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FESPB Newsletter

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Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

FESPB 2010

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XVII Congress of the Federation of European Societies of Plant Biology (FESPB).

4-9 July 2010. Valencia, Spain.

Welcome to FESPB 2010!

REGISTRATION AND CALL FOR ABSTRACTS IS NOW OPEN

ABSTRACT SUBMISSION DEADLINE: 1st March 2010

On behalf of the FESPB 2010 Organising Committee, we are delighted to invite you to participate in the XVII Congress of the Federation of European Societies of Plant Biology (FESPB) to be held in Valencia, Spain on 4-9 July 2010.

The Congress is organised by SEFV, the Sociedad Española de Fisiología Vegetal. SEFV was founded in 1974 and has over 600 members highly active in both, Academia and Education, and promoting knowledge in plant physiology and plant adaptation.

The scientific programme of the FESPB 2010 will cover most aspects of modern plant biology. The aim is to offer a conference with the highest scientific quality in which novelty on multidisciplinary approaches including systems biology, genetics, molecular cell biology and biochemistry, and ecophysiology will be presented.

Valencia is a dazzling destination. A melting pot of 2000 years of diverse cultural influences that mingle with modern trends to create a city of spectacular contrasts. Valencia offers a wide variety of options to the visitor, including beaches, countryside, mountains and areas of cultural interest besides the possibility to enjoy an excellent gastronomy.

The Conference will take place at the "Palacio de Congresos", a building designed by Norman Foster and equipped with the most advanced technologies. The Organising Committee is determined to host a Congress that will be both scientifically rewarding and socially enjoyable.

We look forward to seeing you in Valencia at FESPB 2010.

M^a Dolores Rodríguez (President of SEFV)

José Pío Beltrán (President of FESPB)

Please, visit: <http://www.geyseco.es/fespb>

FESPB homepage

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The FESPB web site has been fully renewed thanks to the effort of the FESPB Secretary General **Prof. K.A. Roubelakis-Angelakis**.

Visit it at : <http://www.fespb.org>

To submit items to FESPB*Newsletter* such as job and studentship vacancies, forthcoming conference details, comments about FESPB etc., please e-mail the details to Prof. Dolores Rodriguez (Chair of the Publications Committee) at mdr@usal.es .

For open letters please click on to the FESPB Web Forum page.

Research News



'Safety Valve' Protects Photosynthesis from Too Much Light

Photosynthetic organisms need to cope with a wide range of light intensities, which can change over timescales of seconds to minutes. Too much light can damage the photosynthetic machinery and cause cell death. Scientists at the Carnegie Institution were part of a team that found that specific proteins in algae can act as a safety valve to dissipate excess absorbed light energy before it can wreak havoc in cells.

Photosynthetic organisms need to cope with a wide range of light intensities, which can change over timescales of seconds to minutes. Too much light can damage the photosynthetic machinery and cause cell death. Scientists at the Carnegie Institution were part of a team that found that specific proteins in algae can act as a safety valve to dissipate excess absorbed light energy before it can wreak havoc in cells.

The research, performed mostly by Graham Peers in the laboratory of Krishna Niyogi from the University of California, Berkeley, included researchers at the University of Münster, Germany, and used a mutant strain of the single-celled green alga *Chlamydomonas reinhardtii*, originally isolated at the Carnegie Institution, to show that a specific protein of the light harvesting family of proteins plays a critical role in eliminating excess absorbed light energy. A mutant lacking this protein, designated LHCSR, suffered severely when exposed to fluctuating light conditions. "Photosynthetic organisms must be able to manage absorbed light energy," says study co-author Arthur Grossman of Carnegie's Department of Plant Biology, "and the LHCSR proteins appear to be critical for algae to eliminate absorbed light energy as heat as light levels in the environment fluctuate, becoming potentially toxic."

Grossman points out that photosynthetic organisms have developed a number of different mechanisms for managing the absorption of light energy and that these different mechanisms may be tailored to the diversity of environments in which organisms have evolved. Some have evolved in deserts where both light levels and temperatures can be very high while others have evolved in alpine environments where the light levels can be very high and temperatures very low.

"As we understand more about the ways in which the environment impacts the evolution of the photosynthetic machinery, we may be able to introduce specific mechanisms into plants that allow them to better manage absorbed light energy, which in turn would let them survive harsher environmental conditions" Grossman says, "which would have obvious benefits for agriculture."

He also notes the current interest in using algae to generate biofuels, and the possibility of cultivating algae in deserts, where solar input can be extremely high. As he states, "If we are going to attempt this we have to make sure that we use the right algae that can thrive and produce oils at high levels under harsh environmental conditions. It's possible that we can also tailor various features of the photosynthetic machinery to let algae use light energy more efficiently and suffer less damage under extremely high light and temperature conditions, but I would emphasize that there are many extreme challenges associated with the creation of such robust, commercially viable strains."

The research appears in the 26 November issue of *Nature*.

Source: ScienceDaily, December 6, 2009.

ABA receptors function as PP2C inhibitors in an ABA-dependent manner.

By Kim Baumann.

Abcisic acid (ABA) is a ubiquitous plant hormone that regulates various aspects of plant growth and development, including seed maturation and dormancy, and has a central role in the adaptation of vegetative tissues to environmental stresses, notably drought. Although many components of the ABA signalling pathway are known, the identity and signalling mechanisms of ABA receptors have remained elusive. Now, six research groups report the mechanism by which the pyrabactin resistance (PYR)/PYR-like (PYL)/regulatory component of ABA receptors (RCAR) family of START proteins, previously identified as ABA receptors, bind ABA and positively regulate ABA signalling.

Previous findings have reported that the *Arabidopsis thaliana* PYR/PYL/RCAR proteins function as ABA receptors that, following ABA binding, inhibit the activity of known negative regulators of ABA signalling — the type 2C protein phosphatases (PP2Cs) ABI1, ABI2, HAB1, HAB2 and PP2CA — in both seeds and vegetative tissues. The suggested model predicts that,

in the presence of ABA, PYR/PYL/RCARs bind to PP2Cs and induce the release of SNRK2 Ser/Thr kinases from PP2Cs, which would otherwise keep SNRK2s in an inactive state. SNRK2s can then phosphorylate downstream substrates, including ABA responsive element-binding protein (AREB) and ABA responsive element-binding factor (ABF) bZIP transcription factors, which activate ABA-responsive genes and ABA-related responses.

In vitro studies by Fujii *et al.* show that combining PYR1, ABI1, SNRK2.6 (also known as SRK2E) and ABF2 is sufficient for ABA triggered ABF2 phosphorylation. This indicates that these four proteins are the core components of the ABA signalling pathway.

The other five groups carried out structural analyses of PYL1, PYL2, PYR1 and PYR2 alone, bound to ABA or in complex with both ABA and PP2Cs. The data reveal how ABA binding induces a conformational change that allows the receptors to stably bind to PP2Cs. PYR and PYL have a seven-stranded curved β -sheet that forms a central cavity resembling that of a folded hand. The surface of the cavity also comprises α -helices, which, together with the inner side of the β -sheet, constitute the ABA-binding site. Two highly conserved β -loops act as cavity 'lids', which, in the absence of ABA, are in an open conformation that allows ABA to access the cavity. On ABA binding, the β -loops adopt a closed-lid conformation. Importantly, this conformational change modifies the lid to create a binding site for PP2C. The receptor-PP2C interaction results in the β -loops covering the PP2C active site, thereby inhibiting its activity. This suggests that ABA receptors function as PP2C inhibitors in an ABA-dependent manner.

Understanding the structural basis of ABA receptor interactions has important implications as it paves the way for the design of agonist molecules that could increase the resistance of crops to water stress.

Journal Reference: Nature Reviews Molecular Cell Biology 11, 2 (1 January 2010).

Original Research Papers:

Fujii, H. *et al.* Nature 462, 660–664 (2009).

Nishimura, N. *et al.* Science 326, 1373–1379 (2009).

Miyazono, K. *et al.* Nature 462, 609–614 (2009).

Melcher, K. *et al.* Nature 462, 602–608 (2009).

Santiago, J. *et al.* Nature 462, 665–668 (2009).

Yin, P. *et al.* Nature Struct. Mol. Biol. 16, 1230–1236 (2009).

How plants 'feel' the temperature rise

Plants are incredibly temperature sensitive and can perceive changes of as little as one degree Celsius. Now, a report in the January 8th issue of the journal Cell, a Cell Press publication, shows how they not only 'feel' the temperature rise, but also coordinate an appropriate response - activating hundreds of genes and deactivating others; it turns out it's all about the way that their DNA is packaged.

The findings may help to explain how plants will respond in the face of climate change and offer scientists new leads in the quest to create crop plants better able to withstand high temperature stress, the researchers say.

'We've uncovered a master regulator of the entire temperature transcriptome,' said Philip Wigge of John Innes Centre in the United Kingdom in reference to the thousands of genes that are differentially activated under warmer versus cooler conditions.

Using the model plant *Arabidopsis thaliana* the researchers show that a key ingredient for plants' temperature sensing ability is a specialised histone protein, dubbed H2A.Z, that wraps DNA into a more tightly packed structure known as a nucleosome. Wigge likens nucleosomes to compact balls of string. As temperatures rise, H2A.Z histones allow DNA to progressively unwrap, leading nucleosomes to loosen up, they show.

'When it gets warmer, the DNA unwraps,' he said, which allows some genes to switch on and others to switch off. They aren't yet sure exactly how all that happens, but Wigge suspects the altered nucleosome structure gives access to sites on the DNA where activators of some genes can bind along with repressors of other genes.

'In addition to H2A.Z containing nucleosomes having more tightly wrapped DNA, our results suggest that the degree of unwrapping may also be responsive to temperature,' the researchers wrote. 'This result suggests a direct mechanism by which temperature may influence gene expression, since it has been shown that RNA Pol II [the enzyme responsible for transcribing DNA into messenger RNA] does not actively invade nucleosomes, but waits for local unwrapping of DNA from nucleosomes before extending transcription. In this way, genes with a paused RNA Pol II will show increased transcription with greater temperature as local unwrapping is increased.' The basic discovery could ultimately prove to have important implications for world food security, the researchers said.

As the number of people and affluence around the world continues to grow, 'it is projected that world agriculture will have to increase yields by 70 to 100 percent in the next 100 years,' Wigge said. 'Under climate change it will be challenging simply to maintain present yields, let alone increase them.' Crops such as wheat are particularly vulnerable to very hot and dry summers, he added, as evidenced by the fact that wheat reserves recently fell to their lowest level in 30 years.

He says the new understanding of plants' temperature sensitivity may prove to be critical for breeding more temperature-resistant crops. His team plans to explore this possibility by studying the role of these H2A.Z histones in a model plant that is more closely related to crops.

'We'd like to engineer a plant where we can control the histones in particular tissues such that it is selectively 'blind' to different temperatures,' Wigge said. 'Obviously you can't make a completely temperature-proof plant, but there is a lot of scope to develop crops that are more resilient to the high temperatures we are increasingly going to experience.'

Source: Science Centric. 11 January 2010

Key Seed Size Gene Identified

Scientists from the John Innes Centre in Norwich, UK and the University of Freiburg in Germany have uncovered a gene in plants that is responsible for controlling the size of seeds, which could lead to ways of improving crops to help ensure food security in the future.

Increasing seed or grain size has been key in the domestication of the crops used in modern agriculture, and with a growing world population, further increasing the yield of crops is one goal of agricultural research. Michael Lenhard, funded by the Biotechnology and Biological Sciences Research Council (BBSRC), has identified a gene in the model plant *Arabidopsis* that determines overall seed size, and is now investigating how this could be used to for the improvement of crops.

Publishing in the Proceedings of the National Academy of Sciences, the team from the John Innes Centre, an institute of the BBSRC, demonstrated that the gene acts locally at the base of the growing seed. It produces an as yet unidentified mobile growth signal that determines final seed size. If the gene is turned off, smaller seeds are produced, but crucially if the gene is turned on at a higher level than normal, seeds a third larger in size and weight are produced. This is the first time such a reciprocal effect on seed size has been observed, and points to the fundamental importance of this gene in plant development.

More work is now needed before this research can be applied to crop plants. One effect of increasing the seed size in the experimental plants was to decrease the total number of seeds produced, so there was no overall increase in yield. The scientists did notice an increase in the relative oil content of the larger seeds, so the effects of altering this gene in oil seed rape is currently being investigated.

Unravelling this gene's role in determining the final seed size will also be important for other strategies for increasing yield, an example of how fundamental plant science can inform and drive efforts to ensure food security.

Professor Mike Bevan, Acting Director of the John Innes Centre, said "This work shows how JIC's focus on understanding the mechanisms controlling plant growth can have immediate useful application for crop improvement."

Journal Reference: Adamski et al. PNAS 106: 20115-20120. 2009

Source: ScienceDaily, December 6, 2009.

Flowering time control and applications in plant breeding

Shifting the seasonal timing of reproduction is a major goal of plant breeding efforts to produce novel varieties that are better adapted to local environments and changing climatic conditions. The key regulators of floral transition have been studied extensively in model species, and in recent years a growing number of related genes have been identified in crop species, with some notable exceptions. These sequences and variants thereof, as well as several major genes which were only identified in crop species, can now be used by breeders as molecular markers and for targeted genetic modification of flowering time. This article reviews the major floral regulatory pathways and discusses current and novel strategies for altering bolting and flowering behavior in crop plants.

C. Jung and A. E. Müller. Trends in Plant Science. Vol. 14: 563-573. October 2009.

Unique Study Isolates DNA From Linnaeus' Botanical Collections

Researchers at Uppsala University has succeeded in extracting long DNA fragments from dried, pressed plant material collected in the 1700s by Linnaeus' apprentice Adam Afzelius. It is hoped that the study, led by Associate Professor Katarina Andreassen, will shed light on whether plants growing today at Linnaeus' Hammarby estate outside Uppsala reflect the species cultivated by Linnaeus himself.

A large number of plants of uncertain provenance grow at Carl Linnaeus' Hammarby estate, a museum and popular tourist destination. Have they been present since Linnaeus' time? In addition to probing this question, the current study will test the limits of DNA-sequencing methods with regard to old plant material and has already demonstrated that it is possible to sequence plant material more than 200 years old. The study is now published in the scientific journal *Taxon*.

"This opens up a number of exciting research possibilities in connection with material from herbaria throughout the world", says Katarina Andreassen.

The researchers hopes to initiate corresponding DNA investigations of plant material from the garden at Hammarby as soon as possible.

"It would be fun, if we can show that the old material is genetically identical with the plants currently growing at Hammarby, to create a living herbarium for summer visitors to the garden", says Katarina Andreassen.

Linnaeus' significance for the science of systematic biology, as reflected in locations in Sweden (Uppsala and Småland) and collection locations in seven other countries, is the focus of a World Heritage Site nomination. The foundations of systematic biology were laid by Carl Linnaeus through the aid of an extensive scientific network. If the nomination is approved by UNESCO preserved animals and plants will for the first time constitute a central aspect of a World Heritage Site.

Source: ScienceDaily (Aug. 31, 2009).

Amazing: Corn genome decoded

In recent years, scientists have decoded the DNA of humans and a menagerie of creatures but none with genes as complex as a stalk of corn, the latest genome to be unraveled.

A team of scientists led by The Genome Centre at Washington University School of Medicine in St. Louis published the completed corn genome in the Nov. 20 journal *Science*, an accomplishment that will speed efforts to develop better crop varieties to meet the world's growing demands for food, livestock feed and fuel.

'Seed companies and maize geneticists will pounce on this data to find their favourite genes,' says senior author Richard K. Wilson, Ph.D., director of Washington University's Genome Centre, who led the multi-institutional sequencing effort. 'Now they'll know exactly where those genes are. Having the complete genome in hand will make it easier to breed new varieties of corn that produce higher yields or are more tolerant to extreme heat, drought, or other conditions.'

Corn, also known as maize, is the top U.S. crop and the basis of products ranging from breakfast cereal to toothpaste, shoe polish and ethanol. The corn genome is a hodgepodge of some 32,000 genes crammed into just 10 chromosomes. In comparison, humans have 20,000 genes dispersed among 23 chromosomes.

The \$29.5 million maize sequencing project began in 2005 and is funded by the National Science Foundation and the U.S. departments of agriculture and energy. The genome was sequenced at Washington University's Genome Centre. The overall effort involved more than 150 U.S. scientists with those at the University of Arizona in Tucson, Cold Spring Harbor Laboratory in New York and Iowa State University in Ames playing key roles.

The group sequenced a variety of corn known as B73, developed at Iowa State decades ago. It is known for its high grain yields and has been used extensively in both commercial corn breeding and in research laboratories.

The genetic code of corn consists of 2 billion bases of DNA, the chemical units that are represented by the letters T, C, G and A, making it similar in size to the human genome, which is 2.9 billion letters long.

But that's where much of the similarity ends. The challenge for Wilson and his colleagues was to string together the order of the letters, an immense and daunting task both because of the corn genome's size and its complex genetic arrangements. About 85 percent of the DNA segments are repeated. Jumping genes, or transposons, that move from place to place make up a significant portion of the genome, further complicating sequencing efforts.

A working draft of the maize genome, unveiled by the same group of scientists in 2008, indicated the plant had 50,000-plus genes. But when they placed the many thousands of DNA segments onto chromosomes in the correct order and closed the remaining gaps, the researchers revised the number of genes to 32,000.

'Sequencing the corn genome was like driving down miles and miles of desolate highway with only sporadically placed sign posts,' says co-investigator Sandra Clifton, Ph.D., of Washington University. 'We had a rudimentary map to guide us, but because of the repetitive nature of the genome, some of the landmarks were erroneous. It took the dedicated efforts of many scientists to identify the correct placement of the genes.'

Interestingly, plants often have more than one genome and corn is no exception. The maize genome is composed of two separate genomes melded into one, with four copies of many genes. As corn evolved over many thousands of years, some of the duplicated genes were lost and others were shuffled around. A number of genes took on new functions.

Corn is the third cereal-based crop after rice and sorghum - and the largest plant genome to date - to have its genome sequenced, and scientists will now be able to look for genetic similarities and differences between the crops. 'For example, rice grows really well in standing water but corn doesn't,' explains co-investigator Robert Fulton, of Washington University. 'Now, scientists can compare the two genomes to find variations of corn genes that are more tolerant to wet conditions.'

The United States is the world's top corn grower, producing 44 percent of the global crop. In 2009, U.S. farmers are expected to produce nearly 13 billion bushels of corn, according to the U.S. Department of Agriculture.

Source: Science Centric, 21 Nov. 2009.

New Discovery May Lead to Heartier, High-Yielding Plants

In a research report published in the November 2009 issue of the journal *Genetics*, scientists show how a family of genes (1-aminocyclopropane-1-carboxylate synthase, or ACS genes) are responsible for production of ethylene. This gas affects many aspects of plant development, and this information lays the foundation for future genetic manipulation that could make plants disease resistant, able to survive and thrive in difficult terrain, increase yields, and other useful agronomical outcomes.

This discovery was made with the weed *Arabidopsis thaliana*, but it will be applicable to plants used in agriculture.

"I hope that this work will provide insights into how a set of genes work together like a finely tuned symphony to regulate plant growth because we may be able to use such knowledge to engineer plants more suited to our changing world," said Athanasios Theologis, a senior scientist at the Plant Gene Expression Center of the U.S. Department of Agriculture and the senior researcher involved in the work. "This is critically important because as the human population grows, we may need to produce more food in the same or in less space."

To understand the function and regulatory roles of each ACS gene in ethylene production during plant development, scientists from Theologis' laboratory analyzed the essential and nonessential roles of each of the family of *Arabidopsis* ACS genes. They found that while loss of any single ACS gene had no visible effect on the plant, it did affect the activity of other genes in the family. They grew different plants that had different combinations of these genes "turned on" and "turned off" and found that the members of this gene family have different but overlapping functions in plant development, such as growth, flowering time, gravitostimulation, and disease resistance.

"Ethylene gas is best known for causing fruit to ripen," said Mark Johnston, Editor-in-Chief of the journal *GENETICS*, "but the molecule is critical to development and growth of plants. By revealing how plants regulate the amount of ethylene they produce, this study gives scientists an entirely new genetic approach for developing heartier, more productive crops. This is becoming increasingly important as our planet warms and our population grows."

Journal Reference: Tsuchisaka et al. *Genetics*, 2009; 183 (3): 979.

Source: ScienceDaily, December 6, 2009.

Banana Plants May Be Used In Production Of Plastic Products

Researchers at Queen's University Belfast are pioneering a new technique for the use of banana plants in the production of plastic products.

The Polymer Processing Research Centre at Queen's is taking part in a €1 million study known as the Badana project. The project will develop new procedures to incorporate by-products from banana plantations in the Canary Islands into the production of rotationally

moulded plastics. In addition to the environmental benefits, the project will increase the profitability of the plantation owners and help job security for those working in the area.

Mark Kearns, Rotational Moulding Manager at the Polymer Processing Research Centre in Queen's School of Mechanical and Aerospace Engineering, said: "Almost 20 per cent of the bananas consumed in Europe are produced in the Canary Islands, with around 10 million banana plants grown annually in Gran Canaria alone.

"Once the fruit has been harvested, the rest of the banana plant goes to waste. An estimated 25,000 tonnes of this natural fibre is dumped in ravines around the Canaries every year.

"The Badana project aims to find a use for these plants. The natural fibres contained within them may be used in the production of rotationally moulded plastics, which are used to make everyday items such as, oil tanks, wheelie bins, water tanks, traffic cones, plastic dolls and many types of boats. The banana plant fibres will be processed, treated and added to a mix of plastic material and sandwiched between two thin layers of pure plastic providing excellent structural properties. The project gives a whole new meaning to 'banana sandwich'.

"This new technique will have substantial environmental benefits. It will hopefully result in a substantial reduction in the amount of Polyethylene used in the rotational moulding process, ushering in a new and more sustainable era in the production of rotationally moulded plastics. The research and development of this new approach will help create jobs and the banana plantations will ultimately benefit financially from the sale of the remains of millions of harvested banana plants, which would otherwise go to waste."

"It is testament to our expertise in rotational moulding, and strong links with several Spanish Universities, that the Polymer Processing Research Centre has been asked to contribute in this groundbreaking project."

The funding for the Badana project has been provided by the European Union's Seventh Framework Programme.

Source: ScienceDaily (Oct. 9, 2009).

If Only The Weeds Would Keep Their Genes To Themselves

Family can be a blessing and a curse, and never more so than in the case of crop plants and their wild relatives. These wild and weedy relatives harbor unique and beneficial genes that may no longer be found in their cultivated siblings, but they also harbor genetic traits that farmers have intentionally selected against in their domesticated brethren. The close genetic relationships between some crop species and their wild relatives allow them to readily hybridize, sharing both the beneficial and problematic genes with each other.

The ecological and economic impacts of gene flow between crops and their weedy relatives are significant. Weedy relatives may acquire beneficial genes from cultivated cousins, potentially increasing their invasive ability. Farmers may find that their crop yields decrease or crops may be more difficult to harvest if they hybridize with a weedy relative. These are only a few consequences of the gene flow that occurs all the time between crops and wild relatives.

A recent article in the October issue of the American Journal of Botany by Dr. Adeline Barnaud and colleagues explores the role of gene flow between cultivated sorghum and its weedy relatives in a village in northern Cameroon. Sorghum is a staple food crop that is essential to food security in semi-arid regions of Asia and Africa.

Barnaud and her colleagues used a multidisciplinary approach involving biologists and social scientists in addressing questions of gene flow among the species and how farmers' practices affect this gene flow. The farmers in northern Cameroon distinguish a variety of types of sorghum—ranging from weedy to cultivated with intermediates in between—but whether there is any genetic basis to these types was a question the researchers addressed. "Farmers have quite accurate perceptions about the genetic nature of their sorghum plants, accurately distinguishing not only domesticated landraces from the others, but also among three classes of introgressed individuals, and classing all four along a continuum that corresponds well to genetic patterns," Barnaud said. "Their practices are fairly effective in limiting gene flow."

The researchers found that farmers actively eradicate weedy types from their fields because their presence lowers yields. However, several of the farmers' practices unintentionally favor gene flow. Although farmers actively select against the weedy types, some are maintained to enhance diversity and lower risks of crop failure due to environmental changes, such as with annual rainfall. Also, despite a desire to remove the weedy sorghums, as any farmer or home gardener knows, it is often difficult to identify weeds when the plants are young, and, even if they are properly identified, it may be difficult to fully remove the weeds. As a result, some seeds from the weedy individuals are able to survive in the field and persist year after

year. Dr. Barnaud and her colleagues discovered that when harvesting seed for the following year, farmers in this village may not select seed from the middle of the fields where plants are less likely to have been pollinated by weedy types. In addition, the presence of intermediate weedy types may facilitate gene flow between the weediest type and the cultivated type due to their intermediate flowering time and the farmers' mode of management.

A multidisciplinary approach is truly necessary when addressing this type of question. "Biologists and social scientists need to work together more often, using their complementary methods to answer shared questions about human-plant interactions," Barnaud said. "Few studies offer really hard, detailed data on how farmers' practices shape patterns in the genetic diversity of their crops. We showed the primary role that farmers continue to play as drivers of crop evolution, in this case by limiting gene flow from wild to crop.

"Such connections between farmers' knowledge and practices and the dynamics of diversity need to be better understood, and taken into account when management plans are being defined."

Journal reference: Barnaud et al. *Am. J. Bot.*, 2009; 96: 1869-1879.

Source: ScienceDaily (Oct. 9, 2009).

'Killer Petunias' Should Join the Ranks of Carnivorous Plants, Scientists Propose

Scientists from the Royal Botanic Gardens, Kew and the Natural History Museum believe that carnivorous behaviour in plants is far more widespread than previously thought, with many commonly grown plants -- such as petunias -- at least part way to being "meat eaters." A review paper, *Murderous plants: Victorian Gothic, Darwin and modern insights into vegetable carnivory*, is published (4 December 2009) in the *Botanical Journal of the Linnean Society*.

Carnivorous plants have caught the imagination of humans since ancient times, and they fitted well into the Victorian interest in Gothic horrors. Accounts of man-eating plants published in 19th century works have long since been discredited, but they continue to appear in different media including films (Audrey II in *Little Shop of Horrors*) and books (Tentacula in the *Harry Potter* series). Even popular Japanese cartoon *Pokémon* includes some characters based on carnivorous plants (Bellsprout, Weepinbell and Victreebell).

Carnivorous plants fascinated Charles Darwin, and he and his friend Sir Joseph Hooker (Director of the Royal Botanic Gardens, Kew at that time) had an extensive correspondence concerning them. Darwin's book *Insectivorous Plants* played a critical role in the idea that plants could eat animals being generally accepted. Before this, many botanists (including Linnaeus) had refused to accept that this could be the case.

Since Darwin's time, several groups have been generally recognised as carnivorous plants (including sundews, Venus flytraps and pitcher plants). Various other plants have been suggested as possible carnivores by some authors, but wide acceptance of these has failed to materialise. Defining what constitutes carnivory in plants is a challenge, and authors include or exclude groups of plants on the basis of different sets of criteria. Professor Mark Chase and co-authors from the Royal Botanic Gardens, Kew and the Natural History Museum contend that carnivory and non-carnivory should not be treated as a black and white situation, and they view plants as being on a sliding scale between those that show no carnivorous characteristics and those that are real "meat eaters" such as the Venus flytrap.

Plants like petunias and potatoes have sticky hairs that trap insects, and some species of campion have the common name catchfly for the same reason. However, some of the commonly accepted carnivores have not been demonstrated to have the ability to digest the insects they trap or to absorb the breakdown products. In their paper, Chase et al. review each of the groups of potential carnivores.

Professor Mark Chase, Keeper of the Jodrell Laboratory at the Royal Botanic Gardens, Kew says, "Although a man-eating tree is fictional, many commonly grown plants may turn out to be cryptic carnivores, at least by absorbing through their roots the breakdown products of the animals that they ensnare. We may be surrounded by many more murderous plants than we think." Vaughan Southgate, President of the Linnean Society of London says, "This scholarly, beautifully illustrated, review of carnivorous plants and the different levels of carnivory that exist in the plant world by botanists at the Royal Botanic Gardens, Kew and the Natural History Museum makes for fascinating reading."

Journal Reference: Chase et al. *Botanical J. of the Linnean Society*, 2009; 161 (4): 329.

Source: ScienceDaily, December 6, 2009.

How Did Flowering Plants Evolve to Dominate Earth?

To Charles Darwin it was an 'abominable mystery' and it is a question which has continued to vex evolutionists to this day: when did flowering plants evolve and how did they come to dominate plant life on earth? A new study in Ecology Letters reveals the evolutionary trigger which led to early flowering plants gaining a major competitive advantage over rival species, leading to their subsequent boom and abundance.

The study, by Dr Tim Brodribb and Dr Taylor Field of the University of Tasmania and University of Tennessee, used plant physiology to reveal how flowering plants, including crops, were able to dominate land by evolving more efficient hydraulics, or 'leaf plumbing', to increase rates of photosynthesis.

"Flowering plants are the most abundant and ecologically successful group of plants on earth," said Brodribb. "One reason for this dominance is the relatively high photosynthetic capacity of their leaves, but when and how this increased photosynthetic capacity evolved has been a mystery."

Using measurements of leaf vein density and a linked hydraulic-photosynthesis model, Brodribb and Field reconstructed the evolution of leaf hydraulic capacity in seed plants. Their results revealed that an evolutionary transformation in the plumbing of angiosperm leaves pushed photosynthetic capacity to new heights.

The reason for the success of this evolutionary step is that under relatively low atmospheric CO₂ conditions, like those existing at present, water transport efficiency and photosynthetic performance are tightly linked. Therefore adaptations that increase water transport will enhance maximum photosynthesis, exerting substantial evolutionary leverage over competing species.

The evolution of dense leaf venation in flowering plants, around 140-100 million years ago, was an event with profound significance for the continued evolution of flowering plants. This step provided a 'cretaceous productivity stimulus package' which reverberated across the biosphere and led to these plants playing the fundamental role in the biological and atmospheric functions of the earth.

"Without this hydraulic system we predict leaf photosynthesis would be two-fold lower than present," concludes Brodribb. "So it is significant to note that without this evolutionary step land plants would not have the physical capacity to drive the high productivity that underpins modern terrestrial biology and human civilisation."

Source: ScienceDaily, December 6, 2009.

Insect Resistance to Bt Crops Can Be Predicted, Monitored and Managed

Since 1996, crop plants genetically modified to produce bacterial proteins that are toxic to certain insects, yet safe for people, have been planted on more than 200 million hectares worldwide. The popularity of these Bt crops, named after the bacterium *Bacillus thuringiensis*, comes from their ability to kill some major pests, allowing farmers to save money and lessen environmental impacts by reducing insecticide sprays.

However, since insects can evolve resistance to toxins, strategies must be implemented to ensure that Bt crops remain effective. A new study published in the December issue of *Journal of Economic Entomology* entitled analyzes insect resistance data from five continents, as reported in 41 studies, and concludes that existing theories and strategies can be used to predict, monitor, and manage insect resistance to Bt crops.

According to lead author Dr. Bruce E. Tabashnik, "Resistance is not something to be afraid of, but something that we expect and can manage if we understand it. Dozens of studies monitoring how pests have responded to Bt crops have created a treasure trove of data showing that resistance has emerged in a few pest populations, but not in most others. By systematically analyzing the extensive data, we can learn what accelerates resistance and what delays it. With this knowledge, we can more effectively predict and thwart pest resistance."

Among the authors' conclusions are:

- The refuge strategy (growing non-Bt crops near the Bt crops) can slow the evolution of insect resistance by increasing the chances of resistant insects mating with non-resistant ones, resulting in non-resistant offspring.
- Crops that are "pyramided" to incorporate two or more Bt toxins are more effective at controlling insect resistance when they are used independently from crops that contain only one Bt toxin.
- Resistance monitoring can be especially effective when insects collected from the field include survivors from Bt crops.

- DNA screening can complement traditional methods for monitoring resistance, such as exposing insects to toxins in the lab.
 - Despite a few documented cases of field-evolved resistance to the Bt toxins in transgenic crops, most insect pest populations are still susceptible. With Bt crop acreage increasing worldwide, incorporating enhanced understanding of observed patterns of field-evolved resistance into future resistance management strategies can help to minimize the drawbacks and maximize the benefits of current and future generations of transgenic crops.
- Journal Reference: Tabashnik et al. *Econ. Entomol.*, 102(6): 2011-2025 (2009).
Source: ScienceDaily, December 6, 2009

New genetic map will speed up plant breeding of the world's most important medicinal crop

Plant scientists at the University of York have published the first genetic map of the medicinal herb *Artemisia annua*. The map is being used to accelerate plant breeding of *Artemisia* and rapidly develop the species into a high-yielding crop. This development is urgently needed to help meet escalating demand for effective malaria treatments. Though preventable and treatable, malaria is a serious global health problem, estimated to kill almost a million people every year. The most effective drugs for treating malaria are Artemisinin Combination Therapies (ACTs). Increased funding for malaria treatments means demand for ACTs is expected to double from last year's figures, to around 200 million treatments, by 2012. However, meeting this increased demand will be a challenge: artemisinin is extracted from the plant *Artemisia annua*, but yields are low, making production expensive. In recent years, *Artemisia* production has been uneconomic and planting areas have declined, raising fears of shortages.

Plant scientists at the Centre for Novel Agricultural Products (CNAP) in the Department of Biology at the University of York are addressing this problem by using molecular technologies to rapidly improve the *Artemisia* crop. In the latest issue of *Science*, they publish the first genetic map of this species, plotting the location on the plant's genome of genes, traits and markers associated with high performance. This will enable scientists to recognise young plants as high performers from their genetics. It will also inform the selection of suitable parent plants for breeding experiments.

The map has been validated in glasshouse experiments that found the top-performing plants had elevated frequencies of genetic indicators for high yield. The project is led by Professor Dianna Bowles and Professor Ian Graham. Professor Graham says "The map is already proving to be an essential tool for us. With our new understanding of *Artemisia* genetics, we can produce improved, non-GM varieties of *Artemisia* much faster than would otherwise be possible." This speed is essential. "We intend to get high-yielding seed to farmers in the next 2-3 years in order to supply soaring demand for malaria treatments" explains Professor Dianna Bowles. "This is a really tight deadline and we can only do it with the benefit of the new knowledge provided by the map." The work demonstrates how modern genetics is shortening the timescales needed to turn a wild plant species into a domesticated crop.

The scientists at York are creating the new varieties for use by many thousands of small scale growers in the developing world, for whom the *Artemisia* crop is an important source of income. The project has just received its second grant from the Bill & Melinda Gates Foundation. This grant will support final development of the new varieties and their delivery to *Artemisia* producers in Africa and Asia.

Source: e! Science News in Biology & Nature, January 14, 2010.

Engineering the cell wall by reducing de-methyl-esterified homogalacturonan improves saccharification of plant tissues for bioconversion

Plant cell walls represent an abundant, renewable source of biofuel and other useful products. The major bottleneck for the industrial scale-up of their conversion to simple sugars (saccharification), to be subsequently converted by microorganisms into ethanol or other products, is their recalcitrance to enzymatic saccharification. We investigated whether the structure of pectin that embeds the cellulose-hemicellulose network affects the exposure of cellulose to enzymes and consequently the process of saccharification. Reduction of de-methyl-esterified homogalacturonan (HGA) in *Arabidopsis* plants through the expression of a fungal polygalacturonase (PG) or an inhibitor of pectin methyl-esterase (PMEI) increased the efficiency of enzymatic saccharification. The improved enzymatic saccharification efficiency

observed in transformed plants could also reduce the need for acid pretreatment. Similar results were obtained in PG-expressing tobacco plants and in PME1-expressing wheat plants, indicating that reduction of de-methyl-esterified HGA may be used in crop species to facilitate the process of biomass saccharification.

Journal Reference: Lionettia et al. PNAS vol. 107 no. 2, 616-621. January 12, 2010.

Cell death occurs in the same way in plants, animals, and humans

Research has previously assumed that animals and plants developed different genetic programs for cell death. Now an international constellation of research teams, including one at the Swedish University of Agricultural Sciences, has shown that parts of the genetic programs that determine programmed cell death in plants and animals are actually evolutionarily related and moreover function in a similar way. The findings were published in Nature Cell Biology 11 October.

For plants and animals, and for humans as well, it is important that cells both can develop and die under controlled forms. The process where cells die under such forms is called programmed cell death. Disruptions of this process can lead to various diseases such as cancer, when too few cells die, or neurological disorders such as Parkinson's, when too many cell die.

The findings are published jointly by research teams at SLU (Swedish University of Agricultural Sciences) and the Karolinska Institute, the universities of Durham (UK), Tampere (Finland), and Malaga (Spain) under the direction of Peter Bozhkov, who works at SLU in Uppsala, Sweden. The research findings are published in the prestigious scientific journal Nature Cell Biology. The scientists have performed comparative studies of an evolutionarily conserved protein called TUDOR-SN in cell lines from mice and humans and in the plants Norway spruce and mouse-ear cress. In both plant and animal cells that undergo programmed cell death, TUDOR-SN is degraded by specific proteins, so-called proteases.

The proteases in animal cells belong to a family of proteins called caspases, which are enzymes. Plants do not have caspases - instead TUDOR-SN is broken down by so-called meta-caspases, which are assumed to be ancestral to the caspases found in animal cells. For the first time, these scientists have been able to demonstrate that a protein, TUDOR-SN, is degraded by similar proteases in both plant and animal cells and that the cleavage of TUDOR-SN abrogate its pro-survival function. The scientists have thereby discovered a further connection between the plant and animal kingdoms. The results now in print will therefore play a major role in future studies of this important protein family.

Cells that lack TUDOR-SN often experience premature programmed cell death. Furthermore, functional studies at the organism level in the model plant mouse-ear cress show that TUDOR-SN is necessary for the development of embryos and pollen. The researchers interpret the results to mean that TUDOR-SN is important in preventing programmed cell death from being activated in cells that are to remain alive.

The research teams maintain that the findings indicate that programmed cell death was established early on in evolution, even before the line that led to the earth's multicellular organisms divided into plants and animals. The work also shows the importance of comparative studies across different species to enhance our understanding of how fundamental mechanisms function at the cellular level in both the plant and animal kingdoms, and by extension in humans.

Journal reference: Sundström et al. Nature Cell Biology. November 2009, Volume 11, No 11, pp1273-1387.

Source: Science Centric .

Mapping and sequencing of soybean genome paves the way for improved soybean crops

Soybean, one of the most important global sources of protein and oil, is now the first major crop legume species with a published complete draft genome sequence. This sequence, which essentially provides a parts list of the soybean genome, will help scientists use the plant's genes to improve its characteristics. The soybean sequencing study appears as the cover story of the January 13 edition of Nature. Value of the new soybean sequence

Scientists will use the new sequence to identify which genes are responsible for particular plant characteristics, and then target specific genes to produce desired characteristics. These desired characteristics may include increases in the plant's oil content to promote the use of soybean oil as a biofuel; bigger crops; improved resistance to pests and diseases that currently claim large percentages of soybean crops; improvements in the digestibility of

soybeans by animals and humans; and reductions in contaminants present in the manure of soybean-fed swine and poultry that may pollute farm runoff.

The research team plans to identify which soybean genes warrant targeting by:

- Comparing the genomes of different varieties of soybean plants to one another.
- Resequencing 20,000 soybean lines that are currently stored in the National Plant Germplasm System to identify desired variances of genes that are not currently captured by domesticated soybean lines.

"When soybeans were domesticated, they were selected for seed size and other traits, but there were a lot of potentially valuable genes left behind," said Scott Jackson of Purdue University--the corresponding author on the soybean genome paper. "There may be valuable genes associated with protein content or disease resistance in the stored lines that are not currently in the cultivated lines."

Having the new soybean sequence as a reference will significantly speed and reduce the costs of resequencing the 20,000 stored soybean lines.

A critical prerequisite to sequencing

The sequencing of the soybean genome was initiated by the production of a physical map of the soybean genome by a research team that was funded by the National Science Foundation (NSF). Production of this map was complicated by the complexities of the soybean genome. These complexities include duplicate copies of genes that account for 70 to 80 percent of the genome's 46,000 genes. These gene copies are scattered throughout the genome and so are particularly difficult to locate.

In addition, the soybean genome contains large numbers of transposable elements, also known as TEs. TEs are mobile DNA pieces that may impact gene expression, but are difficult to distinguish from genes.

The research team conquered the complexities of the soybean genome and produced the map of the soybean genome, which has a lower resolution than the sequence, as a critical prerequisite to the study's sequencing component. The map helped the researchers sequence the genome by enabling them to: 1) distinguish between TEs and genes during sequencing; and 2) break apart and then accurately reassemble the soybean genome as if it were a huge puzzle--as necessary to sequence the genome via the whole genome shotgun strategy.

A closely coordinated project

Because of the importance of the mapping project to the sequencing project, these two components of the study were closely coordinated. "The close coordination of support for this project," said Jane Silverthorne of NSF, "was facilitated by the National Plant Genome Initiative, which is managed by the Interagency Working group on Plant Genomes, whose members include DOE, USDA and NSF." Funding for the mapping/sequencing study was also provided by the United Soybean Board.

A complicated genome

Containing so many TEs and gene duplicates, the soybean genome is "the most complicated genome sequenced to date," said Jackson. And some of the same complexities that complicated the mapping and sequencing of the genome may also complicate the targeting of soybean genes. "If I'm selecting for a gene, I may have difficulty locating all of the necessary duplicates of that gene, explains Jackson. "It has a lot of backup copies."

Confident that such difficulties will be overcome, Silverthorne describes the new soybean sequence as "a valuable tool that will enable research towards a deeper understanding of the impacts of multiple genome copies on genome organization and function." Indeed, Jackson says that techniques developed to map and sequence the soybean genome are already being applied to other sequencing projects.

What's more, the results of the sequencing project have already provided grist for a second paper, which will appear in *The Plant Cell* on January 15, 2010. Jianxin Ma of Purdue University and a member of the sequencing team says that this second paper will explain how TEs thrive in the host genome: "We found that some 'dead' TEs can actually be revived by swapping with their active TE partners, and thus restore or even enhance their ability to proliferate using the amplification machinery encoded by their partners. Although TEs are ubiquitous, what we discovered has not been seen in any other organisms yet."

Source: e! Science News in Biology & Nature. January 13, 2010.

Forthcoming meetings



Keystone Symposia: RNA Silencing Mechanisms in Plants

Hilton Santa Fe, New Mexico, USA

02/21/2010 - 02/26/2010

<http://www.keystonesymposia.org/10B6>

Plant DNA Repair and Recombination 2010

Asilomar Conference Center, Pacific Grove, CA

03/02/2010 - 03/05/2010

Chair: Anne Britt (abbritt@ucdavis.edu)

<http://www.cevs.ucdavis.edu/confreg/index.cfm?confid=451>

Keystone Symposia. Receptors and Signaling in Plant Development and Biotic Interactions.

Granlibakken Resort, Tahoe City, California, USA.

03/14/2010 - 03/19/2010

Scientific Organizers- Thomas Boller and Jen Sheen.

<http://www.keystonesymposia.org/10C2>

Plasmodesmata 2010

Sydney, Australia

03/21/2010 - 03/26/2010

For further information, contact the organizers at pd2010@bio.usyd.edu.au

<http://www.bio.usyd.edu.au/pd2010/home.html>

Trends in Natural Products Research

Leicester, UK.

04/11/2010 - 04/14/2010

For further information contact: Sarah Allen conferences@dmu.ac.uk

<http://www.phytochemicalsociety.org/leicester/>

24th New Phytologist Symposium Plant respiration and climate change: scaling from mitochondria to the globe

St Hugh's College, Oxford, UK.

04/11/2010 - 04/14/2010

Contact Helen Pinfield-Wells newphytsymp@lancaster.ac.uk

<http://www.newphytologist.org/respiration/default.htm>

12th World Congress of the International Association for Plant Biotechnology

America's Center in St. Louis, MO. USA.

06/06/2010 - 06/11/2010

<http://www.iapb2010.org>

21st International Conference on Arabidopsis Research (ICAR2010)

Yokohama, Japan.

06/06/2010 - 06/06/2010

<http://arabidopsis2010.psc.riken.jp/>

Plant Breeding for Drought Tolerance Symposium

Colorado State University; Fort Collins, CO. USA.

06/24/2010 - 06/25/2010

<http://www.droughtadaptation.org/Symposium>

20th International Plant Growth Substances Association (IPGSA) Conference

Universitat Rovira i Virgili, Tarragona, Spain.

06/28/2010 - 07/02/2010

Chair of local organizing committee: Montserrat Pages, CSIC, Barcelona.

Information and scientific program: <http://www.geyseco.es/ipgsa2010/>

SEB Annual Main Meeting 2010

Clarion Congress Hotel, Prague, Czech Republic.

06/30/2010 – 07/03/2010

Enquiries: Talja Dempster t.dempster@sebiology.org

<http://www.sebiology.org/meetings/Prague/Prague.html>

2nd Pan American Congress on Plants and Bioenergy

Sao Paulo, Brazil.

07/06/2010 - 07/10/2010

<http://www.aspb.org/meetings/PCPB2010.pdf>

4th International Conference "from Scientific Computing to Computational Engineering" (4th IC-SCCE)

7-10 July, 2010. Athens, Greece.

Organizer: Professor Demos T. Tsalhalis, Director of Laboratory of Fluid Mechanics and Energy (LFME), University of Patras, Greece.

Conference's website: <http://www.scce.gr/2010/>

3rd Workshop on Molecular Aspects of Seed Dormancy and Germination

July 18-22nd 2010, York, UK.

Contact: Dr Steven Penfield, sdp5@york.ac.uk

<http://www.york.ac.uk/org/cnap/meetings.html>

International Conference on Plant Vascular Biology 2010

Ohio State University, Columbus, Ohio, USA.

07/24/2010 - 07/28/2010

Co-Chairs: Biao Ding and David Hannapel

<http://www.ced.osu.edu/pvb2010conference/index.html>

International Symposium on the Nitrogen Nutrition of Plants (Nitrogen 2010)

Inuyama Int. Sightseeing Center "FREUDE", Aichi, Japan.

07/26/2010 - 07/30/2010

<http://www.agri.tohoku.ac.jp/cellbio/nitrogen2010/nitrogen2010.htm>

Plant Biology 2010

Montreal, Canada.

07/30/2010 - 08/05/2010

<http://www.aspb.org/meetings/pb-2010/>

13th Biennial Cellular and Molecular Biology of the Soybean Conference

Durham, NC. USA.

08/08/2010 - 08/11/2010

<http://continuingeducation.ncsu.edu/MCBS/index.html>

37th Annual Conference of the Plant Growth Regulation Society of America

Portland, Oregon. USA.

08/08/2010 - 08/12/2010

For information contact Dr. Steve McArtney, steve_mcartney@ncsu.edu

<http://www.pgrsa.org>

FASEB - Mechanisms in Plant Development

Saxtons River, Vermont. USA.
08/15/2010 - 08/19/2010
<http://www.faseb.org/meetings/>

The 6th SPPS PhD Student Conference

Espoo, Finland.
09/02/2010 - 09/05/2010
More information: <http://www.phd-spps.com>

SEB Education and Public Affairs Symposium on Food Safety and Security

Lancaster, UK.
09/13/2010 - 09/15/2010
Contact: Talja Dempster - t.dempster@sebiology.org
<http://www.sebiology.org/meetings/Lancaster2010/Lancaster.html>

From Plant Biology to Crop Biotechnology

Cold Spring Harbor Asia Conferences, Suzhou Dushu Lake Conference Center.
China.
10/25/2010 - 10/29/2010
<http://www.csh-asia.org/>

Positions available

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Post-doc Position. Centre for Research in Agricultural Genomics (CRAG) Barcelona, Spain.

A position for a Postdoctoral Fellow is available in the Laboratory of Dr. Paloma Mas, Centre for Research in Agricultural Genomics (CRAG) Barcelona, Spain, to study the cellular and molecular mechanisms underlying circadian clock function in *Arabidopsis thaliana*. The project involves the use of Genomic, Proteomic, Cellular and Molecular approaches to decipher the role of chromatin remodelling on clock progression. A highly motivated PhD with strong interest in science research is required. We offer a competitive salary according to profile and experience (funded by EURYI-EuroHORCS-ESF, EMBO YIP and MICINN) If interested, please submit your application to paloma.mas@cid.csic.es

Post-Doctoral Position. Jean-Pierre Bourgin Institute, INRA, Versailles, France

An INRA financed position is available to work with Helen North on the study of the role of cellulose and its synthesis in Arabidopsis seed mucilage. Work in the group aims to identify key genes required for the synthesis and release of seed mucilage (Macquet et al. Plant Cell 2007). Recent results have shown that Arabidopsis seed mucilage is composed of different layers and domains the most internal of which contains cellulose (Macquet et al. Plant Cell Physiol. 2007). The post- doctoral researcher will use mutants and gene reporter constructs to identify which cellulose synthases are required to produce this cellulose and carry out functional analysis to determine its contribution to mucilage structural organisation. The Jean-Pierre Bourgin Institute (IJPB) is based on the INRA Versailles site. This recently created Institute comprises around 190 permanent staff and 100 non-permanent lab members. The position is open from the 1st of April 2010 with a starting salary a PhD degree and be experienced in plant genetics, molecular biology and biochemistry. Previous work in the domain of plant polysaccharides would be an advantage. Applicants should send a curriculum vitae including the names and addresses of two referees, and a cover letter to helen.north@versailles.inra.fr or Dr Helen North, Institut Jean-Pierre Bourgin, UMR1318 INRA-AgroParisTech, BOftiment 2, INRA Centre de Versailles-Grignon, Route de St-Cyr (RD10), 78026 Versailles Cedex France.

Postdoctoral position in plant molecular biology

Forel Institute, Geneva University, Switzerland

An 18-month post-doctoral position is available starting immediately at the Institute F. A. Forel of Geneva University, Versoix, Switzerland.

<http://www.unige.ch/forel/index.html>

Post-doctoral position Plant Stress Signaling

One post-doctoral position is immediately available in the Plant Stress Signaling group at the Instituto Gulbenkian de Ciencia located near Lisbon, Portugal (<http://www.igc.gulbenkian.pt>).

The position is initially for one year but renewable up to three.

Research in the lab focuses on energy signaling and its connection to environmental changes and growth. The Arabidopsis SnRK1 protein kinases play a central role during the stress response and are required for the proper integration of environmental cues into growth and development. Sensing and signaling stress-associated energy deprivation, SnRK1s trigger global gene expression reprogramming, enabling the adjustment of energy homeostasis necessary for coping with stress. Plant miRNAs, on the other hand, have recently been implicated in adaptive processes, mediating the response to various nutrients as well as to other abiotic and biotic stresses. The present position is aimed to explore the possibility that part of the SnRK1-mediated gene expression program is implemented through miRNAs.

Applicants should have a PhD in genetics, biochemistry or molecular biology, with excellent communication skills and a strong background in molecular biology and biochemistry. Experience in miRNAs/small RNAs and/or traditional biochemical methods (immunopurification, protein complex isolation, cell fractionation, etc) is a plus.

Interested candidates should send CV, a letter of motivation with a brief description of previous research, and three letters of reference to ebaena@igc.gulbenkian.pt

Postdoctoral position. Dusseldorf, Germany

A three-year postdoctoral position is available in the laboratory of Prof. Rudiger Simon at the Institute of Genetics, Heinrich-Heine University, Dusseldorf, Germany. The project is part of a joined research program between 17 partners from academia and industry, aiming at crop plant improvement for generation of renewable energy and chemical resources.

The postholder will investigate the regulation of plant architecture, with a strong emphasis on meristem functions, in model plant species such as Arabidopsis, and employ transgenic strategies to modify plant architecture of crop plant species. Previous experience in plant molecular biology is required.

The position is funded for three years at the german E13 scale.

For applications and enquiries, contact ruediger.simon@uni-duesseldorf.de

Postdoctoral Position. University of California, Riverside, CA, USA

A postdoctoral research associate position is available at the University of California, Riverside. Our lab studies the resistance signaling pathway mediated by the tomato gene Mi-1 against nematodes and aphids. The project entails characterization of genes involved during early pest recognition events. Research opportunities also exist to participate in identification of aphid effectors. The position is available February 1, 2010. We are looking for a highly motivated individual with a PhD and a strong background in molecular genetics. Experience in biochemistry and functional genomics approaches are highly desirable. Oral and written communication skills in English and ability to interact and work with others are essential. Prior work with nematodes or insects is not required.

To apply, please send a cover letter describing research interests, a CV and names and e-mail addresses of three references to: isgouhi.kaloshian@ucr.edu

Postdoc Position

Swedish University of Agricultural Sciences in Uppsala, Sweden

A post-doctoral position is available immediately in the Department of Plant Biology and Forest Genetics, Swedish University of Agricultural Sciences in Uppsala, Sweden. The project will study cytokinin biosynthesis in moss, with special emphasis on tRNA: tRNA cytokinin synthases have been shown to contribute to the cytokinin pools in Arabidopsis. The applicant should have experience in molecular biology and sterile culture. Knowledge of tRNA metabolism is preferred. The position is for 10 months. More info and applications, with cv and references: Bjorn.Nicander@vbsg.slu.se

Postdoctoral Position In Arabidopsis & Canola Seed Coats

McGill University, Montreal, Canada.

We are seeking a highly motivated individual to join a collaborative project aimed at expressing recombinant proteins in the seed coat. This individual will use molecular genetics to create constructs for expression, analyze protein expression and study seed coat-related promoters in the mucilage secretory cells of the Arabidopsis and canola (*Brassica napus*) seed coats.

As the epidermal cells of the developing seed, the mucilage secretory cells undergo a complex process of differentiation that includes the synthesis and secretion of large quantities of polysaccharide as well as modifying enzymes (reviewed in Western, 2006, Can J Bot 84, 622-630; Haughn and Chaudhury, 2005, Trends Plant Sci 10, 474-77).

Applicants should have proven research skills in genetics and molecular biology, and experience in Arabidopsis or Canola genetics, transformation and gene expression analysis is highly desirable. This position requires excellent communication skills and is available starting August 1, 2010.

Applicants should have a PhD degree and relevant experience. Interested candidates should send a cover letter outlining their research experience and interests, a curriculum vitae, and the names, email addresses and phone numbers of 3 referees to Dr. Tamara Western, Biology Department, McGill University, 1205 ave. Docteur Penfield, Montreal, QC, H3A 1B1, Canada; FAX (514) 398-5069;

EMAIL tamara.western@mcgill.ca

Review of applications will commence on January 25, 2010.

Postdoctoral and Experienced Researchers, Germany.

Alexander Von Humboldt Foundation

The Alexander von Humboldt Foundation enables highly-qualified scientists and scholars of all nationalities and fields to conduct extended periods of research in Germany in cooperation with academic hosts at German institutions. Fellowships are awarded solely on the basis of the applicants academic record, the quality and feasibility of the proposed research and the candidates international publications. The Humboldt Foundation particularly welcomes applications from qualified, female junior researchers. Applications may be submitted at any time.

- Research Fellowship for Postdoctoral Researchers. For scientists and scholars who have completed a doctoral degree within the past four years. Allows for a stay of 6-24 months in Germany; monthly stipend of 2250 EUR.

- Research Fellowship for Experienced Researchers. For scientists and scholars who have completed a doctoral degree within the past twelve years. Fellowships may be divided into a maximum of three visits lasting three months or longer; monthly stipend of 2450 EUR

In addition to the monthly stipend, additional allowances are available for accompanying family members, travel expenses, and German language instruction. Applications and details at: www.humboldt-foundation.de

14 PhD Fellowships in Genomics and Molecular Physiology of Fruits

The International GMPF PhD Programme starting in spring 2010

The International PhD programme in Genomics and Molecular Physiology of Fruits, GMPF, consists of 13 highly competitive research institutions spread all over the world. The aim is the establishment of an international network of PhD students working on genomics, bioinformatics, functional genomics, proteomics, metabolomics, genetics and genetic improvement and molecular physiology of fruit trees.

Students joining the GMPF programme have the opportunity to conduct their research project both at the Research and Innovation Centre of the Edmund Mach Foundation (FEM) and at another institution member of the GMPF programme. Students will also receive specialized summer courses aimed at methodological and technological updating (for example bioinformatics; robotics; models of genetic simulation; techniques of genome assembly; phenotyping; chemistry of secondary metabolism).

Talented and motivated candidates who have, or are expecting to obtain by end of July 2010 a Master or equivalent degree in Life Sciences and Bioinformatics, are invited to submit their application by 31st January 2010.

The official language is English

Info: GMPF International PhD Programme. Fondazione Edmund Mach. Innovation and Research Centre. San Michele a/A (TN). Italy.

<http://www.fmach.it/gmpf-phd>

New books



Root Development

Annual Plant Reviews, Volume 37.

Tom Beeckman (Editor)

ISBN: 978-1-4051-6150-3

November 2009, Wiley-Blackwell

The book consists of contributions from author groups based at many of the World's formerst laboratories working in the root development area. The book's editor Tom Beeckman, himself very well known and respected for his work in this area, has drawn together an exceptional set of core cutting edge reviews of the subject, providing a state of the art reference tool for all those researching in this area.

Genes for Plant Abiotic Stress

Matthew A. Jenks, Andrew J. Wood (Eds)

ISBN: 978-0-8138-1502-2

November 2009, Wiley-Blackwell

Abiotic stresses caused by drought, salinity, toxic metals, temperature extremes, and nutrient poor soils are among the major constraints to plant growth and crop production worldwide. While crop breeding strategies to improve yields have progressed, a better understanding of the genetic and biological mechanisms underpinning stress adaptation is needed. Genes For Plant Abiotic Stress presents the latest research on recently examined genes and alleles and guides discussion of the genetic and physiological determinants that will be important for crop improvement in the future.

Fruit Development and Seed Dispersal

Annual Plant Reviews, Volume 38.

Lars Ostergaard (Editor)

ISBN: 978-1-4051-8946-0

January 2010, Wiley-Blackwell

Fruit development and seed dispersal are major topics within plant and crop sciences research with important developments in research being reported regularly. Drawing together reviews by some of the world's leading experts in these areas, Lars Ostergaard has provided a volume essential for all those working in plant and crop sciences worldwide.

The Handbook of Plant Mutation Screening: Mining of Natural and Induced Alleles

Khalid Meksem, Guenter Kahl (Eds)

ISBN: 978-3-527-32604-4

January 2010, Wiley-Blackwell

Induced mutagenesis is a common and promising method for screening for new crops with improved properties. This title introduces the different methods and then focuses on the screening, detection and analysis of the novel mutations. Written by a global team of authors the book is an indispensable tool for all scientists working on crop breeding in industry and academia.

Carotenoids: Physical, Chemical, and Biological Functions and Properties

Editor John T. Landrum

ISBN: 9781420052305

December, 2009. CRC Press.

Carotenoids are of great interest due to their essential biological functions in both plants and animals. However, the properties and functions of carotenoids in natural systems are surprisingly complex. With an emphasis on the chemical aspects of these compounds, Carotenoids: Physical, Chemical, and Biological Functions and Properties presents a broad overview and recent developments with respect to understanding carotenoid structure, electronic and photochemical properties, and the use of novel analytical methods in the detection and characterization of carotenoids and their actions. The text also explores LC/MS and LC/MS/MS techniques as well as new applications of PCR and molecular biology methodologies.

Courses

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EMBO Practical Course: Scientific Programming and Data Visualisation for Structural Biology

Heidelberg, Germany, May 5-7, 2010.

We are pleased to announce our practical course "Scientific Programming and Data Visualisation for Structural Biology" offered at the newly constructed Advanced Training Center, EMBL, Heidelberg, Germany, from May 5-7, 2010.

The course is designed primarily for structural biologists (scientists from other disciplines are welcomed to apply). The goals of the course is to allow students to learn and master computational skills that are frequently required in less routine projects, and to learn methods of data visualization. Lecture sessions will cover data animation, Python programming for Molecular Dynamics and Drug Design, GUI development and high performance computing as well as modern programming tools on OSX.

Three (3) parallel tutorial tracks will be offered (you can only select one):

Molecular Visualization with Maya by Gaël McGill - Expert in Molecular Movies and Animation (to view examples of his work visit MolecularMovies.org).

Scientific Programming with Python - by Ian Stokes-Rees - Harvard University Python programmer, with extensive experience in teaching.

OS X Programming - by Alex Griekspor - Developer of the "Papers".

As part of this course each participant will initiate a project relevant to their own research area, using the newly acquired skills.

Attendees are also invited to present a poster (describing their research), that would benefit from molecular visualization or new software tools. There are several fellowships available!

Joint lectures will be presented by expert programmers with extensive experience in structural biology and computational approaches:

Kathryn Loving - Scientist from Schrodinger, will discuss utilizing Python in docking and macromolecular simulations.

Bernhard Lohkamp - Karolinska Institute, will discuss designing graphical user interfaces with Python.

For additional information please visit the course website and download the poster.

http://www.embl.de/training/courses_conferences/course/2010/APP10-01/index.html

Contact: Daniel Panne. panne@embl.fr. <http://www.embl.fr/>.

Piotrek Sliz. <http://hkl.hms.harvard.edu>

Molecular Techniques In Plant Science

Cold Spring Harbor Laboratory, New York

07/02/2010 - 07/22/2010

This course provides an intensive overview of topics in plant physiology, biochemistry and development, focusing on molecular genetic and analytical approaches to understanding plant biology. It emphasizes recent results from Arabidopsis, maize and a variety of other plants and provides an introduction to current methods used in plant molecular biology. It is designed for scientists with some experience in molecular techniques or in plant biology who wish to work with plants using the latest technologies in genetics, molecular biology and biochemistry. The course consists of a vigorous lecture series, a hands-on laboratory, and informal discussions. Discussions of important topics in plant research will be presented by the instructors and by invited speakers. These seminars will include plant morphology and anatomy; plant development (such as development of flowers, leaves, male and female gametophytes, and roots); perception of light and photomorphogenesis; cell wall biosynthesis, function and perception of hormones and application of research results to addressing current agronomic problems. Lectures describing bioinformatics tools available to the plant community, and the resources provided by plant genome projects are also included. Speakers will provide overviews of their fields, followed by in-depth discussions of their own work. The laboratory sessions will provide an introduction to important techniques currently used in plant research. These include studies of plant development, mutant analysis, histochemical staining, transient gene expression, gene silencing, applications of fluorescent protein fusions, protein interaction and detection, proteomics approaches, several different approaches for quantifying metabolites, transient transformation and techniques commonly used in genetic and physical mapping. The course also includes several short workshops on important themes in plant research.

<http://meetings.cshl.edu/courses/c-plan10.shtml>

Advanced Microscopy

EMBL Heidelberg, Germany

Monday 8 March - Friday 12 March 2010

Registration is now open until 25 January 2010.

This course is aimed at young scientists in life sciences at the pre- or post-doctoral level as well as young investigators with a strong interest to learn more on advanced live cell imaging methods and applying them to their own research. About 40% of the course program covers lectures and tutorials on basic and advanced microscopy methods and applications by experts in the field. The rest of the time will focus on hands on practical work organised in small groups. These practicals will address the following topics: Basic aspects of fluorescence microscopy, characterisation of state of the art imaging detectors, multicolour 3D time-lapse microscopy of living samples, total internal reflection fluorescence microscopy, fluorescence recovery after photobleaching (FRAP), fluorescence resonance energy transfer measurements (FRET), imaging of thick samples such as embryos or tissue sections, basic and advanced image analysis.

http://www.embl.de/training/courses_conferences/course/2010/MIC10-01/index.html

In memoriam: César Gómez-Campo



Professor César Gómez-Campo - a founder figure in wild species seed banking

(Torrelavega-Santander, Spain, 1933 – Madrid, Spain, 2009)

Professor César Gómez-Campo, who passed away on 6 September 2009, was one of the first people to use seed banking for the conservation of wild plant species.

In 1966 Professor César Gómez-Campo established a seed bank primarily for Crucifers at the Universidad Politécnica de Madrid, Spain. He was a contemporary of Dr Peter Thompson who pioneered wild plant species seed banking at Kew not long after, and who passed away in 2008.

Through their visionary work, seed banking has become a mainstream method for conserving plant species away from where they are threatened in the wild. This has paved the way for regional and global activities such as the European Native Seed Conservation Network (ENSCONET) and the Millennium Seed Bank partnership, both of which have involved Kew.

Professor César Gómez-Campo was active to the end on seed banking issues, highlighting the necessity of good quality containers for long-term banking and the value of ultra-dry storage.

The Millennium Seed Bank conserves seeds of wild species. It might not have existed but for early pioneering work in Spain and at Kew.

Source: News, Royal Botanic Gardens, Kew, UK. (19 Nov 2009).