breeding team is illustrated by the number of 'Aber' branded varieties which have excelled in the statutory testing systems and have therefore been placed on all the UK Recommended lists (England & Wales, Scotland and N. Ireland) and the Sports Turf Research Institute recommended lists. These varieties are marketed by Germinal Holdings Ltd.



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## Plant breeding and genetics of forage crops and oats

Athole Marshall leads the Public Good Plant Breeding Group at IBERS. His research focuses on the breeding of improved varieties of forage legumes, particularly white and red clover, the most important forage legumes of temperate Europe. Currently his focus is on

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incorporation of traits associated with improved nutrient use efficiency and drought tolerance into varieties with good agronomic background. A key component of this research is exploitation of novel interspecific hybrids within *Trifolium* and development of appropriate phenotyping approaches that can be used within the breeding programme. Athole Marshall also leads the QUOATS project, funded by the Defra Sustainable Arable LINK programme which harnesses new technologies for the genetic improvement of oats for human consumption, animal feed and for industrial applications.



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### Plant responses to biotic and abiotic stress

The Mur group is researching many aspects of plant stress responses and this involves a large number of international collaborations. A particular interest is in elucidating the responses of *Arabidopsis* and tomato to infection by *Botrytis cinerea*. Resistance to *Botrytis* is linked to the ethylene signalling and (with the Trace Gas Research Group Radboud University, The Netherlands) ethylene effects are being: 1) linked to metabolomic changes in the host; 2) shown to interact with other plant signals; and 3) exploited as marker(s) for post-harvest stress.

The Mur group has shown that nitric oxide (NO) regulates defences in cereal responses to pathogens. With Aarhus University, (Denmark), our group is examining the role of nonsymbiotic haemoglobins in regulating NO production and the plant physiology. More widely, the role of N-nutrition in NO is being characterised (with Rostock University; Germany). The group have also been investigating the mechanisms of stomatal immobilisation ("lock-up") seen with resistance in cereals to fungal pathogen. This work has also been supported by a BBSRC-DEFRA-HGCA LINK programme which is assessing the cost of stomatal lock-up in the field.

*Brachypodium distachyon* is an established model grass species and the Mur group has developed and is exploiting a large germplasm collection in a transnational research effort involving genomic and phenomic approaches.

The Mur group has research links with Universities in India and Pakistan, focusing on: 1) field assessments of the responses of tea and Himalayan grown cereals to infection; or 2) the characterisation of medically active natural products.



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### Evolution and domestication of crop plants

Wayne Powell is Director of IBERS and leads the Breeding Methodologies group ([www.aber.ac.uk/en/ibers/research/gdpb/breeding-methodologies](http://www.aber.ac.uk/en/ibers/research/gdpb/breeding-methodologies)) (<http://www.aber.ac.uk/en/ibers/research/gdpb/breeding-methodologies>). Wayne's interests are in the evolution and domestication of crop plants and the utilisation of genetic diversity to underpin next generation plant breeding. Both family-based mapping and genome-wide association studies are being used in *Lolium* species to identify genes involved in the domestication plasticity and ecological adaptation. Recent collaboration with the National Botanic Garden of Wales (Natasha De Vere) has been initiated to study the conservation genetics of endangered plant species.



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### The role of polyploidy and inter-specific hybridisation in the evolution and adaptation of white clover

White clover (*Trifolium repens*) is an integral component of sustainable agricultural systems because of its high nutritional value and the ability of fixing atmospheric nitrogen. Despite its agronomic advantages, it is not grown as widely as it could be, due to its poor persistency. Improving persistency and tolerance to biotic and abiotic stresses has been the main target of breeding efforts at Aberystwyth since 1919.

White clover is relatively wild compared to more domesticated crop species; however, the continuous use of elite cultivars led to impoverished genetic diversity. Dr Ravagnani's research explores the potential of using wild relatives as a route to manipulation of agriculturally important traits. White clover is a tetraploid of most likely allopolyploid origin from two ancestral genomes. *T. occidentale* is generally accepted as the donor of the paternal genome, while *T. nigrescens* and *T. palleescens* are still under debate as the most likely candidates for the maternal donor. These species are currently being used in an inter-specific crossing program with two main aims:

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1) The white clover putative progenitors display contrasting phenotypes for desirable traits, such as drought and cold tolerance or stoloniferous growth habit. Segregating populations are being generated for mapping these key traits.

2) Hybridisation and polyploidisation have dramatic effects on the making of the genome. Studying its mechanisms has implications in evolutionary terms, as well as crop improvement. Beneficial genetic variants arisen from genome fusion and doubling have to be identified and selected promptly before being eliminated through genome stabilisation.



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### Application of genomics technologies to forage crop breeding and genetics

The advent of more affordable high throughput (next generation) sequencing and genotyping in the last five years has made it possible to make use of molecular markers in a more comprehensive way than hitherto in crop genetics and breeding. Current marker technology allow genome-wide association studies (GWAS) to identify candidate genes governing quantitative traits of biological and agronomic importance. Equally important is the opportunity to apply genomic selection (GS) to crop breeding programmes. GS is already beginning to transform the breeding of livestock such as cattle and pigs, but has yet to make an impact at a practical level in crop plants. GS involves the establishment of a training population for which both phenotypic and genome-wide molecular marker data are available. This information is combined to develop predictive models which will enable us to identify selection candidates in test populations based only on their genotype rather than phenotype. If successful, it will have a profound effect on future plant breeding. It will increase the speed of each breeding cycle, and thus significantly improve the genetic gain per unit time and cost. IBERS is the only university department in the UK with plant breeding programmes, and we will use this unique position by exploiting our perennial ryegrass breeding programme for GS. The ryegrass breeding populations will be used as test beds for studying the importance of various factors such as training population size, marker density and prediction models on the predictive accuracy of GS.



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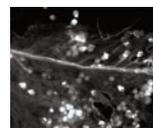
### Plant Genetic Resources

Ian's interests focus on the collection, documentation and management of the IBERS collection of Genetic Resources. This consists of over 25 000 samples of the main temperate forage grass genera important for European agriculture (*Lolium*, *Festuca*, *Dactylis* and *Trifolium*) as well as a variety of species used in amenity, bio-fuel and other research programmes.

The conserved material consists of natural ecotypes collected throughout Europe, breeder's lines, research lines and current and former cultivars as well as accessions donated by Botanical Gardens, universities etc. The material is conserved as seed for the long and medium term in a temperature and humidity controlled environment and is freely available on request.

In addition to documenting our own collections Ian takes an active role in the UK Plant Genetic Resources Group and Ian is also the UK National Inventory Focal Point responsible for the collation of all UK Genetic Resources data and its submission to the European Plant Genetic Resources Information System (Euriscope).

Ian participates in the European Cooperative Programme for Crop Genetic Resources Networks (ECPGR) with responsibility for the European Central Crop Databases for *Lolium* and *Trifolium* (excluding *T. subterraneum*). Ian is also a member of the coordinating groups for the Forages Network and the Documentation and Information Network.



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### Plant breeding

Danny's research focuses on the perennial grass plant *Lolium perenne* as both a perennial outcrossing model and crop. Currently he is leading a mapping approach to identify the genes responsible for the two-locus gametophytic self-incompatibility system common to all grasses with a view to exploiting the system to develop more efficient breeding programmes. Danny has also worked on the single S-locus gametophytic system of *Trifolium repens* and *T. pratense*. Danny is the co-ordinator of a work package in a Marie-Curie ITN program-

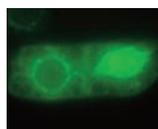
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me investigating the genetic control of leaf lifespan in *Lolium* and barley. He is also interested in developing research areas in the genetic control of grass plant ideotypes for maximising and compartmentalising biomass yield.

### National Plant Phenomics Centre and Computation Sciences Dept

The new NPPC (<http://www.phenomics.org.uk/>) has recently been the subject of an article in GARNet (see Dec 2011 issue) so this section focuses on the people working in the Centre and in closely allied areas within the Computation Sciences Dept intent on developing novel approaches to help close the gap in genotype-phenotype research.

A step-change in plant phenotype measurement is required so that comprehensive “phenomic” information can be recorded rapidly and objectively from large populations and in a format that can be shared. Relevant quantitative information (features) about physical and physiological traits is extracted and integrated with other large ‘omics’ datasets. The NPPC will form a focus for development of multidisciplinary collaborations between computer scientists and biologists with interests in genetics and functional genomics, ecology, genecology, crop improvement, climate change mitigation and adaptation, and global agriculture in an environmental context.



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### Plant growth control

Plant growth underpins the productivity of both natural and agricultural ecosystems. The Doonan group uses both induced (mutants) and natural variation in experimental model systems and wheat to understand how plants grow and respond to their environment. Current research projects include 1) cyclin dependent protein kinase targets and their role in growth and development and 2) understanding the basis of natural variation in crop and model plants. John is also the Director of the National Plant Phenomics Centre, a BBSRC funded National facility that aims to develop high-throughput high-content phenotyping technologies coupled to the exploitation of genomic-type information to accelerate both gene discovery and plant breeding. He also leads

the recently established UK Plant Phenomics Network, which provides a forum for the discussion of issues associated with objective and automated phenotyping.

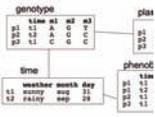


**Anyela Carmargo Rodriguez**  
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### Image analysis and modeling

Anyela’s main interests are understanding the epistatic relationships between genes and how these interactions can affect phenotypes, and on understanding the epigenetic mechanisms that lead via the control of gene expression and protein synthesis to variation in form and function. She develops models that aim at explaining these different levels. Anyela has used these approaches in studies on natural variation and in the analysis of mechanisms underlying plant responses to disease and environmental stresses. At the NPPC, Anyela is using computer vision to compare plant traits in *Arabidopsis thaliana* populations. The techniques developed by working on this plant model will be applied to studies on economically important crops such as oil seed rape and wheat. In addition, she aims to track dynamic aspects of plant architecture under defined environmental conditions and to map variation in these traits against the genome to identify QTLs responsible for simple and complex traits. Explanatory and predictive models for plant architecture, gene-function and their interaction will be developed. To support this, Anyela is responsible for designing a framework that allows the sharing and integration of phenomics data with other information sources. In keeping with worldwide initiatives in this area, a key element is to help create internationally accepted standards in phenomics that facilitate the sharing of knowledge.

## Spotlight on Aberystwyth University



Amanda Clare  
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## Bioinformatics and data mining

Amanda is a lecturer in Bioinformatics in the Department of Computer Science. Her work has previously included developing new data mining techniques to learn more about the functional genomics of Arabidopsis from multi-relational data. The algorithms developed for this earlier work will now form the basis of a recently awarded BBSRC grant to look at data mining for genome wide association studies in Miscanthus. Existing analytical methods tend to underutilise the multiple dependencies and statistical interactions present in GWAS data (e.g. pleiotropy, epistasis, genotype-by-environment interactions).

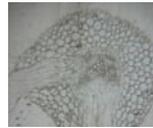
Analysis techniques that can go beyond single-table data (a matrix of individuals and their genotypes, with a corresponding vector of phenotypes as the classes for prediction) are needed. The group aim to make use of the extra relationships present in the data, such as phenotypes and/or genotypes of parents or other relatives of the individuals included in the GWAS population, the confidence of the genotype call, the epigenetic states of genomic regions where markers are located, the proximity and correlation among markers, and information about complex or structured phenotypes measured in multiple environments.



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## Image and video analysis

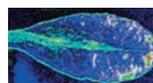
Hannah is a lecturer in the Vision, Graphics and Visualisation group in the Department of Computer Science. Her main interest is time-series analysis of plants using consumer grade cameras (low-cost imaging for shape & growth modeling). She has also been investigating the visual analysis of senescence in images of Miscanthus plants, and, in collaboration with Mark Neal and Paul Robson, laser scanning of field crops for biomass estimation using mobile robots. Her emphasis is on developing techniques which use more than two dimensional imaging modalities – either video (2d+time) or laser (3d + time) – and extracting useful biological information.



John Draper  
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## Enabling technologies

John Draper manages the High Resolution Metabolomics Laboratory and is responsible for oversight and integration of Enabling Technologies within IBERS, including core facilities for Metabolomics, Next Generation Sequencing, Plant Phenomics and Bioinformatics. He has pioneered the development of *Brachypodium distachyon* as a new model system for plant functional genomics. Together with local and international collaborators the group have played a key role in collecting and characterizing *Brachypodium distachyon* germplasm in terms of karyotype, comparative genomics, tissue culture behavior, transformation efficiency and pathogen interactions. The *B. distachyon* 2n = 10 accessions are small, transformable, self compatible annuals. They have a very small genome size (< 250Mbp) which has been sequenced by an international consortium (see [Brachypodium.org](http://Brachypodium.org)). Germplasm collection and characterization continues. Currently he is developing a metabolomics platform for both metabolite identification and high throughput phenotyping in grasses and cereals based on the *Brachypodium* metabolome. A practical application of this research focuses on a study of metabolic reprogramming in *B. distachyon* in response to biotic and abiotic stress. There is a particular emphasis on the validation of an appropriate experimental design to adequately capture and interrogate plant phenomics data. In particular the research uses a range of machine learning methods to quantitatively assess the robustness of phenotype classification and to extract phenotypic variables that discriminate complex attributes.



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## Plant and crop physiologist

Alan's interests include photosynthesis, stomatal responses, senescence, cold hardening, crop modelling and growth measurements. He is currently working on the use of hyperspectral reflectance of leaves as a diagnostic tool in the laboratory and field. This work has been scaled up to analyses of multi-band and hyperspectral data collected from aerial platforms as an aid to environmental, vegetation, crop and forestry monitor-

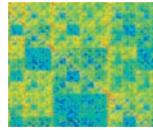
## Spotlight on Aberystwyth University

ing and management. This approach is currently being extended to use Unmanned Aerial Systems as a rapid and flexible means of acquiring these data.

Alan also applies image analyses and interpretation to diverse areas in plant science examples of which are: 1) Determination of necrotic and specifically stained areas of Arabidopsis leaves. 2) Parameterisation of shapes of Arabidopsis rosettes. 3) Analysis of size distributions of oat seeds to quantify distribution of primary and secondary grains. 4) Making quantitative comparisons of particle sizes and viability in vitally stained rumen fluid samples taken from animals fed contrasting grasses.

Because of the central role of image analysis in the emerging science of plant phenomics Alan has also been involved the development of the National Plant Phenomics Centre at Aberystwyth, and has led Aberystwyth's involvement in the European Plant Phenomics Network an European Union Framework 7 project.

Alan's work on stomatal responses concentrates on the disease and host genotype interactions in the Barley mildew pathosystem, work which is currently moving to the field in a LINK programme.



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### Bioinformatics for high-throughput sequencing

Martin's research interests are concerned with data intensive biological applications, with a focus on distributed computing, knowledge discovery and modelling. Most recently he has been concerned with analysing the genomic, transcriptomic and epigenomic data sets generated by next generation sequencing technologies. An on-going concern is with integrating next generation sequencing data with the large volumes of time-dependent images generated by the plant phenomics centre, in order to support data mining applications. Other interests include the development of a post-assembly genome improvement toolkit to obtain annotated genomes (PAGIT), modelling and simulating regulatory and metabolic pathways, and the development of e-Science infrastructure to support these activities.



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### Intelligent robotics

Mark is a senior lecturer in Intelligent Robotics, and specialises in taking intelligent robotics out into the field (or ice sheet). He's currently working on using state of the art laser scanning equipment to model the shape and growth of Miscanthus plants in the field, with a view to moving on to mobile scanning using robots. Models can be constructed of plant height, density and biomass, and machine learning can be applied to automate segmentation (e.g. determining leaf structures from flower heads).

GARNet and Egenis are pleased to present a workshop on

# Making Data Accessible to All

Have you ever had problems accessing data from a paper? Have you ever wondered why some data has to be supplementary and others not? Do you know the correct public database to submit your data to? Should all publicly funded research be open access and freely available to all?

*Organisers: Sabina Leonelli (Egenis), Ruth Bastow (GARNet) and Berris Charnley (Egenis)*

**12 – 13 July 2012**

The focus of this workshop is to discuss issues surrounding data donation, publication and use from the viewpoint of plant biologists, with the aim to produce a series of recommendations about the problems involved in data dissemination in plant science, which could be used to inform funders/publishers' policies.

**The University  
of Exeter**

For more information and **registration** please visit our website:

[www2.warwick.ac.uk/fac/sci/lifesci/news/geworkshop](http://www2.warwick.ac.uk/fac/sci/lifesci/news/geworkshop)

Registration closes  
29<sup>th</sup> June



**Association of Applied Biologists**

**First Announcement and Call for Papers**

# **Crop Genomics and Crop Improvement Conference**

**on 5-6 December 2012**

**at the University of East Anglia, Norwich, UK**

The first sequenced genome of a plant, *Arabidopsis thaliana*, was published c. 12 years (Arabidopsis Genome Initiative, 2000). Since that time, the genome sequences for more than twenty important crops have been completed and these are providing opportunities for both improving our understanding of the history of plant domestication and to accelerate crop improvement. Crop plant genomics is now firmly embedded in the breeding of many crops, improving the precision of breeding and enabling the assembly of multiple traits in new elite breeding lines and varieties. These advances will take plant breeding and trait analysis to a new level of accuracy and productivity that will be needed to meet the major challenges of increased food production in the coming years.

This conference seeks to bring together research in these areas and also focus on the application of markers for genetic improvement of our important crops through molecular marker assisted selection. The conference will focus on the basic and applied aspects of plant genomics, current developments in genome sequencing of our major crop plants in the UK and role of molecular breeding in crop improvement, including marker assisted trait introgression.

Themes for this conference will include:

- Genomics-assisted crop improvement.
  - Genotyping technologies in plant breeding.
  - Molecular marker-assisted breeding for resistance to pathogens, stress tolerance and nutritional quality.
- Bioinformatics: importance and application to genomic approaches to crop improvement.

Presentations and posters from this Conference will be produced together in a volume of the *Aspects of Applied Biology* series (4-8 pages per paper). Further details can be found at our web site: [www.aab.org.uk](http://www.aab.org.uk)

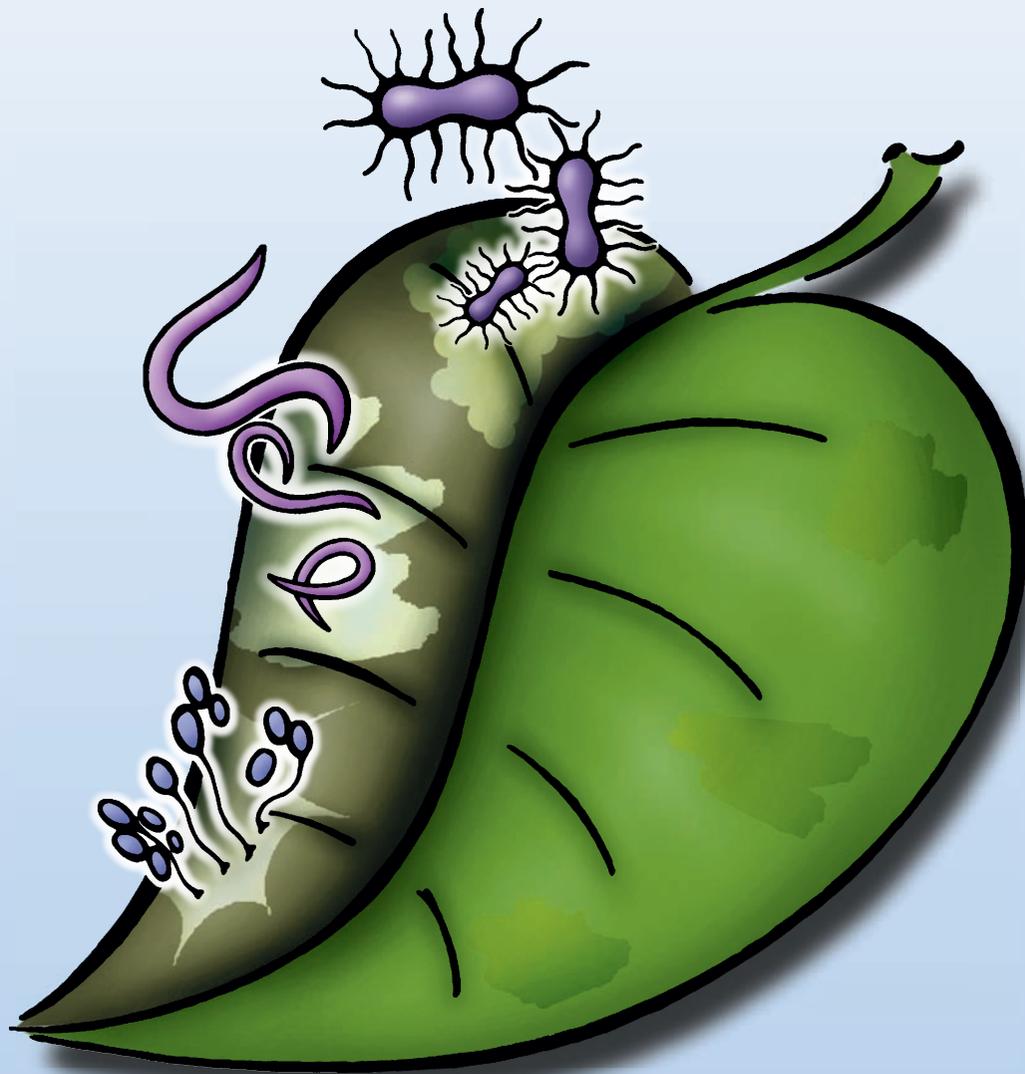
**DEADLINE FOR CALL FOR PAPERS IS 22 JULY 2012**

Association of Applied Biologists, Warwick Enterprise Park, Wellesbourne, Warwick CV35 9EF, UK. Tel: +44 2476 574998; Email: [carol@aab.org.uk](mailto:carol@aab.org.uk)

30th New Phytologist Symposium

# Immunomodulation by plant-associated organisms

Fallen Leaf Lake, California, USA, 16–19 September 2012



## Keynote Speaker

**Jorge Galán** Yale University, CT, USA

## Confirmed Speakers

**Mark Banfield** John Innes Centre, Norwich, UK  
**Adam Bogdanove** Iowa State University, USA  
**Gitta Coaker** UC Davis, CA, USA  
**Jeff Dangl** University of North Carolina, Chapel Hill, USA  
**Peter Dodds** CSIRO Plant Industry, Canberra, Australia  
**Sébastien Duplessis** INRA, Nancy, France  
**David Guttman** University of Toronto, Ontario, Canada  
**Sheng Yang He** Michigan State University, MI, USA  
**Saskia Hogenhout** John Innes Centre, Norwich, UK  
**Jonathan Jones** The Sainsbury Laboratory, Norwich  
**Regine Kahmann** Max Planck Institute, Germany  
**Sophien Kamoun** The Sainsbury Laboratory, Norwich, UK  
**Bostjan Kobe** The University of Queensland, Australia  
**Francis Martin** INRA, Nancy, France  
**Greg Martin** Cornell University, NY, USA  
**Melissa Mitchum** University of Missouri-Columbia, USA  
**Mary Beth Mudgett** Stanford University, CA, USA  
**Natalia Requena** University of Tübingen, Germany  
**Ken Shirasu** RIKEN Plant Science Center, Japan  
**Brian Staskawicz** University of California, Berkeley, USA  
**Nick Talbot** University of Exeter, UK  
**Ryohei Terauchi** Iwate University, Japan  
**Barbara Valent** Kansas State University, USA  
**Pieter van West** University of Aberdeen, UK  
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## New Phytologist Trust

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

Further details and registration at

[www.newphytologist.org](http://www.newphytologist.org)



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