



**FEDERATION OF EUROPEAN SOCIETIES OF
PLANT BIOLOGY**

FESPB Newsletter

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Editor: Prof. Dolores Rodriguez
Chair of Publications Committee



FEDERATION OF EUROPEAN SOCIETY OF PLANT BIOLOGY



Heraklion 16 April 2012

Dear FESPB Members,

As you all know, our Federation is governed by the Executive Committee, the Council and the General Assembly (<http://www.fespb.org/fespb/content/organization>). At the next FESPB Congress, which is co-organized with the European Plant Science Organization (EPSO) and will be held in Freiburg, Germany, from 29 July to 3 August 2012, several members of the Executive Committee will step down. More specifically, the terms of the Secretary General (myself), the Treasurer (Prof. Karl-Josef Dietz), the Chair of the Grants & Awards Committee (Prof. Christine Foyer), and Prof. Anna Rychter, who acted on behalf of Members from the ex-Eastern European Countries are terminated. Therefore, new members shall be elected, except for the last position which is from now on cancelled.

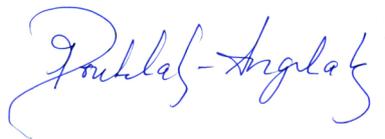
According to the Statutes (<http://www.fespb.org/fespb/content/statutes>), as revised in 2010, candidacies for the positions of Secretary General, Treasurer and Chair of Grants & Awards Committee will be submitted electronically to Secretary General the latest one month before the next FESPB Congress, and voting will be performed electronically, if possible. Thus, the new FESPB EC Officers will be elected by all FESPB members and not only by those present at the General Assembly during the Congress, as it was the case until now.

Therefore, candidacies shall be submitted to me electronically as soon as possible but not later than **25 June 2012** at poproube@biology.uoc.gr. Candidates

must send an Application expressing their interest for one of the positions Secretary General, Treasurer or Chair of Grants & Awards Committee, along with their Curriculum Vitae. Effort will be made for electronic voting, before the next FESPB Congress.

On behalf of the Executive Committee I invite all of you to actively participate in this direct election (for first time) of the Officers of the E.C. by all FESPB members.

With best regards



Prof. Kalliopi (Popy) A. Roubelakis-Angelakis

FESPB Secretary General



The Federation
of European Societies
of Plant Biology

Plant Biology Congress Freiburg 2012

jointly organized by FESPB and EPSO

July 29 to August 3, 2012 at the University of Freiburg

Plant Scientists in Europe are represented by two independent organisations. The FESPB (Federation of European Societies of Plant Biologists) is the umbrella organisation of 27 national botanical societies in Europe, representing more than 24.000 individuals and has in addition several corporate members from the European industry. The EPSO (European Plant Science Organisation) unites more than 220 research institutions and universities from 30 countries representing over 28.000 individuals and over 2.800 personal members. In addition EPSO cooperates with national learned societies, and it has

NGOs and companies as observers. For the first time, both organisations have agreed to hold a joint Plant Biology Congress 2012 at the University of Freiburg, Germany. This congress will highlight all aspects of plant biology with special emphasis on the consequences of global climate change and on feeding the global world population. From July 29 to August 3, 2012 plant scientist from all over the world are cordially invited to meet in the "Green City" of Freiburg.

Heinz Rennenberg and Ralf Reski

For more information, please visit:

<http://www.plant-biology-congress2012.de/home.html>

RESEARCH NEWS



Discovery of plant 'nourishing gene' brings hope for increased crop seed yield and food security

Source: Biotechnology and Biological Sciences Research Council, UK.13 January 2012

University of Warwick scientists have discovered a "nourishing gene" which controls the transfer of nutrients from plant to seed - a significant step which could help increase global food production. The research, funded by BBSRC and led by the University of Warwick in collaboration with the University of Oxford and agricultural biotech research company Biogemma, has identified for the first time a gene, named *Meg1*, which regulates the optimum amount of nutrients flowing from mother to offspring in maize plants.

Unlike the majority of genes that are expressed from both maternal and paternal chromosomes, *Meg1* is expressed only from the maternal chromosomes. This unusual form of uniparental gene expression, called imprinting, is not restricted to plants, but also occurs in some human genes which are known to regulate the development of the placenta to control the supply of maternal nutrients during fetal growth.

While scientists have known for a while of the existence of such imprinted genes in humans and other mammals, this is the first time a parallel gene to regulate nutrient provisioning during seed development has been identified in the plant world. The findings mean that scientists can now focus on using the

gene and understanding the mechanism by which it is expressed to increase seed size and productivity in major crop plants.

Dr Jose Gutierrez-Marcos, Associate Professor in the University of Warwick's School of Life Sciences, said: "These findings have significant implications for global agriculture and food security, as scientists now have the molecular know-how to manipulate this gene by traditional plant breeding or through other methods to improve seed traits, such as increased seed biomass yield. "This understanding of how maize seeds and other cereal grains develop - for example in rice and wheat - is vital as the global population relies on these staple products for sustenance". "To meet the demands of the world's growing population in years to come, scientists and breeders must work together to safeguard and increase agricultural production."

Professor Hugh Dickinson of Oxford University's Department of Plant Sciences added: "While the identification of *MEG1* is an important discovery in its own right, it also represents a real breakthrough in unravelling the complex gene pathways that regulate the provisioning and nutritional content of seeds."

The research, supported by the European Union, the Biotechnology and Biological Sciences Research Council (BBSRC) and the Royal Society, is published in *Current Biology* under the title *Maternal control of nutrient allocation in plant seeds by genomic imprinting*.

A novel sensor to map auxin response and distribution at high spatio-temporal resolution

Source: Centre for Plant Integrative Biology, Univ. Nottingham. UK.

Auxin is a key plant morphogenetic signal but tools to analyse dynamically its distribution and signalling during development are still limited. Auxin perception directly triggers the degradation of Aux/IAA repressor proteins. Here we describe a novel Aux/IAA-based auxin signalling sensor termed DII-VENUS that was engineered in the model plant *Arabidopsis thaliana*. The VENUS fast maturing form of yellow fluorescent protein was fused in-frame to the Aux/IAA auxin-interaction domain (termed domain II; DII) and expressed under a constitutive promoter. We initially show that DII-VENUS abundance is dependent on auxin, its TIR1/AFBs co-receptors and proteasome activities. Next, we demonstrate that DII-VENUS provides a map of relative auxin distribution at cellular resolution in different tissues. DII-VENUS is also rapidly degraded in response to auxin and we used it to successfully visualize dynamic changes in cellular auxin distribution during two developmental responses, the root gravitropic response and lateral organ production at the shoot apex. Our results illustrate the value of developing response input sensors such as DII-VENUS to provide high-resolution spatio-temporal information about hormone distribution and response during plant growth and development.

Reference: Brunoud et al. *Nature* (2012) doi:10.1038/nature10791. Published online 15 January 2012.

Breeding better grasses for food and fuel

Source: BBSRC. 17 January 2012

Researchers from the Biotechnology and Biological Sciences Research Council (BBSRC) Sustainable Bioenergy Centre (BSBEC) have discovered a family of genes that could help us breed grasses with improved properties for diet and bioenergy.

The research was carried out by a team from the University of Cambridge and Rothamsted Research, which receives strategic funding from BBSRC. Their findings are published today (Tuesday 17 January) in the journal *Proceedings of the National Academy of Sciences (PNAS)*.

The genes are important in the development of the fibrous, woody parts of grasses, like rice and wheat. The team hopes that by understanding how these genes work, they might for example be able to breed varieties of cereals where the fibrous parts of the plants confer dietary benefits or crops whose straw requires less energy-intensive processing in order to produce biofuels.

The majority of the energy stored in plants is contained within the woody parts, and billions of tons of this material are produced by global agriculture each year in growing cereals and other grass crops, but this energy is tightly locked away and hard to get at. This research could offer the possibility of multi-use crops where the grain could be used for food and feed and the straw used to produce energy efficiently. This is crucial if we are to ensure that energy can be generated sustainably from plants, without competing with food production.

Plant cells, like these in wheat, are surrounded by thick walls where energy is locked up.

Professor Paul Dupree, of the University of Cambridge, explains "Unlike starchy grains, the energy stored in the woody parts of plants is locked away and difficult to get at. Just as cows have to chew the cud and need a stomach with four compartments to extract enough energy from grass, we need to use energy-intensive mechanical and chemical processing to produce biofuels from straw. "What we hope to do with this research is to produce varieties of plants where the woody parts yield their energy much more readily - but without compromising the structure of the plant. We think that one way to do this might be to modify the genes that are involved in the formation of a molecule called xylan - a crucial structural component of plants."

Xylan is an important, highly-abundant component of the tough walls that surround plant cells. It holds the other molecules in place and so helps to make a plant robust and rigid. This rigidity is important for the plant, but locks in the energy that we need to get at in order to produce bioenergy efficiently.

Grasses contain a substantially different form of xylan to other plants. The team wanted to find out what was responsible for this difference and so looked for genes that were turned on much more regularly in grasses than in the model plant *Arabidopsis*. Once they had identified the gene family in wheat and rice, called *GT61*, they were able to transfer it into *Arabidopsis*, which in turn developed the grass form of xylan.

Dr Rowan Mitchell of Rothamsted Research continues "As well as adding the *GT61* genes to *Arabidopsis*, we also

turned off the genes in wheat grain. Both the *Arabidopsis* plants and the wheat grain appeared normal, despite the changes to xylan. This suggests that we can make modifications to xylan without compromising its ability to hold cell walls together. This is important as it would mean that there is scope to produce plant varieties that strike the right balance of being sturdy enough to grow and thrive, whilst also having other useful properties such as for biofuel production."

The tough, fibrous parts of plants are also an important component of our diet as fibre. Fibre has a well established role in a healthy diet, for example, by lowering blood cholesterol. The team have already demonstrated that changing *GT61* genes in wheat grain affects the dietary fibre properties so this research also offers the possibility of breeding varieties of cereals for producing foods with enhanced health benefits.

Duncan Eggar, BBSRC Bioenergy Champion said: "Recent reports have underlined the important role that bioenergy can play in meeting our future energy needs - but they all emphasise that sustainability must be paramount.

"Central to this will be ensuring that we can get energy efficiently from woody sources that need not compete with food supply. This research demonstrates how, by understanding the fundamental biology of plants, we can think about how to produce varieties of crops with useful traits, specifically for use as a source of energy."

The paper, *Glycosyl transferases in family 61 mediate arabinofuranosyl transfer onto xylan in grasses*, is available online www.pnas.org, January 3, 2012.

'Rules' May Govern Genome Evolution in Young Plant Species

Source: *ScienceDaily*. Jan. 19, 2012.

A new University of Florida study shows a hybrid plant species may experience rapid genome evolution in predictable patterns, meaning evolution repeats itself in populations of independent origin.

Researchers analyzed genes of a naturally occurring hybrid species, *Tragopogon miscellus*, and the study, recently published online in *Current Biology*, suggests genome evolution in hybrid plants may follow a set of "rules" that determine which parental genes are lost. The research may be used to create higher and more stable yields in other hybrid polyploid plants, including agricultural crops such as wheat, corn, coffee and apples.

"The repeatability of gene loss in populations of separate origin is a really exciting result," said co-author Pam Soltis, distinguished professor and curator of molecular systematics and evolutionary genetics at the Florida Museum of Natural History on the UF campus. "Scientists have often wondered if there are 'rules' that govern patterns of evolution, and data for *Tragopogon* polyploids suggest that such rules may actually operate at the genetic level."

Scientists analyzed about 70 of the hybrid plants commonly known as goatsbeard, a species in the daisy family that originated in the northwestern U.S. about 80 years ago. The new species formed naturally when two plants introduced from Europe mated to produce a hybrid offspring, and hybridization was accompanied by polyploidy, or whole genome duplication. Following a polyploidy event, the hybrid

offspring contains twice the number of chromosomes, totaling 24.

Researchers compared the patterns of gene loss in the hybrid to patterns of gene loss in other species from the same family that experienced an ancient polyploidy event about 40 million years ago, and found similar results. The data support an evolutionary hypothesis that genes whose products interact closely with other gene products are more likely to be maintained in duplicate after polyploid formation, meaning some aspects of genome evolution are predictable and repeatable in independent lines.

"We were surprised at the speed at which patterns seemed to form in which genes show loss versus retention," said lead author Richard Buggs of Queen Mary University of London, who worked on the study as a postdoctoral researcher at the Florida Museum.

Soltis said one possible mechanism of gene loss may be linked with changes in chromosome structure, an occurrence documented in a study published Jan. 6 in the *Proceedings of the National Academy of Sciences*. By further researching the connection between specific gene losses and chromosomal changes, researchers hope to better understand how these patterns affect fertility and physical characteristics of hybrid plants.

"Hybridization and chromosome doubling have played a major role in the evolution of flowering plants, and *Tragopogon miscellus* gives us an amazing window into this process," said study co-author Doug Soltis, a distinguished professor in UF's biology department. The polyploid's two parent species, *Tragopogon dubius* and *Tragopogon pratensis*, were introduced to the U.S.

in the 1920s. Because their flowers only bloom for a few hours in the morning, Tragopogon plants are often referred to as "John-go-to-bed-at-noon." It looks like a daisy except for being yellow in color.

Researchers analyzed genes from five natural populations of *T. miscellus*, as well as polyploid plants re-created in UF greenhouses. The DNA was extracted from the leaf tissue. "Although *Tragopogon miscellus* is perfectly positioned to allow examination of genome evolution after hybridization, it is not a traditional research model organism and virtually none of the tools and resources that allow these types of studies had been developed for it," said co-author Brad Barbazuk, a UF associate professor in biology and member of the UF Genetics Institute. "The availability of cost-effective, high-throughput genomics technologies has enabled us to examine this important phenomenon in this young species."

The two-year study was funded by UF and the National Science Foundation. Study co-authors include Srikar Chamala of the UF Genetics Institute, Wei Wu and Pat Schnable of Iowa State University and Jennifer Tate of Massey University in New Zealand.

"Polyploidy, the duplication of whole genomes, is a huge and really important process in plant genetics and plant evolution, and what the Soltises have is a beautiful system for studying these early stages of polyploid formation in nature," said Jeffrey Doyle, a plant biology professor at Cornell University. "If you know something about the rules by which genomes evolve, you may be able to predict what's going to happen when you try to genetically engineer something."

Molecular Structure and Function of Essential Plant Hormone Could Profoundly Change Our Understanding of a Key Cell Process

Source: ScienceDaily. Jan. 23, 2012.

A recent Van Andel Research Institute (VARI) study published in the journal *Science* investigating the molecular structure and function of an essential plant hormone could profoundly change our understanding of a key cell process, and might ultimately lead to the development of new drugs for a variety of diseases.

The study builds on earlier work by the same team of investigators at VARI that was published in the journal *Nature* in 2009. That study shed light on how plants respond when they are under stress from extreme temperatures, drought and other harsh environmental conditions and was later named by *Science* as one of the top scientific breakthroughs of 2009.

In signal transduction -- the basic process of intercellular and intracellular communication -- enzymes known as kinases and phosphatases serve as the opposing partners and key regulators of this process.

VARI scientists mapping the structure of the receptor for Abscisic acid (ABA), a plant hormone that controls growth, development and responses to environmental stress, discovered that ABA regulates the stress-response pathway by affecting an enzyme belonging to the phosphatase family -- which in turn binds to a kinase. "This process has been little understood," said Karsten Melcher, Ph.D., Head of the VARI Laboratory of Structural Biology and Biochemistry and co-author of the study. "We believe that the activation mechanism may in many cases also be

structural. Phosphatases inactivate the active site like a plug -- changing the shape of the kinase."

"The textbook assumption has been that enzymatic phosphatases inhibit kinases only by taking away phosphates from the kinases. There have been few recorded examples of non-enzymatic phosphatases inhibiting kinases." Knowing that these enzymes mimic the structure of the opposing enzyme enables scientists to more accurately develop mechanisms to activate or inhibit intercellular and intracellular communication. Inhibiting or activating this process in plant cells could lead to plants that more readily survive drought or other conditions of stress.

In mammalian cells the ability to impact communication has numerous and far-reaching implications. For example, applications that inhibit or activate cell communication in out-of-control metastasizing cancer cells have enormous potential to affect tumor growth.

Writing in the journal *Science*, where the study was published on January 6, Jeffrey Leung notes that "molecular mimicry might be a common mechanism in many biological processes involving kinase-phosphatase complexes...The structural studies on the core ABA signaling proteins establish a new paradigm for kinase-phosphatase co-regulation and coevolution."

The possibility of broader scientific implications is also noted by Melcher.

"The current studies take a step back from application and focus back on fundamental cellular mechanisms with a broad implication beyond ABA signaling," said Melcher.

In their 2009 study in *Nature*, Melcher and H. Eric Xu, Ph.D., used X-ray

crystallography to detail precisely how ABA works at the molecular level. One of ABA's effects is to cause plant pores to close when plants are stressed so that they can retain as much water as possible.

In a follow-up 2010 study published in *Nature Structural & Molecular Biology*, the VARI team identified several synthetic compounds that fit well with ABA's many receptors to have the same effect. By finding compounds that can close these pores, researchers' findings could lead to sprays that use a plant's natural defenses to help it survive harsh environmental conditions. "This type of finding once again demonstrates the importance of identifying, mapping and understanding fundamental cellular and molecular processes because of the profound implications for human health," said Xu, Director of the VARI Center for Structural Biology and Drug Discovery and co-author of the current *Science* study.

"Proteins with similarities to plant ABA receptors are also found in humans and further studies in this area could reveal important implications for people with cellular stress disorders." The lead authors of the current *Science* study are Fen-Fen Soon, Ley-Moy Ng, and Edward Zhou. The project was carried out in conjunction and collaboration with scientists from the National University of Singapore, Purdue University, The Scripps Research Institute, Scripps Florida, Shanghai Institute of Materia Medica of the Chinese Academy of Sciences, the Synchrotron Research Center of Northwestern University, and University of California at Riverside.

Journal References: Soon et al. *Science*, 2011; 335 (6064): 85. J. Leung. *Science*, 2012; 335 (6064): 46.

Making Poisonous Plants and Seeds Safe and Palatable: Canola Now, Cannabis Next?

Source: ScienceDaily. Jan. 27, 2012.

Every night millions of people go to bed hungry. New genetic technology can help us feed the world by making inedible seeds more edible, researchers say.

There are roughly about a quarter of a million plant species known on Earth. But we only eat between 5,000 and 10,000 of them. Many are poisonous to us -- such as lily of the valley. And many plants have no human nutritional value -- such as grass.

"In fact, there are no more than about 100 known species that can be used as important food crops," says Biology Professor Atle Bones at Norwegian University of Science and Technology.

But Bones and his research team have made a major discovery. They have figured out how a canola plant can be genetically programmed to reduce the toxic substances it produces in its seeds -- thus making it more palatable.

Nobody has done this before, and Bones thinks it could be the beginning of a food revolution.

"The principle could be used with other plant species and plant parts," he says.

Canola, or rape, is one of the fifteen most important crop plants in the world. It contains special cells that produce toxic substances. These "toxic bombs" are part of the plant's defence system and are activated in specific situations - - such as when an insect begins feeding on a leaf. The substance that is released burns like hot mustard, causing animals and insects to move away.

"These 'toxic bombs' are good for the plant, but undesirable in animal feed and human food," says Bones.

When canola seeds are pressed, all the vegetable oil is removed. What is left is a protein-rich flour that can be used in food for animals and humans. But if the seeds are pressed in the wrong way, the plant responds by releasing its toxic compounds. The oil is then flavoured with a taste of strong mustard, and the animals that eat the protein flour have stomach problems and troubles with nutrient uptake.

The NTNU research group has genetically reprogrammed canola cells so that the toxic bomb cells disappear on their own as the seed matures. But the toxin only fully disappears in the mature seeds.

This way, the plant can continue to protect itself, while the toxic compounds are removed from the part of the rapeseed used for food.

Thus, the proportion of rapeseed in the concentrate can be increased, and the seeds can be pressed without the risk of contaminating the oil with unwanted flavours and odours.

There are almost 7 billion people on Earth. Every day, 25,000 people die of malnutrition -- while 800 million are starving. By 2050 there will be more than 9 billion of us. As people become more prosperous, their per-person calorie consumption will grow. This combination of increased prosperity and population growth means that food production will have to double by 2050.

Globally, genetically modified food in production is already cultivated on +130 million hectares. But Bones believes that the production of genetically modified plants will more than double over the next ten years.

Today there are 25 countries that use genetically modified plants on a large scale. More than 50 per cent of the

world's population lives in these countries.

Genetically modified soy already represents 75 per cent of all soybean production. And genetically modified plants are grown in an area that is 40 times the size of Denmark -- mainly in the USA, Argentina, Brazil and China, according to Bones.

Genetically modified food is grown in seven European countries. There is already super broccoli that contains higher doses of the healthy substances in normal broccoli. Next year, producers will introduce soybeans enriched with omega-3 fatty acids.

Among the plants that could be genetically modified by removing their undesirable chemicals is cannabis.

Cannabis is a type of grass that thrives in subtropical and dry climates -- and is best known as the raw material for hashish and marijuana.

But it is one of the world's fastest growing plants, and is exceptionally hardy. Its plant fibres can be used for rope and textiles, or as replacements for trees in the paper industry because they are stronger than wood fibre. The seeds can be used for oil.

"It would be interesting to use our new technology to produce cannabis that does not contain the psychoactive substance THC," says Bones.

It is illegal to grow genetically modified food in Norway, and in principle it may not be imported -- not even for animal feed. But there are cracks in this virtual barrier, and small traces of genetically modified food are seeping in. Because Norway does not allow the sales of goods containing genetically modified contents, there is no provision for labelling this food on the grocery store shelves. But it's there.

The government has set 0.9 percent as the ceiling for how much genetically modified food may be in foods before they must be labelled. Each year, the Norwegian Food Safety Authority finds genetically modified canola, corn or rice in imported foods, which are promptly branded as illegal immigrants and kicked out of the country.

But the test sample size is small -- last year only 131 samples were tested, of which 4 contained genetically modified food.

According to the Norwegian Board of Technology, it is difficult to keep Norway completely free of genetically modified ingredients, which is why the 0.9 per cent limit was set.

"Genetically modified plants can be tailored to tolerate different climatic conditions such as drought or hard winters, and to have increased resistance to insects or fungus. These plants can thus be grown with fewer pesticides.

"This means that farmers are exposed to less pesticides, there are less pesticides in the ecosystem and probably less pesticides in food that is produced," Bones notes.

"There is nothing wrong or unethical about using genetically modified plants - - because, in fact, all crops are modified. They have also been created from wild plants through comprehensive human-controlled breeding programmes and genetic selection," says Bones.

It is no longer possible in the United States to distinguish between ordinary food and genetically modified food, researchers assert.

Some researchers describe the American situation as if people are playing Russian roulette with their health. Fear of allergies is one reason.

Atle Bones believes that these kinds of worries over possible health effects are greatly exaggerated.

"It is obviously not possible to give an ironclad guarantee that no one will be allergic to a new gene in canola or corn. Neither is it possible to guarantee that no one is allergic to traditional modified plants. But this would normally be detected before the plants or the product goes into production.

"The method we have used, however, can remove known allergens, digestive inhibitory substances or toxins in the plant," said Bones.

He also believes that genetically modified plants must be assessed in each situation, and like conventionally modified plants, be tested thoroughly before they are approved for production.

"With our new technology, it is possible to target changes in specific parts of the plant. It is therefore possible to change a strawberry plant without any change in the berry to be eaten. And that is a scientific breakthrough," Bones concludes.

Genetic Information Migrates from Plant to Plant

Source: ScienceDaily. Feb. 1, 2012.

To generate phylogenetic trees and investigate relationships between organisms, scientists usually look for similarities and differences in the DNA. Plant scientists were confounded by the fact that the DNA extracted from the plants' green chloroplasts sometimes showed the greatest similarities when related species grew in the same area. They tried to explain the phenomenon with the assumption that every once in a while those normally sexually incompatible species crossed and

produced offspring with a new combination of nuclear and chloroplast genomes.

They coined the term "chloroplast capture" to illustrate what they thought was happening. Now, scientists around Ralph Bock from the Max Planck Institute of Molecular Plant Physiology in Potsdam discovered that a transfer of entire chloroplasts, or at least their genomes, can occur in contact zones between plants. Inter-species crossing is not necessary. The new chloroplast genome can even be handed down to the next generation and, thereby, give a plant with new traits. These findings are of great importance to the understanding of evolution as well as the breeding of new plant varieties.

Many wooden plants, especially fruit and rose trees, are deliberately damaged by gardeners. They chop off branches or cut dents into the bark in order to put parts of another plant into the slots. The plant whose roots touch the soil is called stock, whereas scion is the technical term for the branch that is put onto it. The reason behind the gardener's atrocities is to reproduce varieties with an especially high yield without the Mendelian Laws messing with their business. According to Mendel, only parts of the progeny show the same traits as their parents. The rest of the offspring will most likely be less valuable. By putting one branch of a successful apple variety onto a new stock, the desired apple tree is easily cloned. But graft junctions do not always have to be human-made. Plants that simply grow in close vicinity to each other can fuse.

In those above mentioned contact zones, so called horizontal gene transfers (HGT), the transfer of genes

without sexual reproduction, can occur. For a long time, scientists believed that HGT was restricted to prokaryotes, organisms without nuclei. It was universally accepted that, for example, bacteria can exchange genes that are crucial to their survival, like the ones that transmit a resistance to antibiotics. Nowadays it is increasingly appreciated that HGT is in fact not restricted to prokaryotes. It can be observed at the contact zone between different animal tissues after an organ transplantation or -- as shown here -- between two fusing plants. In 2009, Ralph Bock and Sandra Stegemann discovered that genetic information stored in the green chloroplasts can be transferred to another plant by means of horizontal gene transfer.

Their results were, at that time, restricted to the transfer of genes between plants of the same species.

"The results from the DNA analyses were especially interesting," says Sandra Stegemann, first author of the paper. "We found a completely identical version of the chloroplast genome from *N. tabacum* in the two other species." When mitochondria, another cell organelle with an individual genome, are transferred across species barriers, the result is often a mixture of the donor and recipient DNA. "The new chloroplasts had kept their entire genetic information and fully ousted the old ones. They were even inherited by the next generation," Stegemann further explains.

Now scientists are trying to find the answer to the question of how exactly the chloroplasts leave their homes and find a new place to live. Do they migrate through the plasmodesmata, the narrow tunnels that connect neighboring plant

cells? Or do enzymes locally remove the cell wall and allow small amounts of cytoplasm and cell organelles to pass from one cell to another? "As of now, we do not know how chloroplasts manage to get from one cell to the other," says group leader Ralph Bock. "But the decisive point is that it happens and the discovery of this process offers a new explanation for important evolutionary processes and opens up new possibilities for plant breeders." After all, the chloroplast DNA vitally contributes to the fitness of a plant and can provide crucial advantages.

Journal Reference: S. Stegemann, M. Keuthe, S. Greiner, R. Bock. Horizontal transfer of chloroplast genomes between plant species. *Proceedings of the National Academy of Sciences*, 2012; DOI: 10.1073/pnas.1114076109.

First plants caused ice ages

Source: John Innes Centre. February 1, 2012.

Research rooted in Norwich science has revealed how the arrival of the first plants 470 million years ago triggered a series of ice ages.

Scientists from the University of East Anglia (UEA) and the John Innes Centre (JIC), now at the Universities of Exeter and Oxford, set out to identify the effects that the first land plants had on the climate during the Ordovician Period, which ended 444 million years ago. During this period the climate gradually cooled, leading to a series of 'ice ages'. This global cooling was caused by a dramatic reduction in atmospheric carbon, which this research, published in *Nature Geoscience*, now suggests was triggered by the arrival of plants.

Among the first plants to grow on land were the ancestors of mosses that grow

today. This study shows that they extracted minerals such as calcium, magnesium, phosphorus and iron from rocks in order to grow. In so doing, they caused chemical weathering of the Earth's surface. This had a dramatic impact on the global carbon cycle and subsequently on the climate. It could also have led to a mass extinction of marine life.

The team used the modern moss, *Physcomitrella patens* for their study. They created 'microcosms' made up of rocks in small incubators with and without moss growing on them. Over three months they were able to measure the effects the moss had on the chemical weathering of the rocks. Much of this work was carried out by former Diss High School student Michael Crouch, as part of studies for a Masters degree.

They then used an Earth system model, developed at UEA, to establish what difference plants could have made to climate change during the Ordovician Period.

The research suggests that the first plants caused the weathering of calcium and magnesium ions from silicate rocks, such as granite, in a process that removed carbon dioxide from the atmosphere, forming new carbonate rocks in the ocean. This cooled global temperatures by around five degrees Celsius.

In addition, by weathering the nutrients phosphorus and iron from rocks, the first plants increased the quantities of both these nutrients going into the oceans, fuelling productivity there and causing organic carbon burial. This removed yet more carbon from the atmosphere, further cooling the climate by another two to three degrees

Celsius. It could also have had a devastating impact on marine life, leading to a mass extinction that has puzzled scientists.

One of the lead researchers, Professor Tim Lenton of the University of Exeter said: "This study demonstrates the powerful effects that plants have on our climate. Although plants are still cooling the Earth's climate by reducing atmospheric carbon levels, they cannot keep up with the speed of today's human-induced climate change. In fact, it would take millions of years for plants to remove current carbon emissions from the atmosphere."

Professor Liam Dolan of Oxford University, one of the lead researchers, said: "For me the most important take-home message is that the invasion of the land by plants - a pivotal time in the history of the planet - brought about huge climate changes. Our discovery emphasises that plants have a central regulatory role in the control of climate: they did yesterday, they do today and they certainly will in the future."

The study was carried out by a team from the Universities of Exeter, Oxford and East Anglia and the John Innes Centre. The project was funded by the Earth and Life Systems Alliance (ELSA) - a major strategic collaboration between the John Innes Centre and the University of East Anglia on the Norwich Research Park integrating world-class expertise in biological, earth and social sciences to tackle the challenges posed by a changing climate.

Reference: First plants cooled the Ordovician, *Nature Geoscience* 5, 86-89 doi:10.1038/ngeo1390

Steroids Control Gas Exchange in Plants

Source: ScienceDaily. Feb. 5, 2012.

Plants leaves are sealed with a gas-tight wax layer to prevent water loss. Plants breathe through microscopic pores called stomata (Greek for mouths) on the surfaces of leaves. Over 40% of the carbon dioxide, CO₂, in the atmosphere passes through stomata each year, as well a water volume twice that of the whole atmosphere. As the key conduits for CO₂ uptake and water evaporation, stomata are critical for both our climate and plant productivity. Thus, not surprisingly, the total number and distribution of stomata are strictly regulated by plants to optimize photosynthesis while minimizing water loss.

The mechanisms for such regulation have remained elusive. New research from Carnegie's Zhiyong Wang, Tae-Wuk Kim and Dominique Bergmann demonstrates that certain plant steroid hormones, called brassinosteroids, play a crucial role in this regulating the number of stomata in the leaf. Their work is published online February 5 by Nature.

Brassinosteroids are found throughout the plant kingdom and regulate many aspects of growth and development, including inhibition of photosynthetic genes when there is insufficient light for photosynthesis. Mutant plants that are deficient in brassinosteroids show defects at many phases of the plant life cycle including reduced seed germination, activation of light-induced genes and growth behavior in the dark, dwarfism, and sterility.

Wang, lead author Kim and their colleagues Marta Michniewicz and Bergmann set out to determine

brassinosteroid's role in stomatal development. They found that mutant plants that are brassinosteroid deficient, or lack sensitivity to brassinosteroids, were observed to have excessive and unevenly-distributed stomata, leading the team to ask what role this class of hormones plays in the developmental process for these crucial plant organs.

Wang and his colleagues had previously determined that when brassinosteroid binds to a receptor on the surface of a plant cell, it initiates a chain of signal transduction that results in certain genes being turned on or off within the cell's nucleus. But this research showed that one of the proteins involved in this chain, called BIN2, is also involved in a completely separate pathway that regulates the development of stomata.

The team found that BIN2--which is similar to a protein found in humans--had an inhibiting effect on a key protein in the stomatal-development regulatory system. This second protein is called YODA and it also has a similar counterpart in humans. In the absence of brassinosteroid, BIN2 inhibits YODA, which allows stomata formation. When brassinosteroid is present, it causes inactivation of BIN2, and this allows YODA to inhibit stomatal development. "This research supports the role of brassinosteroid as a master regulator that coordinates both physiological and development aspects of plant growth," Wang said. "Because brassinosteroid is one of the best-understood chemical pathways in plant physiology, these results could help scientists who are researching many other plant cell systems as well."

Journal Reference: Tae-Wuk Kim, Marta Michniewicz, Dominique C. Bergmann,

Zhi-Yong Wang. Brassinosteroid regulates stomatal development by GSK3-mediated inhibition of a MAPK pathway. *Nature*, 2012; DOI: 10.1038/nature10794.

Ancient Seagrass Holds Secrets of the Oldest Living Organism On Earth

Source: ScienceDaily. Feb. 7, 2012

It's big, it's old and it lives under the sea -- and now an international research collaboration with The University of Western Australia's Ocean's Institute has confirmed that an ancient seagrass holds the secrets of the oldest living organism on Earth.

Ancient giant *Posidonia oceanica* reproduces asexually, generating clones of itself. A single organism -- which has been found to span up to 15 kilometres in width and reach more than 6,000 metric tonnes in mass -- may well be more than 100,000 years old.

"Clonal organisms have an extraordinary capacity to transmit only 'highly competent' genomes, through generations, with potentially no end," said Director of UWA's Oceans' Institute Winthrop Professor Carlos Duarte.

Researchers analysed 40 meadows across 3,500 kilometres of the Mediterranean sea. Computer models helped demonstrate that the clonal spread mode of *Posidonia oceanica*, which as all other seagrasses can reproduce both sexually and asexually, allows them to spread and maintain highly competent clones over millennia, whereas even the most competent genotypes of organisms that can only reproduce sexually are lost at every generation.

"Understanding why those particular genomes have been so adaptable to a

broad range of environmental conditions for so long is the key to some interesting future research," Professor Duarte said.

Seagrasses are the foundation of key coastal ecosystems but have waned globally for the past 20 years. *Posidonia oceanica* meadows are now declining at an estimated rate of five per cent annually.

"The concern is that while *Posidonia oceanica* meadows have thrived for millennia their current decline suggests they may no longer be able to adapt to the unprecedented rate of global climate change."

The genus *Posidonia* occurs only in the Mediterranean and Australian waters.

The findings have been published in the online journal PLoS ONE.

Journal Reference: Sophie Arnaud-Haond, Carlos M. Duarte, Elena Diaz-Almela, Núria Marbà, Tomas Sintes, Ester A. Serrão. Implications of Extreme Life Span in Clonal Organisms: Millenary Clones in Meadows of the Threatened Seagrass *Posidonia oceanica*. PLoS ONE, 2012; 7 (2): e30454.

New Stinky Flower: Our Amorphophallus Is Smaller, but It Stinks Like Its Big Cousin

Source: ScienceDaily. Feb. 7, 2012

The famed "corpse flower" plant -- known for its giant size, rotten-meat odor and phallic shape -- has a new, smaller relative: A University of Utah botanist discovered a new species of *Amorphophallus* that is one-fourth as tall but just as stinky.

The new species, collected on two small islands off Madagascar, brings to about 170 the number of species in the genus *Amorphophallus*, which is Greek for

"misshapen penis" because of the shape of the plants' flower-covered shaft, called the inflorescence or the spadix, says Greg Wahlert, a postdoctoral researcher in biology.

The 4.5-foot-tall plant, *Amorphophallus perrieri*, began reeking Friday, Feb. 3 as it approached the peak of its bloom in a campus greenhouse. A day later, Wahlert began cutting down the plant in stages so the spadix, the surrounding leafy spathe and other parts could be pressed, mounted and submitted to the National Museum of Natural History in Paris as part of the process of designating the plant a new species.

That won't be official until about a year from now after Wahlert publishes a scientific paper formally describing the species, which can grow to 5 feet high, and how it differs from relatives in the genus, including *Amorphophallus titanum* -- also known as the "corpse plant," "corpse flower" and "titan arum" -- which grows to 20 feet high.

After Wahlert first collected specimens of the new plant in 2006 and 2007 and discovered it was a new species, he found the Paris museum's herbarium held a dried specimen collected from one of the same islands by French botanist-geologist Joseph Marie Henri Perrier de la Bâthie (1873-1958), who didn't realize it was a new species. So Wahlert is naming it for Perrier.

"Perrier collected it in 1932, and it sat in the museum until we dug it up and compared it to the other specimens and the plants that I had collected," Wahlert says. "Perrier spent years working on scores of other plant groups [and describing hundreds of other new species] and just never got around to it."

The corpse flower smells like rotting meat to attract the flies and beetles that pollinate it. Wahlert had expected the new species would smell like cheese, which it did briefly when it began blooming Feb. 3. But the odor soon grew worse -- much worse -- and more like its giant relative.

"I smelled rotting roadkill out in the sun reeking," says University of Utah biology Professor Lynn Bohs, in whose lab Wahlert works. "There's also a note of public restroom -- a Porta Potty smell."

Wahlert added: "I would say carrion and feces. When you get right up to it, it's really foul and disgusting."

Another Utah researcher collected volatile gases emitted by the plant "and will identify the components of the smell," Wahlert says. Only a small group of *Amorphophallus* species have been tested for odors, but the known aromas range from rotting meat to anise, cheese, dung, fish, urine, spice and chocolate, he adds.

Two weeks before the plant began to bloom, "it was just a little bud sticking out of the dirt," he says. When it bloomed, the stalk was almost 4 feet tall and the inflorescence or spadix was about 10 inches long. It was yellow, with pollen on the top part. The lower part, hidden by the reddish, leafy spathe, was covered by hundreds of tiny flowers, each a fraction of an inch wide. (Sometimes the entire spadix is referred to informally as the flower.)

"They are just so rude -- their appearance and smell," Bohs says. "Everybody I've talked to says they almost started puking when they smelled it. It's horrid."

Some thought the plants' suggestive genus name was horrid. In 2008, Sir

David Attenborough said he invented the name "titan arum" for the corpse flower for his BBC series "The Private Life of Plants" because he thought it would be inappropriate to repeatedly refer to *Amorphophallus*.

Bohs says the genus belongs to the family Araceae, commonly known as the arum or aroid family. The family includes philodendrons, taro root (from which Hawaiians make poi), skunk cabbage and anthurium, a plant common in floral arrangements, with a yellow spadix surrounded by a leafy, red, heart-shaped spathe.

Wahlert says plants in the genus *Amorphophallus* are found in southern Asia, the South Pacific, Australia and Africa, including Madagascar. Of the 170 or so species in the genus, which first was discovered in 1834, "a lot have been known for 150 years, but one, two or three new species are described every year," he adds.

A. titanum grows naturally only in Sumatra in Indonesia, although it is found around the world in greenhouses that compete for the largest corpse flower plant. The Guinness Book of Records title currently is held by a New Hampshire specimen that had a spadix measuring 10-feet-2.25-inches tall in 2010. Counting the stem and spadix, *A. titanum* can reach 20 feet tall, compared with a 5-foot maximum for *A. perrieri*, which has a longer stem and shorter spadix -- about 10 inches long in the case of the one that bloomed on campus.

Wahlert collected the new species from Nosy Mitsio and Nosy Ankarea -- two islands northwest of Madagascar, which is off the east coast of Africa. "Nosy" means island in the Malagasy language.

The plant since has been found on Madagascar.

He had to obtain permission from a local village to visit Nosy Ankarea, an uninhabited, half-mile-wide island where the Sakalava people buried their rulers. Unlike Ankarea, which is still vegetated, Mitsio is heavily deforested. *A. perrieri* was found there in low scrub behind beach dunes.

"I went there in 2006 to collect tree violets, and when I got there I discovered these *Amorphophallus* in full bloom on the first day in the field," cutting and collecting four or five specimens, Wahlert says. "That night I got malaria. I stayed there a week but was so sick I couldn't do much collecting."

After the trip, Wahlert showed the specimens to Dutch botanist Wilbert Hetterscheid of Wageningen University. Hetterscheid, an expert on *Amorphophallus*, said they were a new species, and is co-authoring the descriptive paper with Wahlert.

In October 2007, Wahlert went back to the islands at the end of the dry season, and once again the new species were in full bloom. He collected 15 tubers -- the roots -- so he could grow the plants.

Wahlert kept the live plants at various institutions where he worked and gave others away, ending up with one left when he moved to Utah last fall.

"It's not high-tech, but it's still important to describe new species, to document biodiversity, particularly in a place like Madagascar, which is one of the world's great biodiversity hotspots," Wahlert says. "It's been severely deforested and is continuing to be deforested. So it's important to document new species before they go extinct."

The Genetics of Rice Metabolism

ScienceDaily. Feb. 8, 2012.

A large-scale study analyzing metabolic compounds in rice grains conducted by researchers at the RIKEN Plant Science Center (PSC) and their collaborators has identified 131 rice metabolites and clarified the genetic and environmental factors that influence their production. As one of the most important staple crops, rice plays a central role in supplying the nutrients needed to keep the world population healthy. The nutritional value of rice crops is determined by the types and quantities of metabolites they contain, which are strongly affected by environmental and genetic factors. Understanding these factors is crucial to increasing nutritional value, but the complex relationship between genes and plant metabolism makes this a formidable challenge.

At the heart of this challenge are so-called quantitative trait loci (QTL), stretches of DNA which contain or link to the genes for a phenotypic trait, in this case metabolite levels. To breed lines of rice which produce more of a specific metabolite (for example one that boosts its nutritional value), you have to know which DNA regions are involved and in what role. This is hard because metabolite levels are controlled by many different QTLs and also strongly influenced by the environment. To solve this problem, researchers at the PSC teamed up with their collaborators at the National Institute of Agrobiological Science (NIAS) to analyze rice grain metabolomic QTL (mQTL) using state-of-the-art mass spectroscopy pipelines developed at the PSC. Analysis of 85 experimental lines of rice specially bred for QTL analysis,

prepared by the NIAS researchers and harvested in 2005 and 2007, yielded a total of 759 metabolite signals. From these, the team identified 131 metabolites, including amino acids, lipids, and flavonoids, and identified a total of 801 mQTLs around the rice genome.

Most important of all, the team showed that while the levels of most metabolites they identified are influenced mainly by environmental factors, genetics can sometimes play a stronger role: coordinated control of amino acids was linked to an mQTL "hotspot" on chromosome 3, while variation of flavonoid levels was linked to genetic factors. Published in *The Plant Journal*, the findings promise a future of faster, more effective breeding techniques for rice, and mark a major step toward a healthier, better-fed world.

Journal Reference: Fumio Matsuda, Yozo Okazaki, Akira Oikawa, Miyako Kusano, Ryo Nakabayashi, Jun Kikuchi, Jun-Ichi Yonemaru, Kaworu Ebana, Masahiro Yano, Kazuki Saito. Dissection of genotype-phenotype associations in rice grains using metabolome quantitative trait loci analysis. *The Plant Journal*, 2012; DOI: 10.1111/j.1365-313X.2012.04903.x.

More grapes, less wrath: Hybrid antimicrobial protein protects grapevines from pathogen

Source: Science Codex. February 21, 2012.

LOS ALAMOS, New Mexico, February 20, 2012—A team of researchers has found a way to ensure that your evening glass of wine will continue to be available, despite the potential attack of *Xylella fastidiosa* (Xf), a bacterium that causes Pierce's Disease and poses a

significant threat to the California wine industry's valuable grapevines.

Researchers from Los Alamos National Laboratory (LANL), University of California at Davis (UCD), and the U.S. Department of Agriculture's Agricultural Research Service have created specially engineered grapevines that produce a hybrid antimicrobial protein that can block Xf infection.

Their research is published in the current edition of Proceedings of the National Academy of Sciences, "An engineered innate immune defense protects grapevines from Pierce's disease," by Abhaya M. Dandekar, et al. The article's online tracking number is 2011-16027R in the PNAS Early Edition to be published the week of Feb. 20, 2012.

By helping the vine fight the microbe with specific proteins, the scientists envision vineyards requiring less reliance on chemicals as growers seek to fend off the bacterium and the glassy-winged sharpshooter (*Homalodisca vitripennis*) insect that carries it. As the insect feeds on various plants, it distributes the microbe widely.

The key to the project's success is the fact that early in an Xf infection, molecules on the outer membrane of the microbe interact with cells of the grapevine. By interfering with that interaction between microbe and vine, scientists can help the vines block the disease and go on to produce a healthy crop of grapes.

"One thing got us started: with almost any pathogen, the major problem is drug resistance," said Goutam Gupta, the corresponding author of the PNAS paper. "We wanted the plant to clear itself of the pathogen before it is infected, much as the body's immune

system naturally recognizes a pathogen and takes action to defeat it."

To make the effective protein, researchers fused two genes: one that encodes a protein to cut a specific molecule on the outer membrane of Xf, and another that triggers the bursting of the Xf bacterium's outer wall, called lysis.

The team inserted the hybrid gene into grapevines and observed the plants' response to Xf infection. "The hybrid protein apparently creates pores in the membrane of the Gram-negative bacterium, Xf," said Gupta, thus allowing the plant to fight back the infection. Sap from the engineered plants successfully killed Xf in laboratory tests, and the whole plants did not exhibit symptoms of Pierce's disease after exposure to the Xf bacterium.

The antimicrobial gene may also protect other economically important plants from Xf-related diseases, and a similar strategy may be effective against a broad range of pathogen-induced plant and human diseases, Gupta said. *X. fastidiosa* is implicated in oleander leaf scorch, phony peach disease, plum leaf scald, almond leaf scorch, Pierce's disease in grapes, and citrus X disease in Brazil.

How photosynthesis originated

Source: Zee News. February 22, 2012.

Washington: Researchers, led by one of Indian origin, have shed light on the early events leading to photosynthesis, the result of the sequencing of 70 million base pair nuclear genome of the one-celled alga *Cyanophora*.

Atmospheric oxygen really took off on our planet about 2.4 billion years ago during the Great Oxygenation Event.

At this key juncture of our planet's evolution, species had either to learn to cope with this poison that was produced by photosynthesizing cyanobacteria or they went extinct.

It now seems strange to think that the gas that sustains much of modern life had such a distasteful beginning.

One of the fundamental steps in the evolution of our planet was the development of photosynthesis in eukaryotes- that include humans, plants, and most recognizable, multicellular life forms - through the process of endosymbiosis.

This crucial step forward occurred about 1.6 billion years ago when a single-celled protist captured and retained a formerly free-living cyanobacterium. This process, termed primary endosymbiosis, gave rise to the plastid, which is the specialized compartment where photosynthesis takes place in cells.

Endosymbiosis is now a well substantiated theory that explains how cells gained their great complexity and was made famous most recently by the work of the late biologist Lynn Margulis, best known for her theory on the origin of eukaryotic organelles.

In the world of plants, "Cyanophora is the equivalent to the lung fish, in that it maintains some primitive characteristics that make it an ideal candidate for genome sequencing," stated Debashish Bhattacharya, evolutionary biologist and Rutgers University professor, who led the study.

Bhattacharya and colleagues consider this study "the final piece of the puzzle to understand the origin of photosynthesis in eukaryotes."

Basic understanding of much of the subsequent evolution of eukaryotes,

including the rise of plants and animals, is emerging from the sequencing of the *Cyanophora paradoxa* genome, a function-rich species that retains much of the ancestral gene diversity shared by algae and plants.

For those unfamiliar with algae, they include the ubiquitous diatoms that are some of the most prodigious primary producers on our planet, accounting for up to 40 percent of the annual fixed carbon in the marine environment.

Bhattacharya leads the Rutgers Genome Cooperative that has spread the use of genome methods among university faculty. Using data generated by the Illumina Genome Analyzer IIX in his lab, Bhattacharya, his lab members Dana C. Price, Cheong Xin Chan, Jeferson Gross, Divino Rajah and collaborators from the U.S., Europe and Canada provided conclusive evidence that all plastids trace their origin to a single primary endosymbiosis.

Now that the blueprint of eukaryotic photosynthesis has come more clearly in sight, researchers will be able to figure out not only what unites all algae as plants but also what key features make them different from each other and the genes underlying these functions.

The study has been published in the journal *Science*.

What Should We Know About Foreign Genes In Our Food?

by Steve Savage. Source: Biofortified. 22 February 2012.

In a recent email exchange about the merits of mandatory "GMO labeling," I was asked this question: "Why shouldn't we be able to know what foreign genes are in our food?" It seems like a reasonable question to most people. After all, we are the customers; don't

we have a right to know what we want to know? The answer to that question is actually a lot more complicated than you might think. Let me explain.

What some people find "creepy" about the idea of "GMO crops" is that they contain genes from organisms other than the crop itself - hence the emotive term, foreign genes. Practical speaking, the novel genes in the commercial biotech crops grown around the world have come from either bacteria or viruses. To your average person, that might still sound creepy, but it needs to be put into perspective. Most people may not know it, but our diet is, and always has been loaded with foreign genes from bacteria and viruses and other living organisms (yeast, other fungi, nematodes, algae...). We don't live in a sterile world. In fact there are a host of microbes whose natural role in the world is to grow in association with plants - including food crops. Except for the case of recently cooked food, these organisms tend to be alive and well when we eat them - genes and all. I'll give a quick survey of the microbes which one finds on plants and whose foreign genes we regularly consume.

The surfaces of all plants, including those used for food, support a rich and diverse community of micro-organisms. Those living on leaves and other above-ground parts of plants make up the Phyllosphere Community (see image above). These organisms live on the nutrients available on the plant's surface, and they thrive in the tiny "boundary layer" of humid air that comes from the water inside the plant. There can easily be between one million and one hundred million microbial cells on every square centimeter of plant

surface. In a salad you are ingesting microbes numbering in the billions. Washing produce only slightly reduces those numbers, and they can reproduce again given a little time. Leaves, stems and fruits are loaded with foreign genes from these residents.

There are also richly diverse communities of microbes that live in association with below ground portions of plants (roots, tubers...). These are called "Rhizosphere inhabitants." Many live in a very close and sometimes even helpful relationship with the plant - protecting its roots from disease causing organisms, helping the plant absorb nutrients, or even supplying certain plants with supplies of usable nitrogen. Some are also just free loaders and some are microbes that cause diseases. The numbers of organisms here are even higher than on the above ground plant surface, and we can only grow and study a small fraction of these microbes in the lab. Some of these common soil bacteria (strains of *Bacillus thuringiensis*) are the source for the Bt genes in insect resistant GMO crops (corn, cotton, sweet corn). Another common soil bacterium (*Agrobacterium*) is the source of the EPSPS gene in most "Roundup Ready" plants. Both of these organisms (and all their genes) have always been present on foods that grow in and near the soil.

Microbes and Their Genes Inside of Plants

The inside of a plant is also far from sterile. There are microbes known as "endophytes" which thrive inside of plants, particularly in the "plumbing" of xylem and phloem. Some cause diseases of the plant (*Fusarium*, *Verticillium*), but many are another class of freeloaders that cause no harm or in a few cases

provide a benefit to the plant. In any case, they and their genes are common elements of our food.

Would You Like Any Viruses With Your Bacteria?

Oh, by the way, our food also carries along lots of genes from viruses (phages) that infect the bacteria that grow on and in it. Many plants are themselves infected with plant viruses (mostly RNA viruses but also some DNA viruses). Any crop in the crucifer family (turnips, broccoli, cabbage...) can be infected with Cauliflower Mosaic virus - a DNA plant virus which is the source of the "promoter" sequence used in many GMO crops. Viruses have only a handful of genes, but they can exist in huge numbers in an infected plant. Farmers try to avoid having plant viruses in their crops because they can be damaging. Even so, there are mild strains that are tolerated in some crops. Viral genes are certainly a regular part of our diet. There are also things called transposons which are natural sequences of foreign DNA that hop in and out of the plant's chromosomes sometimes disrupting working plant genes.

But Isn't That Different? Aren't Those Just "Natural, Foreign Genes"?

Yes and no. The way that plants are cultivated has a big influence on the particular dynamics of microbial associations with the crop above and below ground. Everything from the way the crop is fertilized or irrigated to the microclimate associated with planting density, trellising etc will change the mix of microbes in play. For instance, the pesticides or foliar trace nutrients that are sprayed on the crop effect its microbial suite. There are also quite a few biological control products which comprise live or dead bacteria which are

quite intentionally sprayed on a crop in huge numbers to express some of their genes in a way which wards off a disease or insect. These are celebrated as biological pesticide alternatives to synthetic pesticides. For more than 50 years we've been spraying crops with the same sort of Bt protein that is in a biotech insect resistant plant, but the sprayed form includes the bacterium, its other genes and all its other gene products. There are also viruses that infect insects (Baculoviruses) that are intentionally sprayed on certain crops. When compost is used on an organic or conventional field, one of the express purposes is to bring along a huge and diverse population of microbes. These microbes, and their genes, will then be in abundant supply on the roots, leaves and fruit. These may well be "natural" organisms, but there is no natural system in which such huge amounts of such material and associated bacteria etc. are introduced to a plant community. So, human activity has a profound effect on the range and quantity of foreign genes on and in our food. If it is logical to label genetically modified foods which contain a few foreign genes via genetic engineering, wouldn't it also make sense to label foods that have been intentionally sprayed with a biocontrol product or grown in a compost enhanced soil? Those contain far more foreign genes.

Should Any Of This Be Scary?

Not everything that can be made to sound scary is actually scary. Even though we are eating microbes, their genes, and their gene products on a grand scale, it is almost never a problem. In fact, some of these microbes go on to become part of our own bank of bacteria etc. that live within our

digestive system - often to our benefit. Indeed, we eat many foods that are intentionally loaded with microbes: like the ones that convert milk to yogurt or cheese or seaweed to Nato. This is all just part of our natural food supply. It is a very rare occasion when our incidental bacterial or viral feast includes something that poses a serious threat (certain strains of Salmonella, E.coli, Lysteria...that are actual human pathogens). Generally speaking, the consumption of foreign microbes, foreign genes, and the products of foreign genes is an unavoidable, but still non-issue from a safety point of view.

How Does This Compare To A GMO Crop?

The biggest difference between the foreign genes in GMO crops and the foreign genes that find their way into food by other mechanisms is that the GMO genes are much more of a known entity. Unlike the cocktail of microbes that come along in an uncontrolled, unknown, and almost unknowable way with all food, the microbial genes and gene products in a GMO crop are very well understood. We know the exact sequence of the gene, its location in the plant's chromosomes, what the gene does. We know which proteins are made because of that gene and we have been able to study those proteins in detail to determine their safety. With most of the other microbial genes that we are eating we can't say with certainty what is there, how much is there and what all the possible gene products are or what they do. The foreign genes in GMO crops are different from all the other foreign genes mainly in that we know so much more about them. So in reality, the genes in a GMO crop are the least creepy of such elements in our food.

Turning Off Small RNA: New Tool Designed for Breaking the Epigenetic Code

Source: ScienceDaily (Mar. 1, 2012)

For the last dozen years, scientists have known that minuscule strings of genetic material called small RNA are critically important to our genetic makeup. But finding out what they do hasn't been easy. Now a scientist from Michigan Technological University and his team have developed a way to turn off small RNAs and find out just how important they can be.

When it comes to inheritance, DNA is just the half of it. What we are is also driven by the epigenetic world of RNA: the countless, twisting molecules that DNA churns out. RNA in turn transforms the amino acid soup in our cells into the proteins that are us -- and every other plant and animal on the planet, for that matter.

There's more than one kind of RNA, however. In addition to the long strings that make proteins, there are short, meddling snippets called small RNAs. Sometimes, they can attach to long RNA molecules and break them in two. That obviously has consequences for the organism, but exactly what role the thousands of different small RNAs play has been a puzzle.

Now, Guiliang Tang, an associate professor of biological sciences, has developed a way to put a single small RNA out of commission and observe what happens when it can't do its job.

To do this, Tang and his team threw a wrench into a well-understood process that controls leaf symmetry and the tendency of plants to grow upright.

First they synthesized a sequence of DNA that would make a custom-designed type of small RNA, called a

small tandem target mimic, or STTM. Then they introduced their synthetic DNA in Arabidopsis, a plant often used in genetics research. Once in the Arabidopsis, the synthetic DNA began manufacturing many copies of the STTM.

Then all the little STTMs began locking onto strands of a specific type of RNA, right where the plant's small RNA would normally have cut them in two. That blocked its action, so the long RNA strands remained intact.

Furthermore, the procedure prompted the cell to destroy all of its own small RNAs that would normally have cut the RNA. Together, those two mechanisms allowed the long RNA to make its protein unabated.

The results were dramatic. The control Arabidopsis plants grew upward on a central stem with regularly shaped leaves and stems. The mutant plants were smaller, tangled, and amorphous.

Their method isn't limited to one small RNA involved in leaf symmetry in Arabidopsis.

"You can use this to study the function of any small RNA in the cell," says Tang. In an online commentary, *Plant Cell* senior features editor Nancy Eckardt called their method "a highly effective and versatile tool" for studying the functions of small RNA.

Now, Tang hopes to find out how and why this procedure causes cells to destroy small RNA. And his wife and fellow researcher Xiaoqing Tang, an assistant professor of biological sciences, plans to use this technology to better understand type 2 diabetes.

Their work is funded by the National Science Foundation and described in the article "Effective Small RNA Destruction by the Expression of a

Short Tandem Target Mimic in Arabidopsis," published Feb. 16 online in the journal *Plant Cell*. The lead authors of the paper are students who worked with Tang: Jun Yan, now a postdoctoral researcher at Purdue University, and Yiyu Gu, now an undergraduate at Nanjing Agricultural University, in China. Other coauthors are Xiaoyun Jia, Wenjun Kang and Shangjin Pan of the University of Kentucky and Xuemei Chen of the University of California at Riverside.

Reference: Jun Yan, Yiyu Gu, Xiaoyun Jia, Wenjun Kang, Shangjin Pan, Xiaoqing Tang, Xuemei Chen and Guiliang Tang. Effective Small RNA Destruction by the Expression of a Short Tandem Target Mimic in Arabidopsis. *The Plant Cell*, 2012

The future of plant science - a technology perspective

Source: Carnegie Institution in e/ Science News. March 3, 2012.

Plant science is key to addressing the major challenges facing humanity in the 21st Century, according to Carnegie's David Ehrhardt and Wolf Frommer. In a Perspective published in *The Plant Cell*, the two researchers argue that the development of new technology is key to transforming plant biology in order to meet human needs. Plants serve as the conduit of energy into the biosphere, provide food and materials used by humans, and they shape our environment. According to Ehrhardt and Frommer, the three major challenges facing humanity in our time are food, energy, and environmental degradation. All three are plant related.

All of our food is produced by plants, either directly or indirectly via animals that eat them. Plants are a source of

energy production. And they are intimately involved in climate change and a major factor in a variety of environmental concerns, including agricultural expansion and its impact on habitat destruction and waterway pollution.

What's more, none of these issues are independent of each other. Climate change places additional stresses on the food supply and on various habitats. So plant research is instrumental in addressing all of these problems and moving into the future. For plant research to move significantly forward, Ehrhardt and Frommer say technological development is critical, both to test existing hypotheses and to gain new information and generate fresh hypotheses. If we are to make headway in understanding how these essential organisms function and build the foundation for a sustainable future, then we need to apply the most advanced technologies available to the study of plant life, they say.

They divide the technology into three categories: existing technology that isn't being applied for all of its potential uses; new, readily envisioned technology; and technology we'd like to have, but don't know how to create.

The technological overview includes expanding existing technologies such as DNA sequencing, RNA cataloging, mass spectroscopy, fluorescence-based microscopy, and electron microscopy, among many others. A key focus is on the advances possible through advanced imaging technologies.

Ehrhardt and Frommer point out that many of the most often-cited academic papers related to the development new technology, demonstrating the interest of the scientific community. "We

certainly expect that new technologies will continue to revolutionize biological research," they say. "Plant science has not often been the driver of innovation but often enough has profited from developments made in other areas."

Carbon Nanotubes Spur Plant Cell Growth

By Katherine Bourzac. Source: American Chemical Society. March 6, 2012.

Nanomaterials: Multiwalled nanotubes could improve production in bioreactors based on plant cells, researchers say.

Tobacco cells exposed to multiwalled carbon nanotubes overexpress genes associated with plant growth, researchers report (ACS Nano, DOI: 10.1021/nn204643g). These exposed cells outgrow untreated cells by as much as 64%.

In 2009, Mariya Khodakovskaya, a biotechnology expert at the University of Arkansas, Little Rock, and her colleagues found that multiwalled carbon nanotubes dramatically enhanced growth rates in tomato plants (ACS Nano, DOI: 10.1021/nn900887m). This observation raised the possibility of using the nanomaterials as fertilizers. But, says Khodakovskaya, "if we want to use carbon nanotubes as a fertilizer, we have to understand the mechanism of these positive effects and study the potential risks in detail."

To start to piece together the molecular mechanism behind their observations, the Arkansas researchers grew cells of tobacco plants, which are a commonly studied plant in the lab, in growth media containing varying concentrations of multiwalled carbon nanotubes or activated carbon. They then compared the cells to ones grown without either carbon material. They

measured cell growth rates and expression levels of three growth-associated genes.

As they found in previous studies, the researchers saw that activated carbon increased cell growth rates by 16% at a low concentration of 5 $\mu\text{g}/\text{mL}$. Meanwhile, multiwalled nanotubes increased growth by 55 to 64% over a range of concentrations from 5 to 500 $\mu\text{g}/\text{mL}$. The researchers found that, in the cells grown with nanotubes, expression spiked of all three genes they studied: ones associated with cell division, cell wall formation, and water transport. For example, expression of *cycB*, a gene that regulates the cell cycle, increased 35-fold in cells exposed to 100 $\mu\text{g}/\text{mL}$ of the nanotubes.

Khodakovskaya says it is still too soon to harness these growth-promoting effects by using nanotubes as agricultural fertilizer: Scientists still need to understand how nanotubes and other nanomaterials move through the environment, she says, and how they might accumulate as they move up the food chain (C&EN, Mar. 14, 2011, page 44-46). A potential near-term application, which her group is exploring, would be to use the multiwalled nanotubes to improve production rates in bioreactors that use tobacco cells to make pharmaceuticals and other products.

Tatsiana Ratnikova, a horticulture and physics researcher at Cornell University, cautions against making generalizations based on the study. "We have to study each type of plant, each nanoparticle," she says. The picture is not yet clear even for multiwalled carbon nanotubes, she says, in part because their diameter, length, and number of layers vary widely. In fact,

some studies on the materials have found decreased growth, she says, while other groups reported no effects at all.

Going underground for optimal crops and yields

Source: Cordis. 2012-03-07

Researchers from the University of Nottingham in the United Kingdom have designed an innovative technique to study the underground world of plants. Presented in the journal *Plant Physiology*, the results of this study will lead to improved breeding techniques for crop varieties, as well as better yields.

The novel approach is based on the same X-ray technology used in hospital computed tomography (CT) scans. It integrates new image analysis software that can automatically distinguish the roots of plants from other soil-based materials.

The researchers, from the Centre for Plant Integrative Biology (CPIB), tested this approach on the roots of maize, wheat and tomato. They studied the architecture, what experts refer to as the shape and branching pattern, of roots in soil by using X-ray micro computed tomography (micro CT). The team then entered the information into the new RooTrak software, which enabled them to differentiate between roots and other soil elements.

'This technique is a hugely important advance,' says Dr Sacha Mooney, an expert in soil physics in the School of Biosciences. 'The application of X-ray CT for visualising roots has been limited because we simply couldn't see a large portion of the root structure. RooTrak has enabled us to overcome this and has opened up the use of the technology for exploring the key questions regarding

how we can manipulate plants and soils for improving our food security.'

The innovative software works by obtaining a stack of virtual slices through the root-bearing soil. According to the researchers, RooTrak treats each slice as a movie frame. The slice's static roots are treated as moving objects that can be tracked. So the software can tell the difference between root and water or organic elements in the soil, doing away with any glitches resulting from other techniques. This latest technique offers a three-dimensional (3D) detailed and accurate root architecture.

'Thinking of micro CT data as a sequence of images allows us to solve the problems caused by variations in the appearance of plant roots and the similarity of some roots to the surrounding soil,' says Tony Pridmore, head of data at CPIB and an expert in tracking and analysis software. 'This is important because we can now extract descriptions of root architecture quickly and objectively.'

Adds CPIB's Professor Malcolm Bennet, an expert in root biology: 'Root architecture critically influences nutrient and water uptake. A key impediment to genetic analysis of root architecture in crops grown in soil has been the ability to image live roots. Recent advances in micro CT and RooTrak software at Nottingham now make this possible.'

The Nottingham team has clinched a European Research Council (ERC) Advanced Investigator Grant worth EUR 3.5 million under the EU's Seventh Framework Programme (FP7). They will use this software along with an innovative micro CT-based imaging approach to image the roots of wheat,

and choose new varieties with optimal water and nutrient uptake efficiencies.

The CPIB will lead this new project, supported by experts from Australia, Europe and Mexico.

Reference: Mairhofer, S. et al., 'RooTrak: Automated Recovery of Three-Dimensional Plant Root Architecture in Soil from X-Ray Microcomputed Tomography Images Using Visual Tracking', *Plant Physiology*, 2012.

Petunia Points the Way to Better Harvests: Understanding Plants' Relationships With Helpful Soil Fungi

Source: ScienceDaily. Mar. 8, 2012

Most plants live in symbiosis with soil fungi and are supplied with water and nutrients as a result. Based on the petunia, plant biologists at the University of Zurich have now discovered that a special transport protein is required to establish this symbiotic relationship. The targeted control of this protein could lead to greater harvests.

About 80 percent of all terrestrial plants enter into a symbiotic relationship with fungi living in the soil. The fungi provide the plant with water, important nutrients like phosphate and nitrate, and certain trace elements like zinc; the plant, on the other hand, supplies the fungus with carbohydrates. It is assumed that plants were only able to migrate onto land 400 million years ago thanks to this symbiosis.

The formation of this symbiosis is a strictly regulated process that the plant activates in low nutrient levels. The roots release the hormone strigolactone, which is detected by the fungi. The fungal hyphae grow towards the roots, penetrate the epidermis and

isolated passage cells, and enter the root cortex. There, the fungal hyphae form tiny branch-like networks, which resemble little trees (arbusculum) and gave the symbiotic relationship its name: vesicular-arbuscular mycorrhizal symbiosis.

Until about five years ago, the hormone strigolactone was known to induce and entice parasitic plant seeds in the soil to germinate. At that stage, no-one understood why plants produced this substance, which is harmful to them. Only when the new role of strigolactone in mycorrhiza formation was discovered did it become clear that the attraction of the parasites was a harmful side effect of the symbiosis.

How do strigolactones get into the soil? Exactly how strigolactones are released into the soil from the roots and how the fungi find the specialized entry points in the roots was not known until now. The research group headed by Professor Enrico Martinoia from the University of Zurich has now found the answers to these questions in collaboration with Professor Harro Bouwmeester's team from Wageningen in the Netherlands. "Based on the model plant the petunia, we were able to demonstrate that the protein PhPDR1 transports strigolactones," explains Professor Martinoia. The protein belongs to the ABC-transporter family found in simple organisms like bacteria, but also in humans.

The researchers observed that PhPDR1 is expressed more highly in a low nutrient content in order to attract more symbiotic fungi, which then supply more nutrients. But there are also plants like the model plant *Arabidopsis* (mouse-ear cress) that do not form any mycorrhiza. If the researchers added

PhPDR1, however, the *Arabidopsis* roots transported strigolactones again.

Improvements in yield and weed control "Our results will help to improve the mycorrhization of plants in soils where mycorrhization is delayed," Professor Martinoia is convinced. "Mycorrhization can thus be triggered where it is inhibited due to dryness or flooding of the soils." This would enable the plants to be nourished more effectively and achieve a greater harvest. Moreover, thanks to the discovery of the strigolactone transporter the secretion of strigolactone into the soil can be halted, which prevents parasitic plants that use up the host plants' resources from being attracted. "This is especially important for regions in Africa, where the parasitic weed *Striga* and other parasitic plants regularly destroy over 60 percent of harvests," says Martinoia. Journal Reference: Tobias Kretzschmar, Wouter Kohlen, Joelle Sasse, Lorenzo Borghi, Markus Schlegel, Julien B. Bachelier, Didier Reinhardt, Ralph Bours, Harro J. Bouwmeester, Enrico Martinoia. A petunia ABC protein controls strigolactone-dependent symbiotic signalling and branching. *Nature*, 2012; DOI: 10.1038/nature10873

World breakthrough on salt-tolerant wheat

Source: e! Science News trough University of Adelaide. March 11, 2012

A team of Australian scientists involving the University of Adelaide has bred salt tolerance into a variety of durum wheat that shows improved grain yield by 25% on salty soils. Using 'non-GM' crop breeding techniques, scientists from CSIRO Plant Industry have introduced a salt-tolerant gene into a commercial

durum wheat, with spectacular results shown in field tests. Researchers at the University of Adelaide's Waite Research Institute have led the effort to understand how the gene delivers salinity tolerance to the plants.

The research is the first of its kind in the world to fully describe the improvement in salt tolerance of an agricultural crop -- from understanding the function of the salt-tolerant genes in the lab, to demonstrating increased grain yields in the field.

The results are published March 11 in the journal *Nature Biotechnology*. The paper's senior author is Dr Matthew Gilliam from the University's Waite Research Institute and the ARC Centre of Excellence in Plant Energy Biology. Lead authors are CSIRO Plant Industry scientists Dr Rana Munns and Dr Richard James and University of Adelaide student Bo Xu.

"This work is significant as salinity already affects over 20% of the world's agricultural soils, and salinity poses an increasing threat to food production due to climate change," Dr Munns says.

Dr Gilliam says: "Salinity is a particular issue in the prime wheat-growing areas of Australia, the world's second-largest wheat exporter after the United States. With global population estimated to reach nine billion by 2050, and the demand for food expected to rise by 100% in this time, salt-tolerant crops will be an important tool to ensure future food security."

Domestication and breeding has narrowed the gene pool of modern wheat, leaving it susceptible to environmental stress. Durum wheat, used for making such food products as pasta and couscous, is particularly susceptible to soil salinity.

However, the authors of this study realised that wild relatives of modern-day wheat remain a significant source of genes for a range of traits, including salinity tolerance. They discovered the new salt-tolerant gene in an ancestral cousin of modern-day wheat, *Triticum monococcum*.

"Salty soils are a major problem because if sodium starts to build up in the leaves it will affect important processes such as photosynthesis, which is critical to the plant's success," Dr Gilliam says.

"The salt-tolerant gene (known as TmHKT1;5-A) works by excluding sodium from the leaves. It produces a protein that removes the sodium from the cells lining the xylem, which are the 'pipes' plants use to move water from their roots to their leaves," he says.

Dr James, who led the field trials, says: "While most studies only look at performance under controlled conditions in a laboratory or greenhouse, this is the first study to confirm that the salt-tolerant gene increases yields on a farm with saline soils.

Field trials were conducted at a variety of sites across Australia, including a commercial farm in northern New South Wales.

"Importantly, there was no yield penalty with this gene," Dr James says.

"Under standard conditions, the wheat containing the salt-tolerance gene performed the same in the field as durum that did not have the gene. But under salty conditions, it outperformed its durum wheat parent, with increased yields of up to 25%.

"This is very important for farmers, because it means they would only need to plant one type of seed in a paddock that may have some salty sections," Dr James says.

"The salt-tolerant wheat will now be used by the Australian Durum Wheat Improvement Program (ADWIP) to assess its impact by incorporating this into recently developed varieties as a breeding line."

Dr Munns says new varieties of salt-tolerant durum wheat could be a commercial reality in the near future.

"Although we have used molecular techniques to characterise and understand the salt-tolerant gene, the gene was introduced into the durum wheat through 'non-GM' breeding processes. This means we have produced a novel durum wheat that is not classified as transgenic, or 'GM', and can therefore be planted without restriction," she says.

The researchers are also taking their work a step further and have now crossed the salt-tolerance gene into bread wheat. This is currently being assessed under field conditions.

This research is a collaborative project between CSIRO, NSW Department of Primary Industries, University of Adelaide, the Australian Centre for Plant Functional Genomics and the ARC Centre of Excellence in Plant Energy Biology. It is supported by the Grains Research and Development Corporation (GRDC) and Australian Research Council (ARC).

New research could make it easier to grow health-promoting blood oranges

Source: John Innes Centre News. MARCH 13, 2012

For the red pigmentation to develop, blood oranges normally require a period of cold as they ripen. The only place to reliably grow them on a commercial scale is in the Sicilian area of Italy around Mount Etna. Here, the combination of

sun and cold sunny days and warm nights provides ideal growing conditions.

Scientists have identified the gene responsible for blood orange pigmentation, naming it Ruby, and have discovered how it is controlled.

"Blood oranges contain naturally-occurring pigments associated with improved cardiovascular health, controlling diabetes and reducing obesity," said Professor Cathie Martin from the John Innes Centre on Norwich Research Park. "Our improved understanding of this trait could offer relatively straightforward solutions to growing blood oranges reliably in warmer climates through genetic engineering."

The pigments are anthocyanins, flavonoids that give red, purple and blue fruit their colour. Previous studies have shown that drinking blood orange juice reduces oxidative stress in diabetic patients, protects DNA against oxidative damage and that it may reduce cardiovascular risk factors more generally, as demonstrated for other high-anthocyanin foods.

A 2010 study found that blood orange juice limits the development of fat cells and weight gain in mice and provides resistance to obesity compared to blond orange juice or water.

Blood oranges are grown outside Sicily, for example in Japan, South Africa and Iran. But in some years entire harvests are lost because the right conditions cannot be created during ripening. Or in Florida and Brazil, the anthocyanin content is weak and unreliable.

The scientists isolated the Ruby gene from the flesh of blood and blond oranges. They found that it is controlled by mobile genetic elements that are activated by the stress of cold.

They accessed all globally known blood orange types to analyse whether any produce anthocyanins without cold. Most blood orange cultivars originated directly or indirectly from Sicily, but one old variety, Jingxian, is of Chinese origin. In the Jingxian variety, the production of anthocyanins is dependent on a different mobile element, but again this is activated by cold.

"Our results offer little hope of conventionally breeding or identifying new varieties of blood orange that are free from cold dependency," said Professor Martin.

"We are now experimenting with hooking the Ruby gene up with a specific fruit promoter so it can be induced in another way."

Blood oranges are a derivative of sweet orange, the most commonly grown fruit tree in the world. The current study, to be published in *The Plant Cell*, also confirmed that sweet oranges are a hybrid between the Southeast Asian pummelo and mandarin.

The research was funded by an EU project focused on flavonoids, FLORA, an EU project called ATHENA focussed on anthocyanins and polyphenols, a studentship from the John Innes Foundation, strategic funding from the Biotechnology and Biological Sciences Research Council (BBSRC) and the Italian Agronotech project.

It led the scientists on an historical as well as scientific journey, unearthing the earliest paintings featuring blood oranges, 19th century botanical drawings and their earliest mentions in historic texts.

Reference: Butelli, E., Licciardello, C., Zhang, Y., Liu, J., Mackay, S., Bailey, P., Reforgiato-Recupero, G., and Martin, C. (2012). Retrotransposons control fruit-

specific, cold-dependent accumulation of anthocyanins in blood oranges. *Plant Cell*. 10.1105/tpc.111.095232 in press.

Smoke Signals

Source: Science Signaling, Editor's choice. 13 March 2012

Strigolactones and karrikins are structurally similar butenolides that elicit tissue- and stage-specific growth responses in plants. Whereas strigolactones are endogenously produced hormones that inhibit shoot branching and stimulate branching of mycorrhizal fungi, karrikins are produced by burning plants and aid in revegetation after wildfires by promoting seed germination and improving the responsiveness of seedlings to light. The F-box protein MAX2 is a component of the SCF ubiquitin ligase complex and is required for responses to both classes of butenolides, but how plants distinguish between these compounds is not yet clear. Waters et al. report that two members of the DWARF14 family of α/β hydrolases are differentially required for strigolactone and karrikin responses in *Arabidopsis thaliana*. Mutational analysis coupled with treatment of seeds and seedlings with karrikins or the synthetic strigolactone GR24 revealed that AtD14 (*Arabidopsis thaliana* DWARF14) mediated only strigolactone responses and that the related hydrolase KAI1 (karrikin-insensitive 1) mediated responses to both classes of compounds. AtD14 and kai2 mutants shared distinct subsets of phenotypes with max2 mutants, and genetic interaction experiments suggested that both acted upstream of MAX2 at different stages of development. Because KAI2 does not

exhibit enzymatic activity in vitro, the authors propose that these hydrolases could act as ligand-binding proteins that convey signal-specific information to MAX2 rather than as enzymes that generate active signals from the compounds. *kai2* mutants had impaired responses to light, a phenotype that was not seen in *Atd14* or strigolactone biosynthesis mutants, and plants that are not found in fire-prone environments retain karrikin responsiveness, suggesting that, although smoke is the only reported source of karrikins, there may be endogenous karrikins that regulate germination and seedling development. Citation: A. M. VanHook, Smoke Signals. *Sci. Signal.* **5**, ec76 (2012).

Root-imaging technology could improve crop resilience

By Aleida Rueda. Sci Dev.Net. 13 March 2012

Mexican researchers have welcomed a breakthrough in imaging plant roots, saying it could help breeders develop new varieties of crops that can thrive in harsh conditions.

The technique uses X-ray computed tomography to build up a three-dimensional image by scanning through 360 degrees, a technology commonly used in hospitals to diagnose soft tissue damage.

Scans of plant roots in soil show the shape and branching patterns of the roots, but do not clearly distinguish between the roots and surrounding soil and organic matter.

Now scientists at the Centre for Plant Integrative Biology (CPIB) at the University of Nottingham, United Kingdom, have developed imaging software — called "RooTrak" — to

analyse the scans and display the roots as a distinct three-dimensional structure. Their findings are reported in the February issue of *Plant Physiology*.

"This is the first time this approach has been used for this purpose and the results are very promising," Malcolm Bennett, the project's leader, told SciDev.Net.

As well as providing clearer imaging, the method is fast and non-invasive because roots can be analysed without having to remove the surrounding soil. The technique has passed initial tests on maize, tomato and wheat grown in a range of contrasting soil textures.

The CPIB has been awarded US\$4.5 million by the European Research Council to test the technology in Australia, Europe and Mexico.

The Mexican collaboration is being coordinated by the International Maize and Wheat Improvement Center (CIMMYT), which plans to use the technology to screen wheat for a variety of traits including heat and drought tolerance, and water and nutrient use.

While the technology was welcomed by researchers contacted by SciDev.Net they all expressed concern that it might be too costly for widespread adoption in developing countries.

But the technology could benefit plant breeders, according to Matthew Reynolds, a wheat physiologist at CIMMYT in Mexico who will oversee the collaboration.

"This technique will open enormous possibilities for understanding the interaction between trees and annual crops [such as maize and beans] at the level of their root systems, particularly under conditions of drought and root

competition between species," said Antonio Turrent Fernández, of Mexico's National Institute of Agricultural, Livestock and Forestry Research (INIFAP).

Alejandro Espinosa Calderón, also from INIFAP, said the technology "could help [researchers] select plants with favourable root architecture, shape, depth and size that could thrive in adverse conditions".

Video:

http://www.youtube.com/watch?v=IFX6k9NIFg4&feature=player_embedded

Reference: Plant Physiology 158, 569 (2012)

Plants 'Remember' Drought, Change Responses to Survive

Source: ScienceDaily (Mar. 15, 2012)

Plants subjected to a previous period of drought learn to deal with the stress thanks to their memories of the experience, new research has found. The findings could lead to development of crops better able to withstand drought.

The research also confirms for the first time the scientific basis for what home gardeners and nursery professionals have often learned through hard experience: Transplants do better when water is withheld for a few days to drought harden them before the move.

"This phenomenon of drought hardening is in the common literature but not really in the academic literature," said Michael Fromm, a University of Nebraska-Lincoln plant scientist who was part of the research team. "The mechanisms involved in this process seem to be what we found."

Working with *Arabidopsis*, a member of the mustard family considered an excellent model for plant research, the

team of Fromm, plant molecular biologist Zoya Avramova and post-doctoral fellow Yong Ding compared the reaction of plants that had been previously stressed by withholding water to those not previously stressed.

The pre-stressed plants bounced back more quickly the next time they were dehydrated. Specifically, the nontrained plants wilted faster than trained plants and their leaves lost water at a faster rate than trained plants.

"The plants 'remember' dehydration stress. It will condition them to survive future drought stress and transplanting," Fromm said.

The team found that the trained plants responded to subsequent dehydration by increasing transcription of a certain subset of genes. During recovery periods when water is available, transcription of these genes returns to normal levels, but following subsequent drought periods the plants remember their transcriptional response to stress and induce these genes to higher levels in this subsequent drought stress.

"All of this is driven by events at the molecular level," Avramova said. "We demonstrate that this transcriptional memory is associated with chromatin changes that seem to be involved in maintaining this memory."

Arabidopsis forgets this previous stress after five days of watering, though other plants may differ in that memory time.

This is the first instance of transcriptional memory found in any life form above yeasts. This discovery may lead to breeding or engineering of crops that would better withstand drought, although practical applications of these findings in agriculture are years away, Fromm said.

"We're a long way off. We're just starting to get a basic understanding," Fromm said. "It's possible plants overreact to a first drought stress. They panic, they slow down more than they need to."

Perhaps scientists can modify those instincts in plants to help maintain or improve productivity during times of drought, he added.

But home gardeners can make immediate use of these findings.

"If I was transplanting something, I would deprive it of water for a couple of days, then water overnight, then transplant," Fromm said.

The work is the subject of an article this week in the online journal *Nature Communications* and is funded by the National Science Foundation.

Reference: Yong Ding, Michael Fromm, Zoya Avramova. Multiple exposures to drought 'train' transcriptional responses in *Arabidopsis*. *Nature Communications*, 2012; 3: 740 DOI: 10.1038/ncomms1732

Hotspots for Biogenesis of Small RNA Molecules in Plant Cells Discovered

Source: ScienceDaily (Mar. 15, 2012)

Throughout their life, plants form leaves and side roots. These two types of organs have something in common: their development is finely tuned by small regulatory RNA molecules, the trans-acting short interfering RNAs (ta-siRNAs). Scientists Dr. Alexis Maizel and Virginie Jouannet at Heidelberg University's Centre for Organismal Studies were able to demonstrate how and where within the plant cell these ta-siRNAs are produced. They succeeded in identifying hotspots for the biogenesis of these special RNA molecules.

The results of this study have been published in the *EMBO Journal*.

The formation of plant organs depends on the presence of proteins that allow cells to divide and take on new shapes and characteristics. The most straightforward route to protein production begins when genes are activated and transcribed into messenger RNAs that are then translated into proteins. However, cells often fine-tune their population of proteins by producing short interfering RNAs (siRNAs): small regulatory molecules that dock onto messenger RNA and cause them to be broken down before they can be used for protein production. Researchers already knew that ta-siRNAs, a type of siRNA, fine-tune the formation of leaves and the growth of side roots by blocking the production of specific proteins. What remained unknown, however, was exactly where in the plant cell the ta-siRNAs were produced.

Ta-siRNAs are created from longer RNA molecules that are whittled down by a complex of other molecules. One essential component of this cutting machine is a protein called AGO7. The Heidelberg scientists have uncovered that AGO7 accumulates in foci, called siRNA bodies, located in the cytoplasm of the cells. SiRNA bodies also contain all the other enzymes needed for the formation of ta-siRNAs. "These foci are therefore hotspots for the formation of the siRNAs, that is the small, regulatory RNA molecules," explains Virginie Jouannet, a PhD student in Dr. Maizel's group. In addition, the researchers were able to show that AGO7 could no longer fulfil its functions when released from the siRNA

bodies, resulting in problems in the development of the plant.

Two other observations caught the attention of the researchers. For one thing, the siRNA bodies are closely linked to the network of membranes that the cell uses to transport and secrete proteins. "Interestingly, these foci also host viruses and plants defend themselves against viruses using siRNAs," says Dr. Maizel. "These results reveal a hitherto unknown role for membranes in the biogenesis of RNA and suggest that the generation of siRNA can occur only in specific locations of the cell."

Dr. Maizel leads an independent research group at the Centre for Organismal Studies at Heidelberg University and is a member of the university's CellNetworks Cluster of Excellence. Collaborating on the research project were scientists from the Institut des Sciences du Végétal at the Centre National de la Recherche Scientifique (CNRS) in Gif-sur-Yvette as well as the Institut Jean-Pierre Bourgin at the Institut National de la Recherche Agronomique (INRA) in Versailles (France).

Reference: Virginie Jouannet, Ana Beatriz Moreno, Taline Elmayan, Hervé Vaucheret, Martin D Crespi, Alexis Maizel. Cytoplasmic Arabidopsis AGO7 accumulates in membrane-associated siRNA bodies and is required for ta-siRNA biogenesis. *The EMBO Journal*, 2012; DOI: 10.1038/emboj.2012.20

Study sheds light on plants' 'spring switch'

By Mark Kinver, BBC News. 21 March 2012

Researchers have identified the genetic "switch" that triggers the flowering

process in plants as they respond to warmer temperatures.

They found that a gene, known as PIF4, activated the flowering pathway when a certain temperature was achieved.

The team added that the findings could be used in future research to improve crops' resilience to projected changes in the climate.

Details of the study have been published in the journal *Nature*.

"We have known for hundreds of years that when it gets warmer, plants come into flower," said co-author Philip Wigge from the John Innes Centre, Norwich, UK.

"The question then is... how is it possible that plants are able to control this process with such accuracy and sensitivity."

Dr Wigge said that there were two mechanisms that allowed plants to respond to the arrival of spring: measuring day-length and changes in temperature.

"The switch we discovered is to do with the second one, and helps shed light on how plants know when it is getting warmer," he told BBC News.

"This gene is remarkable because it is only active when it is warm. If you cool the plant down, it has no effect. The gene works in such a way that it is only on in the warm.

"When there are higher temperatures, it activates the target genes and switches on the flowering process."

For their study, the researchers used *Arabidopsis thaliana*, a small flowering plant native to Europe, Asia and northern parts of Africa.

It was the first plant species to have its genome sequenced, Dr Wigge said, making it a "terrific tool" for molecular biologists.

Dr Wigge explained that plants appeared to use a combination of the two trigger mechanisms but to varying degrees, which affects the characteristics of plants' flowering behaviour.

"Some plants will flower at the same time each spring, whereas other plants will flower earlier if it is warmer. Those are the plants that have an active PIF4 pathway," he said.

"Research carried out by a team in the US has shown that plants that use warmer temperatures to control when they flower are out-competing other plants to a considerable degree.

"In the past 100 years or so, many plants that have just used day-length have become locally extinct.

"Yet plants that have used temperature to control when they flower have increased their range considerably and now much more common.

"That makes a lot of sense because those plants will be able to out-compete other species in a climate change scenario."

Phenological studies have shown that plants are flowering and producing fruit earlier than in the past.

Experts warn that the changes will lead to a breakdown in symbiotic relationships within ecosystems, such as plants' dependence on pollinators.

"We have known for some time that wild plant populations are changing, and they are responding in different ways to changes to the climate," Dr Wigge observed.

"But what we have not understood is the underlying mechanism. So now we know some of the genes that are important in the (flowering) process, we can start to make predictions.

"We can look at ecosystems, and based on whether or not the plants use temperature-based signalling, we can start to make predictions about how ecosystems are likely to change in the future."

The findings can also help crop research, allowing scientists to consider possible ways to ensure yields are not adversely affected by projected climate change.

Dr Wigge said it has been estimated that for every 1C (1.8F) rise in mean global temperatures, crop yields would decline by about 10%.

"Many crops are already been grown near the top of their optimal temperature range," he said.

"Temperature basically has a very large and complex effect on yields. We think that the same process that works in Arabidopsis also works in wheat and barley."

This understanding could allow researchers to modify the plants' responses to temperature changes, either genetically or through breeding programmes.

"Identifying these genes gives you a very powerful tool to modify crops to make them more resilient to climate change," he suggested.

Reference: Transcription factor PIF4 controls the thermosensory activation of flowering. S. Vinod Kumar et al. *Nature*, 21 March 2012, doi:10.1038/nature10928

Trace Element Plays Major Role in Tropical Forest Nitrogen Cycle

Source: ScienceDaily (Mar. 22, 2012)

A new paper by researchers from the University of Georgia and Princeton University sheds light on the critical part played by a little-studied element,

molybdenum, in the nutrient cycles of tropical forests. Understanding the role of molybdenum may help scientists more accurately predict how tropical forests will respond to climate change. Nutrient cycles track the movement of essential nutrients as they loop through the environment, into plants and animals and back into the environment. One of the most important of these nutrients is nitrogen.

"The main way that new nitrogen is added to an ecosystem is through a process called nitrogen fixation," said Nina Wurzbarger, assistant professor in the UGA Odum School of Ecology and the paper's lead author. "Bacteria in the soil can pull nitrogen out of the atmosphere and convert it into a form available for themselves and for plants. They do this by creating an enzyme called nitrogenase."

For years, it was assumed that the element phosphorus was the key ingredient bacteria in the soil needed to make this enzyme work. Now Wurzbarger and her colleagues Jean Philippe Bellenger, Anne M.L. Kraepiel and Lars O. Hedin of Princeton University have found that although phosphorus is indeed important to the process, another element-molybdenum-is also crucial. "Our results were quite unexpected," said Hedin, a professor of ecology and evolutionary biology. "We discovered that the trace element molybdenum often was the limiting nutrient, not phosphorus, as most theories would predict."

An earlier study by Princeton researchers revealed that molybdenum might play a previously unsuspected role in nitrogen fixation in tropical forest ecosystems. The researchers wanted to

learn more. Working in lowland Panama, they conducted experiments at six forest sites that had similar climates and plant species but differed in the amount of phosphorus in the soil. "It was fortuitous that we came across this naturally occurring phosphorus gradient," Wurzbarger said. "The only difference between the sites is the geology, so we had a natural range of soil phosphorus levels-from high to low." All the sites had a similar low level of molybdenum.

The researchers took a set of soil samples from each site and treated them by adding phosphorus, molybdenum or a combination of both. They then measured the response of the nitrogen-fixing bacteria in the soil. They expected that nitrogen fixation would increase in phosphorus-rich soils when they added molybdenum and in phosphorus-poor soils when they added phosphorus, but that was not the case. While the phosphorus-rich soils responded as predicted, the phosphorus-poor soils did not. In phosphorus-poor soils, nitrogen fixation did not increase with the addition of phosphorus alone-or, for that matter, molybdenum alone-but only responded when both phosphorus and molybdenum were added together.

"The most surprising result of our work is that phosphorus by itself is not the major constraint we've thought it to be," Wurzbarger said. "This is particularly surprising for tropical forests where the highly weathered soils are thought to be poor in phosphorus."

The reason for this response, the researchers found, was that molybdenum and phosphorus behave very differently with organic matter in

soil. While much of the phosphorus in soil is in a form that plants can use, much of the molybdenum—one of the least abundant of the elements essential to plants—is not. "The chemistry of the leaf litter seems to lock up the molybdenum and make it unavailable to bacteria," Wurzburger said. "Therefore, no matter how abundant or poor phosphorus is in the environment, it's molybdenum that seems to present a consistent constraint for nitrogen-fixing bacteria." The researchers are continuing to pursue their understanding of how this relatively obscure element interacts with other nutrient cycles. "One big question is how this might apply to other ecosystems such as temperate or boreal forests," Wurzburger said. "We just don't know

how important molybdenum might be. I want to know whether these findings relate to these systems too."

The answers to these questions may have widespread implications. "Tropical forests regulate the Earth's climate system," Wurzburger said. "They sequester a large amount of carbon through photosynthesis. Climate models predict that tropical forests may respond to elevated levels of carbon dioxide by sequestering even more carbon, but their ability to do this may be constrained by nitrogen. Since molybdenum constrains nitrogen fixation, it might also determine how much carbon tropical forests can sequester. We really need to know more."

The findings were published March 21 in the journal PLoS ONE.

FORTHCOMING MEETINGS



Gordon Research Conference on: SALT & WATER STRESS IN PLANTS

June 24 – 29, 2012. Hong Kong, China

More info:

<http://www.grc.org/programs.aspx?year=2012&program=salt>

SEB Annual Main Meeting 2012

June 29, 2012. Salzburg, Austria

More info:

<http://www.sebiology.org/meetings/Salzburg2012/Salzburg.html>

Plant Vascular Development 2012

July 1 – 2, 2012. Gregor Mendel

Institute, Vienna, Austria

More info:

<http://www.icar2012.org/Satellite%20Meetings/plant-vascular-development-2012>

2nd International Symposium on Woody

Ornamentals of the Temperate Zone

July 1 – 4, 2012. Ghent, Belgium

Scientists and growers from all over the world will share new developments in hardy nursery stock research.

Visit our **website** for more detailed information:

<http://www.ilvo.vlaanderen.be/woodyornamentals2012>

This symposium will cover all aspects of **woody plant production and management**: crop protection, cultural techniques, multiplication, breeding, biodiversity, effects of climate change on plant physiology, and more.

E-mail:

woodyornamentals@ilvo.vlaanderen.be

Website:

<http://www.ilvo.vlaanderen.be/woodyornamentals2012>

23rd International Conference on Arabidopsis research

July 3 – 7, 2012. Vienna, Austria

More info: <http://www.icar2012.org/>

Malaysia International Biological Symposium: i-SIMBIOMAS 2012

July 11 – 12, 2012. Kajang, Malaysia

MALAYSIA INTERNATIONAL BIOLOGICAL SYMPOSIUM 2012 (i-SIMBIOMAS 2012) has catapulted into international status from the earlier biennial events of SIMBIOMAS 2009, and Kolokium Biologi 2007, 2005 and 2003 organized by the Department of Biology, Faculty of Science, UPM. The symposium is predominantly catered for informal exchange of research findings, ideas and views between postgraduates, researchers and collaborators from local and international. Year 2012 marks SIMBIOMAS goes international and henceforth will be continued biennially. The i-SIMBIOMAS 2012 aims to bridge researchers from various disciplines of Biology, and serves as a platform to foray fundamental biological sciences, applied biology and diversification of research into producing commercially viable knowledge, skill and bioproducts.

<http://www.science.upm.edu.my/biology/i-simbiomas2012/>

Plant Molecular Biology Gordon

Conference Export to Your Calendar

July 15 – 20, 2012. New Hampshire, United States

More info:

<http://www.grc.org/programs.aspx?year=2012&program=plantmolec>

ASPB - Plant Biology 2012
July 20 - 24 , 2012. Austin, TX
Abstract submission is now open.
http://my.aspb.org/?page=Meetings_PB2012

4th Plant Nitric Oxide (NO) Club meeting
July 26 - 27, 2012. Edinburgh, Escocia
Website:
<http://symposium.bio.ed.ac.uk/no2012/>.

FESPB-EPSO 2012 CONGRESS
July 29 - August 3, 2012. Freiburg, Germany
The next FESPB Congress will be jointly organized with EPSO, and will be held in Freiburg, Germany from 29 of July to 3 of August 2012.

Attached please find the relevant Poster and take advantage of the early registration fee.

Also, attached are the Announcements for the **2012 FESPB Student Travel Grants** from ex-eastern european countries and the **FESPB Awards**.

Please notice that EPSO will also sponsor 20 Travel Grants for european students. Information will soon be available at the www.fespb.org and www.epsoweb.eu

28th Congress of the European Society for Comparative Physiology and Biochemistry (28th ESCPB)
September 2 - 5, 2012. Bilbao, Basque Country (Spain).

The congress will bring together researchers and professionals from a broad set of science disciplines with the aim of sharing the latest research results in emerging fields of Cell and Molecular Biology, Biochemistry, Physiology, Genomics, Proteomics and Systems Biology focused on cellular and molecular processes at the basis of physiological adaptation to changing environmental

conditions in a global scenario. Session Topics covered will include:

- Cellular and molecular responses to environmental stress
- Biochemical and physiological adaptation to climate change
- Developmental and reproductive responses to multiple stressors
- Immune responses under multiple stressor challenge
- Cell signalling pathways mediating multiple stressor effects
- Endocrine systems: basic aspects and effects of multiple stress
- Cell cycle regulation, cell death and cell proliferation under multiple stress
- Evolution of receptors and cell protection systems in coping with environmental change
- Integrative neurobiology and behavioural responses to stress
- Acid base regulation and ion transport homeostasis
- Comparative physiology of energy metabolism
- Systems biology of environmental adaptation
- Comparative genomics and next generation sequencing
- From omics to mechanisms and from mechanisms to environmental health

Important Dates

- Deadline for abstract submission: 30th March
- Acceptance of abstracts by the Scientific Committee: 15th April
- Deadline for early registration at reduced fee: 30th June

Registration fees:

- Early registration: 300 €
- Registration after 30th June: 400 €
- Grants available for PhD students: 150 €

Publications

All accepted abstracts will be published as a supplemental issue of Comparative Biochemistry and Physiology - Part A: Molecular & Integrative Physiology (CBA).

A hard copy of this issue will be distributed to all participants at the beginning of the Congress.

Contact details

To keep you informed about all congress details, please visit the congress web page: <http://www.ehu.es/escpb-Bilbao2012>

For any questions or suggestions, please do not hesitate to contact us at gorka.equiguren@ehu.es

9th International Conference "Plant Functioning in Stress Environment" September 12 - 15, 2012. Cracow, Poland

<http://www.ifr-pan.krakow.pl/main.php?lang=eng&page=akt>

Request the 2nd circular by email to: Conf.krakow@gmail.com or m.grzesiak@ifr-pan.krakow.pl

The China - EU Workshop on Phenotypic Profiling and Technology Transfer on Crop Breeding September 17 - 21, 2012. Barcelona, Spain.

China and EU are dedicating great R&D efforts in agriculture, food security and food safety. They both face common challenges, such as the growing demand for safe, nutritive and affordable food given the constraints of land, water, energy and in face of the environmental limits (e.g. soil erosion, and combined effects of climate change impacts and biodiversity loss). The only viable approach to increasing food production is to raise the productivity of existing farmland. The greatest challenge is to increase food production and improve product quality in an environmentally sustainable manner. Crop management and breeding are the pillars of an effort to tackle the present and future challenges on food production. The need to

accelerate plant breeding for increased yield potential and better adaptation to drought and other abiotic stresses is an issue of increasing urgency at the World level. However genetic advance on yield potential and adaptation to major abiotic stresses is constrained in spite the huge advance in the last years on technologies directly related with crop molecular breeding. Phenotyping remains as a bottle neck for future increased plant breeding efforts; particularly when field evaluation is mandatory. That means both high throughput phenotyping technologies, field characterization of experimental sites for environmental variability. Bioinformatic technologies is another key area since it allows to study $G \times E$ interactions, translate phenotyping information into a selection indices and establish links between genomic information and phenotype data. As for the genomic techniques during the last two decades now increasing interest is rising at both public and private sector engaged in crop breeding on the importance of phenotyping very sophisticated albeit expensive state-of-the art approaches on plant phenotyping are emerging (e.g. high-throughput phenotyping platforms). This may represent a constraint for the practical adoption of new technologies by the small companies and NARS. However beside all the glamour related with the adoption of new technologies, breeders experience and common sense may do phenotyping far simpler, cheaper albeit efficient than expected. The EU-China partnership initiative in crop breeding (OPTICHINA) was launched on June, 2011 as a new instrument that may serve as model to reinforce a systematic co-operation on Agricultural Research between Europe and China.

<http://www.ub.edu/optichinagriculture/en/activities/Workshops.php>

**The EMBO Meeting 2012 - Advancing
the life sciences**
September 22 - 25, 2012. Nice,
France
<http://2012.the-embo-meeting.org/>

**17th Meeting of the International
Council for Grapevine Viruses**
October 8 - 12, 2012. Davis,
California (USA)
More information can be found at
<http://ucanr.org/sites/ICVG/>

Genetics of Fagaceae
October 9 - 12, 2012. Agora -
University of Bordeaux. Talence, France
Organized by The IUFRO working group
"2.08.05 - Genetics of Quercus and
Nothofagus"

Website:
<https://colloque.inra.fr/iufro2012>
Contacts: Alexis DUCOUSSO & Laëtitia
PACALY: iufro2012@bordeaux.inra.fr

**INTERNATIONAL SYMPOSIUM ON
BIOCHEMISTRY AND MOLECULAR
BIOLOGY**
October 9 - 12, 2012. HOTEL MELIÁ
HABANA, CUBA
More info:
<http://www.chemistrycuba.com/>

**12th International Citrus Congress (ICC
2012). "Citrus and Health".**
November 18 - 23, 2012. Valencia,
Spain.
[http://www.citruscongress2012.org/web/
?page_id=5](http://www.citruscongress2012.org/web/?page_id=5)

POSITIONS AVAILABLE



PhD STUDENTSHIP in Cereal Flowering time genetics

University of Cambridge - Unilever

Applications are invited for a 4 year PhD studentship starting in October 2012 to work under the supervision of Professor Martin Jones and Dr Harriet Hunt.

Visit: <http://www.jobs.cam.ac.uk/job/-12422/>

Potential applicants are encouraged to contact Dr Harriet Hunt (hvh22@cam.ac.uk) for further information.

Job opportunity for a Germination Specialist in Robin Probert's Conservation & Technology team at the Millennium Seed Bank in Sussex, UK. For more details, please see follow this link:

http://www.kew.org/about-kew/jobs/ref_Jan12_GerminationSpecialist.htm

10 postdoctoral positions in Estonia

Estonian Center of Excellence in Environmental Adaptation (ENVIRON) opens 10 postdoctoral positions in various fields of plant science. For detail see

<http://ec.europa.eu/euraxess/index.cfm/jobs/jobDetails/33754483>

<http://environ.emu.ee/en/>

A number of PhD positions is also available.

Prof Ülo Niinemets, Chair. Dep of Plant Physiology. Centre of Excellence in Environmental Adaptation, Head Estonian University of Life Sciences. ESTONIA

New Job Molecular Breeder / Bioinformatician at Ninsar Agrosciences S.L.

Position as Molecular Breeder / Bioinformatician at Ninsar Agrosciences .

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NEW BOOKS



Abiotic Stress Responses in Plants: Metabolism, Productivity and Sustainability

[Parvaiz Ahmad](#) and [M.N.V. Prasad](#) eds.

Dec 31, 2011.

Springer New York. Hardcover

ISBN 978-1-4614-0633-4

Agricultural Biotechnology and Genetic Engineering

By Qurban Ali

Publisher: LAP LAMBERT Academic Publishing (January 19, 2012)

Paperback: 488 pages

ISBN-10: 3847370359

ISBN-13: 978-3847370352

"Biotechnology," or "biotech" for short, refers to the application of biological research techniques to develop products and processes using biological systems, living organisms, or derivatives of organisms.

Biotech processes have been used for thousands of years, yet the industry we know today is scarcely more than a quarter century old. Bread, cheese and beer all products made from microorganisms have been part of the human diet for 6,000 years. But it was not until the 1970s that scientists began to apply components of these microorganisms at the molecular level to solve human problems in spheres ranging from medicine to agriculture and industry.

Due to this breadth of applications, the term "biotechnology" gradually gave way to the more accurate "biotechnologies" or a collection of techniques that apply cellular and molecular characteristics and processes to solve human problems.

Such techniques are applied at the molecular level and include genetic manipulation, gene transfer, DNA typing and cloning or microorganisms, plants and

animals. Biotech products or "biologics" as they are sometimes called, thus originate from living organisms bacteria, cells or animals.

Environmental Adaptations and Stress Tolerance of Plants in the Era of Climate Change

Ahmad, Parvaiz; Prasad, M.N.V. (Eds.)

2012, Springer New York. Hardcover

ISBN 978-1-4614-0814-7

Functional Biology of Plants

by Martin J. Hodson (Oxford Brookes University, UK) and John A. Bryant (University of Exeter, UK)

Hardcover ISBN: 978-0-470-69940-9

Paperback ISBN: 978-0-470-69939-3

April 2012, ©2011, Wiley-Blackwell

Plant Science text book, taking you from cellular and molecular approaches through whole plant physiology to the environment. This beautifully illustrated book, presents a modern, applied integration of whole plant and molecular approaches to the study of plants.

It is divided into four parts: Part 1: *Genes and Cells*, looks at the origins of plants, cell structure, biochemical processes and genes and development. Part 2: *The Functioning Plant*, describes the structure and function of roots, stems, leaves, flowers and seed and fruit development. Part 3: *Interactions and Adaptations*, examines environmental and biotic stresses and how plants adapt and acclimatise to these conditions. Part 4: *Future Directions*, illustrates the great importance of plant research by looking at some well chosen, topical examples such as *GM* crops, biomass and biofuels, loss of plant biodiversity and the question of how to feed the planet.

Molecular Biology Techniques (Third Edition)

By Susan Carson, Heather Miller and D. Scott Witherow

Elsevier Inc. 2012

ISBN: 978-0-12-385544-2

With content already designed to prepare students for working in a molecular biology lab, the dynamic links into vetted and distilled reference source material greatly enhance the user experience of this book on ScienceDirect.

Plant Biotechnology and Agriculture

Edited By Arie Altman and Paul Michael Hasegawa

Elsevier Inc. 2012

ISBN: 978-0-12-381466-1

This book lays the foundation for understanding the biotechnology interventions in plant and agricultural science rapidly developing over the past ten years and serves as a valuable cross-disciplinary reference source.

PLEASE SEE ALSO:

<http://www.fespb.org/fespb/content/other-conferences>

<http://www.fespb.org/fespb/content/job-vacancies>