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Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

Opinion



How Polyamines act in stress responses and in plant growth and development? Is it the H₂O₂ derived via their PAOs-mediated oxidation/back-conversion?

Polyamines have been correlated with various physiological and developmental processes in plants, including pollen tube growth. Recently, the mechanism of action of polyamines in stress responses and in plant development has started to be resolved by the coordinated action of several groups working in the field. The group of Kalliopi Roubelakis-Angelakis at the University of Crete, Greece, and the graduate student Panagiotis Moschou showed quite recently (Plant Cell 2008: 20:1708-1724.

<http://www.plantcell.org/cgi/content/short/20/6/1708>;

Physiol Plant. 2008:133:2:140-156 <http://Doi:10.1111/j.1399-054.2008.01049.x>

Plant Physiol. 2008:147:1845-1857. <http://www.plantphysiol.org/cgi/content/short/147/4/1845>;

Plant Physiol. 2009: 149(4):1970-1981 http://www.plantphysiol.org/cgi/content/abstract/pp.108.134932_v1?papetoc

that abiotic stress induces secretion of Spermidine (Spd) into the apoplast, where it is oxidized by polyamine oxidase (PAO); depending on its levels, the generated H₂O₂, either induces tolerance events or signals the programmed cell death syndrome, which, in turn, can be reversed by high intracellular polyamine homeostasis. Tobacco plants overexpressing apoplastic PAO showed pre-induced disease tolerance against the

the biotrophic bacterium *Pseudomonas syringae* and to the hemibiotrophic oomycete *Phytophthora parasitica* but not to the Cucumber Mosaic virus and to abiotic stress, such as salinity. This tolerance effect was exerted by the PAO-generated H₂O₂ in the apoplast. Furthermore, collaboration of Roubelakis-Angelakis group with that of Shaoling Zhang at Nanjing Agricultural University, China revealed the mechanism of polyamine action in the pollen tube growth and fertilization (Plant J. DOI: [10.1111/j.1365-313X.2010.04301.x](http://Doi:10.1111/j.1365-313X.2010.04301.x)). It was shown that Spd induces an increase in the cytosolic Ca²⁺ concentration that accompanies pollen tube growth. Using

the whole-cell patch clamp and outside-out single channel patch clamp configurations, it was shown that exogenous Spd induces a hyperpolarization-activated Ca²⁺ current; the addition of Spd cannot induce the channel open probability increase in excised outside-out patches, indicating that the effect of Spd in the induction of Ca²⁺ currents is exerted via a second messenger. This messenger is H₂O₂, and is generated during Spd oxidation, a reaction mediated by PAO. These reactive oxygen species trigger the opening of the hyperpolarization-activated Ca²⁺-permeable channels in pollen. To provide further evidence that PAO is in fact responsible for the effect of Spd on the Ca²⁺-permeable channels, two *Arabidopsis* mutants lacking expression of the peroxisomal encoding *AtPAO3* gene, were isolated and characterized. Pollen from these mutants was unable to induce the opening of the Ca²⁺-permeable channels in the presence of Spd, resulting in reduced pollen tube growth and seed number. However, high Spd concentration triggers a Ca²⁺ influx beyond the optimal, which has a deleterious effect. These findings strongly suggest that the Spd-derived H₂O₂ signals Ca²⁺ influx, thereby regulating pollen tube growth and fertilization. Very recently, further collaboration of Roubelakis-Angelakis group with those of Paraskevi Tavladoraki and Riccardo Angelini, University Tre, Rome, Italy further resolved the biochemical roles of plant PAOs. All the so far characterized PAOs from monocotyledonous plants, such as the apoplastic maize PAO, oxidize Spm and Spd to produce 1,3-diaminopropane, H₂O₂ and an aminoaldehyde and are involved in a terminal catabolic pathway. Mammalian PAOs oxidize Spm or Spd (and/or their acetyl derivatives) differently than monocotyledonous PAOs, producing Spd or Put, respectively, in addition to H₂O₂ and an aminoaldehyde, and therefore involved in a polyamine back-conversion pathway. In *Arabidopsis thaliana*, five PAOs (*AtPAO1-5*) are present with cytosolic or peroxisomal localization and three of them (the peroxisomal *AtPAO2*, *AtPAO3* and *AtPAO4*) form a distinct PAO subfamily. A comparative study of the catalytic properties of recombinant

AtPAO1, AtPAO2, AtPAO3 and AtPAO4 showed that all four enzymes strongly resemble to their mammalian counterparts being able to oxidize the common polyamines Spd and/or Spm through a polyamine back-conversion pathway. The existence of this pathway in *Arabidopsis* plants was also evidenced *in vivo*. In addition, these enzymes are able to oxidize the naturally occurring uncommon polyamines Therm-Spm and Nor-Spm, the latter being involved in important plant developmental processes. Furthermore, some important differences in substrate specificity among the various AtPAOs suggest functional diversity inside the *AtPAO* gene family. These results present a new starting point for further understanding the physiological role(s) of

the polyamine catabolic pathways in plants.

Wu J., H. Qu, Z. Shang, X. Jiang, P. N. Moschou, K. A. Roubelakis-Angelakis, S. Zhang. 2010. Spermidine oxidase-derived H₂O₂ activates downstream Ca²⁺ channels which signal pollen tube growth in *Pyrus pyrifolia*. **Plant J.** 63:1042-1053, DOI: 10.1111/j.1365-313X.2010.04301.x <http://onlinelibrary.wiley.com/doi/10.1111/j.1365313X.2010.04301.x/full>; <http://onlinelibrary.wiley.com/doi/10.1111/j.1365313X.2010.04301.x/abstract>

Fincato P, Moschou P.N., Spedaletti V, Tavazza R, Angelini R, Federico R, Roubelakis-Angelakis K.A., P. Tavladoraki. 2010 *J Exp Bot* 62:1155-1168 doi: 10.1093/jxb/erq341.

Research News



Secrets of symbiosis uncovered

Source: *The Scientist*. October 2010

In order to fix nitrogen, plants form a symbiotic relationship with bacteria such as rhizobia -- now, researchers have uncovered the role of 16 key genes involved in the synchronization of organ formation and rhizobia infection during plant development, by studying *Lotus japonicus* plant mutants.

Journal reference: L. Madsen et al., "The molecular network governing nodule organogenesis and infection in the model legume *Lotus japonicus*," *Nat Commun*, 1:10, 2010.

Prokaryotic Peroxiredoxins Can Be Sensitive

Paper of the Week (*J. Biol. Chem.*). Nov. 2 2010

Hydrogen peroxide has a dual effect in eukaryotic cells; this byproduct of aerobic respiration is an important signaling molecule, but it is also a potential toxin. The signaling activity of hydrogen peroxide involves a transient increase in its concentration due to the inactivation of 2-Cys peroxiredoxin (2-Cys Prx), a thiol-based peroxidase, by overoxidation. This sensitivity to overoxidation depends on GGLG and YF motifs, which are believed to be exclusive to eukaryotic 2-Cys Prxs. In this Paper of the Week, though, María Pascual and colleagues show that 2-Cys Prxs from

several prokaryotes, including two cyanobacteria (*Anabaena* sp. PCC7120 and *Synechocystis* sp. PCC6803), contain these motifs characteristic of sensitive enzymes. Further analysis of the cyanobacterial enzymes confirmed that *Anabaena* 2-Cys Prx is overoxidized at the peroxidatic cysteine residue and furthermore that this enzyme is readily and reversibly overoxidized *in vivo* in response to high light and hydrogen peroxide, more so than the *Synechocystis* enzyme. Interestingly, these two cyanobacterial strains have adapted different strategies to cope with hydrogen peroxide; although *Synechocystis* maintains a low content of less sensitive 2-Cys Prx and high catalase activity, *Anabaena* contains abundant and sensitive 2-Cys Prx but low catalase activity (much like chloroplasts). The results of this study clearly demonstrate that much remains to be learned regarding the mechanisms by which different prokaryotic organisms have evolved to elicit responses to oxidative stresses.

Reference: Pascual M. B., Mata-Cabana A., Florencio F. J., Lindahl M. and Cejudo F. J. (2010) Overoxidation of 2-Cys peroxiredoxin in prokaryotes: cyanobacterial 2-Cys peroxiredoxins sensitive to oxidative stress. *J. Biol. Chem.* 285: 34485-34492 (doi:10.1074/jbc.P110.160465).

Engineered Plants Make Potential Precursor to Raw Material for Plastics

In theory, plants could be the ultimate "green" factories, engineered to pump out the kinds of raw materials we now obtain from petroleum-based chemicals. But in reality, getting plants to accumulate high levels of desired products has been an elusive goal. Now, in a first step toward achieving industrial-scale green production, scientists from the U.S. Department of Energy's (DOE) Brookhaven National Laboratory and collaborators at Dow AgroSciences report engineering a plant that produces industrially relevant levels of compounds that could potentially be used to make plastics.

The research is reported online in *Plant Physiology*, and will appear in print in the December issue.

"We've engineered a new metabolic pathway in plants for producing a kind of fatty acid that could be used as a source of precursors to chemical building blocks for making plastics such as polyethylene," said Brookhaven biochemist John Shanklin, who led the research. "The raw materials for most precursors currently come from petroleum or coal-derived synthetic gas. Our new way of providing a feedstock sourced from fatty acids in plant seeds would be renewable and sustainable indefinitely. Additional technology to efficiently convert the plant fatty acids into chemical building blocks is needed, but our research shows that high levels of the appropriate feedstock can be made in plants."

The method builds on Shanklin's longstanding interest in fatty acids -- the building blocks for plant oils -- and the enzymes that control their production. Discovery of the genes that code for the enzymes responsible for so called "unusual" plant oil production encouraged many researchers to explore ways of expressing these genes and producing certain desired oils in various plants.

"There are plants that naturally produce the desired fatty acids, called 'omega-7 fatty acids,' in their seeds -- for example, cat's claw vine and milkweed -- but their yields and growth characteristics are not suitable for commercial production," Shanklin said. Initial attempts to express the relevant genes in more suitable plant species resulted in much lower levels of the desired oils than are produced in plants from which the genes were isolated. "This suggests that other metabolic modifications might be

necessary to increase the accumulation of the desired plant seed oils," Shanklin said. "To overcome the problem of poor accumulation, we performed a series of systematic metabolic engineering experiments to optimize the accumulation of omega-7 fatty acids in transgenic plants," Shanklin said. For these proof-of-principle experiments, the scientists worked with *Arabidopsis*, a common laboratory plant.

Enzymes that make the unusual fatty acids are variants of enzymes called "desaturases," which remove specific hydrogen atoms from fatty acid chains to form carbon-carbon double bonds, thus desaturating the fatty acid. First the researchers identified naturally occurring variant desaturases with desired specificities, but they worked poorly when introduced into *Arabidopsis*. They next engineered a laboratory-derived variant of a natural plant enzyme that worked faster and with greater specificity than the natural enzymes, which increased the accumulation of the desired fatty acid from less than 2 percent to around 14 percent.

Though an improvement, that level was still insufficient for industrial-scale production. The scientists then assessed a number of additional modifications to the plant's metabolic pathways. For example, they "down-regulated" genes that compete for the introduced enzyme's fatty acid substrate. They also introduced desaturases capable of intercepting substrate that had escaped the first desaturase enzyme as it progressed through the oil-accumulation pathway. In many of these experiments they observed more of the desired product accumulating. Having tested various traits individually, the scientists then combined the most promising traits into a single new plant.

The result was an accumulation of the desired omega-7 fatty acid at levels of about 71 percent in the best-engineered line of *Arabidopsis*. This was much higher than the omega-7 fatty acid levels in milkweed, and equivalent to those seen in cat's claw vine. Growth and development of the engineered *Arabidopsis* plants was unaffected by the genetic modifications and accumulation of omega-7 fatty acid.

"This proof-of-principle experiment is a successful demonstration of a general strategy for metabolically engineering the sustainable production of omega-7 fatty acids as an industrial feedstock source from plants," Shanklin said.

This general approach -- identifying and expressing natural or synthetic enzymes, quantifying incremental improvements

resulting from additional genetic/metabolic modifications, and "stacking" of traits -- may also be fruitful for improving production of a wide range of other unusual fatty acids in plant seeds. Journal Reference: Huu Tam Nguyen, Girish Mishra, Edward Whittle, Scott A. Bevan, Ann Owens Merlo, Terence A. Walsh, and John Shanklin. Metabolic Engineering of Seeds can Achieve Levels of w-7 Fatty Acids Comparable to the Highest Levels Found in Natural Plant Sources. *Plant Physiology*, December 2010.

Source: *ScienceDaily* (Nov. 9, 2010)

Virus Component Helps Improve Gene Expression Without Harming Plant

A virus that normally deforms or kills plants like tomatoes, peppers and eggplants isn't all bad: A gene within the virus has been found useful for allowing foreign genes to be introduced into a plant without harmful effects, according to Texas AgriLife Research scientists.

The technology ultimately could lead the way toward a "cheap, green alternative" for pharmaceutical development, said Dr. Herman Scholthof, AgriLife Research virologist.

Scholthof and colleague Drs. Yi-Cheng Hsieh and Veria Alvarado collaborated with scientists at the John Innes Centre in England on the study which appears in this week's *Plant Biotechnology Journal*.

"Nowadays in the pharmaceutical industry, many protein-based drugs are expressed in and purified from bacteria," Scholthof said. "Plants not only form a cheap and green alternative, but they also have the benefit that they process proteins properly -- something bacteria can not do."

The team worked with tomato bushy stunt virus, which can attack a multitude of plants worldwide but rarely has economically severe consequences. It is model virus that can be safely contained because it does not have an insect vector which could spread it.

For this study, Scholthof said, only one gene of the virus -- called P19 -- was used because it is the one that suppresses RNA silencing.

"RNA silencing is a fairly recently discovered defense that plants use against viruses," he explained. "During this silencing, short strands of RNA serve as signals to alert the plant that a virus is attempting to infect so that all of its tissues start mobilizing to defend.

"The elegance is that the P19 protein forms counter-defense units that are each composed of two protein molecules which form a sort of caliper to measure and capture signal molecules, thereby suppressing the defense to the virus which can infect a plant."

But suppressing the defense might also allow other things, such as allowing desired genes to enter and be expressed. Scholthof said scientists have used other suppressors in plant research in the past to avoid silencing, but "a problem is that these suppressors also cause many developmental defects and severe disease symptoms."

Not so with the P19 variant the group developed, he said.

Scholthof said the process of expressing foreign genes in plants is common in research, but there also is an important practical use.

"It also is used in biotechnology to produce beneficial proteins for medical and veterinary applications," he noted. "By developing this new P19, we have 'tamed' a suppressor because it still works to suppress but does not induce severe disease symptoms in the plant."

"We have provided a proof-of-principle that P19 can be used to protect the silencing of introduced foreign genes in plants."

Source: *ScienceDaily* (Nov. 12, 2010).

Biochemistry of How Plants Resist Insect Attack Determined

Source: *ScienceDaily* (Nov. 15, 2010)

Many plants, including crops, release volatiles in response to insect attack. The chemical compounds can be a defense or can be an aromatic call for help to attract enemies of the attacking insect. Researchers from Virginia Tech, Michigan State University, and Georg-August-University Göttingen have discovered how plants produce the defensive compounds.

The research is reported this week in the online early edition of the *Proceedings of the National Academy of Sciences*. The article is by Sungbeom Lee, postdoctoral associate in biological sciences; Somayesadat Badiyan, Ph.D. student in biological systems engineering; and David R. Bevan, associate professor of biochemistry, all at Virginia Tech; Marco Herde, postdoctoral associate with the Michigan State University, Department of Biochemistry and Molecular Biology; Christiane Gatz, professor and head of the Albrecht-von-Haller-Institute for Plant Sciences at Georg-August-University

Göttingen, Germany, and Dorothea Tholl, assistant professor of biological sciences at Virginia Tech.

To gain detailed insight into volatile defense metabolism and its regulation in plant tissues, the researchers focused on the formation of two common volatile compounds, or homoterpenes -- DMNT (4,8-dimethylnona-1,3,7-triene) and TMTT (4,8,12-trimethyltrideca-1,3,7,11-tetraene). They discovered that formation of both compounds is initiated by the same P450 enzyme -- belonging to a family of enzymes that initiates oxidation of organic compounds in most plants, animals, and bacteria. In plants, the enzyme is specifically activated by insect attack.

"We are excited to finally have elucidated the biosynthesis of these common plant volatiles. The discovered P450 protein was a long-missing enzymatic link in the formation of homoterpenes," said Tholl.

Lee and colleagues created a model using mammalian forms of P450 to study the catalytic specificity of the plant enzyme in greater detail. "The approach supports future efforts to fully understand and optimize the enzymatic reaction," said Tholl. "A primary aim of the study is to engineer the discovered enzymatic pathway in important crop plants to improve their natural pest controls."

"This work illustrates the power of combining computational model-building with experimental methods in elucidating important biochemical activities," said Bevan. "Our detailed understanding of the biology underlying the production of these plant volatiles will now enable us to apply our new knowledge in agriculture in novel ways."

"We now are in the position to use this and previously identified genes of the biosynthetic pathway as tools to change volatile profiles in plants," said Tholl. "This approach can help us to design insect-induced volatile mixtures that are especially attractive to natural enemies used in biological pest control."

Another intriguing aspect of homoterpene volatiles is that they can elicit defensive responses in unattacked neighboring plants. "It may therefore be possible to exploit these signaling activities by priming defenses in crop fields prior to insect attack via specific transgenic 'emitter' plants," Tholl said.

Journal Reference: Sungbeom Lee, Somayesadat Badiyan, David R. Bevan, Marco Herde, Christiane Gatz, and Dorothea Tholl. Herbivore-induced and floral homoterpene volatiles are biosynthesized by a single P450 enzyme

(CYP82G1) in Arabidopsis. PNAS, November 18, 2010 DOI: 10.1073/pnas.1009975107

Mastermind Steroid Found in Plants

Source: *ScienceDaily* (Nov. 15, 2010)

Scientists have known for some time how important plant steroids called brassinosteroids are for regulating plant growth and development. But until now, they did not know how extensive their reach is. Now researchers, including Yu Sun and Zhi-Yong Wang at Carnegie's Department of Plant Biology, have identified about a thousand brassinosteroid target genes, which reveal molecular links between the steroid and numerous cellular functions and other hormonal and light-activated chain reactions.

The study, published in the November 16, 2010, issue of *Developmental Cell*, provides the first comprehensive action map for a plant hormone. The research will help accelerate basic plant science and crop research.

Steroids are important hormones in animals and plants. Unlike animals, plants do not have glands to produce hormones. As a result, each cell has the ability to generate hormones. Animal cells typically respond to steroids using receptor molecules within the cell nucleus. The receptors in plants, called receptor-like kinases, are anchored to the outside surface of the cell membranes. Research has shown that brassinosteroids are involved in acclimation to environmental stresses, promote cell elongation, and enhance resistance to pathogens, thus increasing plant growth and crop yield. But it has been unclear how one steroid hormone controls so many different processes. The breadth of its role has also been incomplete because its target genes have not been identified until now.

"We performed a genome-wide analysis of genes that are direct targets of brassinosteroid in the model plant Arabidopsis, a relative of mustard," explained coauthor Yu Sun. "We identified DNA sequences in the genome where a transcription factor resides -- that is a protein that begins the process of turning a gene on or off. In this case, a protein called BZR1 is the major transcription factor responsible for brassinosteroid-regulated gene expression. It acts at the end of a chain reaction triggered by a steroid binding to the receptor called Brassinosteroid Insensitive 1 (BRI1) at the cell membrane. We were very surprised by the large number of genes involved.

Arabidopsis has about 32,000 genes in total and this hormone appears to be masterminding a lot of different physiological responses."

Scientists have observed a wide range of effects of brassinosteroid on plant growth and plant responses to the environment. They have also worked out the molecular chain that pass the signal from cell surface receptor to BZR1 in the nucleus. How this signaling chain controls various growth and physiological behavior and what cellular machinery it controls was unclear. The scientists found that brassinosteroid target genes turn on a wide range of proteins, including cell-wall enzymes, such as cellulose, a large number of genes concerned with transporting materials throughout plant body and organizing the scaffolding that gives cells their shape, among other developmental processes. Although brassinosteroid has been known to have a close relationship with several other hormones and light signals, the mechanisms involved with the steroid's interactions with them are not known. The researchers found that BZR1 protein directly controls the activity of many genes involved in plant responses to other hormones and light. The brassinosteroid action map provided in this study shows for the first time that multiple hormonal and light signals are integrated into an extensive network to control plant growth and development.

Journal Reference: Yu Sun, Xi-Ying Fan, Dong-Mei Cao, Wenqiang Tang, Kun He, Jia-Ying Zhu, Jun-Xian He, Ming-Yi Bai, Shengwei Zhu, Eunkyoo Oh, Sunita Patil, Tae-Wuk Kim, Hongkai Ji, Wing Hong Wong, Seung Y. Rhee, Zhi-Yong Wang. Integration of Brassinosteroid Signal Transduction with the Transcription Network for Plant Growth Regulation in Arabidopsis. *Developmental Cell*, Volume 19, Issue 5, 765-777, 16 November 2010 DOI: 10.1016/j.devcel.2010.10.010

Gene Discovery Suggests Way to Engineer Fast-Growing Plants

ScienceDaily (Nov. 16, 2010)

Tinkering with a single gene may give perennial grasses more robust roots and speed up the timeline for creating biofuels, according to researchers at the Duke Institute for Genome Sciences & Policy (IGSP).

Perennial grasses, including switchgrass and miscanthus, are important biofuels crops and can be harvested repeatedly, just like lawn grass, said Philip Benfey,

director of the IGSP Center for Systems Biology. But before that can happen, the root system needs time to get established. "These biofuel crops usually can't be harvested until the second or third year," Benfey said. "A method to improve root growth could have a major role in reducing the time to harvest for warm season grasses."

Benfey's team appears to have found a way to do just that. They took a directed genomic approach aimed at identifying genes that become active when cells stop dividing and start taking on the characteristics of the mature, adult cell they are to become. "We systematically looked for those genes that come 'on' precisely when cells transition from proliferation to differentiation and then turn 'off' again just as quickly," Benfey said.

That genome-wide search in the roots of the familiar laboratory plant Arabidopsis and subsequent screening of mutant lines turned up a single gene, which the researchers call UPBEAT1 (UPB1). Further study showed that UPB1 controls the gene expression of enzymes known as peroxidases.

They then showed that these peroxidases control the balance of free radicals between the zone of cell proliferation and the zone of cell elongation where differentiation begins. (Although free radicals are probably most familiar as agents of stress to be combated with antioxidants, Benfey noted that the balance of free radicals has also been implicated in the control of a similar transition from proliferation to differentiation in animals.)

When the researchers experimentally disrupted UPB1 activity in the plant root, it altered the balance of free radicals such that cells delayed their differentiation and continued growing. Those plants ended up with faster-growing roots, having more and larger cells. When UPB1 activity was artificially increased, the growth of plant roots slowed.

"It's possible that by manipulating a single gene, you could get a plant with rapid growth," Benfey said. Interestingly, UPB1 appears to act independently of plant hormones that play well-known roles in the balance between cell division and differentiation.

From an engineering perspective, the prospect of enhancing growth by taking a gene away, as opposed to adding one, is particularly appealing, Benfey notes.

"It also suggests that plants are not growing at their full potential," he says. That makes sense, of course, as plants in

the real world have to make tradeoffs, for example, between growth and reproduction.

In addition to their potential in biofuels production, the findings might also lead to new ways to produce bigger and stronger plants with the capacity to sequester more earth-warming carbon dioxide from the atmosphere, Benfey says. His startup company, GrassRoots Biotechnology Inc., has acquired the patent for this discovery with its potential in mind. The company's primary goals are the development of next-generation biofuels and the use of root systems for carbon sequestration.

Collaborators on the NSF-funded study, which appears in the November 12th issue of the journal *Cell*, include Hironaka Tsukagoshi and Wolfgang Busch, both at Duke.

Journal Reference: Hironaka Tsukagoshi, Wolfgang Busch, Philip N. Benfey. Transcriptional Regulation of ROS Controls Transition from Proliferation to Differentiation in the Root. *Cell*, 2010; 143 (4): 606-616 DOI: 10.1016/j.cell.2010.10.020

Bioscience researchers defeating potato blight

Professor Paul Birch of the University of Dundee and his team at the Scottish Crop Research Institute (SCRI), the University of Dundee, and the University of Aberdeen have developed a new approach to breeding resistance to the mould-like organism *Phytophthora infestans* (*P. infestans*) that causes late blight.

Through their work on the interactions between potato plants and *P. infestans* Professor Birch and his team have come up with a completely new approach to breeding resistance to late blight in potatoes. This approach will be taken forward in a new project working with colleagues at The Sainsbury Laboratory in Norwich to identify resistance in potato plants that could then be used for breeding new resistant varieties. It is also hoped that it will be possible to combine resistance to late blight with resistance to nematodes (another serious problem for potato farming in the UK) in a single GM variety.

Professor Birch said "In the past we have tried to breed resistance to late blight by identifying plants that survive a period infection and could, in future generations, potentially give rise to resistant varieties. This approach is slow, resource intensive and requires a degree of luck that the resistance will last for any prolonged period. So far, all such resistances have

been defeated because of the broad extent of variation in the population of *P. infestans* in the environment. With our discovery, we can use genetic analysis to identify plants for breeding that are inherently resistant to infection. When introduced into cultivated varieties, such disease resistance should be far more durable."

By studying the interactions between *P. infestans* and potato plants the team has identified proteins that are secreted by the invading pathogen and are essential for infection.

Professor Birch continued "We now know a lot more about how *P. infestans* gets round the potato plant's natural defences and therefore what it takes for the plant to resist infection. We can actually look at a potato plant's genetic makeup and say whether it will be sustainably resistant to late blight, which is a huge step forward. Whilst our approaches are suitable for breeding, in future we also hope to use a GM approach to produce a variety that is resistant to both blight and potato cyst nematode."

Dr Mike Storey, Head of Research and Development, AHDB - Potato Council said "Blight is a serious problem for the potato industry in the UK. We are working hard to raise grower awareness and ensure best practice to control the disease but we have the challenge of a continually changing pathogen population. What we need now is the application of this new research to improve variety resistance and identify new crop protection targets and integrate these approaches for sustainable control and to reduce the impact when blight does occur. This will be of great benefit to UK farmers and the economy."

Professor Janet Allen, BBSRC Director of Research and chair of the Global Food Security programme development board said "We know that high quality bioscience research is required if we are to have a sustainable supply of safe, affordable, healthy food to feed a growing world population. Late blight is a significant problem in the UK and elsewhere and so it is particularly good news that the fundamental research carried out under BBSRC's crop science initiative is providing opportunities to move towards application in new varieties."

Provided by Biotechnology and Biological Sciences Research Council (news : web)

Further Information:

<http://www.physorg.com/news/2010-11-bioscience-defeating-potato-blight.html>

Date Posted: Monday, November 22, 2010

How 'bioluminescent' trees that glow like fireflies could one day replace our streetlights

Scientists are developing ways of making trees glow so they can be used as natural streetlights without the need for electricity.

A team of researchers are experimenting with genes to allow the trait that causes fireflies to glow -bioluminescence - to be implanted into a variety of different organisms.

As well as replacing traditional streetlights, bioluminescent plants would be useful for people who are not hooked up to the electricity grid.

And if more lights were ever required, they could simply be grown.

Trees that glow naturally with bioluminescent genes could be used to light streets, as in this artist impression from Cambridge

The scientists at Cambridge University used genes from fireflies and a special form of glowing sea bacteria to create 'BioBricks' – genetic building blocks that can be inserted into a genome.

After inserting the modified genes into a sample of e-coli bacteria they were able to produce a range of colours – and created a living light that was bright enough to read by.

The scientists created the glowing effect by creating a substance known as oxyluciferin which is naturally in a high-energy state at first. However it quickly settles into a more stable, lower-energy state, and when it does so it emits a single photon of light.

Geneticist Theo Sanderson, one of the members of the team, told New Scientist: 'We didn't end up making bioluminescent trees, which was the inspiration for the project.

'But we decided to make a set of parts that would allow future researchers to use bioluminescence more effectively.'

The research was presented at the annual International Genetically Engineered Machines competition (iGEM), held at the Massachusetts Institute of Technology.

The technology could even be used to make glowing signs that do not need to be wired up

The team say that there is huge commercial potential in replacing the street with natural bioluminescent systems.

The idea is also extremely environmentally friendly as no electricity would be required and the process which produces the photons of light is extremely energy-efficient.

The scientists have also considered the possibility that the fuel to fire the chemical reaction in the trees could come from human waste or food waste.

And if the plant species used was a form of algae then energy could be harnessed from sunlight.

The team say on their website: 'We might imagine a system where a bioreactor in the roof of a house - supplied with leftover foodstuffs - could pipe glowing algae through the rooms of the house during the night and across the roof during the day.'

In separate research, Taiwanese scientists have found that inserting gold nanoparticles into the leaves of trees helped the chlorophyll to glow red.

Under ultraviolet light the nanoparticles glowed with blue light, causing the surrounding chlorophyll to glow red.

Source:

<http://www.dailymail.co.uk/sciencetech/article-1333334>: Saturday, November 27, 2010.

Missouri Grapes Hold Key to Improving World Grape Production

Source: *ScienceDaily* (Dec. 6, 2010)

In a few years, a sip of Cabernet Sauvignon, Merlot or Pinot Noir may include a taste of the "Show-Me" State. The state grape of Missouri -- the Norton variety grown at many vineyards around the state -- is resistant to powdery mildew, a fungal pathogen that affects winemaking grapes around the world. Now, researchers at the University of Missouri are working to identify valuable genes from the Norton grape for eventual transfer into other grapes to make them less susceptible to mildew, decrease fungicide use and increase world-wide grape production.

"The hot, humid environment of Missouri is perfect for the growth of fungal pathogens, such as mildew, yet Norton resists the fungus," said Walter Gassmann, a researcher in the Bond Life Sciences Center and associate professor of plant sciences in the College of Agriculture, Food and Natural Resources. "Understanding what makes Norton resistant to fungus, and European varieties, such as Cabernet Sauvignon, susceptible to fungus, can help us improve grape production around the world."

Researchers say the difference between the Norton grape and other varieties is that the Norton grape builds more of a certain protein that is essential to fight fungal pathogens than other grape varieties, which build too little of the protein too late to successfully battle the

fungus. Earlier research has discovered the gene that contains the blueprint for this protein present in both Norton grapes and other varieties that cannot resist the mildew. Gassmann is conducting research on the fast-growing *Arabidopsis* plant, which features a gene similar to the targeted grape gene. His team added the grapevine gene to an *Arabidopsis* plant that was lacking its own gene. Adding the grapevine gene led to plants that resisted the mildew, confirming that the grapevine gene is responsible for orchestrating plant defenses against mildew. The next step in this research is to figure out what in the genetic instructions is different in Norton and other grapevine varieties that leads to the observed difference in protein levels in resistant Norton and susceptible grapevines.

Most wineries must use sulfur to combat the fungus, and Gassmann says that it will be years until fungus-resistant grape varieties can be put into commercial production. He says that research is being conducted, including sequencing the Norton genome, but it will still be technically difficult to make a transgenic grape plant and even more difficult to find consumers accepting of the idea of consuming genetically modified grapes, although he hopes that these attitudes will eventually change.

"Until then, there really is no way to eliminate fungicide use, for economic reasons or to make organic wine, unless you breed the mildew resistant trait into other varieties," Gassmann said. "Many people forget that before Prohibition Missouri was the second largest wine-producing state in the country after New York. We see this work as eventually providing an economic impact through the high-value agriculture and tourism that wineries can provide."

Gassmann worked on the research with Wenping Qiu, professor and director of the Center for Grapevine Biotechnology at Missouri State University. Gassmann and Qiu's study was recently published in the plant sciences journal *Planta*. The research was funded by the U.S. Department of Agriculture.

Genome of Barley Disease Reveals Surprises

Source: The Agricultural Biotechnology Portal. December 08, 2010

Scientists have sequenced the genome of a major fungal disease that affects barley and other cereal crops, a breakthrough that could lead to significant advances in our understanding of how plant diseases

evolve. The research, published in the journal *Science*, suggests that parasites within the genome of the fungus help the disease to adapt and overcome the plant's defences.

The study could help with the development of new agricultural techniques for protecting cereal crops from infection. Barley grains are the basis of many staple foods, and also central to the brewing and malting industries, so keeping the plants disease-free is becoming increasingly important for food security. Today's research, led by Dr Pietro Spanu from the Department of Life Sciences at Imperial College London, decodes the genome of *Blumeria*, which causes powdery mildew on barley.

Powdery mildew affects a wide range of fruit, vegetable and cereal crops in northern Europe. Infected plants become covered in powdery white spots that spread all over the leaves and stems, preventing them from producing crops, and having a devastating impact on the overall agricultural yield. Farmers use fungicides, genetically resistant varieties and crop rotation to prevent mildew epidemics, but the fungi often evolve too rapidly for the techniques to be effective. The mildew is able to evolve so quickly because multiple parasites within the genome, known as 'transposons', help it to disguise itself and go unrecognized by the plant's defences. It is as if the transposons confuse the host plant by changing the target molecules that the plant uses to detect the onset of disease.

The researchers discovered that *Blumeria* had unusually large numbers of transposons within it. "It was a big surprise," said Dr Spanu, "as a genome normally tries to keep its transposons under control. But in these genomes, one of the controls has been lifted. We think it might be an adaptive advantage for them to have these genomic parasites, as it allows the pathogens to respond more rapidly to the plant's evolution and defeat the immune system."

The authors believe that their research will contribute significantly to the design of new fungicides and resistance in food crops, as they now understand how the mildew can adapt so quickly. "With this knowledge of the genome we can now rapidly identify which genes have mutated, and then can select plant varieties that are more resistant," said Dr Spanu. The genetic codes will also help scientists monitor the spread and evolution of fungicide resistance in an emerging epidemic. "We'll be able to develop more efficient ways to monitor

and understand the emergence of resistance, and ultimately to design more effective and durable control measures." Mildew pathogens are a type of 'obligate' parasite, which means they are completely dependent on their plant hosts to survive, and cannot live freely in the soil. Because they are so dependent, the pathogens have devised a way to disguise themselves in order to avoid the immune response of the host plant and overcome its defences.

"We've now found this happening in lots of fungi and fungal-like organisms that are obligate pathogens," said Dr Spanu, adding that the costly genome inflation could therefore be a trade-off that makes these pathogens successful. "Non-obligate pathogens are not so dependent on their hosts, as they can live elsewhere," said Dr Spanu, "so they are less dependent on rapid evolution."

Further Information:

<http://www.imperial.ac.uk>

New discovery about how flowering time of plants can be controlled

Source: Science Centric. 8 December 2010

Researchers at Umea Plant Science Centre in Sweden discovered, in collaboration with the Syngenta company, a previously unknown gene in sugar beets that blocks flowering. The discovery makes it possible to control when sugar beets bloom.

Researchers at Umea Plant Science Centre in Sweden discovered, in collaboration with the Syngenta company, a previously unknown gene in sugar beets that blocks flowering. Only with the cold of winter is the gene shut off, allowing the sugar beet to blossom in its second year. The discovery of this new gene function makes it possible to control when sugar beets bloom. The new findings were recently published in the prestigious journal Science.

Scientists at Umea Plant Science Centre and the international company Syngenta, in a joint study of genetic regulation in the sugar beet, have discovered an entirely new principle for how flowering can be controlled. The study, which was co-directed by Professor Ove Nilsson, of the Swedish University of Agricultural Sciences (SLU), and Syngenta scientist Dr Thomas Kraft, showed that there is a gene in the sugar beet that was previously unknown.

'When we studied a gene in the sugar beet that usually stimulates blooming in other plants, we made a very surprising discovery: in the sugar beet evolution has

developed a 'sister gene' that has taken on the exact opposite function, namely, to inhibit blossoming. For biennial sugar beets this means that they can't flower in their first year. Once the plants have been exposed to the cold of winter at the end of the first year, the 'gene blockade is lifted,' and the sugar beets can bloom in their second year of life,' says Ove Nilsson about the function of the newly discovered flowering gene.

The researchers speculate that the development of the inhibiting sister gene was an important factor in enabling biennial sugar beets to evolve from an annual to a biennial plant. Furthermore, plant researchers in Umea and Landskrona have shown that it is possible to manipulate the 'flowering gene' in such a way as to leave the gene constantly 'turned on,' that is, to block blooming, and thereby prevent it from being turned off after winter.

'In that way it's possible to fully control the flowering time of the sugar beet. This enables us to develop a so-called 'winter beet,' that is, a sugar beet that can be planted in the autumn and then will continue to grow throughout the following growth season without blossoming,' says Thomas Kraft at Syngenta Seeds.

'A winter beet has been a high priority for sugar beet growers, since it is estimated to be able to increase the yield by about 25 percent and at the same time allow a more extended harvesting period. Traditional breeding has failed to produce such a plant. Syngenta Seeds is now going to move on to more in-depth tests of this potential new winter beet.'

Plants 'remember' winter to bloom in spring with help of special molecule

Source: Science Centric. 8 December 2010

The role a key molecule plays in a plant's ability to remember winter, and therefore bloom in the spring, has been identified by University of Texas at Austin scientists.

Many flowering plants bloom in bursts of colour in spring after long periods of cold in the winter. The timing of blooming is critical to ensure pollination, and is important for crop production and for droves of people peeping at wildflowers. One way for the plants to recognise the spring - and not just a warm spell during winter - is that they 'remember' they've gone through a long enough period of cold.

'Plants can't literally remember, of course, because they don't have brains,' says Sibum Sung, assistant professor in the

Section of Molecular Cell and Developmental Biology. 'But they do have a cellular memory of winter, and our research provides details on how this process works.'

The process is known as vernalisation, whereby a plant becomes competent to flower after a period of cold. And though it is common for many plants adapted to temperate climates, including important crops like winter wheat, it has not been until the past decade or so that scientists have begun to understand the process's genetic and molecular underpinnings.

Sung and postdoctoral fellow Jae Bok Heo have now discovered that a long, non-coding RNA molecule, named COLDAIR, is required for plants to set up a memory of winter.

They published their work on the *Arabidopsis* plant in *Science Express* on Dec. 2.

This is how it works: In fall, a gene called FLC actively represses floral production. A random bloom in fall could be a waste of precious energy.

But after a plant has been exposed to 20 days of near-freezing temperatures, the scientists found that COLDAIR becomes active. It silences the FLC gene, a process that is completed after about 30 to 40 days of cold. With the FLC silenced as temperatures warm in the spring, other genes are activated that initiate blooming. COLDAIR helps create a cellular memory for a plant, letting it know it has been through 30 or more days of cold.

But, how does the cold actually turn on COLDAIR?

'That is one of the next questions we have,' says Sung. 'How do plants literally sense the cold?'

Answering these kinds of basic questions could lead to crop improvements and will be important to grasp as climate changes alter the length of the winter season, with possible repercussions to vernalisation in plants around the world.

Researchers unearth plant gene pathogens

Source: CORDIS EU. 2011-01-03

An EU-funded team of researchers, led by the Sainsbury Laboratory, Norwich Research Park in the UK, have discovered the culprit responsible for late blight in potatoes and tomatoes, and downy mildew in cruciferous vegetables and other crops. Presented in the journal *Science*, the study was funded in part by the AVRBLB2-CPT ('Manipulation of host target by the AvrBlb2 effector of the late

blight pathogen *Phytophthora infestans*') project, which received a Marie Curie Intra-European Fellowships grant worth EUR 171,740, under the EU's Seventh Framework Programme (FP7).

The team put the spotlight on the parasitic water fungus and water molds that cause diseases in plants and crops. 'We have been studying the late blight pathogen for a while,' explains Professor Sophien Kamoun, head of the Sainsbury Laboratory at the Norwich Research Park. 'In separate research we are trialling plant genes that mediate blight resistance, while in this latest study we have learnt more about how the pathogen itself evolved and which genes we should focus on to tackle it.'

In their research, the scientists compared the genome of the potato blight pathogen to the genomes of four sister species that infect various plants including the ornamental four o'clock and morning glory. They say these closely related pathogens are from Mexico, the originating hub of the late blight pathogen.

A number of sections of the genome evolve slowly and are very similar between the sister species, the experts found. Other sections enable the pathogen to jump hosts and adapt to and infect new plant species, according to them.

'Our aim is to develop resistance to genes from the stable, slowly-evolving region of the pathogen's genome,' Professor Kamoun says. 'This should be more disruptive to the pathogen's ability to evolve new races.'

The team says the blight pathogen and the parasite responsible for generating downy mildew is a kind of water mold or oomycete, which are fungal-like organisms that evolved from marine algae. Downy mildew triggers fuzzy white mould and yellow patches on the leaves of various crops like maize, lettuce and grapes. Powdery mildew is a fungal disease of barley that causes the greatest damage in cool, wet climates.

'A major focus of our research is sustainable agriculture,' explains Professor Dale Sanders, the Director of the John Innes Centre in the UK. 'We need to help breeders and farmers generate good quality food and other agricultural products in an environmentally sustainable way. One way of doing so will be to develop crops that are resistant to pathogens and pests. Such crops will reduce the need to spray pesticides and fungicides and they will give better yields, as less will be lost to disease.'

The genomes of the parasites were sequenced in two research studies, revealing that the parasites have discarded a number of genes. According to the scientists, the genome sequences show large numbers of effector proteins, the molecules that invade plant cells to stifle a plant's defence mechanism. Researchers from Germany and the US also contributed to this study.

OSU helps decode strawberry genome in bid to improve fruit

Source: Science Centric, 3 January 2011.
Researchers at Oregon State University have helped sequence the genome of a wild strawberry, laying the groundwork for genetic improvements to related fruits like apples, peaches and pears. The advance was published in the journal *Nature Genetics*.
'This will accelerate research that will lead to improved crops, particularly commercial strawberries,' said OSU plant molecular biologist Todd Mockler, one of the lead researchers. 'It could lead to fruit that resists pests, smells better, tolerates heat, requires less fertiliser, has a longer shelf life, tastes better or has an improved appearance.'
An international team of more than 70 researchers, 13 of whom are at OSU, identified 34,809 genes on the seven chromosomes in the woodland strawberry known as *Fragaria vesca*.
They chose the diminutive perennial because it's commonly used in research, is easy to breed, grows quickly and has a small genome. Additionally, it shares a substantial number of genes with apples, peaches, cherries, plums, and commercially cultivated strawberries - a crop that generated \$12.9 million in gross sales for Oregon's farmers in 2009, according to a report by the OSU Extension Service.
As part of their findings, the scientists identified genes that they think might be responsible for some of the berry's characteristics like flavour, aroma, nutritional value, flowering time and response to disease. Knowing what individual genes do will allow researchers to breed crops for those specific traits. And in the case of tree fruits, they won't have to wait years to see if those traits actually show up in the fruit. For example, with molecular breeding they would be able to cross a high-yielding pear tree with one that resists a certain fungal disease, and they'd be certain that the desired genes are actually present.

The woodland strawberry is the smallest plant genome to be sequenced other than *Arabidopsis thaliana*, a small flowering plant in the mustard family, because it has only about 210 million base pairs, Mockler said. Base pairs are the molecules known as adenine, cytosine, guanine and thymine that form a double-stranded DNA helix.

In addition to Mockler, the OSU part of the research was led by Pankaj Jaiswal, Aaron Liston, Sushma Naithani and Nahla Bassil, a plant geneticist with the U.S. Department of Agriculture who holds a courtesy appointment at OSU. Jaiswal's lab assigned functions to about two-thirds of the strawberry's genes. Liston compared the chromosomal locations of 389 genes that the strawberry shares with peaches and found support for the hypothesis that the rose family originally had nine chromosomes. Naithani's lab predicted biochemical functions for various genes, and Liston and Bassil helped assemble the genome for the strawberry's chloroplasts, an organelle that makes sugar and starches through photosynthesis.

The strawberry work is just the latest advance in a series of genome sequencing projects at OSU. In collaboration with experts in other states, Mockler's lab is assembling the genome for the endangered snow leopard in a conservation effort aimed at improving captive breeding programs in zoos and restoring its numbers. His lab is also working with Bassil to sequence the genomes of three more kinds of strawberries as well as various varieties of apples, cherries, peaches, blueberries and black raspberries.

Mockler's lab is also sequencing the genomes of eight hazelnut varieties, a South American carnivorous plant known as *Genlisea aurea*, and duckweed, a tiny plant that looks like pond scum and may have potential as a source of biofuel.

Meanwhile, Liston is sequencing the genome for milkweed, and Jaiswal, who helped create a database of plant genomes, is trying to find genes that control flowering time in rice and corn.

Mockler was part of a global team that sequenced the genome of the wild grass *Brachypodium distachyon*, which scientists hope will serve as a model for improving some grass and cereal crops.

'Food of the gods' genome sequence could make finest chocolate better

Source: Science Centric, 3 January 2011.

The production of high quality chocolate, and the farmers who grow it, will benefit from the recent sequencing and assembly of the chocolate tree genome, according to an international team led by Claire Lanaud of CIRAD, France, with Mark Guiltinan of Penn State, and including scientists from 18 other institutions.

The team sequenced the DNA of a variety of *Theobroma cacao*, considered to produce the world's finest chocolate. The Maya domesticated this variety of *Theobroma cacao*, Criollo, about 3,000 years ago in Central America, and it is one of the oldest domesticated tree crops. Today, many growers prefer to grow hybrid cacao trees that produce chocolate of lower quality but are more resistant to disease.

'Fine cocoa production is estimated to be less than 5 percent of the world cocoa production because of low productivity and disease susceptibility,' said Guiltinan, professor of plant molecular biology.

The researchers report in the current issue of *Nature Genetics* 'consumers have shown an increased interest for high-quality chocolate made with cocoa of good quality and for dark chocolate, containing a higher percentage of cocoa, while also taking into account environmental and ethical criteria for cocoa production.'

Currently, most cacao farmers earn about \$2 per day, but producers of fine cacao earn more. Increasing the productivity and ease of growing cacao can help to develop a sustainable cacao economy. The trees are now also seen as an environmentally beneficial crop because they grow best under forest shade, allowing for land rehabilitation and enriched biodiversity.

The team's work identified a variety of gene families that may have future impact on improving cacao trees and fruit either by enhancing their attributes or providing protection from fungal diseases and insects that effect cacao trees.

'Our analysis of the Criollo genome has uncovered the genetic basis of pathways leading to the most important quality traits of chocolate - oil, flavonoid and terpene biosynthesis,' said Siela Maximova, associate professor of horticulture, Penn State, and a member of the research team. 'It has also led to the discovery of hundreds of genes potentially involved in pathogen resistance, all of which can be used to accelerate the

development of elite varieties of cacao in the future.'

Because the Criollo trees are self-pollinating, they are generally highly homozygous, possessing two identical forms of each gene, making this particular variety a good choice for accurate genome assembly.

The researchers assembled 84 percent of the genome identifying 28,798 genes that code for proteins. They assigned 88 percent or 23,529 of these protein-coding genes to one of the 10 chromosomes in the Criollo cacao tree. They also looked at microRNAs, short noncoding RNAs that regulate genes, and found that microRNAs in Criollo are probably major regulators of gene expression.

'Interestingly, only 20 percent of the genome was made up of transposable elements, one of the natural pathways through which genetic sequences change,' said Guiltinan 'They do this by moving around the chromosomes, changing the order of the genetic material. Smaller amounts of transposons than found in other plant species could lead to slower evolution of the chocolate plant, which was shown to have a relatively simple evolutionary history in terms of genome structure.'

Guiltinan and his colleagues are interested in specific gene families that could link to specific cocoa qualities or disease resistance. They hope that mapping these gene families will lead to a source of genes directly involved in variations in the plant that are useful for acceleration of plant breeding programs.

The researchers identified two types of disease resistance genes in the Criollo genome. They compared these to previously identified regions on the chromosomes that correlate with disease resistance - QTLs - and found that there was a correlation between many the resistance genes' QTL locations. The team suggests that a functional genomics approach, one that looks at what the genes do, is needed to confirm potential disease resistant genes in the Criollo genome.

Hidden in the genome the researchers also found genes that code for the production of cocoa butter, a substance highly prized in chocolate making, confectionary, pharmaceuticals and cosmetics. Most cocoa beans are already about 50 percent fat, but these 84 genes control not only the amounts but quality of the cocoa butter.

Other genes were found that influence the production of flavonoids, natural antioxidants and terpenoids, hormones,

pigments and aromas. Altering the genes for these chemicals might produce chocolate with better flavours, aromas and even healthier chocolate.

Gatekeeper for tomato pollination identified

Source: Science Centric, 4 January 2011.

Tomato plants use similar biochemical mechanisms to reject pollen from their own flowers as well as pollen from foreign but related plant species, thus guarding against both inbreeding and cross-species hybridisation, report plant scientists at the University of California, Davis.

The researchers identified a tomato pollen gene that encodes a protein that is very similar to a protein thought to function in preventing self-pollination in petunias. The tomato gene also was shown to play a role in blocking cross-species fertilisation, suggesting that similar biochemical mechanisms underlie the rejection of a plant's own pollen as well as foreign pollen from another species.

Roger Chetelat, director and curator of UC Davis' Charles M. Rick Tomato Genetics Resource Centre, and Wentao Li, a postdoctoral researcher in the Department of Plant Sciences, report their findings in the Dec. 24 issue of the journal *Science*.

Their discovery will likely find application in plant breeding, particularly for California's \$1.5 billion tomato industry, and in developing a better basic understanding of the biology of pollination.

'Flowering plants have several types of reproductive barriers to prevent accidental hybridisation between species in nature,' Chetelat said. 'We have identified one piece of this puzzle, a gene that helps control whether or not tomato pollen is recognised and rejected by flowers of related wild species.'

'Understanding and manipulating these reproductive barriers might help breeders access desired traits found in wild tomatoes,' he said.

In the mid-1800s, naturalist Charles Darwin observed that many flowering plants reject pollen from their own flowers as well as pollen from foreign plant species - the first because it is too similar and the other because it is too different. They do allow fertilisation, however, between two plants of the same species.

In plants, as well as animals, breeding between closely related individuals is generally considered detrimental because it leads to the expression of harmful mutations and leaves subsequent

generations genetically ill equipped to deal with environmental changes or diseases.

And crossbreeding with individuals from different species can be equally detrimental because it frequently results in hybrid offspring that cannot reproduce.

During the past several decades, scientists have studied the molecular mechanisms that cause plants to reject their own pollen. They have found that in the Solanaceae (nightshade) plant family, which includes tomatoes, prevention of self-pollination is controlled by the 'S-locus.' This is a genetic region responsible for producing distinct proteins in the flower's pollen and in its pistil, the female organ where pollination occurs.

While this mechanism for preventing self-pollination has been relatively well characterised, the mechanism that prevents crossing with plants of other species is much less understood.

To explore these processes in the tomato plant, Chetelat and Li set out to locate the chromosomal regions harbouring genes that control fertilisation and can cause a plant's flower to reject pollen from other species. The researchers identified a gene expressed in pollen known as a 'Cullin1' gene, which interacts genetically with a gene at or near the S-locus to block cross-species pollination.

They found that a mutant (inactive) form of the Cullin1 protein is present in cultivated tomato, as well as in related red- and orange-fruited wild tomato species, all of which are capable of being fertilised by their own pollen. However in the green-fruited tomato species, most of which block self-pollination, the Cullin1 protein is functional.

In short, their findings suggest that the Cullin1 protein is part of a biochemical gatekeeper: An active form of the protein is required for pollen to fertilise plants of another species, if that species is capable of rejecting its own pollen.

While these findings are from a study of tomato hybrids, the researchers suspect that they will be relevant to other members of the Solanaceae family, which also includes potatoes, chilli peppers and eggplant.

Nailing Down a Crucial Plant Signaling System

Source: ScienceDaily, Jan. 23, 2011

Plant biologists have discovered the last major element of the series of chemical signals that one class of plant hormones, called brassinosteroids, send from a protein on the surface of a plant cell to the cell's nucleus. Although many steps of the

pathway were already known, new research from a team including Carnegie's Ying Sun and Zhiyong Wang fills in a missing gap about the mechanism through which brassinosteroids cause plant genes to be expressed.

Their research, which will be published online by Nature Cell Biology on January 23, has implications for agricultural science and, potentially, evolutionary research.

"Brassinosteroids are found throughout the plant kingdom and regulate many aspects of growth and development, as well as resistance from external stresses," said Wang. "Mutant plants that are deficient in brassinosteroids show defects at many phases of the plant life cycle, including reduced seed germination, irregular growth in the absence of light, dwarfism, and sterility."

Previous research had identified a pathway of chemical signals that starts when a brassinosteroid binds to a receptor on the surface of a plant cell and activates a cascade of activity that consists of adding and removing phosphates from a series of proteins.

When brassinosteroids are not present, a protein in this pathway called BIN2 acts to add phosphates to two other proteins called BZR1 and BZR2, which are part of a special class of proteins called transcription factors. The phosphates inhibit the transcription factors. But when a brassinosteroid binds to the cell-surface receptor, BIN2 is deactivated, and as a result phosphates are removed from the two transcription factors. As a result, BZR1 and BZR2 can enter the cell's nucleus, where they bind directly to DNA molecules and promote a wide variety of gene activity.

Before this new research, the protein that detaches the phosphates and allows BZR1 and BZR2 to work was unknown. Using an extensive array of research techniques, the team was able to prove that a protein called protein phosphatase 2A (PP2A) is responsible.

"We discovered that PP2A is a key component of the brassinosteroid signaling pathway," Wang said. "This discovery completes the core signaling module that relays extracellular brassinosteroids to cue activity in the nucleus."

Further research is needed to determine whether brassinosteroid binding activates PP2A, or just deactivates BIN2, thus allowing PP2A to do this job. Additionally, PP2A is involved in a plant's response to gravity and light, among other things.

This aspect of the brassinosteroid signaling pathway bears some surprising resemblances to signaling pathways found in many members of the animal kingdom. More research could demonstrate details of the evolutionary split between non-protzoan animals and plants.

The production of plant pollen is regulated by several signalling pathways

Source: Science Centric, 26 January 2011

Plants producing flower pollen must not leave anything to chance. The model plant thale cress (*Arabidopsis*), for instance, uses three signalling pathways in concert with partially overlapping functions. The yield becomes the greatest when all three processes are active; however, two are sufficient to form an acceptable quantity of flower pollen. In a new study, Peter Huijser and his colleagues at the Max Planck Institute for Plant Breeding Research in Cologne offer fascinating insights into the rich range of proteins that are used by seed plants to develop stamens and form flower pollen. The rule for plant survival is simple: to stay in the game, you have to reproduce.

Flowers are no ornamental luxury to plants; after all, they hold the male and female reproductive organs. The male pollen is produced in the stamens and the carpel bears the female ovule. The fusion of the two produces a germinable embryo that ensures the reproduction of the plant. Plants can only bloom if a radical transition occurs during their development. This stops the production of leaves and instead causes the reproductive cells that are equipped with a single set of chromosomes to form sexually distinctive reproductive organs. For optimal reproduction, this must coincide with certain external conditions, such as light and temperature. However, sensitivity to the external conditions must not be so great that it prevents blooming if the environmental conditions are not optimal.

One of the three signalling pathways that are used to develop male reproductive organs and cells cannot be substituted. This signalling pathway via the SPOROCTELESS gene, which has been known for a long time, is activated as soon as the so-called AGAMOUS protein indicates which cells at the end of the axis of the shoot should form the stamens. Peter Huijser and his colleagues at the Max Planck Institute for Plant Breeding Research have now shown that functional male reproductive organs and cells only

develop if at least one of two further signalling pathways is involved. Together with the central, indispensable signalling pathway, they ensure that not only is the formation of pollen initiated, but also that the right tissue and anatomical structures are developed for the development, maturation and release of the pollen grains. If the central signalling pathway mutates, the flowers become sterile.

Huijser and his colleagues have focussed in particular on investigating mutations in the two other signalling pathways. These lead to highly interesting differences in the plant's fertility during early and late inflorescence. One pathway uses the so-called SPL8 protein; the other uses several proteins that are related to SPL8. The latter is mainly distinguished from SPL8 by the fact that it can be repressed using a short ribonucleid acid, the so-called micro-RNA156. Huijser explains: 'If, due to a mutation, the SPL8 pathway is eliminated, the plant becomes less fertile. However, the alternative signalling pathway ensures that enough mature pollen grains are produced to guarantee the survival of the species, with one important exception: the first flowers of a plant with SPL8 mutation are fully sterile. We think that, in the early floral phase, the second signalling pathway is blocked by a concentration of micro-RNA156 which, at that point, is still too high.'

This conclusion from the scientists in Cologne ties in with an observation by Detlef Weigel and his colleagues at the Max Planck Institute for Developmental Biology in Tuebingen. Weigel has previously shown that a high concentration of micro-RNA156 during the vegetative growth phase blocks one of the two alternative signalling pathways in that phase. The older the plant becomes, the less micro-RNA156 is formed, and thus its effect on the signalling pathway is reduced. When the first flowers form, the effect is still stronger.

Huijser concludes: 'The first flowers are fertile thanks to the two other signalling pathways, that is, SPOROXYTELESS and SPL8. Without SPL8, the thale cress cannot produce mature pollen grains in the first flowers. It is not until a later floral stage that the flowers become fertile: once the retarding effect of micro-RNA156 has completely subsided and the other signalling pathway has been triggered. This also explains why the three signalling pathways together make for the best result in pollen grain production. However, two are sufficient to ensure plant fertility.'

How spring-loaded filaree seeds self launch

Source: Science Centric, 27 January 2011

Even by invading plants' standards, the filaree, or common stork's bill, has been remarkably successful. Introduced into North America in the eighteenth century, it is now endemic in south-western states such as California, and the plant's intriguing seed dispersal mechanism seems to lie at the root of their success. Having launched as far as possible from the mother plant, the seed drills itself into the ground by repeatedly curling and unwinding a strap-like structure, known as an awn, to give it the best chance to germinate. But how do they self-drill? Having watched the seeds bore themselves into the ground in California, research associate Scott Hotton took them back to Jacques Dumais' Harvard laboratory to take a closer look and when Dumais set his introduction to botany class the challenge of making a time-lapse movie, Dennis Evangelista jumped at the opportunity to film the seed's drilling action. Evangelista, Hotton and Dumais publish their discovery that filaree seeds are launched with a spring mechanism that also drills the seeds into the ground in *The Journal of Experimental Biology* at <http://jeb.biologists.org/cgi/content/abstract/214/4/521>.

Setting up a camera in his kitchen, Evangelista wet the dry seeds and filmed them as they uncurled and then rewound when they dried. Evangelista explains that when humidity is low the awn dries, curls and drills the seed into the soil. When the humidity rises the awn uncurls, but backward facing hairs on the awn force the seed to move in one direction so that it continues drilling into the ground even when it uncurls. Plotting the tip's trajectory as it wound round, Evangelista realised that the awn behaved like a beam bending into a stretched logarithmic spiral. He could use engineering physics to calculate the amount of energy stored in the awn as it ripened and dried within the fruit and use it to explain how the seeds launch themselves. 'By knowing how much energy is in the dry awn when it is held straight in the seed head I can estimate the range that it goes,' says Evangelista; but first he needed to find out just how far the seeds could fly.

Setting up a high speed camera in Mimi Koehl's Berkeley laboratory and filming seed heads - formed from clusters of five awns - Evangelista captured the instant when an awn finally tore loose and the speed as it catapulted free, launching the

seed up to 0.5m from the plant. But how well would Evangelista's energy storage model hold up when he used it to calculate how far the seed could be launched?

Calculating the amount of energy that was released as the dry awn curled and broke free of the seed head, Evangelista then subtracted the amount of energy required to tear the awn away and the energy lost to wind resistance as the seed tumbled through the air, before calculating the distance that the seed could be flung. His calculations matched the distance that the filmed seed had flown. So filaree seeds disperse by using energy stored in the dry awns, which act as springs to fling the seeds by up to 0.5m.

Having discovered how filaree seeds are so successful at propagating, Evangelista and Dumais are now keen to find out how other members of the geranium family disperse their seeds. Evangelista explains that all geraniums are thought to use variations of the awn catapult mechanism for seed dispersal and propagation and he is keen to find out how changes in the awn's material properties affect seed dispersal in other members of the geranium family.

Preparing for infection

By Cristina Luiggi. Source: The Scientist.

Plants can predict when common pathogens are most likely to invade and arm themselves for the fight.

Plants can prepare for future infections by turning on the expression of defense genes during the times of day when they are most likely to encounter pathogens, according to a study published this week in *Nature*.

Plants achieve this timing thanks to the synchronization of those resistance genes with their own circadian clock, the daily rhythms that regulate many aspects of plant physiology, the authors report.

"This is a really elegant piece of work," says molecular biologist at the University of Cape Town in South Africa, Laura Roden, who did not participate in the research. "They discovered this circadian component of disease resistance."

With no specialized immune system to speak of, plants rely on a large set of genes that code for receptors and other proteins that specifically recognize molecules, or effectors, from a wide range of pathogens. Known as disease resistance (R) genes, they are responsible for jump starting a series of physiological processes that thwart the progression of infection.

Thanks to the R gene known as RPP4, the model plant *Arabidopsis thaliana* is naturally resistant to the fungus-like parasite, *Hyaloperonospora arabidopsis* (Hpa) that causes downy mildew disease, which stunts plant growth and causes yellow spotting and localized necrosis in leaves.

Lead scientist and molecular biologist from Duke University, Xinnian Dong, was initially interested in finding the other genes that work with RPP4 to enable resistance against the parasite. Using expression data from wildtype and *rpp4* mutants, Dong and her colleagues identified 22 genes that worked downstream of RPP4 to initiate defense mechanisms such as the programmed cell death of infected cells, the accumulation of antimicrobial compounds, and the scarring of the infection site, which helps block the pathogen from moving on to neighboring cells.

But looking more closely at the promoter regions of the 22 downstream genes revealed an unexpected surprise.

It turned out that the majority contained sequences that bind to the major circadian clock transcription factor known as CCA1, as well as other clock elements. This meant that these defense genes were not only regulated by RPP4 in response to downy mildew infection, but they were also intimately tied to the plant's circadian cycle.

When the team went back to monitor the expression of the genes in *Arabidopsis* over the course of 48 hours after infection, they found that indeed, the expression of these genes ebbed and flowed, peaking at dawn and then shutting off during the day. "People had suspected that this was the case," Dong said. "But there were no examples of it. Here we have specific molecules that are involved in immune response but are regulated by the circadian clock."

The team got further evidence of this when they found that *Arabidopsis* plants containing mutant versions of CCA1 were more vulnerable to downy mildew.

Interestingly, even in the control samples (plants that had been sprayed with water instead of the parasite), the genes were expressed in the same oscillatory fashion. "The defense genes have a rhythmic expression even without infection," Dong said, suggesting that the plant was anticipating infection risk.

Sure enough, the genes' most active period at dawn corresponds to the time of day when the downy mildew releases its spores into the air. During the rest of the day, on the other hand, when the genes

are essentially inactive, Hpa infection is highly unlikely.

It wasn't a surprise then, that when the researchers exposed the plants to the pathogen at dusk, the plants were much more susceptible to downy mildew disease.

"When we studied defense gene expression, we would normally take a couple of time points and never really think that these genes would oscillate between day and night," Dong said. If other plants also show cyclical defense strategies against their common parasites, it could have serious implications for understanding and dealing with devastating crop diseases such as the potato blight, she added.

Reference: W. Wang, et al., "Timing of plant immune responses by a central circadian regulator," *Nature*, 470:110-4, 2011.

Fast growth, low defence - plants facing a dilemma

Source: Science Centric, 29 January 2011
Plants are attacked by a multitude of insects and mammals. As defence against these herbivores they developed complex defence mechanisms over the course of evolution: spines, thorns, leaf hairs and a number of toxic chemical substances. For decades it has been controversially discussed whether the production of defence traits incurs costs to the plants. Now, using a new method the ecologists and plant biologists of the University of Zuerich together with their American colleagues demonstrate these costs accurately in a Proceedings of the Royal Society article.

For their study, the researchers planted different 'knockout'-mutants of the same genotype of the model plant *Arabidopsis thaliana*. They then harvested a subset of these plants in evenly distributed intervals to measure the biomass growth over the whole plant life. 'Mutants with suppressed defence mechanisms showed an increased growth rate' Tobias Zuest explains the result of his study. But the faster growth comes at an added cost: aphids reproduce faster on these plants than on slow growing plants with intact defence mechanisms. This is a result of the fact that fast growing plants provide more resources to the herbivore than slow growing plants in the same amount of time.

The study shows that natural resistance is often not compatible with fast growth. This finding is of great importance for agricultural crops: These crops have been

selected for high yield and as a consequence have very low natural resistance to herbivores, consequentially requiring high input of insecticides.

Draft 'Genetic Road Map' of Biofuels Crop

Source: ScienceDaily, Jan. 29, 2011

The first rough draft of a "genetic road map" of a biomass crop, prairie cordgrass, is giving scientists an inside look at the genes of one of the crops that may help produce the next generation of biofuels.

The study already has produced the "transcriptome" of the species, said plant geneticist Jose Gonzalez of South Dakota State University. He said the transcriptome can be used somewhat like a map -- it records the genes the plant uses to reach certain goals.

A transcriptome is the small portion of the DNA of an organism that is transcribed into molecules of ribonucleic acid, or RNA. When DNA is transcribed into what is called "messenger RNA," it enables the organism to carry out instructions about building and maintaining cells. Scientists can decode those instructions to determine what particular DNA sequences do.

In an article in the September 2010 issue of *The Plant Genome*, Gonzalez and his colleagues discussed one of the first studies of the prairie cordgrass transcriptome. Prairie cordgrass is being viewed as a species suitable for producing biomass to make biofuels. One of the reasons scientists are interested in prairie cordgrass is because it yields extraordinarily well while tolerating wet conditions, high salinity or poorly aerated soils in low areas unsuitable for growing conventional crops. But it can also survive in open arid prairies.

Gonzalez said one obvious benefit from studying the transcriptome of a plant such as prairie cordgrass is to enable plant breeders to use marker-assisted selection in order to deliberately include gene sequences that confer desirable traits.

In the study, scientists used four tissues of prairie cordgrass to produce 556,198 expressed sequence tags, or portions of expressed genes. They assembled these into 26,302 "contigs," or overlapping DNA segments from the same gene.

"We calculated probably 40 percent of the genes in prairie cordgrass, or more than 20,000," Gonzalez said. "We're starting to be able to look at the genes involved in particular traits. For example, for biofuels, for cellulosic ethanol production, cell wall composition is very important. We can

actually look at the genes that are related to that cell wall composition so that we can study the variations of those genes. It can help the breeders eventually to select populations of prairie cordgrass with better composition."

Gonzalez said cell walls -- primarily made up of cellulose, hemicellulose, and lignin -- are largely what remains when prairie cordgrass or some other biomass grass has been harvested and allowed to dry.

Cellulose and hemicellulose are carbohydrates that can be transformed into simple sugars that can be fermented. Lignin can't be broken down by fermentation, though it can be isolated by other treatments.

The genes involved in the lignin biosynthesis pathway have been very well studied in other grasses, and the genes across the grasses are very similar. That will be one area of ongoing research for Gonzalez and his colleagues.

The synthesis of cellulose or hemicellulose is much more complex and involves many more enzymes. That is also an area of further research for the group, though those pathways will take longer to unravel, he said.

Scientists are also interested in the morphological development of the plant because that's what supports the yield of the plant through many seasons -- how the plant develops underground and starts growing at beginning of the season, how it goes into dormancy in fall, how it reactivates itself next season.

That is why current research efforts to decipher the plant's genetic information are so important, Gonzalez said.

Journal Reference: Kristene Gedye et al. Investigation of the Transcriptome of Prairie Cord Grass, a New Cellulosic Biomass Crop. *The Plant Genome Journal*, 2010; 3 (2): 69 DOI: 10.3835/plantgenome2010.06.0012

Plants Can Adapt Genetically to Survive Harsh Environments

Source: ScienceDaily, Jan. 31, 2011

A Purdue University scientist has found genetic evidence of how some plants adapt to live in unfavorable conditions, a finding he believes could one day be used to help food crops survive in new or changing environments.

David Salt, a professor of horticulture, noticed several years ago that a variant of the research plant *Arabidopsis thaliana* that could tolerate higher levels of sodium had come from coastal areas. To test the observation, Salt grew more than 300 *Arabidopsis thaliana* plants from seeds

gathered across Europe. The plants were grown in non-saline soil and their leaf-sodium content was measured.

Each plant's origination was mapped, and those with the highest sodium contents were found to have come from seeds collected close to a coast or area with high saline soil. All plants were analyzed using genome-wide association mapping, which compares the genomes of a number of plants with a shared physical trait -- in this case leaf sodium accumulation -- to identify genes that may account for variation in this characteristic. Salt found that the plants that accumulate the highest sodium levels in their leaves had a weak form of the gene *HTK1*, which regulates sodium intake distribution to leaves.

"The major gene that is controlling variation in leaf sodium accumulation across the whole European population of *Arabidopsis thaliana* is *HTK1*," said Salt, whose findings were published in the journal *PLoS Genetics*. "The *Arabidopsis thaliana* plants that accumulated high levels of sodium had a reduced level of *HTK1* gene expression. The populations that have this altered form of *HTK1* are on the coast. There are a few exceptions that prove the rule, such as populations in the Czech Republic, which isn't near the coast, but come from an area containing high saline soils derived from an ancient beach."

It has long been known that plants are adapted to their local soil environments, but the molecular basis of such adaptation has remained elusive. Salt said this is some of the first evidence linking genetic changes with adaptation to specific environmental factors.

"What we're looking at is evolution in action," Salt said. "It looks like natural selection is matching expression of this gene to the local soil conditions."

Salt said crops grown around the world could be affected, possibly negatively, by climate change. It may become important to identify mechanisms to adapt plants to drought conditions, higher temperatures or changes in soil nutrition. Salt believes identifying genetic mechanisms of how plants naturally adapt to their environments will be key to solving those problems.

"Driven by natural selection, plants have been evolving to grow under harsh conditions for millennia," Salt said. "We need to understand genetically what is allowing these plants to survive these conditions."

Salt plans to continue his research to understand at the DNA level how

Arabidopsis thaliana adapts to environmental conditions. The National Institutes of Health funded his work.

Journal Reference: Ivan Baxter, Jessica N. Brazelton, Danni Yu, Yu S. Huang, Brett Lahner, Elena Yakubova, Yan Li, Joy Bergelson, Justin O. Borevitz, Magnus Nordborg, Olga Vitek, David E. Salt. A Coastal Cline in Sodium Accumulation in Arabidopsis thaliana Is Driven by Natural Variation of the Sodium Transporter AtHKT1;1. PLoS Genetics, 2010; 6 (11): e1001193 DOI: 10.1371/journal.pgen.1001193

Two Genes Better Than One for Important Plant Pest

Source: ScienceDaily, Feb. 1, 2011

Researchers funded by the Biotechnology and Biological Sciences Research Council (BBSRC) have revealed a novel molecular mechanism that triggers plant infection by *Pseudomonas syringae*, the bacteria responsible for bacterial speck in tomatoes. The scientists from the Department of Life Sciences at Imperial College London have revealed how two genes in the bacteria work together to launch the infection process that ultimately kills the plant's cells and causes disease, significantly reducing crop quality and yield.

Pseudomonas syringae is responsible for major disease outbreaks in an enormous range of economically important food plants including rice, tomatoes, corn, cucumbers and beans. It is also a problem in wild plants and one *Pseudomonas syringae* type has recently infected half of all chestnut trees in the UK. The researchers hope that by understanding the molecular basis for how the bacteria attack plant cells they will be able to find new targets for pesticides and devise better strategies for disease management. Speaking about the findings, published February 1, 2011 in Nature Communications Dr Jörg Schumacher, the senior author on the study, explains: "These bacteria have quite a sophisticated system for infecting plants. They use remarkable needle-like structures called pili to penetrate and inject a range of proteins into a plant's cells, which then work to suppress its immune response and kill infected cells. *Pseudomonas syringae* are very versatile bacteria and their pili help them to infect a very large range of plants causing numerous symptoms in different plants, for example black/brown specks on tomato fruits."

"From what we know, these bacteria only produce their pili and launch infection

when they have already invaded the plant tissue. It is unclear how they sense the plant tissue environment that triggers infection, but we do know that the regulatory mechanism that controls pili formation is essential in this process."

What distinguishes *Pseudomonas syringae* from other related pathogens that also use pili to infect plants is that it has duplicated a gene during evolution that is involved in producing the pili. Indeed the researchers have found the duplicated gene in all the strains of *Pseudomonas syringae* they have studied, which makes them think that it is very likely to provide some selective advantage in the infection process. It appears, for example, that this innovation may allow for more subtlety when it comes to whether or not to commit to infection.

Dr Schumacher continues: "The motivation for this study was to find out how having a duplicated gene could provide *Pseudomonas syringae* with the 'edge' in terms of evolutionary advantage. We have studied related systems in other bacteria in great detail in the lab of Professor Martin Buck, where this study was carried out. What we have found here is that the two-gene system in *Pseudomonas syringae* is an evolutionary innovation that had not been described in bacteria.

"With our work and that of others we are able to understand how evolution that happens at the molecular level translates to phenomena we observe in our daily lives. When we see brown leaved chestnut trees next spring, chances are that *Pseudomonas syringae* and the duplicated gene are involved."

Professor Douglas Kell, BBSRC Chief Executive said: "With improvements in imaging and modelling we are now able to look deeper into cells at how the molecular machines that underlie all life on earth work. But this is not just knowledge for its own sake; a more detailed understanding of how crop pests interact with their hosts will be important for developing more sophisticated methods of controlling them. This is vital to global food security, ensuring that we can provide safe nutritious food to a growing world population."

Journal Reference: Milija Jovanovic, Ellen H. James, Patricia C. Burrows, Fabiane G. M. Rego, Martin Buck, Jörg Schumacher. Regulation of the co-evolved HrpR and HrpS AAA proteins required for *Pseudomonas syringae* pathogenicity. Nature Communications, 2011; 2: 177 DOI: 10.1038/ncomms1177

Jaume and the Giant Genome

By Daniel Grushkin

The Scientist, Volume 25, Issue 2, Page 18 (2011-02-01)

More than twelve percent of the world's known plant species can be found on the manicured grounds of the Royal Botanic Gardens, Kew. Add 300 acres, 250 years of British history, nearly two million visitors annually, and greenhouses that resemble glass castles, and one can only imagine how overwhelmed Jaume Pellicer, a newly minted PhD originally from a village on Spain's Mediterranean coast, felt when he arrived to work at Kew.

"This was shocking to me," says Pellicer, who's still perfecting his English, "like I was a tiny point in a new world." Surrounded by a staff of 800, mostly plant specialists and scientists, Pellicer was more or less another anonymous technician, but in less than a year the 32-year-old had discovered the largest genome ever recorded. It was sitting in a flowerpot inside Kew's Davies Alpine House. For six months Pellicer had the tedious task of mincing countless leaves with a razor blade to extract DNA and measure genome sizes in the Melanthiaceae family, a group of flowering perennial herbs. His team at Kew was trying to learn exactly when in the plant family's evolution genomes began to expand in size. After measuring a procession of 40 different species, Pellicer arrived at the Japanese canopy plant (*Paris japonica*), native to the mountains surrounding Nagano. From the outside it looked ordinary—an asterisk of deep-green leaves at whose center was a white flower. But inside its cells was a different story.

One summer afternoon, Pellicer hesitantly announced to his boss, plant geneticist Ilia Leitch, "I think we've got something that looks really, really big," bigger than anything they'd ever seen. "Already, there was this sort of bubbling feeling," Leitch recalls. Still doubtful, Pellicer repeated the flow cytometry measurement with three different calibration standards until he was sure.

He found that the canopy plant genome had 150 billion base pairs—50 times as many as human DNA. If the DNA in a human cell were unraveled, it would stretch to two meters. A strand of DNA in the canopy plant would span 100 meters—the difference between a football player's height and a football field's length.

"This is so cool because it tells us we still have interesting things to find out there," says T. Ryan Gregory, a biologist who

studies genome size at the University of Guelph in Canada.

One might expect genome size to correlate with a species' complexity—after all, if one genome codes for a particular number of proteins, then a larger one could potentially code for more. But since the 1970s, scientists have recognized the disparity between number of genes and genome size. In fact, in humans, only about 1.5 percent of the genome's DNA codes for proteins. In the Japanese canopy plant the percentage is sure to be even less. The function of that surplus DNA—or even whether there is a function—is a hotly debated mystery and will likely remain so until the species is sequenced. Noncoding sequences used to go by the derogatory names "selfish" or "junk" DNA, but have more recently acquired milder tags, including "transposable elements" or "jumping genes." Unless somehow restrained, these proliferate across genomes like weeds. One sequence, called Alu, has copied itself a million times and makes up some 10 percent of the human genome. Leitch suspects that though these sequences can run rampant, some may be corralled into contributing to gene regulation at points in a given organism's evolution. Or, according to Gregory, "They could be there just because they're good at being there."

Evolutionarily speaking, "it's not common that a large genome is very advantageous," says Gregory. In both plants and animals, bulky genomes slow an organism's growth simply because copying all that DNA takes so much time. That limits the paths an organism's evolution can take. Two options that are out: being an annual plant or a metamorphosing insect, because larger genomes don't allow enough time to grow or radically change body plan while remaining competitive.

There is, however, some evidence that the canopy plant, despite—or perhaps because of—its huge genome, maintains a competitive edge over plants that share its mountain habitat. In the chilly months of early spring, while neighboring competitors sit dormant, and before overhead trees come into leaf, the plant gets a jump-start on growth by pumping its cells full of water. This cellular expansion allows the canopy plant to increase its size and soak up more sunlight before DNA replication and cell division occur in the warmer summer months.

Back at Kew, Pellicer is enjoying his newfound prestige: "Everybody tells me,

'Wow, good for you.' That's not my usual experience."

Plant's immune defence revs up for the morning attack

Source: Science Centric, 4 February 2011

Timing is everything in the long-standing arms race between the flowering plant *Arabidopsis* and *Hyaloperonospora*, a downy mildew pathogen.

Duke University researchers have found that the little mustard plant cranks up its immune system in the morning to prepare for the greatest onslaught of infectious spores released by the mildew.

It isn't news that plants know what time of day it is and change their activities accordingly, but this is the first time that a plant's defensive systems have been shown to cycle on a daily basis - even when pathogens aren't present. Their work appears in the Feb. 3 edition of *Nature*.

The powerful chemical compounds *Arabidopsis* uses to fight mildew infection are expensive to make and also potentially harmful to the plant itself over the long-term, so a daily, or circadian, cycle of production is safer and more efficient than simply having the chemicals on hand all the time, said Duke biology professor Xinnian Dong.

Morning, just as the dew dries, is the right time to have defences at the ready.

When the mildew has been able to successfully set up housekeeping within *Arabidopsis*, it produces a flowering body that grows upward from the leaf surface. Bearing its spores for the next generation, it looks very much like a tree covered with apples. As the morning dew dries from the leaf, the mildew's flowering body twists violently, flinging the tiny spores in all directions to be carried on air currents until they settle on a potential new host.

Other researchers who have collected the spores had noted that the morning was the most productive time to catch them, but *Arabidopsis* apparently already knew that.

Dong and her graduate students Wei Wang and Jinyoung Barnaby discovered this surprising circadian clock connection during a more general search of *Arabidopsis* immune system genes. They found 22 candidate genes that were a part of the immune response to downy mildew and many of them showed rhythmic expression patterns.

Wang also watched expression patterns of these defence genes in the absence of any pathogens and found them cycling daily. 'It suggests that the plants are

programmed to anticipate infection according to a circadian schedule,' Dong said.

To test this hypothesis, Wang exposed plants to the mildew spores at 'dawn' or 'dusk' in a greenhouse with artificial 12-hour days. He found infection rates were much higher at dusk when spores were not expected in nature.

To identify the clock components that control this immune defence, Wang began a series of experiments on so-called 'clock mutants,' which are *Arabidopsis* plants that lack portions of the circadian time-keeping system. He found that the mutant missing the central clock component CCA1 suffered much higher infection rates than normal plants. Conversely, a plant line expressing CCA1 all the time had heightened resistance.

Over the last decade, plant researchers have identified several systems that work on a circadian clock, including starch metabolism, photosynthesis and frost-resistance, said Robert McClung, a Dartmouth University biologist who was not involved in this research, but is writing an accompanying commentary on the paper for *Nature*. 'This sort of completes the suite of environmental insults that the clock manages,' he said.

Although this finding is specific so far to *Arabidopsis* and its exclusive pathogen *Hyaloperonospora*, it's likely to be a system that will be found in other plants and pathogens, McClung said.

While it makes logical sense that clock mechanisms would be involved with the plant's immune system, this is still 'a remarkable discovery,' said Philip Benfey, the Paul Kramer professor of biology at Duke. 'This required an experimental tour de force combined with inspired insight to make the connection between gene expression patterns and preparation for pathogen attack.'

'It was a huge amount of work, even though the conclusion is quite simple,' Dong said.

SWEET proteins found

Source: The Scientist, 15th February 2011

A new class of proteins, dubbed SWEETs, function as glucose transporters, shuttling sugar molecules out of plant, worm and human cells. In some plants, SWEET proteins are co-opted by bacterial pathogens to deliver nutrition to the invaders.

It is exciting that virulence factors of *Xanthomonas oryzae*, which are known as transcription activator-like type III (TAL) effectors, specifically induce the gene

expression of sugar transporters, SWEETs. The bacterial effectors seem to increase supply of sugars in apoplast and xylem to promote bacterial growth. It is also interesting that other bacterial and fungal pathogens increase the expression of SWEETs. Most of the bacterial effectors characterized to date are shown to suppress plant immune responses; however, TAL effectors induce host susceptibility factors. This paper identified that a major susceptibility factor of rice against *X. oryzae* are the sugar transporters.

This paper identified a new family of sugar transporters named SWEET. First, the authors identified *Arabidopsis* AtSWEET1 as a glucose uniporter by using FRET-glucose sensors, complementation of yeast hexose transporter mutants and kinetic studies of radio labelled sugars. The paralogues of AtSWEET1 have various functions in plant development.

Second, the authors showed that bacterial and fungal infection induces the expression of AtSWEETs. Although they showed that the type III secretion system mutant of *Pseudomonas syringae* does not induce SWEET genes, it is not clear whether SWEET genes are actively induced by bacterial/fungal effectors or if the gene inductions are consequences (plant responses) of bacterial/fungal multiplication. The direct evidence that the pathogen induces SWEETs came from rice-*X. oryzae* interactions where the TAL effector directly induces SWEET genes. SWEET homologues are found in Metazoans. Lastly, the authors showed that the SWEETs from *Caenorhabditis elegans* and humans are also sugar transporters.

Competing interests: Akiko Sugio was previously a student in one of the authors' labs (Prof. F.F White), but had no involvement in this study.

By Sugio A, Hogenhout S: 2011. F1000.com/6785956

Reference: L.Q. Chen et al. *Nature*, 468:527-32, 2010.

New path to water efficient seeds opens as TIP pips PIP as water gatekeeper

Source: Science Centric, 24 February 2011

Research by University of Warwick's School of Life Sciences has opened up a new path to produce water efficient seeds that will be a significant tool to cope with drought resistance, and ensure global food security. The research not only provides

the best map to date of the key protein that appears to be the principal gateway for water intake during seed germination - it also actually provides the right map as it appears much of the research to date was focussed on a much less relevant protein.

The research team led by Dr Lorenzo Frigerio looked at two proteins that are members of the large family of 'Major Intrinsic Proteins,' or MIPs, which are widespread among living organisms and are known to act as water channels governing water uptake.

The first of the types of protein they looked at PIPs - are intrinsic proteins that take the P at the start of their name from being normally found in the 'plasma membrane,' the outer casing of a cell. Because of their normal position on this outer covering these plasma membrane (PM) intrinsic proteins (PIPs) have received much of researcher's attention as the probable prime gatekeepers of the water transport into and out of cells.

The researchers focussed much of their attention on a second group of intrinsic proteins known as 'Tonoplast Intrinsic Proteins' or TIPs as they are most usually found in an inner cell layer called the tonoplast which surrounds a vacuole in a cell (vacuoles are enclosed compartments in a cell filled with water and containing inorganic and organic molecules).

Despite the fact that the TIPs appear to be able to govern water uptake the fact that they are seen as being concentrated in the tonoplast has reduced researchers interest in time as key player in water uptake. This is because the tonoplast itself is generally not considered to present a major problem for intracellular water flow, as its water permeability is thought to be much higher than that of the outer plasma membrane.

This has led to a concentration of study on PIP rather than TIP and meant that virtually nothing was known about how TIPs acted in processes such as seed maturation and germination. The University of Warwick's research team work not only resulted in the most complete plant TIP expression map produced to date - it also threw up a major surprise in that they found that TIP not only had a role to play in water management in seed maturation and germination - in fact they found that it probably plays the crucial water management role, as PIP was almost literally nowhere to be seen.

As PIP, but not TIP, are generally found at the plasma membrane of plant cells, one would expect the involvement of PIP in seed de/rehydration. Intriguingly, however, the Warwick researchers studied

microarray datasets and found that - out of 13 PIPs encoded by the Arabidopsis genome - only 3 (PIP1;2, PIP1;4, PIP1;5) seemed to be detectable in their seeds. They also found that those 3 PIPs did not show up until 60 hours after germination, i.e. only after the end of the most important phases of water uptake in a germinating seed. In contrast the researchers found that very high levels of TIP3 protein appeared to be present in the plasma membrane during seed development and germination.

Dr Frigerio's working hypothesis is that TIP3, besides residing in the tonoplast, is recruited to the plasma membrane to compensate for the absence (or very low concentration) of PIP. We are now on the right path to build a real understanding of how water uptake is regulated in seed development and germination. That understanding will help researchers produce seeds to meet the challenges of Global climate change, and food security through improved drought resistance and increased water use efficiency.

Forthcoming meetings

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10th Conference of the International Society for Seed Science. **April 10 – 15, 2011. Costa do Sauípe, Salvador de Bahía (Brasil)**

Abstracts submission deadline: February 2011.

More info:

<http://www.seedscience2011.com.br/en/index.php>

6th International Symposium on Plant Neurobiology (PNB 2011, Kitakyushu) **May 15 – 19, 2011. Kitakyushu International Conference Center, Kitakyushu (Japan)**

Website: <http://www.dd-plus.net/pnb2011/index.html>

Theme: Discussing the Future of Plant Biology in the City of Environmental Innovation

Topics Covered: Plant biology addressing the physiological and neurobiological basis of adaptive behavior in plants thus covering; Cellular Signaling Mechanism (receptors, calcium, reactive oxygen species, protein phosphorylations, phospholipids, G-proteins, transcription factors, etc.), Cell-to-Cell Communications, Plant Responses to Environmental Factors, Molecular Ecology, Plant-Microbe Interactions, Symbiosis, Regulations of Growth and Development, Membrane Traffics, Metabolic Regulations, Redox Signaling and Regulations, Electro-Physiology, Bioenergetics, Proteomics, Micro-Arrays, Natural and Artificial Photosynthesis, Photobiology (basic biology and agricultural applications), Micro-Robotics and MEMS using Living Cells, Artificial Enzymes, Imaging, Computational Simulation, New Technologies, etc.

26th New Phytologist Symposium: Bioenergy trees

May 17 – 19, 2011. Nancy (France)

More info:

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

Plant pigments and Human Health **May 24 – 26, 2011. Gerona (Spain)**

Organisers: Allan White and Roger Hellens (Plant & Food Research, New Zealand), Cathie Martin (John Innes, UK), Chiara Tonelli (University Milano, IT) and Manuel Rodriguez-Concepcion (CSIC, ES).

Participants will be from academia as well as from private enterprises and national and European research agencies.

The main themes covered will be: Plant pigments with health benefits, Anthocyanins, Delivery of pigments to humans, Human health benefits.

More info:

<http://www.epsoweb.org/workshop-plant-pigments-and-human-health>.

22nd International Conference on Arabidopsis Research **June 22 – 25, 2011. University of Wisconsin-Madison (USA)**

On behalf of the North American Arabidopsis Steering Committee (NAASC) we invite you to attend the 22nd International Conference on Arabidopsis Research (ICAR), June 22-25, 2011. The ICAR is the largest annual international scientific conference focused on cutting-edge research using the reference plant *Arabidopsis thaliana* and also incorporates research on other plants (www.union.wisc.edu/arabidopsis/).

The full program with all confirmed speakers can be found at the conference website.

The low-cost registration fee includes all meals (final banquet optional), and food and beverages at poster sessions and the opening reception. Special reduced rates for students are available.

We look forward to seeing you back in Madison in June, 2011 for an exciting scientific meeting in a beautiful setting.

**11th FEBS Young Scientist Forum
June 23 – 25, 2011. Torino (Italy)**

This event, together with the main FEBS Congress, will encourage young scientists interaction with peers in the field and with the whole scientific community.

We would be honoured if you would promote the 11th YSF and encourage your members to visit the site www.ysf2011.org

10th International Conference on Reactive Oxygen and Nitrogen Species in Plants

July 5 – 8, 2011. Budapest (Hungary)

This conference will be also the official meeting of the Plant Oxygen Group of the Society for Free Radical Research-Europe (SFRR-E).

The conference is designed to present the most recent advances in the metabolism of reactive oxygen and nitrogen species in plants, covering different aspects of plant cell metabolism, plant development, redox signalling, abiotic and biotic stress effects as well as antioxidative defence.

The conference will feature invited presentations by leading experts as well as delegate-contributed oral and poster presentations. For each planned session additional oral presentations will be selected from the submitted abstracts. A major aim of the conference is to bring together young researchers and established scientists from different countries of the world.

The registration is now open.

You can find all necessary information about the conference (topics, registration, abstract submission, accommodation, deadlines, contact information) at the following webpage:

<http://plantros2011.eu>

You are hereby invited to submit an abstract - the deadline is 31 March 2011. Participants with abstracts selected for oral presentations will be contacted in April 2011.

On behalf of all organizers, we are looking forward to seeing you in Budapest
Balazs Barna and Gabor Gullner

**Plant Metabolic Engineering
July 23 – 24, 2011. Waterville Valley,
NH. (USA)**

Gordon Research Seminar on Plant Metabolic Engineering is a pre-meeting of Gordon Research Conference (GRC) specifically designed to facilitate professional development of junior scientists in the field of plant metabolism. The Plant Metabolic Engineering Gordon Research Seminar will be held in conjunction with the Plant Metabolic Engineering Gordon Research Conference. Those interested in attending both meetings must submit an application for the GRC in addition to an application for the GRS. Please refer to the Plant Metabolic Engineering GRC web page for more information.

Applications for this meeting must be submitted by **June 25, 2011**. Please apply early, as some meetings become oversubscribed (full) before this deadline. If the meeting is oversubscribed, it will be stated here. Note: Applications for oversubscribed meetings will only be considered by the Conference Chair if more seats become available due to cancellations.

More info:

http://www.grc.org/programs.aspx?year=2011&program=grs_plant

12th International Symposium on Pre-Harvest Sprouting in Cereals

July 24 – 27, 2011. Alberta (Canada)

More info:

[http://www1.agric.gov.ab.ca/\\$department/deptdocs.nsf/all/fcd12877](http://www1.agric.gov.ab.ca/$department/deptdocs.nsf/all/fcd12877)

Lab Leadership Workshop 2011

**August 4 – 6, 2011. Minneapolis,
Minnesota (USA)**

Contact: ASPB (info@aspb.org)

<http://my.aspb.org/event/LabLeadership2011>

ASPB Plant Biology 2011

**August 6 – 10, 2011. Minneapolis
(USA)**

More info:

http://my.aspb.org/?page=Meetings_Annual

International Conference on Plant Peroxisome Research

**August 11, 2011. Minneapolis,
Minnesota (USA)**

Contact: Jianping Hu, Michigan State University (huji@msu.edu)

<http://my.aspb.org/event/Peroxisome2011>

The second International Conference on Plant Peroxisome Research will be held as a satellite meeting to Plant Biology 2011 (ASPB) in Minneapolis.

XXIV SPPS Congress
August 21 – 25, 2011. Stavanger
(Norway)

More info: <http://www.spps2011.no/>
Registration deadline: 01.05.2011

RNAi & miRNA Europe
September 8 – 9, 2011. Munich
(Germany)

Más info:
info: <http://www.selectbiosciences.com/conferences/qPCRE2011/>

qPCR Europe
September 8 – 9, 2011. Munich
(Germany)

Más info:
<http://www.selectbiosciences.com/conferences/qPCRE2011/>

Epigenetics Europe
September 8 – 9, 2011. Munich
(Germany)

Más info:
<http://www.selectbiosciences.com/conferences/EE2011/>

Plant Growth Biology and Modeling
2011

September 19 – 21, 2011. Elche
(Spain)

Más info: <http://pgbm2011.umh.es>

27th New Phytologist Symposium
September 25 – 28, 2011. Arizona
(USA)

Stoichiometric flexibility in terrestrial ecosystems under global change

More info:
<http://www.newphytologist.org/stoichiometric/default.htm>

2011 International Conference on Computational Biology and Bioinformatics (CBB)
October 28 – 30, 2011. Shanghai
(China)

More info:
<http://www.engii.org/cet2011/CBB2011.aspx>

The 2011 International Conference on Computational Biology and Bioinformatics (CBB) will be held in Shanghai/China, Oct. 28-30, 2011, CBB is part of World

Congress on Engineering and Technology (CET) which will take place in Shanghai China. The CET is composed of several conferences on the frontier topics in the engineering and technological subjects.

The CET conference proceedings will be published by IEEE, and the accepted papers will be indexed by Ei Compendex and ISTP.

Paper Submission Deadline: April. 30, 2011

Acceptance Notification: Jun. 15, 2011

Second International Symposium on Woody Ornamentals of the Temperate Zone

July 1 – 4, 2012. Ghent (Belgium)

Don't miss the Second International Symposium on Woody Ornamentals of the Temperate Zone in Ghent, July 2012. **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.

Join us for these **field trips**: a visit to woody ornamental research centres in Belgium and a post-congress tour of local growers to showcase Belgium's dynamic and innovative woody ornamental industry.

We invite you to share your expertise with us at the symposium. We look forward to seeing you in Ghent in July 2012!

Fax: +32 9 272 29 01

E-mail:

woodyornamentals@ilvo.vlaanderen.be

Website:

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

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/>

Positions available



Call for applications for an Editor in Chief for the Journal of Experimental Botany

The Society for Experimental Biology is seeking to appoint an Editor in Chief to take effect from January 2012. The Journal of Experimental Botany is an established and innovative international journal publishing high quality primary research papers and reviews since 1950 and now includes extra publications such as The Flowering Newsletter. It is wholly owned by the Society for Experimental Biology and published by Oxford University Press. The journal has a novel open access policy and currently an impact factor of 4.27. Under the two previous editors in chief the journal has seen a steady growth in submissions and an increase in the impact factor. Please see <http://jxb.oxfordjournals.org/>

The Society is seeking in the Editor in Chief, a scientist of international standing with a good track record of publishing in high quality international journals, a person with excellent leadership skills and the ambition and vision to drive this innovative journal forward. Funding is available for journal development.

The term is for 5 years and is an honorary post that carries an honorarium (expenses associated with the role will be covered). The position is supported by a managing editor and editorial office currently with three staff. The post may be held by a scientist resident within or outside the UK. Further information can be obtained in the first instance from Professor M. M. Burrell m.burrell@sheffield.ac.uk.

Post-doctoral positions available in Australia

Two post-doctoral positions with an initial funding for at least 2 years is available in the laboratory of Sureshkumar Balasubramanian (SKB Lab - where science is fun!) at the School of Biological Sciences, The University of Queensland, Australia.

SKB lab is interested in deciphering the molecular basis of phenotypic variation and we exploit natural variation in *Arabidopsis thaliana* to address the same (Balasubramanian et al, Nature Genetics, 2006., Balasubramanian et al, PLoS Genetics, 2006, Sureshkumar et al,

Science, 2009). Currently, SKB lab is focussed on two major themes of research. We are interested in thermal adaptation in plants and we are exploring *Arabidopsis thaliana* as a system to study fundamental aspects associated with the genetics of repeat expansions. The postdoctoral researchers will participate in projects that are supported by the Australian Research Council (ARC) and the National Health and Medical Research Council (NHMRC). We are looking for motivated individuals who are interested in exploratory interdisciplinary research.

Interested candidates are requested to contact Dr. Sureshkumar Balasubramanian with their CV, a brief description of their PhD work and names and addresses of 2 referees. For further details please contact at mb.suresh@uq.edu.au. SKB lab can be browsed either at <http://www.uq.edu.au/~uqmsures> or <http://web.me.com/esskay1>.

Postdoctoral position in auxin regulated polarity and division planes

Utrecht University, Utrecht, The Netherlands

The Utrecht University-funded 2-year post-doctoral position is available in the newly established Dhonukshe lab within the Molecular Genetics Section of the Biology Department headed by Prof. Ben Scheres. The Dhonukshe group studies mechanisms driving auxin regulated cell polarity and cell division planes in *Arabidopsis*.

Our lab focuses on the subcellular mechanisms regulating polarity and division planes with a particular emphasis on the role of auxin. We have previously shown that impairment of auxin transport influences cell division planes (Dhonukshe et al. BMC Biology 2005). Recently, we have identified the mechanisms generating cell polarity (Dhonukshe et al., Nature 2008, Dhonukshe et al., Development 2010). The post-doctoral fellow is expected to follow up on this recent work using a combination of molecular cell biology, microscopy and genetics approaches. We are looking for a highly motivated candidate with a strong background in plant molecular biology or a related discipline, as demonstrated by

publications in international peer-reviewed journals.

Experience with plant molecular biology and genetics is obligatory. The project is well

designed based on exciting preliminary data sets and the candidate will have an opportunity to get grip on excellent microscopy and cell biology approaches.

The Dhonukshe lab (website under construction but for reference you can visit the website of the Molecular Genetics Section <http://www.bio.uu.nl/mg/pd>) is situated in the Molecular Genetics Section of the Utrecht University, and has direct access to state-of-the-art facilities for microscopy, molecular cell and developmental biology. Utrecht University offers a renowned international community of scientists in all disciplines of life sciences and interaction between the scientists working on plant and other model species is on a regular basis. Research in our section is embedded in the Graduate School of Experimental Plant Sciences and Graduate School of Developmental Biology those offer an attractive curriculum of courses and workshops.

The position is available immediately. Applications will be accepted until the position has been filled. Please send inquiries for information or your application, including motivation letter, CV and contact information for 2-3 references) to:

Dr. Pankaj Dhonukshe, E mail. P.B.Dhonukshe@uu.nl , Phone: +31-30-2534318

Postdoctoral Research Scientist Position

University of Louisiana, Lafayette
Biology Department
Lafayette, LA. USA

<http://www.AcademicKeys.com/r?job=27438&o=777137&t=SC110124m-8>

A 3 year Postdoctoral Research Scientist position is available for a newly funded NASA project concerning the gravisensing and response mechanisms in plants, which

includes a flight experiment on the Space Shuttle or equivalent orbiter.

The project studies the effect of high-gradient magnetic fields on directional plant growth.

Postdoctoral Fellow

Clafin University
Biology & Chemistry Departments
Orangeburg, SC, USA

<http://www.AcademicKeys.com/r?job=26412&o=777137&t=SC110124m-8>

The Postdoctoral Fellow will test the ability of a sample bank of peats, soybean hulls and rice hulls, to adsorb heavy metals and examine the bioremediation capacity of microbes associated with these materials.

Postdoctoral scholar: Molecular Biology/Gene Regulation

University of Oklahoma, Norman, Oklahoma, United States

I seek a motivated postdoctoral scholar to join our multifaceted study of grass-diverged aspects of cell wall synthesis and degradation

(<http://bomi.ou.edu/bartley/>). Various projects are available related to phenylpropanoid incorporation into grass cell walls, acyltransferase biochemistry, and regulation of cell wall remodeling. Experience with one or more of the following approaches is highly desirable: molecular genetics, molecular biology, bioinformatics, microscopy, high throughput gene expression studies, mass spectroscopy, and/or biochemistry. The position is available immediately with an appointment for a year, renewable by mutual agreement. Compensation will be commensurate with experience (35K+). Position includes health benefits. The research will be conducted in the Botany and Microbiology Department of the University of Oklahoma in Norman, OK, an affordable, mid-sized university town with a vibrant intellectual and cultural community close to Oklahoma City. Interested candidates should send a cover letter explaining interest in the position and career goals and a CV to Dr. Laura Bartley at lbartley@ou.edu.

New books



Annual Plant Reviews, Volume 41, Plant Polysaccharides: Biosynthesis and Bioengineering

Peter Ulvskov
ISBN: 978-1-4051-8172-3
Hardcover
504 pages
December 2010, Wiley-Blackwell
<http://eu.wiley.com/WileyCDA/WileyTitle/productCd-1405181729.html>

Plant Metabolism and Biotechnology

Hiroshi Ashihara (Editor), Alan Crozier (Co-Editor), Atsushi Komamine (Co-Editor)
ISBN: 978-0-470-74703-2
Hardcover
424 pages
March 2011
<http://eu.wiley.com/WileyCDA/WileyTitle/productCd-047074703X.html>

Genetics, Genomics and Breeding of Vegetable Brassicas

Editors: Jan Sadowski: Institute of Molecular Biology and Biotechnology, Adam Mickiewicz University, Poznan, Poland and Institute of Plant Genetics, Polish Academy of Sciences, Poznan, Poland. Chittaranjan Kole: Department of Genetics and Biochemistry, Clemson University, Clemson, SC, USA
ISBN 978-1-57808-706-8; January 2011; ca.450 pages incl. 9 color plates, 6 1/8" X 9 1/4", hc, Price: US \$ 139.95
ISBN: 9781578087068
CRC Press
<http://www.crcpress.com/product/isbn/9781578087068>

Genetics, Genomics, and Breeding of Soybean

Editor(s): Kristin Bilyeu, USDA-ARS, University of Missouri, Columbia, USA; Milind B. Ratnaparkhe, USDA-ARS, University of Missouri, Columbia, USA; Chittaranjan Kole, Clemson University, South Carolina, USA
Cat. #: N10274
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CRC Press
http://www.crcpress.com/product/isbn/9781578086818;jsessionid=X4-WQA-zfclExCcxYW73Iw**

What's New About Crop Plants: Novel Discoveries of the 21st Century

U. S. Gupta, Retired Adj Professor, University of Georgia, Athens, USA
Price: \$179.95
Cat. #: N10329
ISBN: 9781578086993
Publication Date: February 03, 2011
Binding: Hardback
CRC Press
<http://www.crcpress.com/product/isbn/9781578086993>

Growth and Mineral Nutrition of Field Crops, Third Edition

Nand Kumar Fageria, EMBRAPA, San Antonio de Goias, GO, Brazil; Virupax C. Baligar, USDA/ARS SPCL, Beltsville, MD, USA; Charles Allan Jones, Texas A&M University, Dallas, USA
Price: \$149.95
Cat. #: K10875
ISBN: 9781439816950
Publication Date: October 19, 2010
Binding: Hardback
CRC Press
<http://www.crcpress.com/product/isbn/9781439816950>

Handbook of Plant and Crop Stress, Third Edition

Editor(s): Mohammad Pessarakli, University of Arizona, Tucson, USA; Mohammad Pessarakli, University of Arizona, Tucson, USA
Price: \$199.95
Cat. #: K10719
ISBN: 9781439813966
Publication Date: November 16, 2010
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CRC Press
<http://www.crcpress.com/product/isbn/9781439813966>

Recent Advances in Plant Virology

Edited by: Carole Caranta, Miguel A. Aranda, Mark Tepfer and J.J. Lopez-Moya
ISBN: 978-1-904455-75-2
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Publication Date: February 2011
Cover: Hardback
More info:
<http://www.horizonpress.com/plant-virology>