



# FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY

## FESPB Newsletter

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## Letter from the new Secretary General

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**UNIVERSITY OF LEEDS**

Centre for Plant Sciences  
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5<sup>th</sup> of April, 2013

Dear Colleagues

It is my pleasure to write to you as the New Secretary General of FESPB. In addition to our President, Dr Bruce Osborne (Dublin, Ireland), we welcome our new FESPB treasurer, Dr Heinz Rennenberg (Freiburg, Germany) and our new Chair of the FESPB Grants and Awards Committee, Dr Laura De Gara (Rome, Italy). I would like to give my heartfelt thanks to Dr *Kalliopi (Popy) A. Roubelakis-Angelakis, (Heraklion, Greece), who recently stepped down as Secretary General, for her unswerving dedicated service to the FESPB community. I am very pleased that Popy has agreed to continue to undertake her excellent work for FESPB by assisting Executive Committee, particularly in maintaining and enriching the FESPB website. I would also like to thank Dr Karl-Josef Dietz (Bielefeld, Germany), who recently stepped down as FESPB treasurer for all his hard work in steadfastly keeping the FESPB accounts in good order. I am also very grateful for the continued support of Dr Dolores Rodríguez (Salamanca Spain) in her role as FESPB Publications officer on the FESPB Executive Committee. Her dedicated efforts bring the newsletters and other information to the FESPB community. Finally, I look forward to continue working to achieve common goals with the FESPB journals and the National Representatives and Representatives of the FESPB societies.*

Within the coming years Plant Biology will play an increasingly significant role in addressing the looming global challenges to food security and sustainable agriculture, and this is therefore a time of great opportunity for our community. It is my hope that our community will flourish in coming years, and that our new alliances with organizations such as EPSO and the Global Plant Council will grow increasingly stronger. It was recently my pleasure to send a message of congratulations on behalf of FESPB to Dr. Ruth Bastow, as she takes up her new role as Global Plant Council Executive Director.

Our recent agreement with EPSO means that in future we will jointly organize bi-annual conferences based as always on scientific excellence but also mindful of the need to address present and future state of the art directions in plant biology research and education. These joint FESPB-EPSO bi-annual conferences will cover plant biology in its broadest sense, encompassing topics such as agriculture, forestry, horticulture, ecology, and environmental biology and also include science policy and plant science-based societal issues. Our joint

conferences will welcome contributions from students, post-doctoral researchers, senior scientists and policy makers from across Europe and beyond.

I greatly value your membership of FESPB. The contribution of each member enriches the FESPB community, which unites and consolidates scientific excellence across Europe, strengthening capacity building activities in world leading plant science, and our ability to speak with one voice.

I would like to remind you that being part of the FESPB community brings many benefits to its members that are not available in other organisations. For information, I have listed some of the main benefits below:

- Equitability and equality;
- FESPB membership is based on fairness and not legal technicalities.
- Reduced fees at FESPB meetings.
- Access to travel grants to FESPB meetings.
- Access to full information of the website.
- Access to FESPB prizes and awards.
- Membership to Global Plant Council.

The FESPB Executive Committee is in the process of agreeing additional benefits to members, such as support of international meetings on important topics of Plant Biology, as well as other new supporting activities of FESPB. For example, in future years, we hope to make travel grants available to other international meetings.

I look forward to being with you all again at the "Plant Biology FESPB/EPSO2014", Congress" in Dublin.

Yours sincerely

A handwritten signature in black ink, appearing to read 'C. Foyer', written in a cursive style.

Christine Helen Foyer



The Federation  
of European Societies  
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## Research News



### Plant Organ Development Breakthrough

Source: ScienceDaily. Dec. 3, 2012.

Plants grow upward from a tip of undifferentiated tissue called the shoot apical meristem. As the tip extends, stem cells at the center of the meristem divide and increase in numbers. But the cells on the periphery differentiate to form plant organs, such as leaves and flowers. In between these two layers, a group of boundary cells go into a quiescent state and form a barrier that not only separates stem cells from differentiating

cells, but eventually forms the borders that separate the plant's organs.

Because each plant's form and shape is determined by organ formation and organ boundary creation, elucidating the underlying mechanisms that govern these functions could help scientists design the architecture of crop plants to better capture light and ultimately produce more crop yield with less input. New research from two teams led by Carnegie's Zhiyong Wang and Kathryn Barton focuses on the role of the crucial plant hormone

brassinosteroid in the creation of plant-shoot architecture.

Their work is published by Proceedings of the National Academy of Sciences during the week of December 3.

Like all organisms, plant growth and development is regulated by internally produced chemical signals, including hormones like brassinosteroid, which is found throughout the plant kingdom. The brassinosteroid signaling pathway is involved in regulating more than 1,000 plant genes. Mutant plants that are deficient in brassinosteroid that are grown in the dark show features of plants grown in the light. They also have defects at many phases of the plant life cycle, including reduced seed germination, dwarfism, and sterility.

The new study led by Wang and Barton uncovered yet another role of brassinosteroid: the formation of boundaries between organs. Plants made hypersensitive to brassinosteroid displayed fused organs. The team included lead author's Carnegie's Joshua Gendron and Jiang-Shu Liu, as well as Min Fan, Mingyi Bai, and Stephan Wenkel, from Carnegie, and Patricia Springer from the University of California Riverside. Their investigations showed that activation of the brassinosteroid pathway represses a group of genes called the cup-shaped cotyledon, or CUC family, which is responsible for organ boundary formation. Using sophisticated techniques the team demonstrated that the protein in the brassinosteroid pathway that is responsible for binding to DNA and, in this case, for inhibiting CUC genes, is present at high levels in the meristem's undifferentiated stem cells and developing organ primordia, but very low in the boundary cells, suggesting that different levels of brassinosteroid activity contribute to the opposite growth behavior of these three types of cells.

"This work links the plant steroids to growth and development, organ boundary

development, providing a link between the physiology of the plant and its architectural design," Wang and Barton said.

Journal Reference: J. M. Gendron, J.-S. Liu, M. Fan, M.-Y. Bai, S. Wenkel, P. S. Springer, M. K. Barton, Z.-Y. Wang. Brassinosteroids regulate organ boundary formation in the shoot apical meristem of Arabidopsis. Proceedings of the National Academy of Sciences, 2012; DOI: 10.1073/pnas.1210799110

### **Fighting Microbes with Microbes**

By Amy Coombs. Source: The Scientist. January 1, 2013

Doctors turn to good microbes to fight disease. Will the same strategy work with crops?

Like humans, with their complement of microbes that aid in everything from immune responses to nutrition, plants rely on a vast array of bacteria and fungi for health and defense. Over the last decade, research has revealed many new functional aspects of the crosstalk between human-associated microbes and human cells, but plant biologists are only beginning to scratch the surface of the often surprising ways that soil microbiota impact plants, from underground fungus-wired alarm systems to soil bacteria that can trigger defensive plant behavior or even act as a sort of vaccine. But despite these benefits, microbes are still primarily thought of as harbingers of disease.

"Since the discovery of antibiotics, medical research has been dominated by a 'bazooka mentality,'" and so has agricultural research, says Alexandre Jousset, a plant scientist at the Georg-August University in Göttingen, Germany. "Traditionally, microbes have been viewed negatively, and focus has been placed on eradication." Today, scientists and some medical doctors are becoming increasingly aware of their utility, and botanical researchers have also begun to debate whether the same may be true of plants.

While the Human Microbiome Project has discovered that some 10,000 species of microorganisms live in and on the human body, outnumbering our own cells by ten to one, plant scientists have found that any given soil sample contains more than 30,000 taxonomic varieties of microbes. Soil microflora not only provide nutrients for plants, but also suppress disease. In exchange, roots secrete fixed carbon into the soil and feed their bacterial symbionts.

Although the medical community now warns that overprescribing antibiotics kills beneficial organisms and encourages the formation of resistant strains, a similar change in opinion has not occurred in agriculture, where a kill-all approach to plant pathogens has given rise to biocides that indiscriminately wipe out the beneficial along with the pathogenic. “Biocides can nuke the soil, but they never kill everything,” says Mike Cohen, a biologist at Sonoma State University in California. “This creates a biological vacuum that becomes filled by opportunistic survivors and organisms from the surrounding soil.” Biocides create a strong selective pressure: the few pathogens that survive face little competition and proliferate, giving rise to pathogenic communities that can evade standard treatments.

Beneficial soil organisms, however, can protect plants more selectively than biocides do. They displace pathogens and produce toxins that kill pathogenic microbes, and they also trigger plants’ own defense mechanisms. “Native bacteria are the first and most powerful barrier to prevent the establishment of pathogens,” says Jousset. “A diverse community is especially important to keeping pathogens away—this is true in the human gut and in the soil.”

“The idea is that we can reduce pesticide and fungicide use by utilizing the microbiome,” says Harsh Bais, a plant biologist at the University of Delaware in Newark. “But we

need to know more about the mechanisms of action; relationships between microbes and plants are very complex.”

According to a recent study published in PLOS One, underground networks of fungi help tomato plants “eavesdrop” on the alarm signals produced by their neighbors. Even when plants are not able to communicate with chemical cues released through their leaves, they can link up and share vital information under the soil.

Researchers at South China Agricultural University in Guangzhou inoculated tomato plant leaves with the early blight fungus *Alternaria solani*, which creates brown and dead patches on leaves and can rot the tomato fruit. They then covered all research plants with airtight plastic bags, which prevented the transmission of airborne signals. Despite being covered, the tomato plants were able to communicate. Uninoculated plants growing several feet away activated defense-related genes and started making disease-fighting enzymes.

Researchers traced communication back to the fungus *Glomus mosseae*, which forms a symbiotic relationship with plant root hair known as a mycorrhizal network by inserting itself into the root cell’s membrane. Bagged tomato plants grown in soil that lacked this underground network were unable to receive the “activate-defenses!” signal from infected neighbors and did not produce disease-fighting compounds. In contrast, in soils containing *Glomus mosseae*, uninfected plants detected the warning signs of disease and produced higher levels of six defense-related enzymes, including peroxidase (POD), polyphenol oxidase (PPO), chitinase,  $\beta$ -1,3-glucanase, phenylalanine ammonia-lyase (PAL), and lipoxygenase (LOX). (See diagram below.)

Because the mycorrhizal network can extend from one set of plant roots to another, it’s possible that the network of fungal mycelia

acts like telephone wires, allowing the plants to communicate underground. If this hypothesis is proven by identifying compounds that relay the chemical signal through the fungi, it might be possible to prevent plant disease by cultivating an appropriate mix of microbes in the soil. “The problem is that we don’t know how plants and microbes select one another,” says Bais.

To try to answer that question, Bais and his colleagues turned to *Arabidopsis thaliana* plants and *Bacillus subtilis*, a bacterium known to improve plant health. Despite the plant’s antimicrobial defenses, *B. subtilis* somehow becomes established in the soil. The team found that *B. subtilis* secretes an antimicrobial peptide that temporarily suppresses toxins secreted by the root, allowing the beneficial bacterium to colonize the soil around the roots. The peptide secreted by *B. subtilis* may also help ward off soil-borne pathogens while the plant’s defenses are compromised, says Bais.

In a prior study, Bais and his colleagues found that plants can pick and choose the beneficial bacteria species recruited during pathogen attacks. The team infected *Arabidopsis* seedlings with the bacterium *Pseudomonas syringae* pv. tomato, which causes bacterial speck—a major disease of tomato crops. Plant roots soon began secreting L-malic acid, a food source for *B. subtilis*. As a result, *B. subtilis* colonized the roots, which in turn triggered production of the plant’s defense chemical salicylic acid, helping it fight the bacterial infection. “This isn’t a typical symbiotic relationship,” Bais says, “but there is an interesting reciprocity here.” (See diagram below.)

Plants may even be able to recruit different bacterial species as their need for food and water changes. Researchers from Ain Shams University in Cairo, Egypt, recently dissected the root systems of drought-sensitive pepper plants (*Capsicum annuum*) grown with varying

amounts of water. After comparing the structure and diversity of bacterial communities in the rhizosphere, the team found that plants grown in the desert with little water have larger populations of plant growth-promoting (PGB) bacteria which can enhance photosynthesis and biomass synthesis by as much as 40 percent under drought stress. Although PGB’s mechanism of action has not been worked out, the bacteria are known to alleviate salt stress by reducing the production of ethylene in tomato seedlings.

Surprisingly, there is some evidence that the effects of beneficial bacteria can endure across generations. Even after a bacterial community wanes, the biochemical pathways developed by the plants in response to bacterial colonization remain intact. “This suggests the bacteria function as a vaccine of sorts,” says Bais. This heightened disease response can then be passed to the next generation of plants. For example, even when progeny are not exposed to *B. subtilis*, they are better able to fight disease if parent plants fostered a relationship with the bacterium. “The bacteria help prime the plant to respond more quickly to disease, and they pass this memory to the next generation,” says Bais. The effects appear to last the duration of the offspring plant’s life, but are not passed on to a third generation.

Although most microorganisms that are beneficial to plants reside in the soil, their effects are not always localized to the roots. In a third study, published in *The Plant Journal*, Bais and his colleagues showed that beneficial soil microbes encourage the closure of stomatal pores in the leaves of *Arabidopsis* plants. Stomata allow carbon dioxide to diffuse into the leaf and release expired oxygen and water into the air. Hot and dry conditions are known to trigger stomatal closure to preserve a plant’s water, but Bais was the first to show that soil bacteria can

trigger the response—an important finding, as some pathogenic bacteria, such as *P. syringae* pv. tomato, enter the plant through the stomata.

To see if root microbes could help counteract already established plant infections, Bais and his colleagues grew plants infested with *P. syringae* and then inoculated the soil with the beneficial *B. subtilis*. As the roots recruited new colonies of *B. subtilis*, the plants began producing abscisic acid—a chemical known to regulate stomatal closure. After three hours, only 43 percent of stomata were open in *B. subtilis*-treated plants. In control groups, 56 percent of stomata remained open. “This difference was significant and helped reduce disease,” says Bais.

It’s much harder for pathogens to take over the human gut when beneficial microflora coat its surface. A similar mechanism is at play in the soil. When it comes to preventing plant disease, some microbes kill pathogens directly; others consume resources, taking up the niches that invading bacteria might otherwise inhabit.

“When a community is composed of species that use distinct resources, there is less free room for invading species,” says Jousset. He and his colleagues set out to determine whether a broader genetic diversity of beneficial bacterial strains was more important than simply cultivating a large variety of bacteria, regardless of their genetic makeup.

The researchers grew 95 microbial communities, each containing between one and eight strains of *Pseudomonas fluorescens* bacteria—another species known to improve plant health. Each group had varying degrees of genetic similarity. The team then exposed the colonies to the invading bacterial species *Serratia liquefaciens*, which colonizes soil, water, and even the human gut and urinary tract, where pathogenic strains cause infection. After 36 hours, *S. liquefaciens* was

able to invade communities that contained genetically similar species, but it was not able to gain a foothold in more genetically diverse communities. Indeed, as genotypic dissimilarity increased threefold, researchers saw a linear decrease in the colonization by *S. liquefaciens*.

However, the number of beneficial species in the soil was nearly as important as the degree of genetic dissimilarity between them. Communities with four to six species were better able to ward off invasion. Interestingly, communities were more susceptible to invasion by *S. liquefaciens* when a lower or higher number of bacterial species was present. Most likely, says Jousset, this is due to the variety of toxins produced. The colonies containing too many species produced a large amount of toxins, some of which also harmed beneficial strains of bacteria, whereas communities with too few species had low levels of toxin production, thus making invasion more likely.

“This suggests we might be able to encourage disease-fighting bacterial communities by selecting for the right number and combination of species,” says Jousset. Like the gut, the soil is an open system that allows bacteria to come and go, and competition for food and nutrients determines community structure. By manipulating food sources and growing conditions in the soil, it may be possible to select for genetically diverse communities. In a recent field study, Jousset sampled the disease-fighting genes found in the soil and discovered that a diverse mixture of planted herbs and grasses gives rise to the best ratio of disease-fighting genes and helps suppress soil-born pathogens. (See “Down and Dirty,” *The Scientist*, September 2012.)

Just as antibiotics indiscriminately kill both good and bad bacteria in the gut, fungicides and biocides impede the soil’s innate defenses. Studies have shown that gentler practices such as crop rotation, tillage, and

fertilization can influence ecological processes in the soil, and may encourage the establishment of microbial communities capable of suppressing disease.

In search of a way to supplement the soil that encourages the growth of beneficial bacteria, Mike Cohen of Sonoma State University joined colleagues at the US Department of Agriculture to test rapeseed (*Brassica napus*) meal—a waste product from processing rapeseed into cooking oil or biodiesel.

The researchers split the roots of an apple tree seedling so that the plant had roots potted in two different containers. They then introduced the pathogen *Rhizoctonia solani*, which causes root rot, into one container. Rapeseed meal was incorporated into the soil of the other container at about 0.5 percent of the total volume, whereas the soil inoculated with the pathogen was left untreated. “This allowed us to test the indirect impacts of seed meal on the plant,” says Cohen.

The rapeseed meal reduced root rot by about 50 percent relative to control groups grown without the treatment. In fact, the researchers observed that the entire plant benefited from the rapeseed meal even though only half of the roots were exposed. Cohen and colleagues think that rapeseed meal fosters colonization by species of beneficial *Streptomyces*, known to trigger systemic defenses in plants. There were 10 times as many *Streptomyces* bacteria in soils amended by rapeseed meal, a finding that was later corroborated by field trials.

Indeed, when the researchers directly inoculated the split-root soil with *Streptomyces* instead of rapeseed meal, they found that *Streptomyces* encouraged plant defenses much as the seed meal did. “We can’t say for sure how *Streptomyces* benefit the plant,” says Cohen, “but some evidence indicates it’s related to induction of the jasmonic acid signaling pathway,” a hormonal signaling system that triggers plant defenses.

(See “How Plants Feel,” *The Scientist*, December 2012.)

Unfortunately, seed meal can also nourish pathogenic organisms. In some studies, disease-causing microbes proliferated in soils treated with seed meal. However, combining seed meals from mustard, rapeseed, and other plants can help minimize the growth of pathogenic microbes, says Cohen. This is because seed meals contain glucosinolates—chemicals that release pathogen-killing fumigants as they break down in water. As the chemicals released by rapeseed may be slightly different than those of mustard seed, “seed meals are more promising when used in combination,” says Cohen. “One seed meal might target a pathogen, while another will help build beneficial communities of *Streptomyces*.”

As gastroenterologists are now reporting the efficacy of transplanting gut bacteria from healthy individuals into human patients suffering from intestinal inflammation and infection, plant researchers may also find that multiple treatments with different concoctions of beneficial microorganisms will have a great impact on soil ecology. Even if one species doesn’t curtail a pathogen, a full remake of the microbial community might help kick the problem. The goal is to gradually build the soil over time to establish a favorable microbial ecosystem. In rich, healthy soil, the microbial community may be more resistant to disease.

Researchers are now turning to field experiments to test the best combinations of species, and treatments like seed meal are already being used on organic farms in Northern California. If greater microbial diversity improves plant health in large-scale field trials, it could eventually help reduce chemical loads on industrial farms. “It might not work exactly the same way in the gut, but the mechanisms in the soil are very similar,” says Jousset. “If we can protect and cultivate

the soil microbiome rather than kill important species, we might need fewer chemicals in the field.”

### **The state of play: genetically modified rice**

Source: International Rice Research Institute (IRRI), by Adam Barclay and Sophie Clayton. 08 January 2013.

People often argue passionately for or against genetically modified (GM) crops. Rice Today’s aim here is not to take sides in a debate that has often generated more heat than light, but rather to look at the facts—what is actually happening in relation to GM rice with a separate focus on work underway at the International Rice Research Institute (IRRI).

GM crops have been grown commercially since the 1990s. The global coverage of GM crops in 2011 was 160 million hectares in 29 countries reports the International Service for the Acquisition of Agri-biotech Applications. And, they predict that, by 2015, at least 20 million farmers in more than 40 countries will be using the products of biotechnology, including GM crops, on around 200 million hectares.

This article specifically focuses on GM rice—that is, rice that has had a gene or genes from another species or rice variety introduced into its genome using modern biotechnology techniques. This GM rice exhibits the traits conferred by the introduced gene or genes.

As of December 2012, commercialized GM rice had not yet become a reality—which means, farmers aren’t growing it and consumers can’t eat it yet.

The GM Crop Database of the Center for Environmental Risk Assessment shows that two GM rice varieties (LLRice60 and LLRice62, both with herbicide resistance) were approved in the United States in 2000. Subsequent approval of these and other types of herbicide-resistant GM rice occurred across Canada, Australia, Mexico, and Colombia.

However, none of these approvals resulted in commercialization.

In 2009, China granted biosafety approval to GM rice with pest resistance, but no commercial rollout has taken place.

Nevertheless, R&D on GM rice continues to advance in both the public and private sector around the world. GMO Compass notes that Argentina, Australia, Brazil, China, France, India, Indonesia, Italy, Iran, Japan, Mexico, the Philippines, Spain, and the United States have all been involved with GM rice. Bangladesh and South Korea are also engaged in research on GM rice.

Researchers are working on GM rice with higher yield; increased resistance to pests, diseases, and herbicide; better tolerance of drought and salinity; improved nutritional value and health benefits; and higher nitrogen-use efficiency.

IRRI’s approach to its GM rice R&D is based on a premise that genetic modification has the potential to safely deliver to rice farmers and consumers a number of benefits that cannot be achieved through other breeding methods. Genetic modification is used as a research tool—to understand gene function—even when there is no intention to develop a GM rice variety, and to develop new GM varieties with added beneficial traits that cannot be found within the rice gene pool.

“Compared with other major crops such as corn (maize) or wheat, rice has an extraordinarily diverse genetic resource base that spreads across at least 24 different species of rice,” explains Dr. Eero Nissilä, head of IRRI’s Plant Breeding, Genetics, and Biotechnology Division. “This means there is already a very large pool of useful rice genes that breeders can use to develop new varieties of rice with improved traits.

“In fact, less than 5% of our rice breeding focuses on delivering GM rice varieties,” he adds.

The best-known and most advanced example of IRRI's research on GM rice is that of Golden Rice. Unlike other rice, this contains beta carotene—a source of vitamin A (See Golden grains for better nutrition).

By working with a mix of leading agricultural and health organizations, IRRI is helping to further develop and evaluate Golden Rice as a potential new way to help address vitamin-A deficiency. Work on Golden Rice is most advanced in the Philippines, where it is led nationally by Dr. Antonio Alfonso of the Philippine Rice Research Institute.

"We've completed some initial field tests in different locations to evaluate and select breeding lines that potentially would meet farmers' and consumers' expectations, to see how Golden Rice grows in different environments, and to compare any environmental impacts of Golden Rice with those of other rice varieties," said Dr. Alfonso.

#### Turbocharged C4 rice

IRRI's most ambitious attempt to genetically modify rice is its C4 rice project. The project, which brings together a mix of international partners, is attempting to make rice much better at photosynthesis, the process of turning sunlight into grain (see New rice plant could ease threat of hunger for poor).

Rice uses a C3 photosynthetic pathway, which is much less efficient than plants such as maize that use a C4 pathway. Rice already has all the components required for C4 photosynthesis, but they are distributed "differently" within rice cells. By rearranging the photosynthetic structures within the leaves using genetic modification, it is theoretically possible to switch rice over to C4 photosynthesis—potentially increasing productivity by 50%.

In 2012, the C4 rice project got an injection of financial support valued at US\$14 million over 3 years from the Bill & Melinda Gates Foundation, the UK government, and directly from IRRI.

"This is exactly the sort of innovative scientific research that the [UK] Prime Minister was calling for at the Hunger Summit at Downing Street," said Lynne Featherstone, UK Parliamentary undersecretary of state for international development. "This new funding will enable IRRI to begin producing prototypes of this 'super rice' for testing. This could prove a critical breakthrough in feeding an ever-growing number of hungry mouths."

The research still has a long way to go, but the scientists have already identified crucial genes needed to assemble C4 photosynthesis in rice, and they now aim to produce C4 rice prototypes for testing.

#### Iron-clad rice

IRRI senior scientist Dr. Inez Slamet-Loedin is leading two other projects on GM rice. Like Golden Rice, the first of these aims to combat the problem of "hidden hunger," or micronutrient malnutrition, worldwide.

Dr. Slamet-Loedin and her team are developing iron-rich rice. This has the potential to prevent the iron-deficiency anemia that afflicts more than 1 billion people globally, particularly poor women and children (see Iron-clad rice, *Rice Today*, Vol. 10, No. 3). Iron deficiency and iron-deficiency anemia contribute to increased maternal mortality, stifle children's cognitive and physical development, and reduce people's energy.

In its experimental work, IRRI has added two genes to the popular rice variety IR64. One of these is a gene named "ferritin" from soybean, which codes for iron storage. Rice has its own ferritin gene, but adding another increases the plant's iron storage capacity. Ferritin from soybeans is a major source of iron for vegetarians. Crucially, it provides iron that is highly bioavailable—that is, can be easily absorbed and used by the body. The other gene, which comes from another rice variety, helps transport iron to the grain.

"Adding a ferritin gene will increase iron-storage capacity," explains Dr. Slamet-Loedin,

“but you also need to increase the amount of bioavailable iron reaching the grain—hence, the need for the transporter gene, which allows iron in the leaf, where it is abundant, to be moved to the grain, the part of the rice that is eaten.”

As a bonus, she says, the use of a transporter gene will also increase zinc in the grain. In 2012, IRRI and the Colombia-based International Center for Tropical Agriculture (CIAT) each performed the first confined field trials of iron-rich GM rice outside of Japan, to look at iron content in the grain and to check the performance of rice in different conditions.

Non-GM rice varieties that are relatively high in iron have concentrations of 5–8 parts per million. Dr. Slamet-Loedin’s team targets an iron concentration of 13–14.5 parts per million in rice grain. Given average rice consumption, this could provide 30% of women’s and children’s estimated iron requirements. Early trials at IRRI revealed an iron content of 11–13 ppm, on the cusp of the target.

Further growing, bioavailability, and food and environmental safety tests are still needed as the team works toward iron-clad rice.

#### Confirming gene function

Dr. Nissilä explains that one of the most important uses of genetic modification at IRRI is in identifying useful genes and confirming the trait they are responsible for. By using genetic modification, researchers can take a rice gene that they suspect may be responsible for a favorable trait, and insert it into another rice plant to see whether the trait of interest is also transferred. If it is, then they know that is the gene they want to target in their conventional breeding programs—which will result in a regular, non-GM rice variety that includes the beneficial gene and associated trait.

For example, IRRI used genetic modification to confirm the major gene responsible for

phosphorus uptake—PSTOL1. However, the original rice plant with the PSTOL1 gene was not genetically modified and future varieties bred to include the PSTOL1 gene will not be GM.

#### Drought-hardy rice

Dr. Slamet-Loedin is also leading IRRI’s efforts to identify useful drought-tolerance genes that could lead to the development of either GM or non-GM drought-tolerant rice varieties (see *Overcoming the toughest stress in rice: drought*, Rice Today Vol. 8, No. 3). This is more challenging than nutrient-enriched rice because drought itself is complex as well as the way it affects rice crops.

For example, any new variety must be tested in drought conditions of varying severity and length, and at different times during the growing season (drought hitting during the reproductive stage of rice tends to have the worst impact), as well as in different soil types. Furthermore, any new drought-tolerant variety needs to perform well in nondrought conditions too. This project has support from Japan’s Ministry of Agriculture, Forestry, and Fisheries and is a joint effort among the Japan International Research Center for Agricultural Sciences (JIRCAS), which has provided funding; RIKEN, a large public research organization in Japan; and CIAT, which is helping with testing. Promising GM breeding lines with improved drought tolerance have already been developed. Some of these lines include extra rice genes and some have genes from a tiny plant called Arabidopsis. Over the past few years, the performance of these lines has been tested in drought conditions using screenhouses. In 2011 and 2012, it was time to move the testing outdoors and IRRI and CIAT completed confined field tests of the lines at rainfed lowland sites in the Philippines and upland sites in Colombia, respectively. Dr. Slamet-Loedin says that to get a rice variety that tolerates drought at different stages during its life cycle as well as different

types of drought, “stacking” all the genes for drought tolerance into a single variety could get the best results.

The intention of IRRI’s current research on GM rice is that, one day, new GM lines will be passed on to researchers in national agencies for further development and, if approved, eventually to farmers and consumers.

Alongside the development of this research goes training in biotechnology and genetic modification techniques for rice scientists. This gives them specialized skills to conduct biotechnology research and to build up their expertise and understanding of the area, so that they can respond research opportunities back in their home countries and institutes, and meet their own local needs.

In September 2012, IRRI ran the “Advanced Indica Rice Transformation Course”—the first time ever that the Institute provided training on the genetic modification of rice. Indica rice—the rice most widely produced in South and Southeast Asia—is a broad group of many different types of rice that are usually grown in hot climates.

Nine public- and private-sector participants attended the training from China, Colombia, India, Indonesia, Nepal, the Philippines, and the U.S. They got hands-on experience and learned about biosafety issues and international guidelines for biosafety management in research.

Says one of the trainees, Ms. Ritushree Jain, an Indian national who is doing her PhD at the University of Leeds in the UK, “After this training, I hope that I will be able to make a construct and put some genes into rice plants and especially in indica varieties, which are more susceptible to drought and nematodes. A lot of rice cultivation is affected by drought stress and nematode infestation and these are big problems.

“My hope is that I will be able to find some genes to integrate into Indian rice varieties

and develop something new that will help,” she adds.

### **Population genomic and genome-wide association studies of agroclimatic traits in sorghum**

Morris et al. PNAS January 8, 2013 vol. 110 no. 2 453-458

Accelerating crop improvement in sorghum, a staple food for people in semiarid regions across the developing world, is key to ensuring global food security in the context of climate change. To facilitate gene discovery and molecular breeding in sorghum, we have characterized 265,000 single nucleotide polymorphisms (SNPs) in 971 worldwide accessions that have adapted to diverse agroclimatic conditions. Using this genome-wide SNP map, we have characterized population structure with respect to geographic origin and morphological type and identified patterns of ancient crop diffusion to diverse agroclimatic regions across Africa and Asia. To better understand the genomic patterns of diversification in sorghum, we quantified variation in nucleotide diversity, linkage disequilibrium, and recombination rates across the genome. Analyzing nucleotide diversity in landraces, we find evidence of selective sweeps around starch metabolism genes, whereas in landrace-derived introgression lines, we find introgressions around known height and maturity loci. To identify additional loci underlying variation in major agroclimatic traits, we performed genome-wide association studies (GWAS) on plant height components and inflorescence architecture. GWAS maps several classical loci for plant height, candidate genes for inflorescence architecture. Finally, we trace the independent spread of multiple haplotypes carrying alleles for short stature or long inflorescence branches. This genome-wide map of SNP variation in sorghum provides a basis for crop improvement

through marker-assisted breeding and genomic selection.

### **Lower Nitrogen Losses With Perennial Biofuel Crops**

Source: ScienceDaily. Jan. 10, 2013

Perennial biofuel crops such as miscanthus, whose high yields have led them to be considered an eventual alternative to corn in producing ethanol, are now shown to have another beneficial characteristic -- the ability to reduce the escape of nitrogen in the environment. In a 4-year University of Illinois study that compared miscanthus, switchgrass, and mixed prairie species to typical corn-corn-soybean rotations, each of the perennial crops were highly efficient at reducing nitrogen losses, with miscanthus having the greatest yield.

"Our results clearly demonstrate that environmental nitrogen fluxes from row-crop agriculture can be greatly reduced after the establishment of perennial biofuel crops," said U of I postdoctoral research associate Candice Smith. "Because of the establishment variability, we were able to compare annual row crops with perennial crops. Although in the first two years, nitrate leaching remained high in the non-established miscanthus crop, once a dense, productive crop was established in the second year of growth, nitrate leaching in tile drainage quickly decreased."

Smith said that this ability to reduce the loss of nitrogen into the environment will prove to be greatly beneficial.

"Intensive corn production with large fertilizer inputs leads to large losses of nitrogen into the environment, both through gas emissions of nitrous oxide and leaching of nitrate to surface waters through tile drainage systems," added Mark David, U of I biogeochemist. "Nitrous oxide is a greenhouse gas, and nitrate can contaminate drinking water supplies and leads to coastal ocean problems. The hypoxic zone that forms each summer in the Gulf of

Mexico is a result of nitrate leaching from the tile-drained Corn Belt of the midwestern United States -- a likely location for biofuel production," he said.

In the study, funded by the Energy Biosciences Institute, miscanthus, switchgrass, and mixed prairie species were compared against a typical corn-corn-soybean rotation. Harvested biomass and nitrogen, nitrous oxide emissions, and nitrate leaching in the mid-soil profile and through tile drainage lines were all measured.

The researchers found that the perennial crops quickly reduced nitrate leaching in the mid-soil profile as well as from tile lines. "By year four each of the perennial crops had small losses," Smith said. "Nitrous oxide emissions also were much smaller in the perennial crops--including switchgrass, which was fertilized with nitrogen, while prairie and miscanthus were not. Overall, nitrogen levels were higher for the corn and soybean treatment as well as switchgrass, but were lower for prairie and miscanthus. Prairie and miscanthus levels were lower due to harvest of the plant biomass (and nitrogen) each winter, with no fertilizer nitrogen additions to replace it, as occurred in corn and switchgrass," she said.

David added that the miscanthus and mixed prairie also had very wide carbon-to-nitrogen ratios in the harvested material -- as much as 257 to 1 for miscanthus. "Miscanthus efficiently moved nitrogen from leaves to root and rhizome systems after the growing season, where it could be used again the next year," David said. "The lower nitrogen level suggests that the small amount of nitrogen removed by harvest in prairie and miscanthus came from the large pool of soil nitrogen and/or nitrogen fixation. If the soil is the source, this could lead to depletion of this resource without fertilization. If microbial fixation supplied the nitrogen, this would be a more sustainable input," he said.

David said that although more research is needed to fully understand the nitrogen cycle in these new and exciting biofuel crops such as miscanthus, results from this study clearly show these crops have the potential to quickly and greatly reduce nitrogen losses that have important environmental effects, while providing a large biomass harvest.

"Reduced Nitrogen Losses after Conversion of Row Crop Agriculture to Perennial Biofuel Crops" was published in an issue of the *Journal of Environmental Quality*. In addition to Smith and David, Corey Mitchell, Michael Masters, Kristina Anderson-Teixeira, Carl Bernacchi, and Evan DeLucia contributed to the research.

Journal Reference: Candice M. Smith, Mark B. David, Corey A. Mitchell, Michael D. Masters, Kristina J. Anderson-Teixeira, Carl J. Bernacchi, Evan H. DeLucia. Reduced Nitrogen Losses after Conversion of Row Crop Agriculture to Perennial Biofuel Crops. *Journal of Environment Quality*, 2013; 42 (1): 219 DOI: 10.2134/jeq2012.0210

### **Amino Acid Studies May Aid Battle Against Citrus Greening Disease**

Source: ScienceDaily. Jan. 14, 2013.

Amino acids in orange juice might reveal secrets to the successful attack strategy of the plant pathogen that causes citrus greening disease, also known as Huanglongbing or HLB. Studies of these amino acids by U.S. Department of Agriculture (USDA) chemist Andrew P. Breksa III and University of California-Davis professor Carolyn M. Slupsky may pave the way to a safe, effective, environmentally friendly approach to undermine *Candidatus Liberibacter asiaticus*, the microbial culprit behind HLB.

For a 2012 study in the *Journal of Proteome Research*, the scientists used nuclear magnetic resonance spectroscopy to study the amino acid composition of juice from oranges grown on HLB-positive or HLB-negative trees. Their

investigation is apparently the first to use this technology for that purpose, according to the researchers.

The study yielded distinctive profiles of the kinds and amounts of 11 different amino acids in three types of oranges: fruit from healthy trees; symptom-free fruit from HLB-positive trees; and fruit, with HLB symptoms, from HLB-positive trees.

With further research, the profiles may prove to be a reliable, rapid and early indicator of the presence of the HLB pathogen in an orchard, according to Breksa. He is with the Agricultural Research Service (ARS) Western Regional Research Center in Albany, Calif. ARS is the USDA's chief intramural scientific research agency, and this research supports the USDA priority of promoting international food security.

Breksa also noted that the profiles may reveal clues to mechanisms underlying the microbe's mostly unknown mode of attack. For instance, if the HLB pathogen were causing havoc with the trees' ability to create, use and recycle amino acids, scientists might be able to use that information as a starting point for a counterattack strategy.

Phenylalanine may be a case in point. An orange tree can convert this amino acid into cinnamic acid, a precursor to compounds thought to be important to the tree's defense system. But the researchers found that juice squeezed from oranges of HLB-positive trees had significantly higher concentrations of phenylalanine, which suggests that the HLB pathogen may have interfered with the tree's conversion of phenylalanine to cinnamic acid.

Journal Reference: Anne M. Slisz, Andrew P. Breksa, Darya O. Mishchuk, Greg McCollum, Carolyn M. Slupsky. Metabolomic Analysis of Citrus Infection by 'CandidatusLiberibacter' Reveals Insight into Pathogenicity. *Journal of Proteome Research*, 2012; 11 (8): 4223 DOI: 10.1021/pr300350x

## **Fortified by Global Warming, Deadly Fungus Poisons Corn Crops, Causes Cancer**

By Mollie Bloudoff-Indelicato. Scientific American. January 15, 2013

A carcinogenic mold, its growth exacerbated by the warming climate, reached record highs in 2012.

Last year's drought increased the spread of a carcinogenic mold called aspergillus (*Aspergillus flavus*), a fungal pathogen that poisons cattle, kills pets and has infected the 2012 corn crop, rendering significant portions of the harvest unfit for consumption.

Whereas the deadly organism mainly affects countries like China and developing African nations, many U.S. states have experienced an increase in corn contamination since 2011. Farmers are likely to see more of the carcinogen as temperatures continue to rise and droughts become more frequent.

"It's really a climate variable issue," says Barbara Stinson, founding and senior partner of Meridian Institute, a public policy organization. "We're probably looking at an increase in aflatoxin as a result of that."

*A. flavus* releases toxic spores that can be fatal when ingested, prompting symptoms that include jaundice, liver cancer and internal bleeding. The poison is so deadly that in 1995 Iraqi dictator Saddam Hussein confessed to weaponizing the mold spores for use in biological warfare. The high toxicity of the mold means crops with more than 20 parts per billion—the equivalent of about 100 kernels in a truckload of corn—can't cross state lines, says Ronnie Heiniger, professor of cropping systems at North Carolina State University.

That's bad news for the agricultural industry, which suffers annual losses of more than \$190 million due to aspergillus. Last year the green-black mold contaminated more than half the corn harvested in Missouri by October. In contrast, only 8 percent of the 2011 crop

suffered, according to the Missouri Grain Inspection Service.

"We have a big aflatoxin problem," says Charles Woloshuk, a botanist and plant pathologist at Purdue University. "There are loads of corn coming to the [grain] elevators that have been rejected."

Grains like corn and cereals are well documented hosts of aspergillus, although the fungus is also found in oilseed, spices, tree nuts, groundnuts, milk, meat and dried fruit—all staples on which a significant portion of the world's population rely for sustenance. Drought conditions don't cause the mold, but they do help speed its expansion. Unlike the fuzzy stuff that grows on bathroom tiles or in the back of the garage, *A. flavus* prefers hot, dry climes—precisely like the drought afflicting more than half the U.S.

Although the international community has adopted strict legislation to regulate the acceptable amount of aflatoxin for individual countries, cases of poisoning, called aflatoxicosis, still surface regularly. Because the level of aflatoxins found in any given load of corn can be higher than the legal maximum, farmers are allowed to mix contaminated corn with safe corn to dilute the amount—but sometimes contaminants slip through the cracks.

"That's always the problem with a contaminant at these low levels—the distribution of that contaminant in that load," Heiniger says. "The detection of these contaminants is almost more of an art than a science because you're searching for this one little kernel." He adds, "If you selected one bite from that whole area and happened to hit that one kernel you'd get the contaminant."

Aflatoxin contamination is a global food security issue, but it's especially a problem in developing countries, which are often largely populated by subsistence farmers who don't have the resources, technology or infrastructure needed for adequate grain

testing. Lack of education about the effects of the mold also contributes to aflatoxicosis poisoning.

“The average person can’t tell whether the mold contains aflatoxin. You can’t tell if it’s highly toxic or an innocuous fungus,” Stinson says. “So people are used to eating it and don’t know that they’re poisoning themselves or their children.”

To make matters worse, aflatoxins react strongly to the hepatitis B virus (HBV), the most common cause of liver cancer in the world. In countries where HBV is endemic, such as in China and some African nations, ingesting the mold intensifies and speeds liver failure by acting as an immunosuppressant. Consequently, there are over 750,000 new reported cases of primary liver cancer reported yearly worldwide, making it the sixth most common cancer for humankind, according to 2008 statistics from the World Cancer Research Fund International.

The cost in human life is likely due, in part, to international trade issues. Because aspergillus standards in developed countries are so high, African nations export much of their pure commodities overseas, leaving the tainted crops at home for consumption by locals. Natural disasters that increase foreign demand for African products—like floods and droughts in industrialized countries—only compound the issue.

Researchers at the University of Pittsburgh (Pitt) estimate more than five billion people worldwide are at risk for chronic exposure through contaminated foods, according to a March 2012 study published in PLoS One.

“Strict aflatoxin standards mean that many nations will export their best-quality foods and keep contaminated foods domestically, resulting in higher aflatoxin exposure in low- or middle-income nations where hepatitis prevalence is high,” wrote co-authors Felicia Wu and Hasan Guclu, both Pitt faculty members.

Whereas the U.S. is most often spared the cost in human health, the repercussions aren’t nil. Dairy cows and cattle, already stressed from living in close proximity to large numbers of animals, are at particularly high risk for succumbing to aflatoxicosis, though they can handle higher doses of toxin. Pets, too, are susceptible to the poison. In 2007 aflatoxins forced a nationwide pet food recall—but not before dozens of man’s best friends fell ill and died.

Researchers have not yet found an animal species immune to the aspergillus’s effects. The spores are so poisonous that even destroying the contaminated crops is an ordeal. Scientists worldwide keep careful tabs on aflatoxins in a large-scale effort to avoid outbreaks of aflatoxicosis, according to Stinson.

“Our understanding is that in some cases you can’t even incinerate (contaminated food) safely because the aflatoxin can get airborne and be inhaled,” she says. “If there is a high level of aflatoxin...they’re going to be in the position of having to store and destroy crops.”

### **Halfway Between Bacteria and Tree: How the Protein Transport Machinery in the Chloroplasts of Higher Plants Developed**

Source: ScienceDaily. Jan. 15, 2013.

Together with colleagues from Sweden, RUB researchers have studied how the protein transport system of bacteria developed over time to form the system in the chloroplasts of higher plants. They explored the so-called signal recognition particles (SRP) and their receptors. Bioinformatic and biochemical analyses revealed that the moss *Physcomitrella patens* has evolutionarily old and new components of the SRP system, and thus represents an intermediate stage in the development from the bacterial transport system to the chloroplast system in higher plants.

The international team led by Prof. Dr. Danja Schünemann and Dr. Chantal Träger from the Working Group Molecular Biology of Plant Organelles at the Ruhr-Universität reported in the journal *The Plant Cell*.

In the cell fluid, a special transport machinery conveys proteins from their origin to their place of work, for example in the cell membrane. The decisive factor is the so-called SRP system. It binds itself to the protein to be transported, travels with it to the cell membrane and interacts there with the SRP receptor (FtsY). If the SRP system binds to the receptor, cleavage of the energy storage molecule GTP triggers further processes which ultimately anchor the protein in the membrane.

In the cell fluid of bacteria, animals and plants, the SRP system consists of two components: the protein SRP54 and the ribonucleic acid SRP RNA. Several years ago, researchers found that the chloroplasts of higher plants, i.e. the photosynthetically active cell components, possess their own SRP system. It is very different from the system of the cell fluid because it has no SRP RNA. However, alongside SRP54 it also contains the protein SRP43, which occurs exclusively in chloroplasts. Scientists assume that chloroplasts originated from cyanobacteria, which initially lived in symbiosis with plant progenitor cells and were ultimately integrated into the plant cells. The scientists have now explored how the RNA-free SRP system of the chloroplasts originated from the RNA-containing SRP system of the bacteria.

With the aid of bioinformatics, the Bochum biologists and Dr. Magnus Rosenblad of Gothenburg University first examined which representatives in the plant kingdom have which components of the SRP system in their chloroplasts. "We were surprised that many organisms from unicellular green algae to mosses and ferns possess the gene for the SRP RNA in their chloroplasts," says Danja

Schünemann. "The only exceptions are the higher plants, which have lost this gene." For them, the SRP system consists solely of the proteins SRP54 and SRP43. Interestingly though, SRP43 also occurs in the chloroplasts of lower plants, which are still equipped with SRP RNA.

In collaboration with several groups of the Collaborative Research Centre SFB 642 at the RUB, Dr. Chantal Träger investigated the biochemistry of the moss *Physcomitrella patens*, which is among the lower plants. *Physcomitrella* has all the conceivable components of the SRP system in its chloroplasts: both the evolutionarily old components SRP54 and SRP RNA, as well as the more recent evolutionary protein SRP43. However, the SRP RNA of the moss chloroplasts forms a longer loop than the bacterial SRP RNA. This altered structure apparently prevents it from regulating the cleavage of GTP. *Physcomitrella patens* thus contains the evolutionarily old SRP RNA, which has largely lost certain functions. The SRP system of the chloroplasts of *Physcomitrella patens* therefore represents the transition between bacteria and higher plants. An X-ray structure analysis also revealed that the SRP receptor (FtsY) of the moss already has properties of the protein of higher plants.

Journal Reference: C. Trager, M. A. Rosenblad, D. Ziehe, C. Garcia-Petit, L. Schrader, K. Kock, C. Vera Richter, B. Klinkert, F. Narberhaus, C. Herrmann, E. Hofmann, H. Aronsson, D. Schunemann. Evolution from the Prokaryotic to the Higher Plant Chloroplast Signal Recognition Particle: The Signal Recognition Particle RNA Is Conserved in Plastids of a Wide Range of Photosynthetic Organisms. *The Plant Cell*, 2012; DOI: 10.1105/tpc.112.102996

## **Marginal Lands Are Prime Fuel Source for Alternative Energy**

Source: ScienceDaily. Jan. 16, 2013.

Marginal lands -- those unsuited for food crops -- can serve as prime real estate for meeting the nation's alternative energy production goals.

In the current issue of *Nature*, a team of researchers led by Michigan State University shows that marginal lands represent a huge untapped resource to grow mixed species cellulosic biomass, plants grown specifically for fuel production, which could annually produce up to 5.5 billion gallons of ethanol in the Midwest alone.

"Understanding the environmental impact of widespread biofuel production is a major unanswered question both in the U.S. and worldwide," said Ilya Gelfand, lead author and MSU postdoctoral researcher. "We estimate that using marginal lands for growing cellulosic biomass crops could provide up to 215 gallons of ethanol per acre with substantial greenhouse gas mitigation."

The notion of making better use of marginal land has been around for nearly 15 years. However, this is the first study to provide an estimate for the greenhouse gas benefits as well as an assessment of the total potential for these lands to produce significant amounts of biomass, he added.

Focusing on 10 Midwest states, Great Lakes Bioenergy researchers from MSU and the Pacific Northwest National Laboratory used 20 years of data from MSU's Kellogg Biological Station LTER Site to characterize the comparative productivity and greenhouse gas impacts of different crops, including corn, poplar, alfalfa and old field vegetation.

They then used a supercomputer to identify and model biomass production that could grow enough feedstock to support a local biorefinery with a capacity of at least 24 million gallons per year. The final tally of 5.5 billion gallons of ethanol represents about 25

percent of Congress' 2022 cellulosic biofuels target, said Phil Robertson, co-author and MSU professor of crop, soil and microbial sciences.

"The value of marginal land for energy production has been long-sSpeculated and often discounted," he said. "This study shows that these lands could make a major contribution to transportation energy needs while providing substantial climate and -- if managed properly -- conservation benefits."

This also is the first study to show that grasses and other non-woody plants that grow naturally on unmanaged lands are sufficiently productive to make ethanol production worthwhile. Conservative numbers were used in the study, and production efficiency could be increased by carefully selecting the mix of plant species, Robertson added.

"With conservation in mind, these marginal lands can be made productive for bioenergy production and, in so doing, contribute to avoid the conflict between food and fuel production," said Cesar Izaurralde, PNNL soil scientist and University of Maryland adjunct professor.

Additional benefits for using marginal lands include:

- New revenue for farmers and other land owners.
- No indirect land-use effects, where land in another part of the globe is cleared to replace land lost here to food production.
- No carbon debt from land conversion if existing vegetation is used or if new perennial crops are planted directly into existing vegetation.

Journal Reference: Ilya Gelfand, Ritvik Sahajpal, Xuesong Zhang, R. César Izaurralde, Katherine L. Gross, G. Philip Robertson. Sustainable bioenergy production from marginal lands in the US Midwest. *Nature*, 2013; DOI: 10.1038/nature11811

### **Breakthrough: How salt stops plant growth**

Source: Carnegie Institution, Washington, D.C., USA. January 23, 2013.

Until now it has not been clear how salt, a scourge to agriculture, halts the growth of the plant-root system. A team of researchers, led by the Carnegie Institution's José Dinneny and Lina Duan, found that not all types of roots are equally inhibited. They discovered that an inner layer of tissue in the branching roots that anchor the plant is sensitive to salt and activates a stress hormone, which stops root growth. The study, published in the current issue of *The Plant Cell*, is a boon for understanding the stress response and for developing salt-resistant crops.

Salt accumulates in irrigated soils due to the evaporation of water, which leaves salt behind. The United Nations estimates that salinity affects crops on about 200 million acres (80 million hectares) of arable land and not just in developing countries, but areas such as California as well.

As Dinneny explained: "An important missing piece of the puzzle to understanding how plants cope with stressful environments is knowing when and where stressors act to affect growth."

Roots are intimately associated with their environment and develop highly intricate branched networks that enable them to explore the soil. The branching roots grow horizontally off the main root and are important for water and nutrient uptake.

The scientists grew seedlings of a laboratory plant (*Arabidopsis*) that is a relative of mustard using a custom imaging system, which enabled them to measure the dynamic process of root growth throughout the salt response. This ability to track root growth in real time led the scientists to observe that branching roots entered a dormant phase of growth as salt was introduced. To determine how dormancy might be regulated, Lina Duan surveyed the role of different plant hormones

in this process and found that Abscisic Acid was the key signaling molecule.

"We are familiar with how animals use a fight or flight strategy to face external challenges. While plants can't run for safety, they can control how much they grow into dangerous territory," commented Dinneny. It turns out that Abscisic Acid, a stress hormone produced in the plant when it is exposed to drought or salty environments, is important in controlling the plant equivalent of fight or flight."

To understand how Abscisic Acid controls growth, the investigators devised a strategy to inhibit the response to this hormone in different tissue layers of the root. They developed several mutants in which the response to the hormone was suppressed in different root layers. They found that a significant portion of the salt response was dependent upon how a single cell layer sensed the hormone. The live imaging allowed them to watch what happened to root growth in these mutant plants.

"Interestingly, the 'inner-skin' of the root, called the endodermis, was most critical for this process. This tissue layer is particularly important as it acts like a semipermeable barrier limiting which substances can enter the root system from the soil environment." remarked lead author Duan.

"Our results mean that in addition to acting as a filter for substances in the soil, the endodermis also acts as a guard, with Abscisic Acid, to prevent a plant from growing in dangerous environments," said Dinneny.

"Irrigation of agricultural land is a major contributor to soil salinity. And as sea levels rise with climate change, understanding how plants, particularly crops, react to salt might allow us to develop plant varieties that can grow in the saltier soils that will likely occur in coastal zones."

Reference: Duan et al. Endodermal ABA Signaling Promotes Lateral Root Quiescence

during Salt Stress in Arabidopsis Seedlings. The Plant Cell. January 2013 tpc.112.107227

### **'Scarecrow' Gene: Key to Efficient Crops, Could Lead to Staple Crops With Much Higher Yields**

Source: ScienceDaily. Jan. 24, 2013.

With projections of 9.5 billion people by 2050, humankind faces the challenge of feeding modern diets to additional mouths while using the same amounts of water, fertilizer and arable land as today.

Cornell researchers have taken a leap toward meeting those needs by discovering a gene that could lead to new varieties of staple crops with 50 percent higher yields.

The gene, called Scarecrow, is the first discovered to control a special leaf structure, known as Kranz anatomy, which leads to more efficient photosynthesis. Plants photosynthesize using one of two methods: C3, a less efficient, ancient method found in most plants, including wheat and rice; and C4, a more efficient adaptation employed by grasses, maize, sorghum and sugarcane that is better suited to drought, intense sunlight, heat and low nitrogen.

"Researchers have been trying to find the underlying genetics of Kranz anatomy so we can engineer it into C3 crops," said Thomas Slewinski, lead author of a paper that appeared online in November in the journal Plant and Cell Physiology. Slewinski is a postdoctoral researcher in the lab of senior author Robert Turgeon, professor of plant biology in the College of Arts and Sciences.

The finding "provides a clue as to how this whole anatomical key is regulated," said Turgeon. "There's still a lot to be learned, but now the barn door is open and you are going to see people working on this Scarecrow pathway." The promise of transferring C4 mechanisms into C3 plants has been fervently pursued and funded on a global scale for decades, he added.

If C4 photosynthesis is successfully transferred to C3 plants through genetic engineering, farmers could grow wheat and rice in hotter, dryer environments with less fertilizer, while possibly increasing yields by half, the researchers said.

C3 photosynthesis originated at a time in Earth's history when the atmosphere had a high proportion of carbon dioxide. C4 plants have independently evolved from C3 plants some 60 times at different times and places. The C4 adaptation involves Kranz anatomy in the leaves, which includes a layer of special bundle sheath cells surrounding the veins and an outer layer of cells called mesophyll. Bundle sheath cells and mesophyll cells cooperate in a two-step version of photosynthesis, using different kinds of chloroplasts.

By looking closely at plant evolution and anatomy, Slewinski recognized that the bundle sheath cells in leaves of C4 plants were similar to endodermal cells that surrounded vascular tissue in roots and stems.

Slewinski suspected that if C4 leaves shared endodermal genes with roots and stems, the genetics that controlled those cell types may also be shared. Slewinski looked for experimental maize lines with mutant Scarecrow genes, which he knew governed endodermal cells in roots. When the researchers grew those plants, they first identified problems in the roots, then checked for abnormalities in the bundle sheath. They found that the leaves of Scarecrow mutants had abnormal and proliferated bundle sheath cells and irregular veins.

In all plants, an enzyme called RuBisCo facilitates a reaction that captures carbon dioxide from the air, the first step in producing sucrose, the energy-rich product of photosynthesis that powers the plant. But in C3 plants RuBisCo also facilitates a competing reaction with oxygen, creating a byproduct that has to be degraded, at a cost of about 30-

40 percent overall efficiency. In C4 plants, carbon dioxide fixation takes place in two stages. The first step occurs in the mesophyll, and the product of this reaction is shuttled to the bundle sheath for the RuBisCo step. The RuBisCo step is very efficient because in the bundle sheath cells, the oxygen concentration is low and the carbon dioxide concentration is high. This eliminates the problem of the competing oxygen reaction, making the plant far more efficient.

Journal Reference: T. L. Slewinski, A. A. Anderson, C. Zhang, R. Turgeon. Scarecrow Plays a Role in Establishing Kranz Anatomy in Maize Leaves. *Plant and Cell Physiology*, 2012; 53 (12): 2030 DOI: 10.1093/pcp/pcs147

### **After 30 years, is a GM food breakthrough finally here?**

Source: The Observer, 2 February 2013.

Golden rice, a new strain that boosts vitamin A levels and reduces blindness in developing countries, is about to be sown in the Philippines – and is the new battleground crop.

Scientists say they have seen the future of genetically modified foods and have concluded that it is orange or, more precisely, golden. In a few months, golden rice – normal rice that has been genetically modified to provide vitamin A to counter blindness and other diseases in children in the developing world – will be given to farmers in the Philippines for planting in paddy fields.

Thirty years after scientists first revealed they had created the world's first GM crop, hopes that their potential to ease global malnutrition problems may be realised at last. Bangladesh and Indonesia have indicated they are ready to accept golden rice in the wake of the Philippines' decision, and other nations, including India, have also said that they are considering planting it.

"Vitamin A deficiency is deadly," said Adrian Dubock, a member of the Golden Rice project.

"It affects children's immune systems and kills around two million every year in developing countries. It is also a major cause of blindness in the third world. Boosting levels of vitamin A in rice provides a simple, straightforward way to put that right."

Recent tests have revealed that a substantial amount of vitamin A can be obtained by eating only 60g of cooked golden rice. "This has enormous potential," said Dubock.

But scientists' satisfaction over the Golden Rice project has been tempered by the fact that it has taken an extraordinarily long time for the GM crop to be approved. Golden rice was first developed in 1999, but its development and cultivation has been opposed vehemently by campaigners who have flatly refused to accept that it could deliver enough vitamin A, and who have also argued that the crop's introduction in the developing world would make farmers increasingly dependent on western industry. The crop has become the cause célèbre of the anti-GM movement, which sees golden rice as a tool of global capitalism.

This view is rejected by the scientists involved. "We have developed this in conjunction with organisations such as the Bill and Melinda Gates Foundation as a way of alleviating a real health problem in the developing world," says Dubock. "No one is going to make money out of it. The companies involved in developing some of the technologies have waived their licences just to get this off the ground."

This view is shared by Mark Lynas, an environmental campaigner and one of the founders of the anti-GM crop movement. He has publicly apologised for opposing the planting of GM crops in Britain. "The first generation of GM crops were suspect, I believed then, but the case for continued opposition to new generations – which provide life-saving vitamins for starving people – is no longer justifiable. You cannot

call yourself a humanitarian and be opposed to GM crops today."

Golden rice was created by Peter Beyer, professor for cell biology at Freiburg University in Germany, and Ingo Potrykus of the Institute of Plant Sciences in Switzerland, in the late 1990s. They inserted genes for a chemical known as beta-carotene into the DNA of normal rice. In this way they modified the rice genes so that the plants started to make beta-carotene, a rich orange-coloured pigment that is also a key precursor chemical used by the body to make vitamin A.

By 2000 the plant was ready for trials. However, it took another five years before test fields were grown, such was the resistance to the idea of introducing GM plants in many countries. These trials showed golden rice could stimulate vitamin A uptake but at a low level. New research was launched to create varieties that would provide enhanced amounts of the vitamins.

"All the time, opponents to golden rice insisted, year after year, that it would not be able to produce vitamin A in those who ate it," said Beyer, golden rice's co-creator. "For example, it was alleged by Greenpeace that people would have to eat several kilograms of the stuff to get any benefit."

Two studies, both published in the American Journal of Clinical Nutrition, demolished this claim. The first, in 2009, was based on a group of healthy adult volunteers in the US and showed that golden rice's beta-carotene was easily taken up into the bloodstream. The second trial was carried out by American and Chinese researchers and published last year. It was carried out on Chinese children, aged between six and eight, and showed that a bowl of cooked golden rice, between 100g and 150g, could provide 60% of the recommended intake of vitamin A for young people. The study also revealed that golden rice is better than spinach at providing vitamin A.

"Given that normal rice has no vitamin A to speak of, that shows the importance of what has been achieved," said Dubock.

The latter study has since been immersed in controversy after it was claimed in a Greenpeace press release that the parents of the Chinese children had not been informed they were being given GM food and had been used as guinea pigs. An investigation by the Chinese authorities led to the sacking of the three Chinese scientists named by Greenpeace, which described the incident as "another example of big business hustling in on one the world's most sacred things: our food supply". For his part, Lynas has described Greenpeace's actions as "immoral and inhumane" because it deprives "the needy of something that would help them and their children because of the aesthetic preferences of rich people far away".

The reactions of bureaucracies to golden rice were also described by Beyer as "hard to believe". "We have had to undergo endless trials and tests and endure endless amounts of bureaucracy. Yet new breeds of standard crops have no such problems, even though they are often created by exposing them to doses of radiation. This is done to create new mutant breeds which you can then grow to see if any have features you like. None of the regulations that we had to meet in creating golden rice were imposed on these plant breeders. Yet this is the standard means by which new crops, including organic crops, are created. It is manifestly unbalanced."

This point was backed by Dubock. "All the time we have been required to show that there are no risks associated with growing golden rice, but at no point did we get a chance to point out its benefits. Everything is about risk assessment and nothing is about benefits assessment." Of course, some doubts about the technology still remain, as my colleague John Vidal makes clear here.

Nevertheless, a warning about consequences of imposing regulations on GM crops and not others was provided by Professor Cathie Martin of the John Innes Centre in Norwich. "At institutes like ours, we can prioritise research to bring new consumer health benefits and environmental benefits to market [via GM], as long as the regulatory process is not prohibitively expensive for publicly funded organisations."

The fate of golden rice is therefore important, as Professor Jonathan Jones of the John Innes Centre points out. "When I started making GM plants 30 years ago I did wonder if there might be unknown unknowns. But the evidence now is clear. GM food and crops are as safe as non-GM food and crops."

The prospect of further delays preventing future life-saving GM plants going to the field because of carefully orchestrated campaigns of opposition is therefore viewed with concern.

The Golden Rice project has had one beneficial knock-on effect, however. It has triggered a series of similar crop modification programmes that aim to tackle vitamin A deficiency through use of other GM foodstuffs. One example is provided by the golden banana, which has been created by scientists led by Professor James Dale of Queensland University in Australia.

"In Uganda, where the banana is a key source of nutrition, there is considerable vitamin A deficiency and also iron deficiency in diets," he said. "The former not only causes blindness but leaves children less able to fight disease which, in Africa, is particularly serious. The latter, iron deficiency, causes blood disorders."

To put this right, Dale and his team have found ways to boost beta-carotene levels in bananas. Now they are working on boosting iron levels as well. The team expects to have developed a golden banana, that will raise

both iron and vitamin A levels, by the end of the decade.

"People in Uganda eat up to a kilogram of mashed banana a day, so we don't need to get a great deal of beta-carotene in our bananas," said Dale.

The result of the team's work will be similar to golden rice: peeled, the pale fruit will be carrot-coloured. And if that sounds strange, it is worth noting that carrots were not originally orange. In the 17th century they were mostly yellow or purple, but were bred to be orange by Dutch farmers in tribute to the ruling House of Orange.

### **How plants sense gravity -- a new look at the roles of genetics and the cytoskeleton**

Source: American Journal of Botany. 4-Feb-2013.

Gravity affects the ecology and evolution of every living organism. In plants, the general response to gravity is well known: their roots respond positively, growing down, into the soil, and their stems respond negatively, growing upward, to reach the sunlight. But how do plants sense gravity and how do they direct or signal their cells to grow in response to it? Although botanists understand a great deal about how this works, a recent article in the recent issue of the American Journal of Botany reviews what we know so far, from mechanical to genetic approaches; it reveals that there are still substantial gaps in our knowledge of the molecular details and highlights new ideas for potential regulating mechanisms.

One of the most constant environmental stimuli that a plant encounters is gravity. Elison Blancaflor, author of the article and a Professor in the Plant Biology Division at the Samuel Roberts Noble Foundation, Oklahoma, is particularly interested in the effects that gravity has on plant development, and especially in its pivotal role in the evolution of a plant's sensory and signaling system.

"Although the process of gravitropism—defined as the downward growth of the plant root so it can explore the soil better for nutrients and water and the upward growth of the plant shoots to maximize light absorption—appears to be a simple plant response that we observe here on earth, the biological processes that control it are rather complex," notes Blancaflor.

Indeed, Blancaflor explains in his review article that gravitropism requires the coordinated activity of different cell and tissue types. In plants, the area where gravity is sensed is often spatially distinct from the area of growth. So how do these two discrete areas communicate with each other and direct the plant to where it should grow?

To date, gravity sensing in plants has been explained by the starch-statolith hypothesis. For example, in roots, gravity-sensing cells at the tip of the root contain dense, starch-filled organelles known as amyloplasts. Amyloplasts settle to the bottom of the cells in response to gravity, which then triggers the hormone auxin to move to another, distinct, area of cells and causes them to elongate and bend toward gravity. However, the molecular details of exactly how the physical movement and settling of amyloplasts in one set of cells triggers the accumulation of auxin in another, physically distant, set of cells in a plant remains a mystery.

The most prevalent current hypothesis is that the cytoskeleton, or cellular scaffolding, plays a major role in this gravity-sensing, intercellular communication; the cytoskeleton is made up of filaments, consisting of the proteins actin or tubulin, that allow movement of materials along strands, such as is seen in meiosis or mitosis. However, there is a major controversy in the field regarding the role of actin in gravitropism primarily due to contradictory outcomes in studies where actin was inhibited—the most interesting ones, according to Blancaflor, being those where

actin disruption actually led to enhanced gravitropism.

Blancaflor tackles this controversy by reviewing what we know regarding how amyloplasts work, what affects actin, and how recent genetic studies have discovered that proteins may regulate actin and therefore auxin distribution. For example, recent genetic work using the model plant, *Arabidopsis*, reveals potential mechanisms as to how the actin cytoskeleton connects the gravity sensing cells to auxin in the growing cells.

Although Blancaflor's review article specifically discusses, based on years of research, how one component of the plant cell, namely the cytoskeleton, controls the process of plant gravitropism, he notes that understanding gravitropism has important implications for agriculture as well.

"Information from basic studies on the cytoskeleton and how plants respond to gravity," he comments, "can inform and provide strategies for genetically engineering crop plants with improved root systems or overall plant architecture."

Blancaflor's interest in gravitropism goes even beyond this earth's atmosphere and into space: "The research I discuss in this article has led me to explore how minimal gravity impacts plant growth and development, and to ask if, like on earth, the actin cytoskeleton also contributes to plant growth in space where gravity is reduced."

Indeed, Blancaflor has conducted research on the Space Shuttle and will have some upcoming experiments on the International Space Station (ISS) this year related to the topic he reviews in this special issue article.

Reference: Blancaflor E. B. 2013. Regulation of plant gravity sensing and signaling by the actin cytoskeleton. *American Journal of Botany* 100(1): 143-152. DOI: 10.3732/ajb.1200283

**Pointing PINs in the right directions: a potassium transporter is required for the polar localization of auxin efflux carriers**

Source: *New Phytologist*, by Liam Dolan, 4 FEB 2013.

The polar transport of auxin is critical for development and growth of plants, and understanding how the directional movement of this hormone is controlled is a major challenge in plant biology. In this issue of *New Phytologist*, Rigas et al. (pp. 1130–1141) demonstrate that the polar localization of PIN-FORMED (PIN) proteins, which are responsible for the polar transport of auxin, requires the activity of TINY ROOT HAIR1 (TRH1), a putative plasma membrane potassium transporter.

‘The discovery that TRH1 is required for the localization of PIN1 is an important step forward in understanding how polar auxin transport is regulated.’

Auxin, synthesized in the shoot system, moves to the root tip through the stele and endodermis at the centre of the root. This ‘downward’ flow is facilitated by PIN proteins that transport auxin across the plasma membrane, and which are located on the face of the cell that is nearest to the root tip. PIN proteins accumulate in this plasma membrane domain in auxin-transporting cells and are excluded from other membrane domains on the sides or the domain facing the shoot.

The auxin transported across the plasma membrane may then be taken up by the neighbouring cell before being ‘effluxed’ across the membrane nearest the root tip again. Auxin is thus passed from cell to cell from the shoot to the root tip. Once at the root tip some auxin is channelled away from the tip in the outer layers of the root by a similar mechanism, except this time PIN proteins are located at the opposite end of the cell, nearest the shoot. This root-tip directed movement through the central regions of the root, and shootward movement through the

peripheral tissues, has been likened to an upside-down fountain.

The accumulation of PIN proteins to specific membrane domains is thus central to polar auxin transport and identifying proteins that are required for the polar localization of PIN proteins in cells is an active field of enquiry. The paper by Rigas et al. shows that TRH1 activity is required for the polar localization of PIN1 proteins in roots.

This flux of auxin in and around the root tip coordinates development and growth responses including root-hair growth and gravitropism (the growth of roots relative to the gravity vector). Plants that lack TRH1 function have defects in both root-hair development and gravitropism, which can be suppressed by auxin treatment suggesting that TRH1 is active in a process involving auxin (Fig. 1a). Furthermore there is evidence that TRH1 plays a role in auxin transport itself. Nevertheless the precise mechanism of TRH1's involvement in auxin transport has remained elusive.

Rigas et al. set out to determine the way in which TRH1 facilitates auxin transport. They predicted that if TRH1 is required for the transport of auxin towards the root tip, then auxin would back up along this route in *trh1* mutants. Such a blockage would be expected to result in higher levels of auxin behind the root tip. Indeed the levels of auxin in these regions were higher in *trh1* mutants than in wild type. They then demonstrated that the levels of the auxin-responsive promoter DR5, were higher in this region of the root. Together these data are consistent with the hypothesis that TRH1 is required for the movement of auxin from shoot to root.

Given that the movement of auxin to the root tip is defective in *trh1* mutants the authors hypothesized that TRH1 would either itself be asymmetrically localized in auxin-transporting cells or that it would control the polar localization of PIN1. They first demonstrated

that TRH1:YFP is not uniformly distributed around the plasma membranes of cells; it is located on the plasma membrane domain nearest the root tip. This corresponds to the site of PIN1 protein accumulation, that is, TRH1 and PIN1 co-localize (Fig. 1b). To ascertain if TRH1 has a role in the regulation of PIN1 they determined the location of PIN1 in *trh1* mutants. PIN1 is present in the membrane domain nearest the root tip in wild type but PIN1 is delocalized in the *trh1* mutants – it accumulates in the plasma membrane nearest the root tip as in wild type but it also accumulates at the opposite end of the cell, closest to the shoot. TRH1 is therefore required for the localization of PIN1 protein to the plasma membrane domain nearest the root tip in stele cells.

Rigas et al. hypothesized that the delocalization of PIN1 proteins in *trh1* mutants was sufficient to account for the defective root-hair and gravitropism phenotypes observed in *trh1* mutants. To test the hypothesis, plants were generated in which PIN1 accumulated throughout the plasma membrane of stele cells (such delocalized PIN1 accumulation is found in plants that accumulate large amounts of PIN1 proteins). This can be done experimentally by expressing PIN1 at high levels using the cauliflower mosaic virus 35S (35S) promoter. Just as predicted, the roots of 35S:PIN1 roots were phenotypically similar to *trh1* mutant roots – few root hairs developed and gravitropic responses were defective (Fig. 1). To independently verify this conclusion the authors treated roots with hypaphorine, a fungal drug that blocks the localization of PIN proteins to restricted domains in the plasma membrane. Hypaphorine treatment both reduced root-hair growth and caused gravitropic defects. Together these data support the hypothesis that delocalization of PIN1 proteins causes defects in root-hair growth and gravitropism, and is consistent

with a model in which TRH1 regulates PIN1 localization during wild type development.

The paper by Rigas et al. demonstrates that TRH1 is a regulator of PIN1 localization and polar auxin transport. The discovery that TRH1 is required for the localization of PIN1 is an important step forward in understanding how polar auxin transport is regulated. Nevertheless, this discovery raises many new questions. Given that PIN1 and TRH1 co-localize, it is possible that these proteins physically interact in the target membrane. If they do, is this interaction required for localization of both? It is nevertheless formally possible that these proteins control auxin transport independently. TRH1 may itself modulate auxin transport, and this would in turn modulate PIN localization. Intriguingly TRH1 is likely to be a cation transporter. Is TRH1 cation transport activity required for its own localization and the localization of PIN1? Characterization of new *trh1* alleles may provide us with the answers to these questions.

Reference: Rigas S, Ditengou FA, Ljung K, Daras G, Tietz O, Palme K, Hatzopoulos P. 2013. Root gravitropism and root-hair development constitute coupled developmental responses regulated by auxin homeostasis in the Arabidopsis root apex. *New Phytologist* 197: 1130–1141.

### **Healthy Seeds -- Treated Environmentally Friendly**

Source: ScienceDaily through Fraunhofer-Gesellschaft. Feb. 5, 2013

Farmers treat seeds chemically in order to rid them of pest infestation. Now researchers have developed a method that kills pathogens without harming the environment. Pioneering seed suppliers are already implementing the procedure commercially.

Seeds are home to molds and fungi, bacteria and viruses. To kill them off and to thereby prevent plant diseases from spreading, the

seeds are, as a rule, treated chemically. However, recently this method has been discredited. The permits for some chemical treating agents have been withdrawn, but the granting of new permits has declined markedly as well. And lastly, a severe case of E-coli infection which was caused by beansprout seeds and which made headlines in summer 2011, also resulted in calls for alternatives. The scientists of the Fraunhofer Institute for Electron Beam and Plasma Technology FEP in Dresden, Germany have developed an environmentally friendly method for removing germs from seeds. They treat the seeds with electrons, which within milliseconds destroy the DNA of the harmful organisms. Due to a special device setup, the elementary particles only act on the surface and in seed coat. The embryo in the interior of the seed is not affected so that the ability of the seeds to germinate is not impaired.

"In cereal seed you will find almost exclusively fungal pathogens but due to climate change it has been affected increasingly by bacteria from the south, against which there are no chemical agents as yet. Our treatment with low-energy accelerated electrons on the other hand is effective against bacterial and fungal pathogens. Also, the pathogens cannot build up a resistance against this process," says Frank-Holm Rögnér, holder of a master's degree in physics and department head at the FEP. Since the scientist and his team do not use any chemical additives, they destroy the pathogens in an environmentally friendly fashion with their method. Any leftover seed can be used as feed without any concerns.

Experts have long been able to prove that the germination ability of seeds treated in this manner is equal to that of chemically treated seeds. For two decades they have been attempting to establish and further develop their method. In 2002, they built a mobile demonstration unit which they use to provide test treatments all across Germany. However,

even though the EPPO (European and Mediterranean Plant Protection Organization) recommends the process for conventional as well as for ecological farming, the technology has been unable to significantly penetrate the market and has not progressed beyond demonstration status. According to Rögnér, one of the reasons, among others, for the lack of economic success is said to be the farmers, who can be convinced only if good results have occurred over many years, in conjunction with the recommendations of the supplier of their seeds or specialist advisor, but who rarely would take new ideas by scientists, who are not working in their field, seriously.

Now the researchers are working with the company Nordkorn Saaten GmbH. In 2010, Nordkorn had them demonstrate the process for the first time using the mobile demonstrator -- a truck on which the unit is mounted -- directly on site at their headquarters in Güstrow, Germany. The seed producer was impressed as the prototype ran for hundreds of hours with a throughput of up to 30 tonnes per hour -- the durability of the technology had inspired his confidence. In the meantime Nordkorn has bought the pilot plant, together with the long-standing seed partner company of the FEP, BayWa AG, and has commissioned the FEP with the building a second, custom-fit unit. This unique system is to start operations in Güstrow in late June 2013. Together with BayWa and Nordkorn as well as a plant manufacturer, the further development of the unit has also been planned. Among other things, the technology should become more affordable and more compact. The scientists and their partners are currently looking for project sponsors.

The scientists from the FEP are confident that, in the long term, the treatment with electrons will prove to be a success story. There is some support for this: Starting in 2015, farmers must prove that they are trying to reduce their CO2 footprint and lower the use of chemical

pesticides. "With our unit, we are able to contribute significantly to this," says Rögner. Should the treatment with electrons gain greater acceptance, the scientists from FEP could license their process to plant construction companies.

The scientists are currently promoting their activities abroad. The FEP is endeavoring to introduce the electron treatment process into the Chinese and Indian markets. "Due to the large amounts of seed produced, we see good opportunities there," says Rögner.

### **Preserving Biodiversity Can Be Compatible With Intensive Agriculture**

Source: ScienceDaily. Feb. 6, 2013

Preserving genetically diverse local crops in areas where small-scale farms are rapidly modernizing is possible, according to a Penn State geographer, who is part of an international research project investigating the biodiversity of maize, or corn, in hotspots of Bolivia, Peru and Mexico.

Hotspots are areas where cultivation of peaches and other non-traditional crops has exploded over the past decade, noted Karl Zimmerer, professor and head of the Department of Geography, and where small-scale farms are often female-run and have been previously regarded as marginal to mainstream agriculture.

"Peach-growing in central Bolivia is a vitally important income-generating strategy, even while farmers also desire and succeed in producing their Andean maize, both for eating and seed, as well as some sale," said Zimmerer, whose findings were recently published in the Proceedings of the National Academy of Sciences.

The researcher analyzed small-scale farm, or smallholder, landscapes and their farming and livelihood practices, including labor migration and irrigation issues, from 2000 to 2010 over three areas within Bolivia's Valle Alto region.

Farmers had low-to-moderate incomes by national standards.

Zimmerer and his colleagues surveyed land use among 174 smallholder households to assess production inputs and outputs of maize and peach crops. Among the factors they examined were farm-level management, varietal choices and water and soil management. Zimmerer designed this data collection and analysis to use with high-resolution satellite imagery and Geographic Information Systems. These techniques enabled him to create geographic models, maps and estimates of the areas devoted to intensified peach- and maize-growing.

Zimmerer also interviewed diverse groups of land users and officials to determine similarities and differences of perspectives on biodiversity in changing farming and food systems.

In addition to determining the compatibility of traditional plants, or landrace, diversity and intensified agriculture, Zimmerer also addressed important links between migrant communities and smallholder farms.

"Many of these farmers rely on money sent back home from relatives abroad, primarily in the United States and Spain," he said. "This money is key to the farmers' ability to run successful smallholder farms and grow high agrobiodiversity maize."

The farmers' families tend to become better educated, and local non-profit groups currently supporting food security, health, and agrobiodiversity see the migrants as potential major allies for their projects and policies they advocate, according to Zimmerer.

"Migrants are adept at global and other long-distance opportunities on the one hand, and still well aware of the value of their local agrobiodiversity traditions on the other hand," he said. "The migrant communities also are developing international outlets for these products. For example parched or toasted maize and a kind of popular fermented

beverage from Bolivian maize are both readily available in Washington, D.C., and in northern Virginia, where there is a community of 60,000 Bolivians."

In recent years, several prominent summits on ecological concerns have identified biodiversity in agricultural ecosystems as a major sustainability issue with implications for food security, conservation, health and well-being and adaptation to such global concerns as climate change.

"Sustainable development is crucial in Bolivia and other places in hotspots worldwide," Zimmerer said, "since it's these landscapes and peoples' livelihoods there that will ultimately determine the fate of humankind's global centers of biodiversity and agrobiodiversity in particular--unequaled and unique types of many major food plants, as well as minor and increasingly familiar ones. Sustainable development means protecting the future of these environments through the social-ecological systems in which they exist and change."

Maize agriculture, for example, is both a subsistence crop -- ideal for helping to ensure food security, which is most important among the rural poor -- and a cash crop.

"Women farmers, food-preparers and small-scale commercial processors are vitally important as those responsible for a majority of the management and knowledge of the diverse types of maize," Zimmerer noted, "and they have the highest levels of expertise in this knowledge and management."

Zimmerer's project included activities with Bolivian non-governmental organizations, and faculty and institute colleagues at Penn State and the University of Wisconsin, Madison. Grants from the Biocomplexity and Human-Social Dynamics programs at the National Science Foundation supported the research.

Journal Reference: K. S. Zimmerer. The compatibility of agricultural intensification in a global hotspot of smallholder agrobiodiversity

(Bolivia). Proceedings of the National Academy of Sciences, 2013; DOI: 10.1073/pnas.1216294110

### **Desert bacteria could help boost crop yields**

Source: SciDev.Net – the Science and Development Network. 6 February 2013.

Desert soil microbes could help halt desertification and boost agriculture in arid regions of the Middle East and North Africa, according to a study.

Scientists from the United Arab Emirates [UAE] have isolated local salt- and drought-tolerant strains of Rhizobia, soil bacteria that fix nitrogen when they become established inside the root nodules of legumes.

Rhizobia bacteria establish a mutually beneficial relationship with their host plant in which they exchange nitrogen they fix for nutrients plants produce through photosynthesis, and could be integral to improving the quality and nitrogen content of soil.

The discoveries could pave the way to improving the production of leguminous plants cultivated in arid environments, says the study published in the February issue of the Emirates Journal of Food and Agriculture.

The study was carried out by scientists from the Dubai-based International Center for Biosaline Agriculture (ICBA) in collaboration with the Dubai branch of the Birla Institute of Technology and Science.

"The project was conceived when I noticed, at a research farm in Dubai, some leguminous crops forming nodules to fix atmospheric nitrogen," lead author Nanduri Rao, a researcher at ICBA, tells SciDev.Net.

Rao's team began isolating several naturally occurring Rhizobia strains from the root nodules of three leguminous plants: sesbania (*Sesbania sesban*), lablab (*Lablab purpureus*) and pigeon pea (*Cajanus cajan*).

Rao explains that the team has also been studying the Rhizobia strains' tolerance to

environmental stresses such as high temperature, salinity, acidity and heavy metal concentrations in laboratory tests.

"The strains, native to the United Arab Emirates desert, were found to have a high tolerance to such stresses," Rao says, adding that a full length journal article based on this additional research is currently being prepared.

Daniele Daffonchio, professor of microbiology at the University of Milan, Italy, tells SciDev.Net that the identification of microbes capable of surviving in stressful conditions has important implications for agriculture in arid regions.

Philippe Normand, professor of microbial ecology at the University of Claude Bernard Lyon 1, France, tells SciDev.Net that the UAE project "has great potential for improving plant productivity under extreme environments," and is "an interesting approach for deserts".

Normand is also a collaborator with the EU-funded BIODESERT project, which is planning a research project in North Africa that aims to exploit microbes from deserts and arid environments to improve farming practices.

To facilitate this, the project will establish research laboratories with an advanced capacity for microbiology and microbial ecology studies at the University of Tunis in Tunisia.

Daffonchio, who is also coordinator for BIODESERT, says the project will aim to identify microbes that can improve the resistance of plants to water stress and drought, and could therefore make "a major contribution to saving water by decreasing water consumption".

Some of this work was published in PLOS ONE in October.

Ameur Cherif, professor of microbial biotechnology at the University of Manouba, Tunisia, and co-author of the PLOS ONE study, says that isolated bacteria or whole

communities of these desert microbes that are "adapted to water scarcity and drought conditions constitute a key element in a larger anti-desertification strategy that could be planned for southern countries".

Reference: Marasco et al. 2012. PLoS ONE 7(10): e48479.  
doi:10.1371/journal.pone.0048479

### **Do plants 'veto' bad genes?**

By Heidi Ledford. Source: Nature News. 08 February 2013

Latest evidence fails to quell doubt about whether plants can access 'ancestral' genes outside their parents' DNA.

Two publications are seeking to resurrect claims that plants can reject the inheritance of a mutated gene from their parents, in favour of a healthier 'ancestral' copy from their grandparents.

Susan Lolle, a plant geneticist now at the University of Waterloo in Canada, and her colleagues first published evidence in 2005 that plants had passed on genes correctly two generations down, even though the genome of the generation in between had only a mutated version<sup>1</sup>. This type of inheritance would require some hidden reservoir of genetic information outside of DNA, some suggested — perhaps in RNA transcribed from the healthy gene, which the plant would then use to correct the mutated one. If true, those findings would upend the modern concept of genetic inheritance, and predictably they have met with considerable scepticism.

Two groups of researchers later reported that attempts to reproduce those findings had failed<sup>2, 3</sup>. The original results did not signal a new form of inheritance, these researchers argued: rather, the original experiments were simply contaminated by pollen from other plants bearing the ancestral gene. "Everyone backed away after that," says Raphaël Mercier, a plant biologist at the French

National Institute for Agricultural Research in Versailles.

But Lolle has now collected more data that she says strengthens her position. In a paper published last month by F1000Research4, Lolle reports that cells in parts of a single adult thale cress (*Arabidopsis thaliana*) plant can bear an ancestral gene, rather than the parental version found in the rest of the plant. That, she says, supports her theory that plants somehow maintain a cache of ancestral genetic information beyond their DNA sequence, and abolishes concerns about polluting pollen.

"If we believe in the veracity of the experiments, these are very intriguing observations," says Animesh Ray, a systems biologist at the Keck Graduate Institute of Applied Life Sciences in Claremont, California.

The next concern, however, is contamination of a different sort. The assays used to characterize the cells rely on the polymerase chain reaction (PCR), a method for producing lots of copies of one DNA sample. But PCR is notoriously prone to contamination. Lolle says that she has taken steps to limit contamination and has repeated her experiments often enough to make the odds of a spurious result vanishingly small. But Ray says that he would be more comfortable with the data if Lolle and her team performed additional control experiments to make sure contamination is not the issue.

Luca Comai, a plant biologist at the University of California, Davis, doesn't discount the new results, but remains dubious. "Is there a magical genetic cache that allows the ancient memories of DNA past to come through?" he says. "I don't see compelling evidence for it."

To further back her claims, Lolle points to the publication of a second paper, also in F1000Research5, by an independent group asserting to have found evidence of the same phenomenon, this time while studying vitamin-C synthesis in *A. thaliana*. But Comai

and others say that this paper does less to convince them, because it has not ruled out possible contamination by errant seeds.

Despite the rampant scepticism, Lolle and her colleagues deserve credit for pursuing a difficult problem, says Ray. "It takes courage to actually try to figure out these complex events," he says. "And they may be on to something."

Nature doi:10.1038/nature.2013.12401

### **New Insights Into Plant Evolution**

Source: ScienceDaily. Feb. 28, 2013

New research has uncovered a mechanism that regulates the reproduction of plants, providing a possible tool for engineering higher yielding crops. In a study published today in *Science*, researchers from Monash University and collaborators in Japan and the US, identified for the first time a particular gene that regulates the transition between stages of the life cycle in land plants.

Professor John Bowman, of the Monash School of Biological Sciences said plants, in contrast to animals, take different forms in alternating generations -- one with one set of genes and one with two sets.

"In animals, the bodies we think of are our diploid bodies -- where each cell has two sets of DNA. The haploid phase of our life cycle consists of only eggs if we are female and sperm if we are male. In contrast, plants have large complex bodies in both haploid and diploid generations," Professor Bowman said.

These two plant bodies often have such different characteristics that until the mid-1800s, when better microscopes allowed further research, they were sometimes thought to be separate species.

Professor Bowman and Dr Keiko Sakakibara, formerly of the Monash School of Biological Sciences and now at Hiroshima University, removed a gene, known as KNOX2 from moss. They found that this caused the diploid generation to develop as if it was a haploid, a

phenomenon termed apospory. The equivalent mutations in humans would be if our entire bodies were transformed into either eggs or sperm.

"Our study provides insights into how land plants evolved two complex generations, strongly supporting one theory put forward at the beginning of last century proposing that the complex diploid body was a novel evolutionary invention," Professor Bowman said.

While Professor Bowman's laboratory in the School of Biological Sciences is focused on basic research exploring the evolution and development of land plants, he said there were possible applications for the results as mutations in the gene cause the plant to skip a generation.

One goal in agriculture is apomixis, where a plant produces seeds clonally by skipping the haploid generation and thereby maintaining the characteristics, such as a high yielding hybrid, of the mother plant. Apomixis would mean crops with desirable qualities could be produced more easily and cheaply.

"Gaining a better understanding of the molecular basis of plant reproduction and the regulations of the alternation of generations could provide tools to engineer apomixis -- a breakthrough that would be highly beneficial, especially in developing countries," Professor Bowman said.

Journal Reference: K. Sakakibara, S. Ando, H. K. Yip, Y. Tamada, Y. Hiwatashi, T. Murata, H. Deguchi, M. Hasebe, J. L. Bowman. KNOX2 Genes Regulate the Haploid-to-Diploid Morphological Transition in Land Plants. *Science*, 2013; 339 (6123): 1067 DOI: 10.1126/science.1230082

### **Key Developmental Mechanism in Plants Explained for First Time**

Source: ScienceDaily. Mar. 6, 2013

When a stem cell commits to becoming a leaf cell, how does a polycomb gene-repressing

protein complex know where in the genome to go, and when? The normal development of an animal or plant can be compared in at least two ways with the successful performance of a great symphony. The whole is the product of a great number of events involving contributions by many different "players"; and these contributions must occur in a precise and almost perfectly coordinated temporal and spatial sequence.

In simple animals like the fruit fly and more recently in plants and mammals, scientists have been able to identify some of the principal players in the developmental symphony. Today, a team of researchers from Cold Spring Harbor Laboratory (CSHL) explains for the first time the operation of a mechanism in plants that controls a class of key developmental regulatory genes, called homeobox genes.

The homeobox genes under study, called BREVIPEDICELLUS (BP) and KNAT2, need to be active in plant stem cells in order for the cells to maintain their non-specialized character. Stem cells are totipotent: they can develop, or "differentiate," into any plant cell type, depending on signals they receive which send them down the developmental path. When the moment is just right for plant organs such as leaves to begin to grow, BP and KNAT2 are switched off so that development can proceed.

"We were already familiar with the players in this regulatory mechanism, which have been conserved, or preserved, by evolution across species from flies to plants to animals," says CSHL Professor Marja Timmermans, who led the research team. "What we have not understood until now is how, in plants, the action of the players is very precisely coordinated in time and space."

It turns out that a highly conserved assembly of polycomb proteins, called Polycomb-repressive complex2 (PRC2), spurs a process called epigenetic regulation that physically

marks targeted genes -- in this case, BP and KNAT2 -- for repression. But how do these protein complexes know where along the plant cell's genome to go, and when, in order to induce this gene-repressing effect?

The key discovery by the Timmermans team, which appears online today in the journal *Genes & Development*, is the identification of the mechanism that brings PRC2 to specific sites along the genome precisely in those cells committed to become a leaf.

Timmermans' team showed that PRC2 physically interacts with DNA binding proteins that attach to plant DNA in specific genome regions just ahead of where the homeobox genes are situated. In the plant they studied, *Arabidopsis*, those DNA binding proteins are ASYMMETRIC LEAVES1 (AS1) and AS2. When a stem cell commits to becoming a leaf cell, AS1 and AS2 become active, attach at the DNA sites near BP and KNAT2, and recruit PRC2 to repress these homeobox genes. The epigenetic mark made by PRC2, which acts like a cellular memory, is heritable, and is essential in order for leaves and other plant organs to develop.

In other locations along the genome, other analogous mechanisms are surely at work, says Timmermans, whose broad interest in this research concerns its implications for patterning in development.

Timmermans is intrigued to learn the effects of tweaking with the timing of regulatory gene expression and repression. She suspects small adjustments to expression of master regulators during development are one of the means by which evolution proceeds over vast stretches of time.

She also notes that by tweaking these developmental regulatory systems, it might be possible to beneficially affect plant regeneration -- the process in which a new plant is generated from the leaf of an existing one. This process involves de-differentiating a mature cell and returning it to a primitive

developmental state before once again allowing it to proceed down a developmental path -- a process akin to that employed in the making of human IPS (induced pluripotent stem) cells.

Journal Reference: M. Lodha, C. F. Marco, M. C. P. Timmermans. The ASYMMETRIC LEAVES complex maintains repression of KNOX homeobox genes via direct recruitment of Polycomb-repressive complex2. *Genes & Development*, 2013; DOI: 10.1101/gad.211425.112

### **When a Gene Is Worth Two: Same Gene Fulfills Different Biological Roles in Plants**

Source: ScienceDaily. Mar. 22, 2013

The notion that each gene can only codify for a single protein has been challenged for some years. Yet, the functional outcomes that may result from genes encoding more than one protein are still largely unknown. Now, in a study published in the latest issue of *The Plant Cell* journal, a group of scientists led by Paula Duque at the Instituto Gulbenkian de Ciência (IGC, Portugal) discovered a gene -- ZIFL1 -- that has the particularity of producing two different proteins with completely distinct locations and functions in the plant. The researchers observed that in the root ZIFL1 codifies a protein that is important for the transport of auxin, a hormone essential for the correct growth and development of the plant. However, in the leaves the same gene originates a protein that promotes tolerance to drought. The gene presented in this study is one of the few identified to produce two proteins with such different biological roles.

ZIFL1 belongs to a family of transporter genes known to be present in all classes of organisms, but the functional role of most of its members remains unknown. What is known is that these transporter genes encode proteins that are integrated into cell membranes and act by allowing the passage of small molecules across them. By

undergoing genetic and cell biology studies in the plant model *Arabidopsis thaliana*, Paula Duque's team was able to study the role of the ZIFL1 gene. What surprised the scientists was that mutant plants unable to produce the ZIFL1 transporter presented specific defects in different organs and functions. On one hand, their roots exhibited problems of growth, ramification and orientation when compared to normal plants.

These observations suggested that the ZIFL1 gene was involved in the transport of the auxin hormone, which plays an important role in the development of the root. But the researchers also found out that the mutant plants had problems in tolerating drought. They realized that the leaf pores that regulate transpiration -- the stomata -- were more open in the mutants than in normal plants, resulting in the loss of higher quantities of water. This suggested a role for ZIFL1 in the closure of stomata and in the control of water loss by the plant, which can be critical under drought conditions.

Intrigued by these observations, the researchers investigated whether the ZIFL1 gene could be originating two proteins that would act differently in distinct tissues. Alternative splicing is a key mechanism allowing the same gene to produce multiple proteins. When genes are activated to give rise to proteins, they first originate an intermediate molecule of RNA that can be processed differently, with some parts being removed. This cut and paste process may originate different RNA molecules that can then be converted into different proteins. Estelle Remy, investigator at Duque's laboratory and first author of this work, observed that in the case of the ZIFL1 gene, alternative splicing originates two RNA molecules that differ in just two chemical residues. However, this small difference has a huge impact on the proteins that are generated, with one of them being shortened

by 67 amino acids. In collaboration with Isabel Sá-Correia's group at Instituto Superior Técnico, the researchers then tested the activity of the two proteins in yeast cells and found that both transport potassium ions.

Having different size but similar transport activity, Estelle looked for the reason why these two proteins had such distinct biological functions. Surprisingly, she observed that root tissues only present the longer form of the protein, whereas the shorter protein can only be found in the leaves. Furthermore, the location of these two proteins also differs inside the cells of the root and leaves, being integrated into different cell membranes. According to Estelle, "the fact that we cannot find both proteins being expressed either in roots or leaves suggests that these tissues may have specific factors that somehow influence the splicing of the ZIFL1 RNA into the form that confers the biological role necessary for that tissue."

Says Paula Duque, "To our knowledge, there are not many known cases of proteins with such different biological functions being codified by the same gene. What is most fascinating is how the inclusion or removal of just two chemical residues in the RNA molecule results in the production of two proteins that play essential roles either in hormone transport or in tolerance to drought."

Alternative splicing is a crucial mechanism to generate protein diversity. In humans, about 20,000 to 25,000 genes codify proteins. However, recent studies indicate that over 90% of these genes undergo alternative splicing, with scientists estimating that there may be up to 500,000 or more different proteins in the human body.

Journal Reference: E. Remy, T. R. Cabrito, P. Baster, R. A. Batista, M. C. Teixeira, J. Friml, I. Sa-Correia, P. Duque. A Major Facilitator Superfamily Transporter Plays a Dual Role in Polar Auxin Transport and Drought Stress

Tolerance in Arabidopsis. *The Plant Cell*, 2013;  
DOI: 10.1105/tpc.113.110353

### **Gene Discovery May Yield Lettuce That Will Sprout in Hot Weather**

Source: ScienceDaily. Mar. 28, 2013

A team of researchers, led by a University of California, Davis, plant scientist, has identified a lettuce gene and related enzyme that put the brakes on germination during hot weather -- a discovery that could lead to lettuces that can sprout year-round, even at high temperatures.

The study also included researchers from Arcadia Biosciences and Acharya N.G. Ranga Agricultural University, India.

The finding is particularly important to the nearly \$2 billion lettuce industries of California and Arizona, which together produce more than 90 percent of the nation's lettuce. The study results appear online in the journal *The Plant Cell*.

"Discovery of the genes will enable plant breeders to develop lettuce varieties that can better germinate and grow to maturity under high temperatures," said the study's lead author Kent Bradford, a professor of plant sciences and director of the UC Davis Seed Biotechnology Center.

"And because this mechanism that inhibits hot-weather germination in lettuce seeds appears to be quite common in many plant species, we suspect that other crops also could be modified to improve their germination," he said. "This could be increasingly important as global temperatures are predicted to rise."

Most lettuce varieties flower in spring or early summer and then drop their seeds -- a trait that is likely linked to their origin in the Mediterranean region, which, like California, characteristically has dry summers. Scientists have observed for years that a built-in dormancy mechanism seems to prevent lettuce seeds from germinating under

conditions that would be too hot and dry to sustain growth. While this naturally occurring inhibition works well in the wild, it is an obstacle to commercial lettuce production.

In the California and Arizona lettuce industries, lettuce seeds are planted somewhere every day of the year -- even in September in the Imperial Valley of California and near Yuma, Ariz., where fall temperatures frequently reach 110 degrees.

In order to jump-start seed germination for a winter crop in these hot climates, lettuce growers have turned to cooling the soil with sprinkler irrigation or priming the seeds to germinate by pre-soaking them at cool temperatures and re-drying them before planting -- methods that are expensive and not always successful.

In the new study, researchers turned to lettuce genetics to better understand the temperature-related mechanisms governing seed germination. They identified a region of chromosome six in a wild ancestor of commercial lettuce varieties that enables seeds to germinate in warm temperatures. When that chromosome region was crossed into cultivated lettuce varieties, those varieties gained the ability to germinate in warm temperatures.

Further genetic mapping studies zeroed in on a specific gene that governs production of a plant hormone called abscisic acid -- known to inhibit seed germination. The newly identified gene "turns on" in most lettuce seeds when the seed is exposed to moisture at warm temperatures, increasing production of abscisic acid. In the wild ancestor that the researchers were studying, however, this gene does not turn on at high temperatures. As a result, abscisic acid is not produced and the seeds can still germinate.

The researchers then demonstrated that they could either "silence" or mutate the germination-inhibiting gene in cultivated lettuce varieties, thus enabling those varieties

to germinate and grow even in high temperatures.

Other researchers on the study were: Post-doctoral researcher Heqiang Huo and staff researcher Peetambar Dahal, both of the UC Davis Department of Plant Sciences; Keshavulu Kunusoth of Acharya N.G. Ranga Agricultural University, India; and Claire McCallum of Arcadia Biosciences, which provided the lettuce lines with variants of the target gene to help confirm the study's findings.

Journal Reference: H. Huo, P. Dahal, K. Kunusoth, C. M. McCallum, K. J. Bradford. Expression of 9-cis-EPOXYCAROTENOID DIOXYGENASE4 Is Essential for Thermoinhibition of Lettuce Seed Germination but Not for Seed Development or Stress Tolerance. *The Plant Cell*, 2013; DOI: 10.1105/tpc.112.108902

### **Gene Responsible for Short Stature of Dwarf Pearl Millet Identified**

Source: ScienceDaily. Mar. 29, 2013

While pearl millet is a major food staple in some of the fastest growing regions on Earth, relatively little is known about the drought-hardy grain.

Recently, plant geneticists at the University of Georgia successfully isolated the gene that creates dwarfed varieties of pearl millet. It is the first time a gene controlling an important agronomic trait has been isolated in the pearl millet genome. Their work appeared in the March edition of the journal *G3: Genes, Genomics, Genetics*.

The dwarf varieties are economically important in the U.S., India and Africa, in particular.

The researchers, led by UGA's Katrien Devos, also were able to trace the dwarf gene to plants bred 50 years ago by Glenn Burton, a UGA plant breeder who worked on the College of Agricultural and Environmental Sciences' Tifton campus.

Knowing which gene controls the dwarfing trait will help plant breeders create more efficient, sustainable varieties of millet that have the short stature some farmers and ranchers want.

"Knowing the actual gene that reduces plant height has allowed us to develop markers that can be used by breeders to screen for the presence of the gene long before the effects of the gene can be visually observed," said Devos, a professor in the College of Agricultural and Environmental Sciences' Institute of Plant Breeding, Genetics and Genomics, housed in the department of crop and soil sciences, and the Franklin College of Arts and Sciences' department of plant biology.

"In the longer term, the knowledge gained in pearl millet will help to develop semi-dwarf lines with high agronomic performance in other cereal crops," she said.

Rajiv K. Parvathaneni, a doctoral student working in Devos' lab, was in charge of tracking down the gene, which works by controlling the flow of the growth hormone auxin through the plant.

He also wanted to understand the mechanism by which the gene controls auxin and to develop plant-breeder-friendly markers that would allow breeders to screen for the dwarfing gene before their plants matured.

The gene that Parvathaneni found affects the downward transport of auxin, which is made in the top part of the plant. If this gene is on, the auxin flows freely, and millet will grow to its full height, about 10 feet. If it is off, the millet plant may only grow to be 3 to 5 feet in height.

Parvathaneni and Devos' team first found which region of the pearl millet's genome contributed to growth and then compared that section to a similar section of DNA from sorghum. Sorghum is a grain related to pearl millet, and a complete map of its genome

recently was released by Devos' UGA colleague Andy Patterson.

The comparison revealed that ABCB1, a gene controlling auxin transport and causing reduced plant height in sorghum, was the prime gene candidate controlling pearl millet dwarf stature, Devos said.

Comparative genome analysis, a process in which an unmapped genome is compared to the genome of a similar and more thoroughly described plant genome, is a common method to help identify the functions of specific genes, especially in crops for which little genetic resources are available.

The next step for Devos' team is to work with researchers in other states to understand more fully how auxin transport differs in tall and dwarf millet plants and to verify that ABCB1 is in fact the gene that controls dwarfism.

After Devos and Parvathaneni located the dwarfing gene, they tested pearl millet dwarfs from around the world. All dwarfs caused by a nonfunctional ABCB1 gene have the same mutation as the dwarfs that were first bred by Burton in the 1960s.

Dwarf varieties of pearl millet are not ideal for every planting situation. In Africa, many farmers prefer taller varieties because they use the long stalks for roofing thatch and other applications.

However, where millet is intensively cultivated, dwarf millet allows farmers to harvest the grain with mechanical threshers. Ranchers like dwarf millet as a forage plant because it has a high leaf-to-stem ratio, Devos said.

Knowing more about the plant in general is key to broadening production of the very drought-resistant, hardy grain.

"The crop itself has a future, a bright one—especially in regions where climate change may lead to more erratic rainfall patterns as pearl millet is highly drought tolerant. It already is a popular food crop in semi-arid

regions of India and Africa and will likely gain interest from drought-prone regions of the developed world as an alternative to corn in animal feed," Parvathaneni said.

Journal Reference: R. K. Parvathaneni, V. Jakkula, F. K. Padi, S. Faure, N. Nagarajappa, A. C. Pontaroli, X. Wu, J. L. Bennetzen, K. M. Devos. Fine-Mapping and Identification of a Candidate Gene Underlying the d2 Dwarfing Phenotype in Pearl Millet, *Cenchrus americanus* (L.) Morrone. *G3: Genes|Genomes|Genetics*, 2013; 3 (3): 563 DOI: 10.1534/g3.113.005587

### **Total Buzz Kill: Metals in Flowers May Play Role in Bumblebee Decline**

Source: ScienceDaily. Apr. 2, 2013

Beekeepers and researchers nationally are reporting growing evidence that a powerful new class of pesticides may be killing off bumblebees. Now, research at the University of Pittsburgh points toward another potential cause: metal pollution from aluminum and nickel.

Published in the journal *Environmental Pollution*, the Pitt study finds that bumblebees are at risk of ingesting toxic amounts of metals like aluminum and nickel found in flowers growing in soil that has been contaminated by exhaust from vehicles, industrial machinery, and farming equipment. The Pitt study finds that bumblebees have the ability to taste -- and later ignore -- certain metals such as nickel, but can do so only after they visit a contaminated flower.

Therefore, the insects are exposed to toxins before they even sense the presence of metals.

"Although many metals are required by living organisms in small amounts, they can be toxic to both plants and animals when found in moderate to high concentrations," said Tia-Lynn Ashman, principal investigator of the study and professor and associate chair in Pitt's Department of Biological Sciences in the

Kenneth P. Dietrich School of Arts and Sciences. "Beyond leading to mortality, these metals can interfere with insect taste perception, agility, and working memory -- all necessary attributes for busy bumblebee workers."

Ashman and George Meindl, coauthor of the study and a PhD candidate in Ashman's lab, studied bumblebee behavior using the *Impatiens capensis*, a North American flower that blooms in summer. Its flowers are large, producing a high volume of sugar-rich nectar each day -- an ideal place for bumblebees to forage. The blooms were collected from the field each morning of the two-week study and were of a similar age, color, and size.

To determine whether nickel and aluminum in the flowers' nectar influenced bumblebee behavior, Ashman and Meindl used two groups of uncontaminated flowers, one group of flowers contaminated by nickel, and another contaminated by aluminum. When a bumblebee visited a flower in an array, the entire visitation was recorded as well as the time spent (in seconds) foraging on each individual flower. This included monitoring whether the bee moved from a contaminated to a noncontaminated flower, whether the bee moved to the same group it had just sampled, or whether the bee left the flower group without visiting other individual blooms. Following each observed visit, all flowers in the array were replaced with new flowers, to ensure accurate results.

"We found that the bees still visited those flowers contaminated by metal, indicating

that they can't detect metal from afar," said Ashman. "However, once bumblebees arrive at flowers and sample the nectar, they are able to discriminate against certain metals."

In the study, the bees were able to taste, discriminate against, and leave flowers containing nickel. However, this was not the case for the aluminum-treated flowers, as the bees foraged on the contaminated flowers for time periods equal to those of the noncontaminated flowers.

"It's unclear why the bees didn't sense the aluminum," said Meindl. "However, past studies show that the concentrations of aluminum found throughout blooms tend to be higher than concentrations of nickel. This suggests that the bees may be more tolerant or immune to its presence."

These results also have implications for environmentally friendly efforts to decontaminate soil, in particular a method called phytoremediation -- a promising approach that involves growing metal-accumulating plants on polluted soil to remove such contaminants. Ashman says this approach should be considered with caution because the bees observed in the study foraged on metal-rich flowers. She states that further research is needed to identify plants that are ecologically safe and won't pose threats to local animals that pollinate.

Journal Reference: George A. Meindl, Tia-Lynn Ashman. The effects of aluminum and nickel in nectar on the foraging behavior of bumblebees. *Environmental Pollution*, 2013; 177: 78 DOI: 10.1016/j.envpol.2013.02.017

## Forthcoming meetings

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### **8<sup>th</sup> International Symposium on In Vitro culture and Horticultural Breeding**

*Highlighting in vitro morphogenesis to improve plant breeding*

**June 2 – 7, 2013. Coimbra, Portugal**

<http://www.uc.pt/en/congressos/IVCHB2013/>

The next IVCHB2013 will be held at the Department of Life Sciences, University of Coimbra, Portugal, from 2-7 June 2013. The main aim of the symposium is to bring together specialists and stakeholders interested in different areas of plant tissue culture to exchange ideas and information and to establish new lines of research for the future. Main topics of the symposium will be: plant cloning, plant conservation, somatic embryogenesis, rooting, haploid research, genetic transformation and physiological, biochemical and molecular aspects of in vitro culture. A technical tour and several cultural and social events (dinner and a serenade of Fado included!) will take place. The convener of this symposium (Prof. Jorge Canhoto) and his team have the pleasure to invite all the colleagues working in this field to join this meeting which will be held, for the first time, in Portugal.

For more information contact:  
[jorgecan@ci.uc.pt](mailto:jorgecan@ci.uc.pt)

### **International Symposium of Plant Photobiology (ISPP)**

**June 3, 2013. Edinburgh, Scotland**

More info:

<http://www.plantsci.org.uk/events/international-symposium-plant-photobiology-ispp-2013-conference>

### **30<sup>th</sup> ISTA Congress Seed Symposium**

**June 12 - 14, 2013. Antalya, Turkey**

### **21<sup>st</sup> IPGSA meeting**

**June 18 – 22, 2013. Shanghai, China.**

Web site: <http://www.ipgsa.org>

Contact: **Sheri Strydhorst, PhD**

Project Manager - Plant Hormone Technology  
Agricultural, Food and Nutritional Science  
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[sheri.strydhorst@ualberta.ca](mailto:sheri.strydhorst@ualberta.ca)

### **Seed Ecology IV: 4th International Society for Seed Science Meeting on Seeds and the Environment.**

**June 22 – 26, 2013. Shenyang, China**

More info Website:

<http://seed2013.csp.escience.cn/dct/page/1>

E-mail: [seedecology4@iae.ac.cn](mailto:seedecology4@iae.ac.cn)

### **Society for Experimental Biology (SEB) Annual Main Meeting 2013**

**July 3 – 6, 2013. Valencia, Spain**

More info:

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

### **9<sup>th</sup> European Conference on Precision Agriculture (ECPA)**

**July 7<sup>th</sup> – 11<sup>th</sup>, 2013. Lleida, Spain**

More info: <http://www.ecpa2013.udl.cat/>

### **4<sup>th</sup> Workshop on the Molecular Aspects of Seed Dormancy and Germination**

**July 9<sup>th</sup> -12<sup>th</sup>, 2013. Paris, France**

University Pierre et Marie Curie, Paris, France.

<http://www.congres.upmc.fr/paris-iss2013/>

### **11<sup>th</sup> International Conference on Reactive Oxygen and Nitrogen Species in Plants**

**July 17 – 19, 2013. Warsaw, Poland**

We are pleased to announce that many distinguished scientists confirmed their participation at the upcoming 11th POG meeting in Warsaw.

The list of Invited Speakers can be found at the conference website:

<http://www.pogwarsaw2013.org/>

### **XIII Portuguese-Spanish Congress of Plant Physiology (FV2013)**

**July 24 – 28, 2013. Lisbon, Portugal**

The Portuguese Society of Plant Physiology (SPFV) in collaboration with its counterpart Spanish (SEFV) is organizing the "XIII Portuguese-Spanish Congress of Plant Physiology (FV2013)", <http://fisiologiavegetal2013.itqb.unl.pt> that will take place in Lisbon, Faculdade de Ciências da Universidade de Lisboa (Campo Grande), from 24 to 28 July 2013.

The SPFV invited world-renowned scientists from Portugal, Spain, USA, Chile, Germany and the UK, who will contribute to this conference with six plenary lectures. It will be a comprehensive and exciting program including ten sessions (each with a guest speaker) and 4-6 oral presentations of selected abstracts, covering subjects ranging from "Cell biology and development" to "Biotechnology and innovation." Other sessions include "Plant-Microorganism Interactions and Plant-Environment", "Metabolism and Bioenergy", "Evolution and Biodiversity", "Applied Physiology", "Systems Biology and Omics", "Education and Training" and "Entrepreneurship / Opportunities Financing".

While aiming for a scientific meeting of high international level, we are also targeting high schools, promoting research in plants among young students and teachers and bringing some to participate in this conference (contest "**VIP - Vamos Investigar as Plantas** Let's Investigate Plants"). During this meeting we will promote high quality research and raise public awareness of the importance of plants and their research for global food security, renewable resources, bio-energy, environment and sustainability, health and wellbeing and for the global economy. We are offering special conditions to facilitate the participation of scientists from the Community of Portuguese Speaking Countries (CPLP) and the participation of students.

We would like to invite to participate in the FV2013 all those who are involved in research on plants or in the teaching of Plant Biology.

<http://fisiologiavegetal2013.itqb.unl.pt>

### **Third International Conference on Plant Vascular Biology**

**July 26 – 30, 2013. Helsinki, Finland.**

<http://www.pvb2013.org>

### **25<sup>th</sup> Congress of the Scandinavian Plant Physiology Society (SPPS 2013)**

**August 11 – 15, 2013. Elsinore, Denmark.**

The overall theme of the congress is Post-Genomic Plant Science.

Website: <http://spps2013.org/>

### **7<sup>th</sup> EPSO Conference: Plants for a Greening Economy**

**September 1 – 4, 2013. Porto Heli, Greece**

<http://www.epsoweb.org/7th-epsa-conference-1-4-september-2013-greece>.

#### **ONLINE REGISTRATION STARTED!**

**AIM:** The 7<sup>th</sup> EPSO Conference Plants for a Greening Economy will be held at the beautiful coast of Porto Heli, at the east side of the Peloponnese, in Greece, from 1 to 4 September 2013. The Conference will address many of the challenges faced by the plant research community in an evolving world: basic research as well as applied research on climate change, preservation of the environment and of natural biodiversity, as well as the food and feed demands of a growing world population. Non-food crops for energy, biomaterials, biopharmaceuticals and other new products will also be an important focus of the conference.

**TOPICS:** Regulatory networks in plants – Plant response and adaptation to biotic stresses – Plant response and adaptation to abiotic stress – Plant response and adaptation to low resource availability – Climate change – the mitigating role of plants – Global food security – sufficiency and affordability – Global food security – nutritional quality and safety – Plant breeding and sustainability – Plant

driven bioeconomy–bioenergy, biofuels, molecular farming, biomaterials – Plant evolution–biodiversity and ecosystems – Science policy – plant science and environment – Two dedicated poster sessions

#### **LIST OF CONFIRMED SPEAKERS AND CHAIRS:**

Eva-Mari Aro, David Beerling, Jose-Pio Beltran, Philip Benfey, Malcolm Bennett, Ton Bisseling, Marc de Block, Alain Charcosset, Jan Delcour, Xinnian Dong, Matthias Erb, Eckhard George, Jean-Christophe Glaszmann, Wilhelm Gruissem, Jacek Hennig, Heribert Hirt, Jonathan Jones, Angela Karp, Sandy Knapp, Mauricio A. Lopes, Cathie Martin, Karin Metzloff, Maurice Moloney, John Mundy, Bruce Osborne, Javier Paz-Ares, Merja Penttil , Christophe Plomion, Marcel Prins, Edward Rybicki, Uli Schurr, George Skaracis, Chiara Tonelli, Athanasios Tsiftaris, Rens Voesenek, Olivier Voinnet, Tom Whitham, Dan Yakir, Kazuko Yamaguchi-Shinozaki and Jian-Kang Zhu.

**CONTACT EPSO Conference officer at:**  
[Katerina.Karkala@epsomail.org](mailto:Katerina.Karkala@epsomail.org)

#### **The 5<sup>th</sup> EMBO Meeting**

**September 21 – 24, 2013. Amsterdam**  
<http://www.the-embo-meeting.org/>

#### **Plant Dormancy Symposium**

**November 4 – 7, 2013. Auckland, New Zealand**  
Please see the website for more information:  
<http://www.dormancy2013.com/>  
Abstract submission is open at:  
<http://www.dormancy2013.com/page/registration/abstract-submission/>

#### **32<sup>nd</sup> New Phytologist Symposium: Plant interactions with other organisms: molecules, ecology and evolution**

**November 20 – 23, 2013. Buenos Aires, Argentina**

The goal of this symposium is to bring together researchers working in a wide range of disciplines in plant biology, ecology and evolution in the field of plant interactions with other organisms. The central objective is to discuss and integrate information from different

approaches and perspectives in order to create a synthetic framework for understanding these interactions. Our hope is to have a diverse and dynamic group of scientists, who are willing to step out of their disciplinary comfort zone and engage in an effort to participate in discussions spanning the range from molecular approaches to ecosystem implications.

<http://www.newphytologist.org/symposiums/view/2>

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

**March 18 – 21, 2014. Hue, Vietnam**

This is a joint conference of the recently formed IUFRO Working Party WP 2.08.07 on **Acacia Genetics and Silviculture**, WP1.02.06 on **Ecology and Silviculture of Acacia** and WP 2.04.01 on **Population, Ecological and Conservation Genetics** and will be hosted by the Vietnamese Academy of Forest Sciences (VAFS). The conference will include invited and contributed presentations and posters, discussion sessions, satellite and business meetings, and in-conference and post-conference tours.

This 4 days' conference with the theme, **"Sustaining the Future of Acacia Plantation Forestry"** will be structured so as to promote discussion between geneticists, breeders and scientists concerned with management regime development and interactions of the crop with its biotic and abiotic environment. This broad ranging review should provide scientific support to those responsible for developing and implementing forest plantation management policies. While our primary interest is in tropical acacias we recognize that there is a much more established tradition of planting temperate species such as *A. mearnsii*, and we will welcome contributions from scientists working on those crops.

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

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

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

## Positions available



### PREDOC

#### PhD studentship in Plant Science/Developmental Biology

PhD studentship available to work in Anthony Bishopp's lab at the University of Nottingham, UK. This is a newly established laboratory focused on understanding the genetic regulation of vascular patterning in Arabidopsis roots and transferring this to crop species. As the xylem provides the main mechanism for the long distance transport of water, we reason that manipulating xylem properties will have positive benefits for water use efficiency.

Outline The embryonic root initially forms as a radially symmetric organ. The specification of xylem cells generates the positional information to create bilateral symmetry. This is coordinated by small differences in the spatial response patterns of two hormones, auxin and cytokinin. Using the model plant Arabidopsis, we have identified a mutually inhibitory interaction that sets vascular pattern. In this mechanism auxin directly promotes the expression of the cytokinin signalling inhibitor AHP6 and (through an unknown mechanism) cytokinin regulates the activity of the PIN class of auxin transporters.

The successful applicant will investigate the mechanism through which cytokinin regulates the activity of one of the PIN proteins, PIN7. The

applicant will use a combination of genomic tools (including microarrays and yeast one hybrid screens) alongside a genetic screen to identify novel cytokinin-dependent factors regulating PIN7.

Details This project will be based at the Centre for Plant Integrative Biology, a world-renowned centre for plant biology with state of the art equipment. We are taking an interdisciplinary approach to investigating root vascular patterning and combine experimental biology with mathematical modelling of vascular patterning. A suitable candidate will have good communication skills and be willing to work in an interdisciplinary team. Applicants are required to have the equivalent of a 2(i) class degree in biology (or related subject) and a desire to research plant development. Experience in some of the following areas would be desirable; plant science, molecular biology, genomics or microscopy. Good proficiency in English is required.

This studentship is available from 1 September 2013 for a period of three years with a postgraduate stipend of £13,726 per year. Due to funding restrictions this project is only available to EU/UK students.

Applications by email to [anthony.bishopp@nottingham.ac.uk](mailto:anthony.bishopp@nottingham.ac.uk)