



=====

**FESPB Newsletter**

=====

No. 03.13. December 2013

**PLANT BIOLOGY EUROPE  
FESPB/EPSO 2014 Congress**

**22nd - 26th June 2014, Dublin, Ireland  
Convention Centre Dublin**

**MERRY CHRISTMAS**

 **The Federation  
of European Societies  
of Plant Biology**

 **www.europlantbiology.org**  
contact: [info@europlantbiology.org](mailto:info@europlantbiology.org)

**In this issue:**

- FESPB/EPSO 2014 Congress.....	2
- The GlobalPlant Council.....	3
- Overview	
- Meeting Summary	
- Brief News	
- Research news.....	8
- Forthcoming meetings.....	22
- Positions available.....	25
- Courses .....	25

Editor: Prof. Dolores Rodriguez  
**Chair of Publications Committee**

**FESPB/EPSO 2014 Congress**

=====

# **PLANT BIOLOGY EUROPE FESPB/EPSO 2014 Congress**

**June 22 - June 26, 2014** The Convention Centre, Dublin, Ireland

## **Abstract Submissions Now Open!**

We are now accepting abstracts for the Plant Biology Europe FESPB/EPSO 2014 Congress. Be a part of this exciting event and present your work/research on an international platform, with colleagues from around the globe. [Click here for more information including details on how to submit an abstract, submission categories and deadlines.](#)

## **FESPB Travel Grants**

The Federation of European Societies of Plant Biology (FESPB) offers Travel Grants for graduate students from member countries in Europe to attend the 2014 FESPB/EPSO Congress in Dublin, Ireland. Thirty grants will be available on a competitive basis.

Applicants should be registered at a European University as graduate students (masters or doctorate) in Plant Biology. Their country should be a FESPB member and should have paid the respective fees.

[Click here to find out more information and to download an application form.](#)

## **EPSO Conference Support Grants for the 2014 FESPB/EPSO Conference**

Students from any European country and scientists (junior & senior) from the recent EU Member States and Eastern European countries can apply to EPSO for an EPSO Conference Support Grant. The number of grants will be distributed equally between the two groups. Preference will be given to applicants from EPSO member institutions and personal members.

The EPSO Conference Support Grant covers 4 nights' accommodation in shared rooms (booked by EPSO) and the conference registration fee will be waived. Recipients of a support grant will have to pay their own travel costs. Students must also include a copy of their student card when submitting

the support grant application form.

Students and scientists receiving an EPSO Conference Support Grant are required to submit a poster abstract and encouraged to use social media to communicate about the conference.

The Application form will be available from the 14th November 2013 on at **MailScanner has detected a possible fraud attempt from "europlantbiology.org" claiming to be** [www.epsoweb.org](http://www.epsoweb.org) and <http://europlantbiology.org/>.

### FESPB Awards

The FESPB Awards are the Federation's most prestigious awards. Two FESPB Awards are normally presented at each FESPB Congress to young scientists under the age of 35 chosen from nominations put forward by each of the constituent societies of the FESPB or the applications directly submitted to FESPB. [Click here for more information.](#)

### Exhibition and Sponsorship

The congress invites companies and organisations to participate in this important meeting as sponsors and exhibitors. A range of sponsorship & exhibition opportunities are available. Please email [expo@europlantbiology.org](mailto:expo@europlantbiology.org) for more information.

## The Global Plant Council



### Global Plant Council Overview

#### What is the Global Plant Council (GPC)?

The GPC is a coalition of 25 plant and crop organizations and societies from across the globe. Through its member organizations the GPC represents at least 40,000 researchers spread over 5 continents.

#### GPC PriorityAreas

- Agricultural Productivity and Sustainability
  - GPC Initiative: Capturing Crop Biodiversity – Digital Seed Bank
- Food and Human Health

GPC Initiative: Dealing with Malnutrition – Biofortification

- Adaptation to Climate Change

GPC Initiative: Towards Yield Stability – Stress Resilience

- Data, Knowledge and Resources

Cross-cutting theme throughout all initiatives

### Unique Role of GPC

1. Provide a voice for plant and crop science at the global level that is not possible at the national/regional level. For example, the GPC has the ambition to be consulted by the UN, G8 G20 and FAO on global plant and crop research.

2. Bring plant and crop scientists together at the global level to pool expertise and knowledge in order to define and engage in coordinated strategies that impact the most critical global issues. This will be achieved via GPC Initiatives for Global Challenges.

3. Generate a critical mass for plant and crop science at the global level to undertake activities and generate greater leverage than one organization could achieve on its own. For example, the GPC plans to undertake an economic assessment of the global value of plant and crop science.

### What Does GPC Hope to Achieve?

1. Be an **advocate** for plant science at the global level

2. Act as a **catalyst** to initiate plant-based solutions to global problems

### GPC Advocacy Activities

1. To be consulted by the UN, G8, G20 and FAO on global plant and crop research

2. Organise an economic assessment of the value of plant and crop science

3. Generate policy/advocacy papers to promote awareness of plant science

4. Provide commentary articles for key journals to promote the importance of plant science.

5. Collate and promote success stories in plant science across the globe

### GPC Catalyst Activities

1. Digital Seed Bank and Seed Seq Workshop Jan 2014 San Diego

2. Global Plant Council Forum on Biofortification July 2014 China

3. Global Plant Council Forum on Stress Resilience 2015 in collaboration with SEB

4. Explore the possibility of African Agricultural Workshop with the International Crop Science Society

## Summary Report of the 2013 GPC Annual Meeting October

The 2013 GPC Annual Meeting was graciously hosted by the Howard Hughes Medical Institute (<http://www.hhmi.org>) on October 20–22 2013 at its headquarters in Washington DC, USA.

25 delegates representing 20 GPC member societies and organizations from 16 different countries gathered together to discuss progress during the last year as well as future strategies and initiatives.

Those present at the meeting agreed that the main functions of the GPC are:

1. To be an **advocate** for plant science at the global level

2. Act as a **catalyst** to initiate plant-based solutions to global problems

3. To serve as a **platform** through which national organizations can increase their own visibility, impact and membership.

Through its 25 member organizations and societies the GPC currently represents over 40,000 plant and crop science researchers spread over five continents.

This wide geographical distribution and wealth of experience allows the GPC to fulfil a unique role by:

1. Providing a voice for plant and crop science at the global level that is not possible at the national/regional level.

For example, the GPC has the ambition to be consulted by the UN, G8, G20 and FAO on global plant and crop research.

2. Bringing plant and crop scientists together at the global level to pool expertise and knowledge in order to define and engage in coordinated strategies that impact the most critical global issues. This will be achieved via GPC Initiatives for Global Challenges.

3. Forming a critical mass for plant and crop science at the global level to undertake activities and generate greater leverage than one organization could achieve on its own.

For example, the GPC plans to undertake an economic assessment of the global value of plant and crop science.

## Looking Forward

In the coming years the GPC's central aim will be to define and coordinate research programmes to **provide food and feedstocks for 10 billion people in a sustainable manner.**

To achieve this the GPC has decided on four main priority areas:

### •Agricultural Productivity and Sustainability

To begin with this will be achieved via the **Digital Seed Bank** GPC Initiative, which focuses on capturing and exploiting the wealth of crop biodiversity to find new genes, alleles and genetic networks. These will make our crop plants more resilient to climate change and pathogens while increasing nutrient use efficiency and yield.

### •Food and Human Health

The initial focus in this area will be the **Biofortification** GPC Initiative, which aims to generate plant-based solutions for dealing with malnutrition.

### •Adaptation to Climate Change

Activities in this area will be centred on the **Stress Resilience** GPC Initiative.

This will concentrate on understanding how plants grow, develop and interact with their environments in order to develop crops that can generate a stable yield under fluctuating and unpredictable environmental conditions.

### •Data, Knowledge and Resources

To make informed decisions regarding the most appropriate solutions and approaches to current global problems, it is essential that all stakeholders have access to the most up-to-date evidence and relevant information.

The sharing of data, knowledge and resources will therefore be a common foundation of all GPC initiatives.

## Planned Activities

### Advocate for plant science at the global level

1. Ambition to be consulted by the UN, G8, G20 and FAO on global plant and crop research.

– Initiated contact with FAO Agriculture and Consumer Protection department, planned meeting in Rome.

– Utilise GPC member organizations that are based in G20 countries to become involved in preparatory discussion in advance of G20 Agriculture Ministers meeting in 2014.

GPC will provide a draft letter to be sent to each agriculture ministry and minister via a GPC representative.

2. Organise an economic assessment of the value of plant and crop science.

3. Generate policy/advocacy papers to be utilized by each national/regional organisation, to help promote awareness of plant science and the role it plays in everyone's life.

4. Provide commentary articles for key journals such as Nature and Science to promote the importance of plant science.

5. Collate and promote success stories in plant science across the globe.

6. Promote global scientific prizes for which plant and crop scientists are eligible.

### **Catalyst to initiate plant-based solutions to global problems**

#### 1. Immediate GPC Initiatives for Grand Challenges

These initiatives will bring together expertise from across the globe via the **GPC Forums** to define and engage in coordinated research programmes.

The GPC will focus its efforts on the following three Initiatives:

##### – Capturing Crop Biodiversity – Digital Seed Bank

Initial Workshop to be held in collaboration with the Seed Seq project and the Global Diversity Trust, in San Diego, USA, Jan 2014.

##### – Dealing with Malnutrition – Biofortification

Global Plant Council Forum to be held after the third international conference on plant metabolism in Xiamen, China, July 2014

##### – Towards Yield Stability – Stress Resilience

Potential Global Plant Council Forum in collaboration with the SEB plant section during 2015.

#### 2. Aspirational initiatives

These initiatives will be kick-started by the GPC and driven forward by the community.

Planned topics to include: Perennial Crops, Plant Environment Metagenome, Towards a Green Economy, and Enhancing Crop Diversity

– For each initiative the GPC will request experts from each member organisation/society that is interested in the area and willing to be actively involved, to drive the initiative forward.

– The GPC will facilitate the formation of working groups (at least one lead scientist from each continent) to drive initiatives forward.

– Working groups will organize a meeting of experts in discussion with the GPC executive to kick-start the initiative.

– Continuation of the initiative will be the responsibility of the grouping/community with a request to report back to the annual GPC meeting.

#### 3. New initiatives

Further initiatives from member organizations and individual scientists will be requested each year and considered at the annual GPC meeting.

#### 4. Sustainable African Agricultural Workshop

The feasibility of a potential workshop in collaboration with the International Crop Science Society will be explored during 2014.

### **Increasing Awareness of the GPC**

To provide a strong voice for plant science in the world debate the GPC must establish itself as a prominent network at the global level. To help achieve this the GPC will:

1. Provide a monthly e---bulletin to which all members can contribute information and to which individual scientists can subscribe
2. Provide quarterly updates to all members on GPC activities
3. Request that GPC members organizations and societies promote the GPC at their meetings for example via a poster, a presentation or a booth
4. Utilise online media such as the GPC website and Twitter to reach a wider audience

### **Active Involvement of GPC Members**

The GPC is a coalition of member organizations and societies, each of which represents distinct competencies and knowledge areas that are critical for the mission and operations of the Council. For the future success of the GPC, it is therefore essential that all members are actively involved in GPC activities.

The GPC outlined the following responsibilities of each member organisation/society

- Respect the constitution and bylaws
- Promote the GPC whenever possible, e.g. at annual meetings, organisation/society newsletters
- Distribute the GPC monthly e---bulletin and quarterly reports to all members
- Provide the GPC with relevant information for the GPC website and newsletter
- Provide experts for GPC Initiatives as requested
- Become actively involved in and support GPC activities
- Provide the relevant contact details of society members such as GPC representatives and the financial officer
- Payment of membership fees

### **Brief News from the 2013 Annual Meeting of the Global Plant Council**

The 2013 Global Plant Council (GPC) Annual Meeting was graciously hosted by the Howard Hughes Medical Institute on October 20–22 2013 at its headquarters in Washington DC, USA. 25 delegates representing 20 GPC member societies and organisations from 16 different countries gathered together to discuss progress during the last year as well as future strategies and initiatives.

The GPC will focus its current activities on two main areas. Firstly, it will be an advocate for plant and crop science at the global level with the ambition to be consulted by bodies such as the FAO, G8, G20 and the United Nations, on global problems facing humankind. Secondly, it will act as a catalyst to initiate plant-based solutions to global problems via the GPC Initiatives for Grand Challenges.

The GPC looks forward to working with all its members and other partners during the next 12 months when it will be actively pursuing its Digital Seed Bank initiative. In collaboration with colleagues from the Seed Seq project and the Global Crop Diversity Trust, these activities include a workshop to be

held in January 2014 in San Diego, USA. At this workshop we will discuss the potential of untapped variation from plant and crop biodiversity that exists in seed banks across the world to help us feed the growing population in a sustainable manner.

Council members will also be working together to progress its initiative in biofortification via a GPC Forum in China during the summer of 2014.

If you would like further information on the Global Plant Council please contact Executive Director Ruth Bastow: [ruth@globalplantcouncil.org](mailto:ruth@globalplantcouncil.org)

[Please visit the Global Plant Council at http://globalplantcouncil.org.](http://globalplantcouncil.org)

## Research News



### **Pondering Photosynthesis**

*By Tracy Vence. The Scientist. September 30, 2013*

New research uncovers previously unappreciated insights into the evolution of the well-studied energy-producing process. One of the most widely studied biological processes, photosynthesis is fairly well understood. Now, two recent studies suggest that a certain variation of photosynthesis has evolved several times independently, and that the energy-producing process may have evolved earlier than scientists once believed. In a paper published in *eLife* last week (September 28), researchers from the University of Cambridge and Imperial College London used computational approaches to predict how plants that perform C4 photosynthesis—which fix carbon more efficiently than plants that use the C3 version of the process—diverged from their C3 ancestors. The researchers found that C4 photosynthesis evolved through multiple distinct trajectories, including in the diverging monocot and eudicot clades. “C4 photosynthesis provides an excellent example of how independent lineages with a wide range of ancestral phenotypes can converge upon similar complex traits,” Cambridge’s Julian Hibberd and his colleagues wrote in their paper.

Meanwhile, a separate team led by investigators at the University of Southern Denmark unearthed from an ancient South African soil sample evidence that atmospheric oxygen appeared about 3 billion years ago—around 300 million to 400 million years earlier than previous estimates. The team presented its results in *Nature* last week (September 25). The discovery has implications for the emergence of ancient photosynthetic organisms. “Because we capture oxygen in the atmosphere 3 billion years ago, the likelihood is that oxygen-producing organisms evolved before that—very early in Earth’s history,” lead author Sean Crowe, who is now at the University of British Columbia, told CBC News. The University of Washington’s Roger Buick told *Science News* that the study “adds greater complexity to our picture of how and when the Earth got its oxygen. It suggests that oxygenic photosynthesis, the ultimate source of most oxygen, evolved long before the Great Oxidation Event”—when biologically induced free oxygen appeared in Earth’s atmosphere, around 2.4 billion years ago.

### **Team uses a cellulosic biofuels byproduct to increase ethanol yield**

*Source: Science Newsletter, October 8, 2013.*

Scientists report in *Nature Communications* that they have engineered yeast to consume acetic acid, a previously unwanted byproduct

of the process of converting plant leaves, stems and other tissues into biofuels. The innovation increases ethanol yield from lignocellulosic sources by about 10 percent. The new advance will streamline the fermentation process and will simplify plant breeding and pretreatment of the cellulose, the researchers say. | Photo courtesy of U.S. Department of Energy Joint Genome Institute

Lignocellulose is the fibrous material that makes up the structural tissues of plants. It is one of the most abundant raw materials on the planet and, because it is rich in carbon it is an attractive source of renewable biomass for biofuels production.

The yeast *Saccharomyces cerevisiae* is good at fermenting simple sugars (such as those found in corn kernels and sugarcane) to produce ethanol. But coaxing the yeast to feast on plant stems and leaves is not so easy. Doing it on an industrial scale requires a number of costly steps, one of which involves breaking down hemicellulose, a key component of lignocellulose.

"If we decompose hemicellulose, we obtain xylose and acetic acid," said University of Illinois food science and human nutrition professor Yong-Su Jin, who led the research with principal investigator Jamie Cate, of the University of California at Berkeley and the Lawrence Berkeley National Laboratory. Jin and Cate are affiliates of the Energy Biosciences Institute (EBI), which funded the research. Jin is an affiliate of the Institute for Genomic Biology at the U. of I.

"Xylose is a sugar; we can engineer yeast to ferment xylose," Jin said. "However, acetic acid is a toxic compound that kills yeast. That is one of the biggest problems in cellulosic ethanol production."

In an earlier study, graduate student Soo Rin Kim (now an EBI fellow) engineered *S. cerevisiae* to more efficiently consume xylose. This improved ethanol output, but the process generated an excess of NADH, an electron-transfer molecule that is part of the energy currency of all cells. The buildup of acetic acid also killed off much of the yeast.

After discussing the problem with Jin, Cate had an idea -- perhaps the team could induce the yeast to consume acetic acid. It later occurred to Jin that that process might also

use up the surplus NADH from xylose metabolism.

By reviewing earlier studies, postdoctoral researcher Na Wei found that another organism, a bacterium, could consume acetic acid. She identified the enzymes that catalyzed this process and saw that one of them not only converted acetic acid into ethanol, but also would use the surplus NADH from xylose metabolism.

The team was not ready to start putting the genes into their yeast, however. They first had to determine whether their efforts were likely to succeed.

"One challenge with yeast is it has evolved to do one thing really well," Cate said. "When you start adding these new modules into what it's already doing, it's not obvious that it's going to work up front."

To get a better idea of the feasibility of the idea, graduate student Josh Quarterman used computer simulations to see how adding the new genes to the yeast's metabolic repertoire would affect its ethanol output. His calculations indicated that the pathway Wei had identified would boost ethanol production.

Next, Wei did the painstaking work of inserting the desirable genes into the yeast, a process that took several months. When she tested the yeast, she saw that it produced about 10 percent more ethanol than before, in line with Quarterman's calculations. In further experiments, she demonstrated that the new yeast was in fact making some of the ethanol from acetate, a first for *S. cerevisiae*.

"We sort of rebuilt how yeast uses carbon," Cate said.

The breakthrough also will help those who focus on other steps in the biofuels production process, Jin said. Plant geneticists and those involved in pretreatment can stop worrying about finding ways to eliminate acetic acid from lignocellulose, he said.

"Many people are curious about why we don't have cellulosic biofuel right now," Jin said.

"But it's not because of one limiting step. We have many limiting steps in growing the biomass, storing, moving, harvesting, decomposing the biomass to the sugar, fermentation and then separation (of the ethanol). The advance that we are reporting

involves one of those steps -- fermentation. But it also will make other steps in the process a little easier."

### **Scientists identify key genes for increasing oil content in plant leaves**

*Source: Science Codex. October 18, 2013*

UPTON, NY -- Scientists at the U.S. Department of Energy's Brookhaven National Laboratory have identified the key genes required for oil production and accumulation in plant leaves and other vegetative plant tissues. Enhancing expression of these genes resulted in vastly increased oil content in leaves, the most abundant sources of plant biomass—a finding that could have important implications for increasing the energy content of plant-based foods and renewable biofuel feedstocks. The research is described in two new publications in *The Plant Journal* and *Plant Cell*.

"If we can transfer this strategy to crop plants being used to generate renewable energy or to feed livestock, it would significantly increase their energy content and nutritional values," said Brookhaven biochemist Changcheng Xu, who led the research. The experiments were carried out in large part by Xu's group members Jilian Fan and Chengshi Yan.

Think about it in the familiar terms of calories: Oil is twice as energy-dense as carbohydrates, which make up the bulk of leaves, stems, and other vegetative plant matter. "If you want to cut calories from your diet, you cut fat and oils. Conversely, if you want to increase the caloric output of your biofuel or feed for livestock, you want more oil," said Xu.

But plants don't normally store much oil in their leaves and other vegetative tissues. In nature, oil storage is the job of seeds, where the energy-dense compounds provide nourishment for developing plant embryos. The idea behind Xu's studies was to find a way to "reprogram" plants to store oil in their more abundant forms of biomass.

The first step was to identify the genes responsible for oil production in vegetative plant tissues. Though oil isn't stored in these tissues, almost all plant cells have the capacity to make oil. But until these studies, the

pathway for oil biosynthesis in leaves was unknown.

"Many people assumed it was similar to what happens in seeds, but we tried to look also at different genes and enzymes," said Xu.

The scientists used a series of genetic tricks to test the effects of overexpressing or disabling genes that enable cells to make certain enzymes involved in oil production. Pumping up the factors that normally increase oil production in seeds had no effect on oil production in leaves, and one of these, when overexpressed in leaves, caused growth and developmental problems in the plants. Altering the expression of a different oil-producing enzyme, however, had dramatic effects on leaf oil production.

"If you knock out (disable) the gene for an enzyme known as PDAT, it doesn't affect oil synthesis in seeds or cause any problems to plants, but it dramatically decreases oil production and accumulation in leaves," Xu said. In contrast, overexpressing the gene for PDAT—that is, getting cells to make more of this enzyme—resulted in a 60-fold increase in leaf oil production.

An important observation was that the excess oil did not mix with cellular membrane lipids, but was found in oil droplets within the leaf cells. These droplets were somewhat similar to those found in seeds, only much, much larger. "It was as if many small oil droplets like those found in seeds had fused together to form huge globules," Xu said.

Bigger droplets may seem better, but they're not, explained Xu. Oil in these oversized droplets is easily broken down by other enzymes in the cells. In seeds, he said, oil droplets are coated with a protein called oleosin, which prevents the droplets from fusing together, keeping them smaller while also protecting the oil inside. What would happen in leaves, the scientists wondered, if they activated the gene for oleosin along with PDAT?

The result: Overexpression of the two genes together resulted in a 130-fold increase in production of leaf oil compared with control plants. This time the oil accumulated in large clusters of tiny oleosin-coated oil droplets.

Next the scientists used radio-labeled carbon (C-14) to decipher the biochemical mechanism

by which PDAT increases oil production. They traced the uptake of C-14-labeled acetate into fatty acids, the building blocks of membrane lipids and oils. These studies showed that PDAT drastically increased the rate at which these fatty acids were made.

Then the scientists decided to test the effects of overexpressing the newly identified oil-increasing genes (PDAT and oleosin) in a variant of test plants that already had an elevated rate of fatty acid synthesis. In this case, the genetic boost resulted in even greater oil production and accumulation-170-fold compared with control plants-to the point where oil accounted for nearly 10 percent of the leaf's dry weight.

"That potentially equals almost twice the oil yield, by weight, that you can get from canola seeds, which right now is one of the highest oil-yielding crops used for food and biodiesel production," said Xu. Burning plant biomass with such energy density to generate electricity would release 30 to 40 percent more energy, and the nutritional value of feed made from such energy-dense biomass would also be greatly enhanced.

"These studies were done in laboratory plants, so we still need to see if this strategy would work in bioenergy or feed crops," said Xu. "And there are challenges in finding ways to extract oil from leaves so it can be converted to biofuels. But our research provides a very promising path to improving the use of plants as a source of feed and feedstocks for producing renewable energy," he said.

Xu is now collaborating with Brookhaven biochemist John Shanklin to explore the potential effect of overexpressing these key genes on oil production in dedicated biomass crops such as sugarcane.

### **Barley Crops Affected by Disease Found On Common Wild Grass**

*Source: ScienceDaily. Oct. 16, 2013*

A major fungal pathogen which affects barley crops is also present on a common wild grass according to a new study by leading agricultural researchers including the University of Hertfordshire.

Barley is the second most important cereal crop grown in the UK -- used as animal fodder,

in human foods such as health foods, soups and stews, and also in the drinks production industry. High quality malting barley underpins beer and whisky production and is worth around £20 billion to the UK economy. However, barley is susceptible to a number of diseases, the most important of which is called leaf blotch and is caused by a fungal pathogen. This disease affects the leaves, ears and stems of the barley -- decreasing grain quality and reducing crop yields by up to forty per cent.

Bruce Fitt, professor of plant pathology at the University of Hertfordshire, said: "Crops that appear to be clear of disease can suddenly develop leaf blotch symptoms unexpectedly. The source of the disease is unclear and this has puzzled farmers and researchers alike.

"However, our research shows that the fungal pathogen that causes barley leaf blotch can be found on wild ryegrasses which are common both as weeds within cereal crop fields and in the surrounding field margins."

In the study, both DNA and plant testing showed that the leaf blotch pathogen that affects barley can be found on the wild grasses and was virulent on commonly grown varieties of barley.

Professor Fitt continued: "Field margins play an important role in creating areas of habitat to support wildlife and wild plants species. But the increasing demand for agricultural land to provide enough crops to feed and support the growing population is putting pressure on these little pockets of wild nature.

"And if this pathogen species can be spread from wild grasses onto barley crops and back again, further investigation is needed to identify how widespread this species is and also the role that wild grasses play as sources of disease for other crops such as wheat."

Journal Reference: Kevin M. King, Jonathan S. West, Patrick C. Brunner, Paul S. Dyer, Bruce D. L. Fitt. Evolutionary Relationships between *Rhynchosporium lolii* sp. nov. and Other *Rhynchosporium* Species on Grasses. *PLoS ONE*, 2013; 8 (10): e72536 DOI: 10.1371/journal.pone.0072536

### **Model Plant Misled Scientists About Multicellular Growth**

*Source: ScienceDaily. Oct. 22, 2013*

Scientists have misunderstood one of the most fundamental processes in the life of plants because they have been looking at the wrong flower, according to University of Leeds researchers.

*Arabidopsis thaliana* -- also known as thale cress or mouse-ear cress -- grows abundantly in cracks in pavements all over Europe and Asia, but the small white flower leads a second life as the lab rat of the plant world.

It has become the dominant "model plant" in genetics research because of its simple genetics and ease of use in a research environment. Thousands of trays of the humble weed are cultivated in laboratories across the world, but it turns out they may actually contain a rather oddball plant.

A study by researchers at the University of Leeds found that *Arabidopsis thaliana* was exceptional in not having a "censorship" protein called SMG1.

SMG1 was known to play a vital role in the growth of animals as multicellular organisms, but scientists thought that plants built their complex life fundamentally differently. That conclusion, it turns out, was built on a dummy sold by *Arabidopsis thaliana*.

Professor Brendan Davies from the University of Leeds' School of Biology, who led the study, said: "Everybody thought that this protein was only in animals. They thought that because, basically, most of the world studies one plant: *Arabidopsis thaliana*."

Gene expression -- the process by which the information from a genome is converted into the differentiated cells that make up complex life -- relies on processes that turn genes on, when their genetic messages are required, and off when they are not.

"Switching genes on and off is really what life is about. If you can't do that, you can't have life," said Professor Davies. "There are various ways this is done, but one way in more complex life such as animals and plants is through a sort of 'censorship' process. The system looks at the messages that come out of the nucleus and effectively makes a judgement on them. It says 'I am going to destroy that message now' and intervenes to destroy it before it takes effect."

Scientists know that this "censorship" process -- called Nonsense Mediated mRNA Decay (NMD) -- is used by both plants and animals, but thought the two types of organism did it in different ways.

Because *Arabidopsis thaliana* does not have SMG1, which plays a key role in triggering the censorship system in animals, scientists had concluded that SMG1 was not present in any plant.

However, the Leeds researchers discovered that the plant that has established itself as the standard reference plant for all of biology is in fact an anomaly.

"We have found that SMG1 is in every plant for which we have the genome apart from *Arabidopsis* and we have established that it is being used in NMD. Rather than being just in animals, we are suggesting that the last common ancestor of animals and plants had SMG1," Professor Davies said.

The study also found SMG1 in *Arabidopsis lyrata*, a close relative of *Arabidopsis thaliana*, which suggests that the missing protein has been lost relatively recently in evolutionary time, perhaps in the last 5-10 million years.

The next key question for researchers is to explain how organisms without SMG1, such as fungi and *Arabidopsis thaliana*, work without the protein.

As for *Arabidopsis thaliana*, it may not have met its Waterloo just yet. "It is still a fantastically useful model. We would not be anywhere close to where we are in understanding plant biology without it, but this is a lesson to us all about the dangers of extrapolating from a single model, however successful that model has been, and the importance of studying processes in a range of models. Evolution does strange and unpredictable things," Professor Davies said.

The flower, which is a member of the mustard family, was first recorded by Johannes Thal in the Harz mountains of northern Germany in the 16th century, but its scientific career really took off at the very end of the 1970s and the early 1980s when molecular geneticists chose it as the ideal model.

Its simple genome, small size, ease of cultivation, and rapid life cycle have since made it an institution in plant genetics with books, web sites and academic conferences

devoted to it. In 2008 alone, 3,500 papers on *Arabidopsis thaliana* were added to the PubMed database, which logs important publications in the life sciences.

The plant has a history of leaving scientists scratching their heads. In the 18th century, it was categorised as one of the *Arabis* genus but had to be renamed "*Arabidopsis*," meaning "resembling *Arabis*" after the original classification was found to be incorrect.

Journal Reference: James P. B. Lloyd, Brendan Davies. SMG1 is an ancient nonsense-mediated mRNA decay effector. *The Plant Journal*, 2013; DOI: 10.1111/tpj.12329

### **Surprises discovered in decoded kiwifruit genome**

*Source: Phys.org. Oct 22, 2013 by Amanda Gurung*

A new study that decoded the DNA sequence of the kiwifruit has concluded that the fruit has many genetic similarities between its 39,040 genes and other plant species, including potatoes and tomatoes. The study also has unveiled two major evolutionary events that occurred millions of years ago in the kiwifruit genome.

The kiwifruit is an economically and nutritionally important fruit crop. It has long been called 'the king of fruits' because of its remarkably high vitamin C content and balanced nutritional composition of minerals, dietary fiber and other health-benefits," says Zhangjun Fei, a scientist from the Boyce Thompson Institute at Cornell who contributed heavily to study, which was conducted by a team of plant scientists from the United States and China and published Oct. 18 in *Nature Communications*.

"The genome sequence will serve as a valuable resource for kiwifruit research and may facilitate the breeding program for improved fruit quality and disease resistance," Fei says.

Kiwifruit originated from the mountains and ranges of southwestern China and was not really known to the world until the early 20th century, when farmers in New Zealand discovered the fruit and began breeding it as a commercial crop. It is a form of berry that grows on woody vines, much like grapes, and

belongs to the order of Ericales, where blueberries, tea bushes and Brazil nuts are also classified.

One of the most remarkable findings of the study was uncovered when scientists observed a high percentage of similarities within the kiwifruit DNA. The data revealed two unusual mishaps that occurred in the process of cell division about 27 and 80 million years ago, when an extensive expansion of genes arose from an entire extra copy of the genome, followed by extensive gene loss.

Fei explains, "The kiwifruit genome has undergone two recent whole-genome duplication events."

When genes are duplicated, the extra genes can mutate to perform entirely new functions that were not previously present in the organism. This process, called neofunctionalization, can occur with no adverse effects in plants and, in the case of kiwifruit, was quite beneficial.

"The duplication contributed to adding additional members of gene families that are involved in regulating important kiwifruit characteristics, such as fruit vitamin C, flavonoid and carotenoid metabolism," says Fei.

For the sequencing, the scientists used a Chinese variety called "Hongyang," which is widely grown in China, to produce the draft sequence. They then compared kiwifruit to the genomes of other representative plant species including tomato, rice, grape and the mustard weed *Arabidopsis*. They uncovered about 8,000 genes that were common among all five species. The comparison revealed important evolutionary relationships, including the development genes related to fruit growth, ripening, nutrient metabolism, and disease resistance.

Prior to the study, extensive research on the metabolic accumulation of vitamin C, carotenoids and flavonoids had been reported in kiwifruits, but genome sequence data, critical for its breeding and improvement, had never been available.

"The kiwifruit genome sequence represents the first of a member in the order Ericales, thus providing a valuable resource for comparative genomics and evolutionary studies," Fei says. "We expect to continue

generating genome sequences from other kiwifruit varieties to investigate the genetic diversity of kiwifruit and elucidate regulatory networks of important biological processes." The sequence is accessible online at the Kiwifruit Genome Database.

### **Key Genes for Increasing Oil Content in Plant Leaves Identified**

*ScienceDaily. Oct. 18, 2013.*

Scientists at the U.S. Department of Energy's Brookhaven National Laboratory have identified the key genes required for oil production and accumulation in plant leaves and other vegetative plant tissues. Enhancing expression of these genes resulted in vastly increased oil content in leaves, the most abundant sources of plant biomass—a finding that could have important implications for increasing the energy content of plant-based foods and renewable biofuel feedstocks.

The research is described in two new publications in *The Plant Journal* and *Plant Cell*.

"If we can transfer this strategy to crop plants being used to generate renewable energy or to feed livestock, it would significantly increase their energy content and nutritional values," said Brookhaven biochemist Changcheng Xu, who led the research. The experiments were carried out in large part by Xu's group members Jilian Fan and Chengshi Yan.

Think about it in the familiar terms of calories: Oil is twice as energy-dense as carbohydrates, which make up the bulk of leaves, stems, and other vegetative plant matter. "If you want to cut calories from your diet, you cut fat and oils. Conversely, if you want to increase the caloric output of your biofuel or feed for livestock, you want more oil," said Xu.

But plants don't normally store much oil in their leaves and other vegetative tissues. In nature, oil storage is the job of seeds, where the energy-dense compounds provide nourishment for developing plant embryos. The idea behind Xu's studies was to find a way to "reprogram" plants to store oil in their more abundant forms of biomass.

The first step was to identify the genes responsible for oil production in vegetative

plant tissues. Though oil isn't stored in these tissues, almost all plant cells have the capacity to make oil. But until these studies, the pathway for oil biosynthesis in leaves was unknown.

"Many people assumed it was similar to what happens in seeds, but we tried to look also at different genes and enzymes," said Xu.

The scientists used a series of genetic tricks to test the effects of overexpressing or disabling genes that enable cells to make certain enzymes involved in oil production. Pumping up the factors that normally increase oil production in seeds had no effect on oil production in leaves, and one of these, when overexpressed in leaves, caused growth and developmental problems in the plants. Altering the expression of a different oil-producing enzyme, however, had dramatic effects on leaf oil production.

"If you knock out (disable) the gene for an enzyme known as PDAT, it doesn't affect oil synthesis in seeds or cause any problems to plants, but it dramatically decreases oil production and accumulation in leaves," Xu said. In contrast, overexpressing the gene for PDAT—that is, getting cells to make more of this enzyme—resulted in a 60-fold increase in leaf oil production.

An important observation was that the excess oil did not mix with cellular membrane lipids, but was found in oil droplets within the leaf cells. These droplets were somewhat similar to those found in seeds, only much, much larger. "It was as if many small oil droplets like those found in seeds had fused together to form huge globules," Xu said.

Bigger droplets may seem better, but they're not, explained Xu. Oil in these oversized droplets is easily broken down by other enzymes in the cells. In seeds, he said, oil droplets are coated with a protein called oleosin, which prevents the droplets from fusing together, keeping them smaller while also protecting the oil inside. What would happen in leaves, the scientists wondered, if they activated the gene for oleosin along with PDAT?

The result: Overexpression of the two genes together resulted in a 130-fold increase in production of leaf oil compared with control

plants. This time the oil accumulated in large clusters of tiny oleosin-coated oil droplets.

Next the scientists used radio-labeled carbon (C-14) to decipher the biochemical mechanism by which PDAT increases oil production. They traced the uptake of C-14-labeled acetate into fatty acids, the building blocks of membrane lipids and oils. These studies showed that PDAT drastically increased the rate at which these fatty acids were made.

Then the scientists decided to test the effects of overexpressing the newly identified oil-increasing genes (PDAT and oleosin) in a variant of test plants that already had an elevated rate of fatty acid synthesis. In this case, the genetic boost resulted in even greater oil production and accumulation-170-fold compared with control plants-to the point where oil accounted for nearly 10 percent of the leaf's dry weight.

"That potentially equals almost twice the oil yield, by weight, that you can get from canola seeds, which right now is one of the highest oil-yielding crops used for food and biodiesel production," said Xu. Burning plant biomass with such energy density to generate electricity would release 30 to 40 percent more energy, and the nutritional value of feed made from such energy-dense biomass would also be greatly enhanced.

"These studies were done in laboratory plants, so we still need to see if this strategy would work in bioenergy or feed crops," said Xu. "And there are challenges in finding ways to extract oil from leaves so it can be converted to biofuels. But our research provides a very promising path to improving the use of plants as a source of feed and feedstocks for producing renewable energy," he said.

Xu is now collaborating with Brookhaven biochemist John Shanklin to explore the potential effect of overexpressing these key genes on oil production in dedicated biomass crops such as sugarcane.

Journal References: Fan et al. Phospholipid:diacylglycerol acyltransferase-mediated triacylglycerol biosynthesis is crucial for protection against fatty acid-induced cell death in growing tissues of Arabidopsis. The Plant Journal, 2013; DOI: 10.1111/tpj.12343. Fan et al. Dual Role for Phospholipid:Diacylglycerol Acyltransferase:

Enhancing Fatty Acid Synthesis and Diverting Fatty Acids from Membrane Lipids to Triacylglycerol in Arabidopsis Leaves. The Plant Cell, 2013 DOI: 10.1105/tpc.113.117358

### **Why Plants Usually Live Longer Than Animals** *ScienceDaily. Oct. 24, 2013*

Stem cells are crucial for the continuous generation of new cells. Although the importance of stem cells in fuelling plant growth and development still many questions on their tight molecular control remain unanswered. Plant researchers at VIB and Ghent University discovered a new step in the complex regulation of stem cells.

Today, their results are published online in this week's issue of Science Express.

Lieven De Veylder said, "Our data suggest that certain organizing stem cells in plant roots are less sensitive for DNA-damage. Those cells hold an original and intact DNA copy which can be used to replace damaged cells if necessary. Animals rely on a similar mechanism but most likely plants have employed this in a more optimized manner. This could explain why many plants can live for more than hundreds of years, while this is quite exceptional for animals."

Plant growth and development depend on the continuous generation of new cells. A small group of specialized cells present in the growth axes of a plant is driving this. These so-called stem cells divide at a high frequency and have the unique characteristic that the original mother cell keeps the stem cell activity while the daughter cell acquires a certain specialization. Besides these stem cells, plant roots also harbor organizing cells. These organizing cells divide with a three- to ten-fold lower frequency, therefore often referred to as quiescent center cells. The organizing cells control the action of the surrounding stem cells and can replace them if necessary.

For almost 20 years, scientists all over the world have been studying the action of the stem cells and that of their controlling organizing cells. Until now it was not known how quiescent and actively dividing cells could co-exist so closely and which mechanisms are at the basis of the quiescent character. Plant

researchers at VIB and Ghent University have now identified a new molecular network that increases our understanding of stem cell regulation and activity.

Central in this process is the discovery of a new protein, the ERF115 transcription factor. The scientists demonstrated that the organizing cells barely divide because of the inhibition of ERF115 activity. When the organizing cells need to divide to replace damaged surrounding stem cells, ERF115 gets activated. ERF115 then stimulates the production of the plant hormone phytoalexin which in turn activates the division of the organizing cells. Thus, the ERF115-phytoalexin network acts as a back-up system during stress conditions which are detrimental for the activity of stem cells.

Journal Reference: Heyman et al. ERF115 Controls Root Quiescent Center Cell Division and Stem Cell Replenishment. *Science*, 24 October 2013 DOI: 10.1126/science.1240667

### **Surprises Discovered in Decoded Kiwifruit Genome**

*Source: ScienceDaily. Oct. 25, 2013*

A new study that decoded the DNA sequence of the kiwifruit has concluded that the fruit has many genetic similarities between its 39,040 genes and other plant species, including potatoes and tomatoes. The study also has unveiled two major evolutionary events that occurred millions of years ago in the kiwifruit genome.

"The kiwifruit is an economically and nutritionally important fruit crop. It has long been called 'the king of fruits' because of its remarkably high vitamin C content and balanced nutritional composition of minerals, dietary fiber and other health-benefits," says Zhangjun Fei, a scientist from the Boyce Thompson Institute at Cornell University. Fei contributed heavily to the study, which was conducted by a team of plant scientists from the United States and China and published Oct. 18 in *Nature Communications*.

"The genome sequence will serve as a valuable resource for kiwifruit research and may facilitate the breeding program for improved fruit quality and disease resistance," Fei says.

Kiwifruit originated from the mountains and ranges of southwestern China and was not really known to the world until the early 20th century, when farmers in New Zealand discovered the fruit and began breeding it as a commercial crop. It is a form of berry that grows on woody vines, much like grapes, and belongs to the order of Ericales, where blueberries, tea bushes and Brazil nuts are also classified.

One of the most remarkable findings of the study was uncovered when scientists observed a high percentage of similarities within the kiwifruit DNA. The data revealed two unusual mishaps that occurred in the process of cell division about 27 and 80 million years ago, when an extensive expansion of genes arose from an entire extra copy of the genome, followed by extensive gene loss.

Fei explains, "The kiwifruit genome has undergone two recent whole-genome duplication events."

When genes are duplicated, the extra genes can mutate to perform entirely new functions that were not previously present in the organism. This process, called neofunctionalization, can occur with no adverse effects in plants and, in the case of kiwifruit, was quite beneficial.

"The duplication contributed to adding additional members of gene families that are involved in regulating important kiwifruit characteristics, such as fruit vitamin C, flavonoid and carotenoid metabolism," says Fei.

For the sequencing, the scientists used a Chinese variety called "Hongyang," which is widely grown in China, to produce the draft sequence. They then compared kiwifruit to the genomes of other representative plant species including tomato, rice, grape and the mustard weed *Arabidopsis*. They uncovered about 8,000 genes that were common among all five species. The comparison revealed important evolutionary relationships, including the development genes related to fruit growth, ripening, nutrient metabolism, and disease resistance.

Prior to the study, extensive research on the metabolic accumulation of vitamin C, carotenoids and flavonoids had been reported in kiwifruits, but genome sequence data,

critical for its breeding and improvement, had never been available.

"The kiwifruit genome sequence represents the first of a member in the order Ericales, thus providing a valuable resource for comparative genomics and evolutionary studies," Fei says. "We expect to continue generating genome sequences from other kiwifruit varieties to investigate the genetic diversity of kiwifruit and elucidate regulatory networks of important biological processes."

The sequence is accessible online at the Kiwifruit Genome Database. Cornell University has television and ISDN radio studios available for media interviews.

Journal Reference: Huang et al. Draft genome of the kiwifruit *Actinidia chinensis*. *Nature Communications*, 2013; 4 DOI: 10.1038/ncomms3640

### **Plant Cell Architecture: Growth Toward a Light Source**

*Source: ScienceDaily. Nov. 7, 2013*

Inside every plant cell, a cytoskeleton provides an interior scaffolding to direct construction of the cell's walls, and thus the growth of the organism as a whole. Environmental and hormonal signals that modulate cell growth cause reorganization of this scaffolding. New research led by Carnegie's David Ehrhardt provides surprising evidence as to how this reorganization process works, with important evidence as to how the direction of a light source influences a plant's growth pattern.

It is published by Science Express.

The cytoskeleton undergirding each cell includes an array of tubule-shaped protein fibers called microtubules. By directing cell growth and development, this scaffold is crucial for supporting important plant functions such as photosynthesis, nutrient gathering, and reproduction.

The cytoskeleton does not appear to be remodeled by moving these microtubules around in the cell. Rather, it is altered by changes to the way these fiber arrays are assembled or disassembled. Ehrhardt's team--including lead author Jelmer Lindeboom, Masayoshi Nakamura, Ryan Gutierrez and Viktor Kirik, all from Carnegie--used advanced tools to watch the reorganization process of

these microtubule arrays under different conditions.

These imaging data, combined with the results of genetic experiments, revealed a mechanism by which plants orient microtubule arrays. A protein called katanin drives this mechanism, which it achieves by redirecting microtubule growth in response to blue light. It does so by severing the microtubules where they intersect with each other, creating new ends that can regrow and themselves be severed, resulting in a rapid amplification of new microtubules lying in another, more desired, direction.

"Our genetic data, together with previous studies that tie microtubule organization to cell growth, indicate that this restructuring is required for the plant to bend toward a light source as it grows, a phenomenon called phototropism," Ehrhardt explained. "Our findings also have broader implications for the construction of cytoskeletons in other types of cells, including human cells, because katanin is conserved between animals and plants."

"This is exceptional work, which draws upon decades of pioneering discoveries made by Carnegie's Winslow Briggs on blue light perception. For the first time Ehrhardt's group demonstrates how blue light drives changes in cytoskeleton organization, which underlies the architecture and mechanical properties of the cell walls. These properties are critical for the light-induced bending" says Wolf B. Frommer, Director of the department. He terms the study: "fantastic work, a milestone in the history of blue light research."

Journal Reference: Jelmer J. Lindeboom, Masayoshi Nakamura, Anneke Hibbel, Kostya Shundyak, Ryan Gutierrez, Tijs Ketelaar, Anne Mie C. Emons, Bela M. Mulder, Viktor Kirik, and David W. Ehrhardt. A Mechanism for Reorientation of Cortical Microtubule Arrays Driven by Microtubule Severing. *Science*, 7 November 2013 DOI: 10.1126/science.1245533

### **Defending Food Crops: Whitefly Experimentation to Prevent Contamination of Agriculture**

*Source: ScienceDaily. Nov. 8, 2013*

On November 8th, JoVE, the Journal of Visualized Experiments, will introduce a new technique to aid in the development of defenses against diseases threatening food crops worldwide. The method, published under the title Transmitting Plant Viruses Using Whiteflies, is applicable to such at-risk crops as tomatoes and common bean plants. The whitefly method provides a means of interfering with the plant-contamination process as well as the cultivation of plants that are altogether resistant to infection.

"For example, the described technique is used to develop tomatoes with resistance to tomato yellow leaf curl virus, which is a big problem in tomato production in the southern U.S. and in many parts of the world," said Jane Polston, the principle investigator at the University of Florida's Department of Plant Pathology. In the article accompanying their JoVE video, Polston and her colleagues write that numerous genera of whitefly-transmitted plant viruses (such as Begomovirus, Carlavirus, Crinivirus, Ipomovirus, Torradovirus) are part of an emerging and economically significant group of pathogens affecting important food and fiber crops.

The technique includes reliably rearing whiteflies with a specific virus while omitting the possibility of cross-contamination to other viruses -- an easily encountered problem because of the sheer number of whiteflies used in testing. Such contamination would jeopardize the results of an entire experiment. After exposing large numbers of a particular plant species to a specific whitefly-transmitted virus, a researcher can then note which individual plants resisted infection and why. This article outlines how to generate hundreds or thousands of infected plants year-round by exposing them to whiteflies each week. Therefore, the whitefly-assisted transmission method provides researchers with a powerful means for continued experimentation in developing plant defenses against the threat of whitefly-transmitted disease.

Polston said that she published this technique through JoVE's video format because it was difficult to explain it through traditional text-only journals. "I have never published like this before and wanted to try it," she said, "And it

was very difficult to describe some of the details of this technique in writing. Video was a better approach."

Journal Reference: Polston, J. E., Capobianco, H. Transmitting Plant Viruses Using Whiteflies. *J. Vis. Exp.*, 2013; (81), e4332 DOI: 10.3791/4332

### **Why Seedlings Always Grow Towards the Light**

*ScienceDaily. Nov. 14, 2013 —*

Scientists from the Carnegie Institution at Stanford University and Wageningen University have discovered how cells in the stems of seedlings use blue light to grow towards the light. During earlier research the discovery was made that the cells in the seedling stems responded to blue light used in the microscope.

The scientists have now discovered how the blue light causes small structures in the cell, the microtubules, to grow perpendicular to their normal growth direction. As a result, the growth direction of seedlings also changes, making them head towards the light. The scientists discovered which protein is responsible for making the microtubules grow perpendicular to the normal direction.

The results were published in *Science*.

Most people know that seedlings grow towards the light. But do they do that? It is a question that many scientists have wrestled with over the years. In earlier studies, scientists were looking into the cells of seedlings. Using special microscopes with blue laser light, they visualized the structures that are important for the growth direction of plant cells. Something surprising happened: within ten minutes, the arrangement of the microtubules changed completely under the microscope.

Through smart use of image analysis techniques, the scientists were able to show that -- within a few minutes -- blue light results in generation of large numbers of new microtubules which are all perpendicular to the pre-existing microtubules. They also discovered how the cells in seedlings detect the light in these conditions, namely through phototropin, one of the proteins that allow plants to detect light.

In addition, it was determined that the generation of large numbers of microtubules that are perpendicular to pre-existing microtubules is caused by the protein katanin. Seedlings that do not contain the katanin protein cannot make their microtubules change direction and are unable to grow towards the light. Katanin is activated by phototropin and can sever microtubules in half where they intersect other microtubules. Severing results in two microtubules each of which grow in the same orientation. Microtubules that are perpendicular to the pre-existing microtubules make many intersections. Every time new microtubules intersect with other microtubules positioned in the original direction, katanin can sever the new microtubules to create new branches. Within a few minutes, this results in 'trees' of microtubules within the cells that are perpendicular to the original direction. The growth and development of plants depends strongly on the quality and quantity of light they detect. Plants depend on light for photosynthesis but are unable to move themselves. Instead, they grow towards the light. This study shows that the reorganisation of microtubules plays an essential role in this process.

Journal Reference: J. J. Lindeboom, M. Nakamura, A. Hibbel, K. Shundyak, R. Gutierrez, T. Ketelaar, A. M. C. Emons, B. M. Mulder, V. Kirik, D. W. Ehrhardt. A Mechanism for Reorientation of Cortical Microtubule Arrays Driven by Microtubule Severing. *Science*, 2013; DOI: 10.1126/science.1245533

#### **How Onions Recognize When to Bulb**

*Source: ScienceDaily. Dec. 3, 2013*

Onions, the third largest vegetable crop in the world, form a bulb in response to lengthening days, however the molecular mechanisms controlling this response were not previously known.

Research undertaken by Plant & Food Research and the University of Otago has identified the gene controlling bulb development, the first step in discovering genetic markers that can be used as tools to screen conventional breeding programmes for

new onion varieties with the right genetic profile.

The research is published in the online journal *Nature Communications* with related research published in *Theoretical and Applied Genetics*. "This research is an excellent example of how new genome technologies can enable major discoveries that, in the past, have been difficult," says Associate Professor Richard Macknight of the University of Otago Department of Biochemistry. "By understanding how these plants control development of the bulb, we can support the breeding of new cultivars that have the right genetic profile to respond to specific growing conditions, ensuring each plant produces a bulb for sale on the market."

"Commercial production of onions relies on cultivars tailored to the environment they are grow in, responding to the right combination of day length and temperature to form a bulb," says John McCallum of Plant & Food Research. "Around 90 million tonnes of onions are produced globally each year, but genetic studies of onions have been limited. Our research is now beginning to link genetics and physiology of onions, allowing industry to tap into more diverse genetic resources and breed products adapted to different and changing environments."

Onion is the second largest vegetable crop in New Zealand, with 586,000 tonnes produced each year and generating \$62 million in export revenues.

Journal References: Robyn Lee, Samantha Baldwin, Fernand Kenel, John McCallum, Richard Macknight. FLOWERING LOCUS T genes control onion bulb formation and flowering. *Nature Communications*, 2013; 4 DOI: 10.1038/ncomms3884. Samantha Baldwin, Roopashree Revanna, Meeghan Pither-Joyce, Martin Shaw, Kathryn Wright, Susan Thomson, Leire Moya, Robyn Lee, Richard Macknight, John McCallum. Genetic analyses of bolting in bulb onion (*Allium cepa* L.). *Theoretical and Applied Genetics*, 2013; DOI: 10.1007/s00122-013-2232-4

#### **4 degree temperature rise will end vegetation 'carbon sink'**

*Source: University of Cambridge. 17 Dec 2013*

New research suggests that a temperature increase of 4 degrees is likely to “saturate” areas of dense vegetation with carbon, preventing plants from helping to balance CO2 escalation - and consequently accelerating climate change.

Latest climate and biosphere modelling suggests that the length of time carbon remains in vegetation during the global carbon cycle - known as ‘residence time’ - is the key “uncertainty” in predicting how Earth’s plant life on land - and consequently almost all life - will respond to higher CO2 levels and global warming, say researchers.

Carbon will spend increasingly less time in vegetation as the negative impacts of climate change take their toll through factors such as increased drought levels - with carbon rapidly released back into the atmosphere where it will continue to add to global warming.

Researchers say that extensive modelling shows a 4 degree temperature rise will be the threshold beyond which CO2 will start to increase more rapidly, as natural carbon ‘sinks’ of global vegetation become “saturated” and unable to sequester any more CO2 from the Earth’s atmosphere.

They call for a “change in research priorities” away from the broad-stroke production of plants and towards carbon ‘residence time’ - which is little understood - and the interaction of different kinds of vegetation in ecosystems such as carbon sinks.

Carbon sinks are natural systems that drain and store CO2 from the atmosphere, with vegetation providing many of the key sinks that help chemically balance the world - such as the Amazon rainforest and the vast, circumpolar Boreal forest.

As the world continues to warm, consequent events such as Boreal forest fires and mid-latitude droughts will release increasing amounts of carbon into the atmosphere - pushing temperatures ever higher.

Initially, higher atmospheric CO2 will encourage plant growth as more CO2 stimulates photosynthesis, say researchers. But the impact of a warmer world through drought will start to negate this natural balance until it reaches a saturation point.

The modelling shows that global warming of 4 degree will result in Earth’s vegetation

becoming “dominated” by negative impacts - such as ‘moisture stress’, when plant cells have too little water - on a global scale.

Carbon-filled vegetation ‘sinks’ will likely become saturated at this point, they say, flat-lining further absorption of atmospheric CO2. Without such major natural CO2 drains, atmospheric carbon will start to increase more rapidly - driving further climate change.

The researchers say that, in light of the new evidence, scientific focus must shift away from productivity outputs - the generation of biological material - and towards the “mechanistic levels” of vegetation function, such as how plant populations interact and how different types of photosyntheses will react to temperature escalation.

Particular attention needs to be paid to the varying rates of carbon ‘residence time’ across the spectrum of flora in major carbon sinks - and how this impacts the “carbon turnover”, they say.

The Cambridge research, led by Dr Andrew Friend from the University’s Department of Geography, is part of the ‘Inter-Sectoral Impact Model Intercomparison Project’ (ISI-MIP) - a unique community-driven effort to bring research on climate change impacts to a new level, with the first wave of research published today in a special issue of the journal *Proceedings of the National Academy of Sciences*.

“Global vegetation contains large carbon reserves that are vulnerable to climate change, and so will determine future atmospheric CO2,” said Friend, lead author of this paper. “The impacts of climate on vegetation will affect biodiversity and ecosystem status around the world.”

“This work pulls together all the latest understanding of climate change and its impacts on global vegetation - it really captures our understanding at the global level.”

The ISI-MIP team used seven global vegetation models, including Hybrid - the model that Friend has been honing for fifteen years - and the latest IPCC (Intergovernmental Panel on Climate Change) modelling. These were run exhaustively using supercomputers - including Cambridge’s own Darwin computer, which can easily accomplish overnight what would take a

PC months - to create simulations of future scenarios:

"We use data to work out the mathematics of how the plant grows - how it photosynthesises, takes-up carbon and nitrogen, competes with other plants, and is affected by soil nutrients and water - and we do this for different vegetation types," explained Friend.

"The whole of the land surface is understood in 2,500 km<sup>2</sup> portions. We then input real climate data up to the present and look at what might happen every 30 minutes right up until 2099."

While there are differences in the outcomes of some of the models, most concur that the amount of time carbon lingers in vegetation is the key issue, and that global warming of 4 degrees or more - currently predicted by the end of this century - marks the point at which carbon in vegetation reaches capacity.

"In heatwaves, ecosystems can emit more CO<sub>2</sub> than they absorb from the atmosphere," said Friend. "We saw this in the 2003 European heatwave when temperatures rose 6°C above average - and the amount of CO<sub>2</sub> produced was sufficient to reverse the effect of four years of net ecosystem carbon sequestration."

For Friend, this research should feed into policy: "To make policy you need to understand the impact of decisions.

"The idea here is to understand at what point the increase in global temperature starts to have serious effects across all the sectors, so that policy makers can weigh up impacts of allowing emissions to go above a certain level, and what mitigation strategies are necessary."

The ISI-MIP team is coordinated by the Potsdam Institute for Climate Impact Research in Germany and the International Institute for Applied Systems Analysis in Austria, and involves two-dozen research groups from eight countries.

See <http://www.cam.ac.uk/research/news/4-degree-temperature-rise-will-end-vegetation-carbon-sink#sthash.YTan321e.dpuf>

### **Silver Banksia plants excel at phosphate saving**

*Source: Phys.org. Dec 10, 2013*

Plants in the leached soils of Western Australia have developed a special strategy for coping with the scarcity of phosphorus. Together with colleagues from the University of Western Australia, Perth, scientists from the Max Planck Institute of Molecular Plant Physiology in Golm near Potsdam have discovered that plants from the Banksia genus of the Proteaceae family make severe cutbacks, in particular to the RNA found in the ribosomes (rRNA). The cell's protein factories are the biggest consumers of phosphorus; in this way, the plants save on both phosphorus and water. As global phosphorous reserves are in severe decline, the strategies of the Proteaceae could be of interest from the perspective of optimising crop plants through breeding.

Plants in Western Australia have to be very tough to survive. The heat is oppressive there, rain is extremely rare, and phosphorous in the form of phosphate is virtually nowhere to be found in the soil. However, this element is crucial to the survival of plants. It attaches itself to sugar and proteins and is a component of DNA, the cell membrane and the energy currency ATP. When phosphorous is scarce, photosynthesis declines and plants hardly grow.

This is not, however, the case with some of the plants from the Banksia genus of the Proteaceae family. "These plants grow on soils which contain a hundred times less phosphate than unfertilised soils in Europe," explains Mark Stitt, one of the authors of the study. This is due to their roots, on the one hand, which resemble toilet brushes and suck every phosphorous atom from the soil with their fine hairs. On the other hand, the plants are extremely prudent in their use of the little phosphorous available to them.

They save most in the nucleic acids, which combine between 30 and 50 percent of the cell's total phosphorous. Cutbacks are applied in particular to ribosomal RNA, a component of the cell's protein factories. Compared to Proteaceae, the model plant *Arabidopsis thaliana* has two to four times more ribosomes in its fully-grown leaves and, in the case of young leaves, it has 10 to 40 times more. Fewer ribosomes produce fewer proteins and enzymes. The plant grows more

slowly as a result, but does not present any symptoms of phosphorous deficiency. In fact, only too much phosphorus could prove dangerous for them.

"The plants can be fertilised to death, as they cannot halt the absorption of phosphate," explains Mark Stitt. Other plants simply close down when over-fertilised. "Up to now, we did not know why the Proteaceae, which have adapted to phosphorous deficiency, are no longer able to do this." Presumably, they have simply never been in such a situation, as the soils of Western Australia are very old and weathered and did not acquire additional phosphate in the past from volcanic eruptions, people or animals.

The plants are also extremely economic when they form new leaves. Instead of investing simultaneously in the growth and formation of the photosynthesis equipment, which would bind huge volumes of ribosomes and, thus phosphorous, they focus first on the formation of the leaf and later on the production of the green chlorophyll.

In the next phase of their study, the researchers would like to establish whether humans could implement the strategies of the Proteaceae for the efficient use of phosphorous in crop plants, or whether this

approach could be associated with disadvantageous characteristics, for example lower yields.

Phosphorous is very rarely found on the Earth and deposits are concentrated in very small geographical areas: almost 75 percent of the world's total phosphate rock is found in Morocco and the Western Sahara and a further 15 percent is distributed between China, Algeria, Syria, South Africa and Jordan.

Read more at: <http://phys.org/news/2013-12-silver-banksia-excel-phosphate.html#jCp>

More information: Ronan Sulpice, Hirofumi Ishihara, Armin Schlereth, Gregory R. Cawthray, Beatrice Encke, Patrick Giavalisco, Alexander Ivakov, Stéphanie Arrivault, Ricarda Jost, Nicole Krohn, John Kuo, Etienne Laliberté, Stuart J. Pearce, John A. Raven, Wolf-Rüdiger Scheible, François Teste, Erik J. Veneklaas, Mark Stitt, Hans Lambers, Low levels of ribosomal RNA partly account for the very high photosynthetic phosphorus-use efficiency of Proteaceae species, *Plant Cell Environment*, Online Pub DOI: 10.1111/pce.12240

Read more at: <http://phys.org/news/2013-12-silver-banksia-excel-phosphate.html#jCp>

## Forthcoming meetings



### **Keystone Symposia Conference on "Plant Signaling: Dynamic Properties"**

**February 5 - 10, 2014. Breckenridge, CO, USA.**

<http://www.keystonesymposia.org/index.cfm?e=web.RegisterSelf&MeetingID=1305>

### **Sustaining the Future of Acacia Plantation Forestry**

**March 18 – 21, 2014. Hue, Vietnam**

This is a joint conference of the recently formed IUFRO Working Party WP 2.08.07 on **Acacia Genetics and Silviculture**, WP1.02.06 on **Ecology and Silviculture of Acacia** and WP 2.04.01 on **Population, Ecological and**

**Conservation Genetics** and will be hosted by the Vietnamese Academy of Forest Sciences (VAFS). The conference will include invited and contributed presentations and posters, discussion sessions, satellite and business meetings, and in-conference and post-conference tours.

This 4 days' conference with the theme, **"Sustaining the Future of Acacia Plantation Forestry"** will be structured so as to promote discussion between geneticists, breeders and scientists concerned with management regime development and interactions of the crop with its biotic and abiotic environment. This broad ranging review should provide scientific

support to those responsible for developing and implementing forest plantation management policies. While our primary interest is in tropical acacias we recognize that there is a much more established tradition of planting temperate species such as *A. mearnsii*, and we will welcome contributions from scientists working on those crops.

To be included in the mailing list for updates on the conference, please contact:

Email: [J.L.Harbard@utas.edu.au](mailto:J.L.Harbard@utas.edu.au)

For more information please follow the link: <http://www.iufro.org/science/divisions/division-2/20000/20800/20807/>

**9<sup>th</sup> International Workshop: Sulfur Metabolism in Plants.**

**April 14 – 17, 2014. Freiburg. Germany**

Molecular Physiology and Ecophysiology of Sulfur.

Registration, Abstract Submission and detailed programme on our congress website:

[www.sulfur-workshop.com](http://www.sulfur-workshop.com)

**2014 Spring International Conference on Agriculture and Food Engineering (AFE-S)**

**April 16 – 18, 2014. Shanghai China,**

More info:

<http://www.engii.org/scet2014/Home.aspx>

**ICREA Workshop: From model systems to crops, challenges for a new era in plant biology**

**May 7 – 8, 2014. Barcelona, Spain**

More info:

<http://icreaworkshop2014.cragenomica.es/>

**33<sup>rd</sup> New Phytologist Symposium**

**May 14 – 16, 2014. Zurich, Switzerland**

**Title:** Networks of Power and Influence: A symposium on the ecology and evolution of symbiotic associations between plants and mycorrhizal fungi

**Website:**

<http://www.newphytologist.org/symposiums/view/4>

**SEB Manchester 2014.**

**July 1 – 4, 2014. Manchester, UK.**

The main Meeting of the [Society for Experimental Biology](#)

<http://www.sebiology.org/meetings/Manchester/sessions.html>

**34<sup>th</sup> New Phytologist Symposium**

**July 15 – 18, 2014. Lake Tahoe - Tahoe City, USA**

**Title:** Systems biology and ecology of CAM plants

**Description:** We aim to promote basic research in crassulacean acid metabolism (CAM) by integrating functional genomics with biochemistry, physiology, development, ecology, and evolutionary studies to gain new insights into the regulatory mechanisms and evolutionary origins of the pathway. We will highlight the potential of CAM research for tackling bioenergy and environmental challenges pertaining to water security and resource limitation and the maintenance of productivity and ecosystems services in a changing world. In addition to this, specific talks will look at new research areas and address the big questions for future research.

**Website:**

<http://www.newphytologist.org/symposiums/view/5>

**EMBO workshop on Intercellular Communication in Plant Development and Disease**

**August 24 – 29, 2014, Bischoffsheim near Strasbourg, France**

More info: <http://events.embo.org/coming-soon/index.php?EventID=w14-11>



# Seed Science Conference 2014

15-19 September 2014  
Changsha  
China

## The 11<sup>th</sup> Conference of the International Society for Seed Science ( ISSS )



Seed science plays an increasingly important role in ensuring future food security in a sustainable environment and is therefore a subject of expanding international interest.

This 11<sup>th</sup> ISSS conference will build upon the success of previous conferences to bring together international experts and young scientists from around the world with an interest in the field of seed science.

The conference aims to provide a forum for the exchange of information and ideas on seed science and the development of new scientific collaborations. It will encompass the latest research progress in key areas of seed science including: seed development, dormancy, germination, stress tolerance, germplasm preservation, seed ecology, seed engineering and biotechnology to improve seed quality and hybrid seed.

Details of the programme, registration, venue and accommodation will appear on the website <http://2014seed.doevent.com> as the event draws closer. Please send your name and e-mail address to [seedscience2014@hhrc.ac.cn](mailto:seedscience2014@hhrc.ac.cn) if you would like to be added to our mailing list and receive notification of the web site launch.



## Positions available

---

### **Biologist / Research Assistant to join our client in Wichita, KS.**

Research Assistant to work as a team member in their Wheat Breeding Program. This position will assist in developing and executing a program in Doubled-Haploids for Wheat Improvement, and will report to the Wheat Double Haploid Lead. Assistance with all activities entailed in execution of a doubled haploid program, including but not limited to care and maintenance of plants, tissue culture, ordering and preparation of supplies, data collection, and reporting.

#### Job Qualifications:

The successful candidate will have experience in the above, plus demonstrate aptitude and willingness to learn, to teach others and to carry out diverse technical activities in the lab, growth chamber and greenhouse.

Bachelor degree in plant sciences / biology or closely related field. Experience with accurate data collection and management. Computer proficiency, particularly with Microsoft Office, database and data analysis software.

- More info:

<http://careers.the-scientist.com/jobdetails.cfm/397677/Research-Assistant-Plant-Biology-Science-Job#sthash.Q36CNwpU.dpuf>

## Courses

---

**EMBO PRACTICAL COURSE ON METABOLOMICS BIOINFORMATICS FOR LIFE SCIENTISTS.** 17 - 21 March 2014 L. Emery, R. Salek, C. Steinbeck. [Application deadline 17 January 2014](#)

More info:

<http://www.ebi.ac.uk/training/course/metabolomics-2014>

**Networks and Pathways Bioinformatics for Biologists.** 9-13 June 2014. European Bioinformatics Institute, CB10 1SD. United Kingdom

More info:

<http://www.ebi.ac.uk/training/course/networks-and-pathways-2014>