



# FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY



## FESPB Newsletter



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Chair of Publications Committee

## FESPB/EPSO 2014 Congress

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# PLANT BIOLOGY EUROPE FESPB/EPSO 2014 Congress

22<sup>nd</sup> - 26<sup>th</sup> June 2014, Dublin, Ireland  
Convention Centre Dublin



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of Plant Biology



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## Research News

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### Genomes Gone Wild

By Megan Scudellari. *The Scientist*.  
January 1, 2014

Weird and wonderful, plant DNA is challenging preconceptions about the evolution of life, including our own species. What do cells, genes, mutations, transposons, RNA silencing, and DNA recombination have in common? All were discovered first in plants.

It sounds grandiose, but it's true, and plant biologists delight in reminding others of these plant-derived breakthroughs. The first cell observed under a microscope,

back in the mid-1660s by physicist Robert Hooke, was a plant cell in a slice of cork. Botanist Robert Brown first named the nucleus after observing opaque spots inside orchid cells. The saintly father of genetics, Gregor Mendel, defined the laws of inheritance by studying pea plants. The list goes on.

Today, with the advent of high-throughput sequencing, that legacy of firsts in the plant field is extending to genomics research. In the tens of millions of nucleic acids of familiar and not-so-familiar plant species—from fluffy, domesticated cotton to aquatic, carnivorous bladderwort—plant

biologists are uncovering surprising principles about how genomes are organized and how they evolved.

In the last two years, researchers have stumbled upon some “mind-blowing” phenomena in plant genomics, including genomes so strange that “we didn’t think [they] could be like that,” says R. Keith Slotkin, a geneticist at Ohio State University. Examples include the peaceful coexistence of two different genomes in a single nucleus and the willy-nilly way plants swap genes among species. And just as with Hooke’s, Brown’s, and Mendel’s fundamental discoveries in plant biology, the bizarre behavior of plant genomes often applies to animals as well.

In 2010, a young technician picked his way through a sea of plants at the Royal Botanic Gardens, Kew, in London and clipped a leaf from a Japanese canopy plant (*Paris japonica*), a pretty, umbrella-like perennial with a perky white flower at its apex. Jaume Pellicer was conducting a survey of plant genome sizes, removing small pieces of leaves to stain for the cells’ nuclei and estimate the amount of DNA inside.

There was nothing extraordinary about the Japanese canopy plant—that is, until Pellicer analyzed the stained cells using flow cytometry, a high-throughput technique to detect features of cells suspended in liquid. To Pellicer’s eye, the balls of DNA inside *P. japonica*’s nuclei looked “really, really big,” he recalls. Soon, he confirmed that *P. japonica* carries the largest known eukaryotic genome on the planet, with a whopping 150 billion base pairs—50 times the size of the human genome.<sup>1</sup> “We were astonished,” says Pellicer. Plants in general are known to have sizable genomes, often as a result of whole-genome duplications, so “we were expecting to find big genomes, but nothing that big.” (See “Jaume and the Giant Genome,” *The Scientist*, April 2011.)

Two years later, Victor Albert at the University of Buffalo decided to investigate a group of plant cells with nuclei that looked quite different: they appeared to harbor especially tiny genomes. When Albert and colleague Luis Herrera Estrella sequenced the genome of *Utricularia gibba*, a bladderwort that forms free-

floating mats with hidden underwater bladders that suck in unsuspecting prey, they found that it has one of the smallest genomes ever to be sequenced from a plant—just 82 million base pairs. Even more interesting, the genome is small not because it has fewer genes than other plants. In fact, it has more genes than grapes, papaya, or *Arabidopsis*. Rather, 97 percent of the plant’s genome is protein-coding genes and gene regulatory regions, with only 3 percent having no known function—what scientists often call “junk” DNA.<sup>2</sup> That’s the complete opposite of the human genome, which is made up of 98 percent junk and 2 percent protein-coding genes.

“The implications are that you can make a perfectly good complex, multicellular plant with a gigantic genome or a tiny genome,” says Albert. “You probably need approximately the same number of genes, but the ‘junk’ or lack of ‘junk’ probably doesn’t matter much, if it even matters at all.”

Albert’s findings challenge recent papers from the ENCODE project published in September 2012, which concluded that 80 percent of the human genome contains “functional elements.” Even non-protein-coding sequences should be considered “functional” if they are transcribed into RNA, the ENCODE researchers argued. But Albert and other comparative genomicists don’t buy it. “Biologically active is not the same thing as functional,” says Albert. Just because DNA is transcribed doesn’t mean it is being used.

But much research on noncoding DNA has focused on mammalian genomes, which are all similar in size, around 3 to 4 billion base pairs, says T. Ryan Gregory, who studies animal genomes at the University of Guelph in Ontario, Canada. “Throw a salamander in there, or a pufferfish, and now you’ve got 200- to 300-fold variation in genome size. Now explain [noncoding DNA],” he challenges.

From the vast range of genome sizes within plants, researchers are getting a better grasp not only of noncoding DNA, but of how and why a genome grows or shrinks in the first place.

An increase in genome size is typically a consequence of one of two mechanisms:

the duplication of the entire genome, or the multiplication of transposable elements (TEs) within a genome. The former is common in plants and results in polyploidy, a state in which an organism harbors multiple copies of a genome. But the latter is a far more common cause of size increase in animal genomes. The human genome, for example, is swollen with more than 1 million copies of a single, typically nonfunctional TE called ALU.

But how and why TEs, which are often compared to parasites, multiply in genomes had remained mysterious, despite decades of study in animals. Then Sue Wessler decided to study rice.

To study how TEs might be influencing genome evolution, Wessler, a molecular biologist now at the University of California, Riverside, sought out organisms harboring TEs that were still moving around and increasing their copy number in the genome. They weren't easy to find. Most plants and animals have elaborate and strict mechanisms for keeping TEs quiet. If they didn't, these upstart elements could pop themselves into important promoters and genes all over the place, throwing cellular processes awry. (See illustration.)

Then, in the early 1990s, Wessler discovered a new type of TE. These small elements, called MITEs (for miniature inverted repeat transposable element), were peppered throughout noncoding regions of plant genomes, including the DNA of rice (*Oryza sativa*). And in 2003, her team found that one particular MITE, called mPing, was increasing its copy number by 25 to 40 new insertions per rice plant every generation.<sup>3</sup> Wessler immediately wondered how this could happen without disrupting the physiology of the plant harboring the rapidly enlarging genome.

She found her answer in 2009: although mPing tends to insert into or nearby genes, it avoids exons, meaning it rarely disrupts gene function. Specifically, the element has an insertion preference for AT rich sequences, and rice exons are GC rich.<sup>4</sup> The same is not true in other plants, however, and when Wayne Parrott's lab at the University of Georgia inserted mPing into the soybean genome, the TE inserted

into gene exons far more frequently. "It points out the intimate association between a successful element and its host," says Wessler, who collaborated on the study.

But are TEs just miniparasites, or could they serve a biological purpose in the genome? Some have suggested TEs work as built-in diversity-generating factors in stressed populations. Wessler's laboratory, for example, has found that the insertion of mPing in the rice genome has, in several instances, made the transcription of an adjacent gene stress-inducible. By inserting themselves into promoter regions and even genes themselves, TEs can create new alleles in populations, Wessler adds. And this phenomenon is not just occurring in plants. There are also clear examples of TEs generating diversity within animal genomes. The human adaptive immune system, for example, only has enough genes in a given cell to produce about 20 different antibodies. Thanks to TEs that reshuffle our small deck of antibody genes, however, human immune cells can produce up to 2 million different antibodies to fight foreign invaders. Animal TEs are also particularly active during early brain development, which may help create genetic diversity within a population, despite every member of that population using essentially the same DNA as raw material.

Though TEs can contribute to genome size, the main cause of behemoth plant genomes is polyploidy: when an organism contains more than two sets of paired chromosomes. In most cases, polyploidy occurs due to an error in cell division, resulting in a whole genome, rather than half, being retained in a gamete. When two such diploid gametes join to form a zygote, it yields tetraploid offspring. (See illustration.) For reasons that are unclear, this appears particularly common among plant species. All flowering plants, in fact, have had a genome doubling sometime in their history, and most have had more than one. The Japanese canopy plant, for example, is an octaploid, says Pellicer—with four genome duplications in its history. "There are lots of [plant] groups where you find polyploidy," says Jonathan

Wendel, who studies cotton's tetraploid genome at Iowa State University. "It's clearly important, but finding the smoking gun of how it's important is really hard."

In some cases, genome doubling is a misnomer—it's not a doubling of a single genome, but a genomic union of two different species in a single organism. When a diploid gamete from one species combines with a diploid gamete from another species and the resulting organism survives, a new species is born—one with two full genomes. (See illustration.) This is speciation at its most dramatic, and it is far more common than one might think.

Cotton, the soft, malleable fiber you may be wearing as you read this, is the result of one such "illicit affair," as Wendel likes to call it. At some point in history, the genome from an old-world cotton species and the genome from a new-world cotton species joined together, resulting in cotton as we know it today, with double the number of chromosomes of either parent species. Although such cross-species hybridization is much rarer in animal species, says Wendel, it happens there too. For example, the Lonicera fly (genus *Rhagoletis*), discovered in the U.S. in 2005, is a hybrid of two existing insects, the blueberry maggot and the snowberry maggot.

The effect of such genomic combining on the fitness and phenotype of an organism, however, had been unclear. "It's really difficult to catch this ecological angle in action, to show differential fitness between a polyploid and a diploid in the same environment under the same conditions," says Wendel. But just in the last few years, this has been accomplished.

In 1949, while walking around the campus of Washington State University (WSU) in Pullman, botanist Marion Ownbey noticed an oddly colored species of *Tragopogon*, a weedy flower also known as salsify or goatsbeard. Upon further investigation, he discovered that the species, which he named *T. mirus*, was a hybrid of two *Tragopogon* species, and that it had double the chromosomes of either parent. And since the parent species had not arrived in the Pacific Northwest from Europe until the 1920s, Ownbey realized

that *T. mirus* was a brand-new polyploid species.

In the mid-1990s, while working at WSU, husband-and-wife team Douglas and Pamela Soltis began to analyze the new *Tragopogon* species, realizing they had a chance to watch the combination of two genomes in action. When they moved across the country in 2000 to take jobs at the University of Florida, they brought *Tragopogon* with them, and remade the polyploid in the lab.<sup>5</sup> Within a few generations, the Soltises observed a genomic shakedown in the nucleus of *T. mirus*, including changes in gene expression, rapid reshuffling of chromosomes, translocations of genes, and changes in methylation to activate or deactivate genes.

In addition to observing molecular changes, the Soltises observed some of the only direct evidence of polyploidy being favored by natural selection. Although *T. mirus* individuals have been created from its two parent species multiple times in the western U.S., and in numerous locations where both parents once thrived, now only the polyploid lives: it outcompeted its parents. "It's like the North American success story: the parents get here, eke out an existence, give rise to children of North American origin, and those children are highly successful," says Douglas Soltis.

This and other evidence suggest that a large genome can be beneficial. In many cases, polyploid plants, especially cultivated crops, appear to be hardier than their diploid relatives. This may be because if a gene is accidentally deleted or mutated in an individual, a spare copy can take over.

Imagine borrowing a few genes from a lion to improve your night vision, sneaking a couple from a salmon to breathe underwater, and swiping one or two more from a salamander in case you need to grow back a finger.

Yes, it sounds crazy, because animals don't normally swap genes. But plants do, even between species as different as humans and salamanders. Plants that intermingle physically can trade DNA—typically mitochondrial DNA—but not always. This gene swapping can happen

when a parasitic plant latches onto a host, like a vine wrapping around the trunk of an oak tree, or when two plants grow close together and graft onto each other, says Indiana University's Jeffrey Palmer, who studies horizontal gene transfer in plants. Recently, Palmer demonstrated that land plants take up foreign mitochondrial DNA from other land plants and green algae, but not from animals or fungi. He hypothesizes that this is because plants and green algae share a mechanism to fuse mitochondria together, while animals and fungi have a completely different, noncomplementary fusing mechanism. "Species barriers go deep between plants and animals," says Palmer.

The king of gene stealing is *Amborella*, a nondescript flowering plant that grows only in New Caledonia, an island off the east coast of Australia. *Amborella* can often be found draped with mosses, lichens, and other organisms, and apparently the crafty plant extracts a genetic tax from each one. Sequencing the *Amborella* mitochondrial genome "just knocked our socks off," says Palmer. "For every native gene, it contains six foreign copies of that gene, acquired from a range of land plants and green algae." (D.W. Rice et al., *Science*, in press)

In most cases, horizontal gene transfer in plants appears to be neutral—it doesn't affect an organism's phenotype. But in a few cases, foreign genes supplant or replace native genes and assume an active role in the genome. In one transfer of a key mitochondrial gene for respiration from the blueberry family to *Ternstroemia*, a genus of flowering plants from the tropics, the native and foreign copies of the gene began to recombine, leading to the diversification of mosaic genes across a group of *Ternstroemia* species. And in 2012, researchers found that some species of grasses in the genus *Alloteropsis* had acquired nuclear genes from other grasses that are essential for C4 photosynthesis, which employs a more efficient form of carbon fixation. Only those *Alloteropsis* species that possessed these genes were able to perform C4 photosynthesis.<sup>6</sup>

Plants don't rely only on horizontal gene transfer for new alleles; they also gain new

genes through the traditional route of mutation. But here, once again, plants go to the extreme, boasting some of the fastest and slowest mutation rates on Earth.

Several years ago, while studying the organization of chloroplast genomes in geraniums, Robert Jansen of the University of Texas at Austin noticed that mutation rates appeared to be exceptionally high compared to other plant species.<sup>7</sup> He shared his findings with Indiana University's Palmer and Jeff Mower at the University of Nebraska, both of whom studied the mitochondrial genomes of the same family of plants, Geraniaceae. Lo and behold, the two also identified highly accelerated genetic mutation rates in the mitochondria. The three researchers decided to work together to find out if the geranium family's three genomes—nuclear, mitochondrial, and chloroplast—were mutating in coordination.

Geraniaceae is "a natural system for looking at mutation, because there's so much variation," says Jansen. The plant family could offer insight as to how multiple genomes in one organism coevolve, including human nuclear and mitochondrial genomes. With a grant from the National Science Foundation, the team has so far generated sequence data for the mitochondrial and chloroplast genomes of more than 100 Geraniaceae species (which are shorter and easier to sequence than nuclear genomes), and will be sequencing the transcriptomes of 30 species from the group. They've just begun to analyze the data, but they hypothesize that the geranium's DNA repair system, which fixes breaks in all three genomes, experienced some type of mutation or alteration, speeding up the mutation rate across the organism's three genomes.

One way to tell if the geranium DNA repair system is faulty would be to compare it to an especially slow mutator, such as the tulip tree. The tulip tree's mitochondrial genome—which Palmer sequenced because "it happens to be a tree that I love"—turns out to have one of the slowest mutation rates of any known mitochondrial genome.<sup>8</sup> It's essentially a living fossil,

says Palmer, who believes that the tree may have an especially good system for repairing DNA damage, and that studying it could help us learn how to prevent deleterious mutations in our own DNA.

"Plants are a model system for comparative genomics and other processes," says Palmer. In polyploidy, transposable elements, and rates of mutation, plants lead the way. And there's plenty more exciting work coming down the pipeline from plants, he adds, but you have to keep your eye out for it. "Furry animals get on the covers of *Science* and *Nature* a lot more than plants do," he says with a laugh.

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### **Sniffed out: 'Gas detectors' of the plant world**

Source: ScienceDaily. January 23, 2014

The elusive trigger that allows plants to 'see' the gas nitric oxide (NO), an

important signalling molecule, has been tracked down by scientists at The University of Nottingham. It is the first time that a central mechanism for the detection of NO in plants has been identified.

Led by Professor Michael Holdsworth in the School of Biosciences, a team of experts, including researchers from UK and EU Universities and government research institutes, have found the 'master regulators' that control the detection of NO by plants and that regulate many important aspects of plant growth and response to environmental stress.

Their research "Nitric oxide sensing in plants is mediated by proteolytic control of GroupVII ERF transcription factors" is published in the academic journal *Molecular Cell*.

Plants fine-tune their growth and survival in response to various signals, including internal hormones and external factors such as light or temperature. Nitric oxide gas is one such signal.

Professor Holdsworth said: "In plants, NO regulates many different processes throughout the plant's lifetime from seeds to flowering and responses to the environment. Although the effect of NO on plants has been known for many years, a general mechanism for the initial sensing of this important molecule has remained elusive. We have identified a small number of key proteins, called transcription factors, which act as 'master sensors' to control NO responses throughout the plant life cycle."

A specific structure at the beginning of these proteins means that they are rapidly degraded in the presence of NO. However, when NO is absent they become stable, resulting in changed growth and development. This mechanism allows plants to sense the NO signal and alter its growth accordingly.

Interestingly, these proteins had previously been shown to control the plant response to low oxygen stress, which occurs when plants are flooded. Therefore they appear to act as central "gas detectors," providing plants with an inbuilt mechanism for sensing and responding to different gas signals.

Due to the importance of both NO and oxygen in plant development and stress

responses, these proteins represent promising targets in the development of crops that have improved agricultural traits, particularly in relation to climate change.

The above story is based on materials provided by University of Nottingham.

Journal Reference: Gibbs et al. Nitric Oxide Sensing in Plants Is Mediated by Proteolytic Control of Group VII ERF Transcription Factors. *Molecular Cell*, January 2014.

### **Brazilian beans and Japanese barley shipped to Svalbard seed vault**

Jonathan Watts. *The Guardian*, 26 February 2014

Some 20,000 plant species from more than 100 countries and institutions will be added to the global seed bank in Norway.

A Noah's Ark of 20,000 plant species will unload this week at a remote Arctic port to deposit humanity's latest insurance payment against an agricultural apocalypse or a man-made cock-up.

Brazilian beans and Japanese barley are among the botanical varieties that are carried aboard the ship that is shortly expected to dock near the Svalbard global seed vault, that celebrates its sixth anniversary this week.

The facility, which is bored into the side of a mountain by the Barents Sea, is primarily designed as a back-up for the many gene banks around the world that keep samples of crop diversity for agricultural businesses.

But its operators, the Global Crop Diversity Trust, say the "Doomsday Vault" could also help to reboot the world's farms in the event of a climate catastrophe or a collapse of genetically modified crops.

Built to withstand a nuclear strike, a tectonic shift or rising sea levels, the vault has the capacity to store 4.5m different seed varieties for centuries.

Currently, it holds 820,619 samples of food crops and their natural relatives, but this is steadily increasing with one or two shipments each year, according to the trust, which maintains the seed vault in partnership with the Norwegian government and the Nordic Genetic Resources Centre.

The latest shipment contains deposits from more than 100 countries and institutions, including the International Potato Centre, the Australian Tropical Crops Collection and the International Maize and Wheat Improvement Centre.

A first collaboration with the Barley Germplasm Centre of Okayama will see the addition of the plant widely used for Japanese whisky and shochu. The Brazilian Agricultural Research Corporation is sending 514 samples of "the common bean" which is the primary ingredient in the national dish of feijoada.

Eventually it is thought that the vault may serve as a repository for every plant species used by humans.

"Each and every single deposit into the vault provides an option for the future," said Marie Haga, the Crop Trust's executive director. "At a time of unprecedented demands on our natural environment, it is critical to conserve plant genetic resources for food and agriculture. This will guarantee farmers and plant breeders continued access to the raw materials they need to improve and adapt crops."

### **Pheromone Factories**

By Kerry Grens. *The Scientist*. February 26, 2014

Genetically modified tobacco plants produce pheromones that can trap pests. Rather than relying on industrial labs to synthesize pheromones to attract or repel crop pests, researchers have genetically engineered plants to do such work for them. Writing in *Nature Communications* this week (February 25), plant biologists report on genetically engineered tobacco plants that produce a moth sex pheromone. Once extracted from the plant, the pheromone can be used to trap male moths.

"It will change the way that commercial pheromone outfits do business and will significantly enhance the quality and potentially lower the cost of the products that they provide," Steve Seybold of the US Department of Agriculture Forest Service's Pacific Southwest Research Station in Davis, California, told *ScienceNow*.



Plant-produced pheromones might also reduce the use of harmful chemicals in pheromone production. “What we demonstrated in this study is a more environmentally friendly approach that avoids the need to use toxic chemicals and eliminates hazardous byproducts from producing synthetic pheromones. The plant just handles everything,” study coauthor Timothy Durrett, a biochemist at Kansas State University, said in a press release.

Tobacco is used in a variety of so-called “molecular farming” (or biopharming) pursuits, including the development of an HIV medicine and vaccines.

Christer Löfstedt, a chemical ecologist at Lund University in Sweden who led the pheromone project, told ScienceNow that next he’d like to bypass the extraction step and have plants do the rest. “Right now, we derive pheromone components from plants and prepare baits for trapping from these products, but our next goal is to develop [genetically modified] plants that can release these pheromones into the environment.”

### **Plants Without Plastid Genomes**

By Ed Yong. The Scientist. February 28, 2014

Two independent teams point to different plants that may have lost their plastid genomes.

Plant cells photosynthesize using chloroplasts—small structures that were once free-living bacteria and retain their own DNA. Even when plants lose the ability to photosynthesize, they retain a genome in their plastids, and some scientists have argued that these genes are indispensable.

But two teams have now independently found the first examples of plants whose plastids seem to lack a genome, including a giant rot-scented flower and a group of single-celled algae. Neither case is iron-cast yet, but given the teams’ intense searches, these plants’ plastid genomes are either missing, well-hidden, or can be found only at very low levels.

Jeanmaire Molina from Long Island University and Michael Purugganan from New York University focused on *Rafflesia*

*lagascae*—a Philippine parasite that does not photosynthesize, and lacks stems, roots, and leaves. The only sign of its existence is a huge red flower, which protrudes from its host vine and looks and smells like rotting flesh.

*R. lagascae* still has plastid-like structures in its cells but, despite using a variety of methods, the team could not find any hints of an intact plastid genome. “It’s hard to prove a negative, but we came up with controls to make sure we got it right,” said Purugganan. They tried different methods for assembling fragments of sequenced DNA or identifying plastid genes. They easily found *R. lagascae*’s mitochondrial genome, which also derived from ancient bacteria. And they showed that in other plants, like *Arabidopsis thaliana*, non-photosynthetic tissues like roots still contain huge amounts of plastid DNA.

Molina and Purugganan did detect 46 small fragments of plastid DNA, but none of them amounted to full genes. Even if they were, these genes would have so many mutations that they would not be functional. These plastid DNA fragments remain a mystery, although a third of them may have come from the host vine, the researchers proposed.

Meanwhile, David Smith from the University of Western Ontario and Robert Lee from Dalhousie University found similar results in *Polytomella*—a genus of single-celled, colorless, freshwater algae. It too has a plastid but not a trace of a plastid genome. Smith and Lee also showed that while the alga’s nucleus produces proteins that are used in its plastids, none of these are involved in expressing plastid genes—another sign that such genes do not exist.

If these plants have genuinely lost their plastid genomes, neither team knows why. “One possibility is that *Rafflesia* parasitism started in the mid-Cretaceous,” said Purugganan. “It may be that it just took some time to evolve the mechanisms whereby you can safely get rid of the chloroplast genome.” Smith and Lee suggested that *Polytomella* may be generally prone to gene loss in its organelles—its mitochondria have among the smallest genomes of any plant.

“These studies show that plastids can at least lose their genome given the right circumstances, which opens up the big question: Why do they have genomes at all?” said Smith. “We don’t know the answer to that.”

After all, non-photosynthetic plants, including parasites like *Rafflesia*, still retain plastid genomes, albeit heavily reduced ones. Even the malaria parasite *Plasmodium*, which descended from the same photosynthetic ancestor as plants, still clings onto its plastid genome.

Some scientists have argued that plastid genomes include essential genes with metabolic roles, such as making heme. But *Rafflesia* and *Polytomella* suggest that such genes are either not vital or have been relocated. Both teams now want to completely sequence the nuclear genomes of their respective plants, to see if they contain the missing plastid genes. Smith said he hopes that other scientists will investigate these plants using microscopy and stains that bind to DNA. “The final verdict will come in when lots of people try lots of approaches,” he said.

“Showing convincingly that something does not exist is always a challenge in science,” says Kirsten Krause from The Arctic University of Norway, who has investigated plastid evolution but was not involved in the studies. “The authors of both publications were wise to leave a back door open by indicating that plastid genome loss is a possible conclusion of their findings but not—not yet?—a new fact.”

In an e-mail, she added, “I am nevertheless convinced that that the publications will ignite a new wave of scientific dispute and, hopefully, of research in this field.”

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## **Fire-blight resistant apples**

Source: ETH Zurich. 13.03.2014

Researchers from ETH Zurich and the Julius Kühn Institute in Germany have created the first fire-blight-resistant apple. With the aid of so-called cis-genetic engineering, they transferred a resistance gene from a wild apple into the genome of a Gala apple. Tests in the greenhouse indicate that the gene is effective in protecting the tree against the disease.

Fruit farmers dread fire blight. The infection keeps flaring up again and causes considerable damage to apple plantations. In 2007, when the last major epidemic hit Switzerland, the damage the country suffered cost CHF 50 million and 250,000 trees had to be destroyed. Farmers primarily use sprays containing the antibiotic streptomycin against the pathogen, the bacterium *Erwinia amylovora* – a controversial method to save fruit trees and harvests.

A team of researchers headed by ETH-Zurich plant pathologist Cesar Gessler and from the Julius Kühne Institute in Germany report a genetically modified apple of the popular Gala variety in the latest issue of *Plant Biotechnology Journal* that is resistant to fire blight. In an earlier issue of this journal, the researchers presented an apple tree of the same variety that can ward off scab, a common fungal disease, thanks to the insertion of a scab resistance gene of a wild apple.

The researchers succeeded in identifying and isolating the gene for fire-blight resistance in a wild apple for the first time and confirming its function as a resistance-mediating gene. The gene carries the genetic code for a protein that recognises a surface protein of the pathogen, triggering a defence response in the plant affected. This one, single gene is sufficient to protect the plant against the disease.

Gessler and his collaborators were using so-called cis-genetic engineering. Additional genes are incorporated into cis-gene organisms using the biotechnological methods available. However, these are not foreign to the species, as in the case of so-called transgenic organisms. Instead, the apple only receives genes from another variety of apple. Although the

gene was marked with other genes that were foreign to the species to discern whether the gene transfer was successful, the researchers managed to remove these foreign genes from the genome of the Gala apple afterwards so that only the wild-apple genes remained.

The researchers tested the fire blight resistance properties of the cis-gene apple trees in the greenhouse at the Agroscope research facility in Wädenswil and in Germany by infecting them with fire blight. The results revealed that the resistance gene took effect and prevented the trees from becoming infected.

Although Gessler has now been able to reap the fruits of his years of research and development work, he does not believe that fruit farmers will ever grow these cis-gene apples. On the one hand, there is still a moratorium on genetic engineering in Switzerland, banning the cultivation of genetically modified organisms (GMO), which also affects cis-gene crops. "Moreover, there is still too much opposition to GMO in Switzerland," he says. And, unlike in the USA, here in this country and the EU we don't assess individual products for approval, but rather the technology used while growing them. "Unless the attitudes and legislation change, the cis-gene Gala apple will never be grown," the plant pathologist sums up.

Gessler is not a GMO hardliner looking to push genetically modified crops at all cost. "In the case of crops like the banana, cassava or apples, which can be reproduced via clones, however, the use of genetic engineering makes sense," he says. Consumers have to realise that an organically grown Gala apple is treated with copper and sulphur at least twenty-five times, which has a serious impact on the soils, air and groundwater. Scab and fire-blight-resistant cis-gene Gala apples do not have to be treated in this way, making them more environmentally friendly than their bio-counterparts.

Breeding in the resistance gene via conventional cultivation, however, takes too long, says Gessler. The Gala variety would have to be crossed with a wild apple and the undesired properties of the wild apple bred out again in subsequent generations, which can take many

decades and ultimately results in a new variety.

Another obstacle stands in the way of growing cis-gene apple trees in the foreseeable future: "Although the gene now implanted works, it only takes one mutation for the pathogens to get around this resistance, which can happen very quickly," Gessler points out. Consequently, more resistance genes need to be added to the cis-gene Gala apple to have a cumulative effect. As a result, the probability of the pathogen circumventing the infection protection drops exponentially. Only then can we really begin to consider planting cis-gene trees on open land. Agroscope will continue to conduct research into this multiple resistance as Gessler is retiring from ETH Zurich in April 2014.

This means that the threat to fruit cultures from fire blight has not been averted in the short run. "Another epidemic might break out this spring," warns Gessler. Warm and wet weather shortly before the flowering season are ideal conditions for the bacteria that cause fire blight to multiply at an explosive rate.

### **Elusive Receptor ID'd**

By Kerry Grens. *The Scientist*. April 1, 2014

Scientists identify an extracellular ATP receptor in plants.

The membrane receptors that help mammalian cells respond to extracellular ATP have been known for two decades. Over the years, evidence that plants also use extracellular ATP had bubbled up in the literature, but no one had identified the receptor until a determined team of plant scientists spent five years working on a massive genetic screen in *Arabidopsis*.

Gary Stacey's group at the University of Missouri analyzed 50,000 mutagenized seedlings to find one that did not respond to the addition of extracellular ATP. The gene responsible encodes a lectin receptor kinase, a finding that surprised Stacey, given that lectins are usually associated with proteins that bind sugars. "When we found this, it made me worry," he says, "but then we found it bound ATP with high affinity."

Knowing the receptor's identity can help uncover the role of extracellular ATP, which Stacey suspects to be important in stress responses. His group showed in the study that many of the genes whose expression is induced by ATP signaling are also expressed following wounding. "Everyone assumed it was wounding" causing this upregulation, he says. "But now we showed it's the ATP coming out of the wound that's inducing this response."

"Their data [are] quite convincing" that the lectin receptor kinase is an extracellular ATP receptor, but there might be others waiting to be found, says Stephen Chivasa, who studies extracellular ATP in plants at Durham University in the U.K. "My suspicion is that there will be even more coming out."

Reference: J. Choi et al., "Identification of a plant receptor for extracellular ATP," *Science*, 343:290-94, 2014.

### **Cheaper Fuel From Self-Destructing Trees**

Source: *Science Now*. 3 April 2014

Wood is great for building and heating homes, but it's the bane of biofuels. When converting plants to fuels, engineers must remove a key component of wood, known as lignin, to get to the sugary cellulose that's fermented into alcohols and other energy-rich compounds. That's costly because it normally requires high temperatures and caustic chemicals. Now, researchers in the United States and Canada have modified the lignin in poplar trees to self-destruct under mild processing conditions—a trick that could slash the cost of turning plant biomass into biofuels.

"This work has the potential to fundamentally change the economics of lignin degradation," says Ronald Sederoff, a plant geneticist at North Carolina State University in Raleigh. If researchers can add the same self-destructing lignin to agricultural plants such as corn and energy crops such as switchgrass—an effort already under way—that could open the spigots for cellulosic ethanol, made from plant waste rather than food. The U.S. Department of Energy has backed a number of cellulosic ethanol producers,

and in 2007 it forecast that by this year they would be making more than 6 billion liters of cellulosic ethanol. Yet this year's actual production is expected to be just 1% of that volume.

The problem is the lignin. More than two-thirds of plant matter consists of cellulose and hemicellulose fibers, both made up of long chains of glucose and other sugar molecules. Much of the rest is the lignin that wedges between the other fibers and glues them together, providing rigidity and preventing pathogens from lurching on the sugary materials. To remove that glue, engineers typically heat biomass to 170°C for several hours in the presence of sodium hydroxide or other alkaline compounds that break lignin apart. This "pretreatment" accounts for between one-quarter and one-third of the cost of making cellulosic ethanol, says Bruce Dale, a chemical engineer and biomass pretreatment expert at Michigan State University in East Lansing.

Plant biologists have tried for decades to work around their troubles with lignin. One early approach decreased the expression of plants' lignin-producing genes. But that backfired, as the plants either wound up with stunted growth or keeled over when hit with a gust of wind. "Plants really need lignin," says John Ralph, a plant biochemist at the University of Wisconsin, Madison.

Among the strategies for dealing with lignin, numerous teams have tried altering the chemicals that make up lignin. Although the structure of lignin varies from species to species, most plants assemble it from three main building blocks called coniferyl alcohol (CA), sinapyl alcohol (SA), and p-coumaryl alcohol, producing chains abbreviated G lignin, S lignin, and H lignin, respectively. Several teams have manipulated plant genes to change the proportions of building blocks, hoping to create a lignin that degrades more easily. Researchers led by Clint Chapple of Purdue University reported in *Nature* last month, for example, that plants engineered to produce only H lignin wound up dwarfed, but knocking out certain regulatory genes enabled them to grow to a near-normal size. H lignins give up their sugars with less pretreatment, but the

chemical bonds between the remaining lignin molecules are still hard to break.

Ralph and his colleagues opted for another path. Instead of altering the proportions of lignin building blocks, they added a new one—ferulic acid (FA)—that pairs up with CA and SA building blocks. These pairs then form bonds with their neighbors that are easier for chemists to break. (A few plants naturally use these FA-containing pairs in making lignins that serve as plant defense compounds, Ralph says.) They hoped that by introducing paired building blocks throughout the lignin, they could later “unzip” the lignin’s structure during pretreatment.

The feat took several years to pull off. Ralph’s team had to isolate the genes for the synthesis of FA-containing building blocks, insert them into plants, show that the plants could make the compounds, send them to the cell walls, and incorporate them into lignins. But online today in *Science*, Ralph and his colleagues report that they’ve now produced “zip-lignins” in young poplar trees. The plants appear healthy and show every sign of normal growth in the greenhouse. But when ground up and subjected to a mild base at 100°C, the lignins readily fall apart, releasing twice as many sugars as their wild-type kin do under the same conditions. “It’s the most promising method of changing lignin that I’ve seen so far,” Sederoff says.

Ralph says his team is already working to insert zip-lignins into corn plants. If the effort succeeds, it could save cellulosic biofuel companies serious cash and may even propel them to profitability, Dale says. It could also spawn a new generation of biorefineries that convert plant cellulose into plastics and other industrial materials. But Dale and others caution that it could take a decade or more. Any newly engineered plants and trees must still be field-tested to show that they grow normally and aren’t more susceptible to pests, among other things. Then researchers must also show that they pass economic muster in pilot-scale and demonstration biorefineries. But if the strategy works, biofuel-makers may finally find a way out of the glue that has trapped them for decades.

## **Calcium waves help the roots tell the shoots**

Source: Science Codex. April 3, 2014

For Simon Gilroy, sometimes seeing is believing. In this case, it was seeing the wave of calcium sweep root-to-shoot in the plants the University of Wisconsin-Madison professor of botany is studying that made him a believer.

Gilroy and colleagues, in a March 24, 2014 paper in the *Proceedings of the National Academy of Sciences*, showed what long had been suspected but long had eluded scientists: that calcium is involved in rapid plant cell communication. It’s a finding that has implications for those interested in how plants adapt to and thrive in changing environments. For instance, it may help agricultural scientists understand how to make more salt- or drought-tolerant plants.

“How do you think plants live?” Gilroy asks. “If I poke you, I see an instant response. You move away. Plants live in a slightly different world. They are rooted to the ground, literally, and they respond to the world either by growing or creating chemicals.”

Calcium is involved in transmitting information in the cells of humans and other animals, contracting muscles, sending nerve signals and more.

In plants, scientists believed it had to also play a role in processing information and sending rapid signals so that plants can respond quickly to their environments.

Imagine you are a plant being eaten by a caterpillar: “It’s like a lion chewing your leg,” says Gilroy. “If an insect is chewing your leaf, you’re gone unless you determine something effective immediately.”

But no one had ever been able to see it before. Even Gilroy’s team found it by accident.

The team was using a specific calcium sensor they thought wasn’t going to work. They speculated it could serve as a control in their studies.

The sensor’s brightness changes in the presence of calcium, displayed on screen as a change from green to red through a process known as fluorescence resonance energy transfer, or FRET. Typically, this

particular sensor is so sensitive to calcium it is nearly always red.

But when researchers applied stress to the tip of a plant's roots — a high concentration of sodium chloride salt — it triggered a wave of red that traveled rapidly from the root to the top of the plant. "We were kind of like, 'Why is it even working?' says Gilroy. "It was probably telling us we were looking in the wrong realm. It's like we could only hear the people shouting and we couldn't hear the talking."

The calcium wave, a flush of red on an otherwise green palette, traveled on a scale of milliseconds, traversing about eight plant cells per second — too quick to be explained by simple diffusion of salt.

"It fit with a lot of our models," Gilroy says. "But the idea that it's a wave is one step beyond what our models would predict."

Within 10 minutes of applying a small amount of salt to the plants' roots, typical stress response genes were turned on in the plant.

Also turned on was the machinery to make more of a protein channel called two pore channel 1 (TPC1). Within one-to-two minutes, there was 10 times more of the building blocks needed to make the channel, which is thought to be involved in calcium signaling.

Gilroy and his team then looked at plants with a defect in TPC1. They had a much slower calcium wave — about 25 times slower — than plants with normal TPC1. When they studied plants expressing more of the TPC1 protein, the calcium wave moved 1.7 times faster.

Plants with more channels also grew larger and contained more chlorophyll than plants with normal or mutated TPC1 when grown in salt water.

The protein channel is present in all land plants, says Gilroy, and it's found throughout the plant. This is one of the many reasons it surprised the team to learn the calcium wave moves only through specific cells in the plant, like electrical signals moving through nerve cells in humans and other animals.

"We weren't expecting that," Gilroy says. "It means specific cell types have specific functions ... there must be something

special about those cells. We're really at the beginning."

The lab is now looking at the molecular machinery that makes up TPC1, to figure out how the parts of the channel work.

And now that the scientists know that calcium talks, the volume is turned up. The work is just getting started.

"We can hear the screaming," says Gilroy. "Now we're trying to see what the vocal chords are doing."

### **Worm Subverts Plant Attack**

By Ed Yong. The Scientist. April 3, 2014

A parasitic nematode relies on a plant's defense mechanism to invade and grow.

Plants defend themselves against infectious bacteria and fungi by releasing a storm of reactive oxygen species (ROS), which kill the invaders. But for the sugarbeet nematode (*Heterodera schachtii*), this defensive attack is actually the key to its success.

Shahid Siddique and Christiane Matera from the University of Bonn in Germany have found that the nematode switches on plant genes that produce ROS. Without these molecules, the parasite cannot properly grow within its host. Their results are published April 3 in *Science Signaling*. *H. schachtii* targets sugar beets, cabbages, broccoli, and related plants. It enters their roots as a larva and burrows its way toward the plant's vascular cylinder, which runs down the middle of each root. The larval nematode then gently stabs the host's cells with its mouthparts, causing them to partially dissolve and fuse with one another. The result is a giant nurse cell made of more than 200 merged plant cells—an all-you-can-eat buffet that the nematode taps into for nourishment while it matures into adulthood.

This sequence of events plays out differently in mutant *Arabidopsis* plants with faulty copies of the *RbohD* and *RbohF* genes, which protect against infections by producing ROS. These mutants are generally more susceptible to fungal or bacterial infections. But to Siddique and Matera's surprise, these plants are more resistant to *H. schachtii*. While the nematodes can still invade, they

make slower progress toward the vascular cylinders and create smaller nurse cells. Their eventual numbers are lower and their adult bodies smaller.

The researchers suggested that when the nematode first invades and wounds a root, it triggers an immune response that kills off local cells. The ROS contribute to this process, but also restrict it to the zone of infection. "They are executing cells, but also controlling the degree of cell death so it doesn't get out of hand," said Siddique.

In the mutant plants, which do not produce ROS, the wave of dying cells spreads faster than the nematode. This prevents the worms from successfully setting up the nurse cells that they need to feed from.

Jeff Dangl from the University of North Carolina at Chapel Hill, who studies plant-pathogen interactions but was not involved in the work, praised the study. In an e-mail to *The Scientist*, he said that it supports the idea that two responses to infections—an ROS burst and a wave of programmed cell death—can be antagonistic, rather than the former driving the latter.

It is unclear whether the nematodes actively release substances that stimulate the produce of ROS, or if they are simply relying on the plant's natural response. The team next wants to understand how the nematode's presence triggers cell death, and how the ROS suppress this.

"This work gives us new clues as to how we might inhibit the ROS-producing machinery in the root to inhibit nematode infection, which is a huge agricultural problem in many crops," said Dangl.

Reference: S. Siddique et al., "Parasitic worms stimulate host NADPH oxidases to produce reactive oxygen Species that limit plant cell death and promote infection," *Science Signaling*, 7:ra33, 2014.

### **'Noah's Ark' of the fruit world where the banana seeds of 1,600 varieties are grown**

Source: *The Independent*. 05 April 2014

Behind a locked door in a basement on a Belgian university campus lie row after row of yellow-capped test tubes on brightly lit, refrigerated racks. Inside each of the 15,000 or so tubes sits a tiny, fragile green plant.

In space-age surroundings about as removed far from the jungles of Thailand or Malaysia, the farms of Ghana or Tanzania and the plantations of Costa Rica or Guatemala as it is possible to be - sits the world's largest collection of a crop responsible for sustaining 410 million people - the banana.

The test tubes of the World Banana Collection - held under the auspices of the United Nations at Leuven University, near Brussels - hold seedlings from each of 1,400 different varieties of edible bananas and plantains painstakingly gathered from across the world to be preserved for humanity.

Each is bred and re-bred on a constant cycle to produce small "master plants" from which, if needed, millions of copies can be propagated to be returned to nature or horticulture.

But the collection, overseen by Professor Rony Swennen, one of the world's leading banana scientists, has recently taken on a more vital purpose: Within its serried racks could lie the answers to the raft of diseases which threatens to decimate the global banana supply.

Early last year, workers on a commercial banana farm in Mozambique noticed a tell-tale yellowing of leaves on some of their plants. Within weeks the stems had started to collapse and by last December the worst fears of scientists had been confirmed - the worst of these diseases, Panama Disease Tropical Race 4 (TR4), had arrived in Africa.

Following confirmation of the outbreak, limited to a small number of fields, the plants were destroyed and a strict sanitary cordon placed around the farm in the hope it would stop the spread of the disease across Mozambique and beyond.

It is likely to be a forlorn hope.

TR4 is the natural born killer of the banana world, capable of wiping out entire plantations within two to three years and then spreading "sleeper" spores into the soil which will last for decades and decimate any new crop.

Once it takes hold, passing through the roots into the stems of the banana plant, the fungus effectively chokes it to death, blocking the paths through which water and nutrients pass. TR4 is so potent that it

has earned the nickname “banana AIDS” and there is currently no proven cure.

Since it emerged in Malaysia and Indonesia in the 1990s, scientists and plant protection experts have battled to prevent the spread of TR4 from south east Asia to the world’s other banana-producing regions. In Malaysia, it wiped out a thriving export industry while in Indonesia it choked off the export trade before it could begin. It has also devastated crops in the Philippines and reached China.

But its appearance in Mozambique, at the southern end of a continent where the banana is one of the most important staple foods, opens a new front in the battle against TR4 which has set alarm bells ringing across the world, in particular at the Rome headquarters of the Food and Agriculture Organisation (FAO), the United Nations body whose goal is the defeat of hunger.

In a briefing obtained by The Independent, the FAO will this week warn that the disease poses a risk to “the global banana supply” and united action is needed by governments, the big banana producers and research bodies to prevent the spread of TR4, also known as *Fusarium oxysporum cubense*, and its grim implications for tropical countries where bananas are both a vital source of food and income.

The document states: “Virtually all export banana plantations... and also a considerable part of the bananas cultivated for local markets are vulnerable to this race [of Panama Disease].

“Once present in the soil the disease cannot be controlled. The social consequences of the fusarium wilt can be severe as bananas are an important source of food, income, employment and government revenues in many tropical countries.”

The scenario which is concerning the authorities and many scientists most is the spread of TR4 to Latin America, where at least 70 per cent of the bananas used for the global export trade, worth some \$9bn (£5.4bn), are grown.

The export trade is dominated by a single variety, Cavendish, which was introduced in the 1950s after an earlier version of

Panama Disease wiped out plantations growing Gros Michel, a sweeter, tastier banana considered vastly superior to its successor but unable to resist the fungus. It was the disappearance of the Gros Michel which inspired the song, “Yes, we have no bananas”.

The Cavendish proved resistant to the original versions of Panama and, though it was less palatable and bruised more easily than Gros Michel, it kept well and became the banana of choice for the big growing companies such as Fyffes and Chiquita (which last month announced a merger to create the world’s largest grower), Dole and Del Monte.

Today, some 95 per cent of bananas grown for export are Cavendish to meet the world’s insatiable demand for this nutritious fruit.

Some 17 million tonnes of Cavendish are traded internationally each year (up from 12m tonnes in 2001), making it the world’s most lucrative fruit. Americans eat more bananas than apples and oranges combined.

In cash terms, bananas are the most important export for Costa Rica, Ecuador, Panama and Belize, and in the top three for five other countries ranging from Colombia to Cameroon.

But now history is repeating itself and Panama Disease is once more on the march, only this time there is no new “Cavendish” waiting in the wings to replace the disease-susceptible variety. The world’s banana trade is based on billions of clones of the same plant which has no resistance to its fast-spreading fungal nemesis.

The multinational growing companies hope that the march of TR4 towards Latin America can be slowed or even halted by stringent quarantine and biological-control measures, despite proof in Jordan and Mozambique, where it is thought to have been transferred via plantation workers from the Philippines or Latin America, that it can now leap continents.

Experts agree that TR4’s destruction of Cavendish could take years or even decades to reach its zenith but warn Latin America has almost no chance of avoiding its grip.



Prof Swennen, who curates the banana collection on behalf of the charity Bioversity International, said: "This is a gigantic threat to the Cavendish industry."

Gert Kema, an expert on Panama Disease at Wageningen University in the Netherlands, said: "It's not a question of whether it will appear [in Latin America]. It's a question of when."

A contagion of fear is also spreading in Latin American countries themselves. Romano Orlich, Costa Rica's former agriculture minister, said: "Should TR4 invade our plantations, we would lose \$800m of export income. Misery, unemployment, drugs and delinquency would be the result. I'd better stop here as I will not be able to sleep from now on."

According to scientists and development experts, the world is paying the price for allowing the international banana trade to become a vast monoculture, rigorously managed to provide uniform, perfect bananas to consumers in the developed world.

There are signs that another pest, a fungus called Black Sigatoka, which is prevented from spreading on commercial plantations by weekly pesticide spraying, may also be developing resistance.

But while first world consumers face at worst the threat of the disappearance of one item from their fruit bowls, banana disease has far more profound implications for those that rely on it for both income and food.

The vast majority of the 135 million tonnes of bananas grown each year are produced by small holders or subsistence farmers and used to either feed themselves or sold locally, funding additional purchases from food to school fees.

Bananas and plantains are the world's fourth most important staple crop after rice, wheat and maize and some 410m people rely on them for between 15-32 per cent of their daily calories.

Ongoing work suggests TR4 affects many of the different, non-Cavendish banana varieties grown in Africa, Asia and the Caribbean. Other diseases - a virus called Bunchy Top which stops banana production and a bacterial infection, BXW - also pose a long-term risk to the crop in Africa.

According to Professor Randy Ploetz, the California-based disease expert who discovered TR4, between 80-85 per cent of all bananas grown by volume are at risk of destruction by the fungus.

He told The Independent: "There is a great need for additional research, especially on the development of new, TR4-resistant bananas. Unfortunately, we are years away from that objective."

It is here that the test tubes sitting in a basement at the 589-year-old Leuven University come in.

It is more than likely that sitting within the chiller room sit banana varieties which could be inter-bred to offer natural resistance to TR4 or whose DNA could be tweaked to provide a genetically-modified fruit resistant to some, many or all of the pests plaguing global banana production.

Already, certain breeds of East African cooking banana, known as matoke, and plantains have been shown to grow in land in the Philippines previously infected by TR4. Researchers in Taiwan believe they have perfected a variant of Cavendish which could offer resistance to TR4 over a number of years, though a more long-term resistance is yet to be found.

But other argue that the problems posed by TR4 and other diseases are an opportunity to switch to a more sustainable model based on growing several banana varieties commercially rather than accepting the tyranny of a "Cavendish".

According to Prof Swennen, the world has forgotten the sheer diversity of a fruit which can be red or blue, taste of apple or lime and grow in climates from the tropics to snowy hills in China.

He is pioneering work in Tanzania and Uganda which encourages farmers to harness methods such as growing bananas among nitrogen-fixing groundcover crops such as beans and under trees, massively increasing yields and reducing disease.

He said: "There are about 300,000 plant species in the world and yet we use only about 100 to feed ourselves. There are around 2,000 varieties of cultivated banana but in the developed world we eat only one.

"If we could bring that diversity to our plates we would increase access to

markets for developing countries and get away from the monoculture of the Cavendish banana.

"To reach the recommended daily amount of vitamin A, you need to eat 80 Cavendish bananas. I have varieties in the collection which would give you all your vitamin A from just two bananas. We should harness this potential."

### **Food quality will suffer with rising carbon dioxide, field study shows**

Source: ScienceDaily, 6 April 2014.

Summary: Climate change is hitting home -- in the pantry, this time. A field study of wheat demonstrates how the nutritional quality of food crops can be diminished when elevated levels of atmospheric carbon dioxide interfere with a plant's ability to process nitrate into proteins. "Several explanations for this decline have been put forward, but this is the first study to demonstrate that elevated carbon dioxide inhibits the conversion of nitrate into protein in a field-grown crop," the lead researcher said.

For the first time, a field test has demonstrated that elevated levels of carbon dioxide inhibit plants' assimilation of nitrate into proteins, indicating that the nutritional quality of food crops is at risk as climate change intensifies.

Findings from this wheat field-test study, led by a UC Davis plant scientist, will be reported online April 6 in the journal *Nature Climate Change*.

"Food quality is declining under the rising levels of atmospheric carbon dioxide that we are experiencing," said lead author Arnold Bloom, a professor in the Department of Plant Sciences.

"Several explanations for this decline have been put forward, but this is the first study to demonstrate that elevated carbon dioxide inhibits the conversion of nitrate into protein in a field-grown crop," he said. The assimilation, or processing, of nitrogen plays a key role in the plant's growth and productivity. In food crops, it is especially important because plants use nitrogen to produce the proteins that are vital for human nutrition. Wheat, in particular, provides nearly one-fourth of all protein in the global human diet.

Many previous laboratory studies had demonstrated that elevated levels of atmospheric carbon dioxide inhibited nitrate assimilation in the leaves of grain and non-legume plants; however there had been no verification of this relationship in field-grown plants.

To observe the response of wheat to different levels of atmospheric carbon dioxide, the researchers examined samples of wheat that had been grown in 1996 and 1997 in the Maricopa Agricultural Center near Phoenix, Ariz.

At that time, carbon dioxide-enriched air was released in the fields, creating an elevated level of atmospheric carbon at the test plots, similar to what is now expected to be present in the next few decades. Control plantings of wheat were also grown in the ambient, untreated level of carbon dioxide.

Leaf material harvested from the various wheat tests plots was immediately placed on ice, and then was oven dried and stored in vacuum-sealed containers to minimize changes over time in various nitrogen compounds.

A fast-forward through more than a decade found Bloom and the current research team able to conduct chemical analyses that were not available at the time the experimental wheat plants were harvested.

In the recent study, the researchers documented that three different measures of nitrate assimilation affirmed that the elevated level of atmospheric carbon dioxide had inhibited nitrate assimilation into protein in the field-grown wheat.

"These field results are consistent with findings from previous laboratory studies, which showed that there are several physiological mechanisms responsible for carbon dioxide's inhibition of nitrate assimilation in leaves," Bloom said.

Bloom noted that other studies also have shown that protein concentrations in the grain of wheat, rice and barley -- as well as in potato tubers -- decline, on average, by approximately 8 percent under elevated levels of atmospheric carbon dioxide.

"When this decline is factored into the respective portion of dietary protein that humans derive from these various crops, it becomes clear that the overall amount of

protein available for human consumption may drop by about 3 percent as atmospheric carbon dioxide reaches the levels anticipated to occur during the next few decades," Bloom said.

While heavy nitrogen fertilization could partially compensate for this decline in food quality, it would also have negative consequences including higher costs, more nitrate leaching into groundwater and increased emissions of the greenhouse gas nitrous oxide, he said.

Story Source:

The above story is based on materials provided by University of California - Davis. Note: Materials may be edited for content and length.

Journal Reference: Arnold J. Bloom, Martin Burger, Bruce A. Kimball, Paul J. Pinter, Jr. Nitrate assimilation is inhibited by elevated CO<sub>2</sub> in field-grown wheat. *Nature Climate Change*, 2014; DOI: 10.1038/nclimate2183

### **Agriculture's Greenhouse Gas Emissions On The Rise**

Source: Newsroom America. 12 Apr 2014

From farming to forestry and fisheries, agriculture greenhouse emissions have nearly doubled over the past 50 years and may increase by another 30 per cent by 2050, according to new estimates from the Food and Agricultural Organization (FAO). "FAO's new data represent the most comprehensive source of information on agriculture's contribution to global warming made to date," said Francesco Tubiello of the agency's Climate, Energy and Tenure Division.

For the first time, FAO has used its own FAOSTAT emissions database to estimate global greenhouse gas emissions from agriculture, forestry and other land use in contributing to the Fifth Assessment Report of the Intergovernmental Panel on Climate Change (IPCC).

Emissions from crop and livestock production grew in 2001 from 4.7 billion tonnes of carbon dioxide equivalents (CO<sub>2</sub> eq) to more than 5.3 billion tonnes in 2011 – a 14 per cent increase.

"The increase occurred mainly in developing countries, due to an expansion of total agricultural outputs," FAO said

Meanwhile, net greenhouse gas emissions due to land use change and deforestation registered a nearly 10 percent decrease over the 2001-2010 period – averaging some 3 billion tonnes CO<sub>2</sub> eq year over the decade.

"This was the result of reduced levels of deforestation and increases in the amount of atmospheric carbon being sequestered in many countries," explained FAO, adding that, "as a result of carbon sequestration in forest sinks, some two billion tonnes of carbon dioxide were removed from the atmosphere during the same timeframe."

FAO's data based on country reports show that while those emissions continue to increase, they are not growing as fast as emissions from fossil fuel use in other sectors – actually decreasing over time the share of agriculture and other land use out of total anthropogenic emissions.

The largest source of emissions within agriculture is enteric fermentation – methane produced by livestock during digestion and released via belches. In 2011, this accounted for 39 per cent of the sector's total greenhouse gas outputs and increased 11 per cent between 2001 and 2011.

In 2011, 14 per cent of agricultural emissions (725 Mt CO<sub>2</sub> eq.) were generated while applying synthetic fertilizers – the fastest growing emissions source in agriculture – having increased some 37 per cent since 2001.

Greenhouse gases resulting from biological processes in rice paddies that generate methane make up 10 per cent of total agricultural emissions, while burning savannahs accounts for 5 per cent.

FAO data revealed that in 2011, 45 per cent of agriculture-related greenhouse gas outputs occurred in Asia – followed by 25 per cent in the Americas, five per cent in Africa, eleven per cent in Europe and four per cent in Oceania.

"This regional distribution was fairly constant over the last decade," the agency noted, adding "in 1990 however, Asia's contribution to the global total [38 per cent] was smaller than at present, while Europe's was much larger [21 per cent]."

The new FAO data also provide a detailed view of emissions from energy use in the agriculture sector generated from

traditional fuel sources – including electricity and fossil fuels burned to power agricultural machinery, irrigation pumps and fishing vessels.

"Up to now, information gaps have made it extremely difficult for scientists and policymakers to make strategic decisions regarding how to respond to climate change and has hampered efforts to mitigate agriculture's emissions," said Mr. Tubiello.

FAO is already generating disaggregated assessments along supply chains and analyzing the effectiveness of comprehensive mitigation interventions in the livestock sector.

Mr. Tubiello explained, "Data on emissions for agriculture, forests and other land use activities support member countries in better identifying their mitigation options and enable their farmers to take faster and more targeted climate-smart responses."

This improves their overall resilience and their food security and allows the countries to tap into international climate funding and accomplish their rural development goals.

"We also see much interest in capacity development on these topics at country level and respond to these needs through regional and country-level activities around the globe," he added.

### **Plants evolve ways to control embryo growth**

Source: Smallholder News. 11th April 2014

A new generation of high yield plants could be created following a fundamental change in our understanding of how plants develop.

The research, led by the University of Warwick and published in the journal *Science*, provides the first evidence that plants have evolved ways to control embryo growth and development by emitting information from surrounding cells.

The international study, headed by Dr Jose Gutierrez-Marcos from Warwick's School of Life Sciences, revealed that female sex cells and the placenta-like endosperm contained within plant seeds

send out specific signals to developing embryos to help direct their growth.

"This new information fundamentally changes our understanding of plant development and opens up exciting avenues of research, which could allow for the breeding and propagation of plants that incorporate the most successful characteristics of existing species", said Dr Gutierrez-Marcos.

"With rising global populations and changing climates, there is an increasing need for more robust plant varieties that provide higher yields and can grow under a wide set of environmental conditions. By understanding how plants control embryo growth we have opened up the possibility of breeding a new generation of plants that potentially meet these requirements."

Plant embryos are found within seeds and, once germinated, give rise to the adult plant. It was previously thought that embryo development was determined by the genetic make-up of the embryo alone.

The new research has however shown that specific cell-types present in the embryo environment can send out protein signals to also influence this process. This situation mirrors a similar scenario in mammals, whereby embryo development is regulated by signals sent out by neighbouring placental cells.

Understanding how these cells of non-embryonic origin can influence developing plant embryos, the researchers argue, is key to creating new, improved plant species including advantageous hybrid crops, where at present embryos often fail to develop properly when distantly-related parents are used.

"Before our discovery, the ability of non-embryonic plant cells to direct embryo growth was unrecognised, but we now have valuable information that neighbouring cells can directly interact with and influence embryos, most likely via a cascade of protein signals. The next step is to identify the embryonic factors that respond to these non-embryonic signals and understand their mode of action" commented Dr Gutierrez-Marcos.

## **Chloroplasts, the plant powerhouses, send signals to roots**

Source: The Conversation Apr 13 2014

We don't know what it is, but it controls the expression of nuclear genes.

For more than a billion years, plants have had an internal dialogue, and we are just beginning to learn the words. The unusual conversation occurs between two compartments within plant cells—the nucleus and the chloroplast. It is a dialogue that continues today, and, according to research just published in *Science*, it shapes the productivity of plants.

All living organisms are made of cells. These cells contain many compartments, a bit like organs in an animal body. Each plant cell contains many chloroplasts, which are responsible for producing energy. A billion years ago, the ancestors of chloroplasts existed as free-living individual cells, able to convert energy from light into sugar. But in a spectacular evolutionary event, these early chloroplasts were consumed by larger cells, where they eventually took up residence, supplying the larger cells with sugar. The legacy of that merger is evident around us every day in the green tissues of plants.

The fate of every plant cell is inextricably tied to the interaction between chloroplasts and other compartments of the plant cell. The most important of these interactions is with the nucleus.

The nucleus is the home of the genetic material for the plant—its genome. The genome contains all of the plant's genes, written in DNA code. Like human beings, plants have tens of thousands of genes in the nucleus. Each gene encodes a specific set of instructions—a recipe of sorts—for a particular cell component. The nucleus is like a non-circulating library for all of the plant's genetic recipes. All the information is there, but it can't leave the nucleus to be used elsewhere in the cell. In order to use the information in the library, it has to be transcribed into a different kind of information molecule—an RNA transcript. The transcript is then transported out of the nucleus, where it is used as

instructions to create a particular piece of cellular machinery.

Some of the genes in the nucleus are recipes for cellular machinery needed for the chloroplast to do its job—to undertake photosynthesis. It is important that the nucleus transcribes these genes in response to appropriate cues, especially daylight.

Light affects the transcription of one in every five plant genes. Intriguingly, some genes are transcribed based on a signal that comes from the chloroplast itself. Signaling from the chloroplast to the nucleus is called retrograde signalling. It has fascinated scientists for decades because the nature of the signal from the chloroplast is unknown.

Now this story has become even more intriguing. According to the *Science* paper, authored by Ezequiel Petrillo at the University of Buenos Aires and his colleagues, it seems that this form of signalling from chloroplasts can do more than direct the transcription of genes—it can also direct modifications of the RNA transcribed from the genes. These transcripts are modified by splicing the RNA, which removes bits of superfluous information from them. Without splicing, most RNAs wouldn't be able to encode proteins.

Petrillo and colleagues found a transcript that is spliced in different ways depending on whether light is present or not, and showed that the switch depended on the chloroplast's signalling. The transcript in question encodes part of the cell's splicing machinery, so the splicing process itself is regulated by a retrograde signal. That means that the effects can be broader than simply this one protein.

Whatever signal the chloroplast is producing, it must be able to move not just within the cell but also throughout the plant. If they shined light on the leaves, cells in the roots contained the spliced transcript. If they shined light on roots that do not contain active chloroplasts, the root cells did not contain the spliced transcript. This implies that the signal must travel from other tissues to the roots—so that the entire plant body is informed that the leaves have perceived light.

Finding out what this signal is would help researchers understand more about the process and perhaps exploit it for applications such as engineering plants that work in low light. One hypothesis was that the signal could be the sugars produced by chloroplasts, but that idea was shot down. Sugar-starved plants growing in the dark failed to produce any spliced transcript, as expected. But supplying them with sugars didn't restore the splicing.

The signal has to be something new. Some have suggested candidate retrograde signals involved in other aspects of chloroplast communication with

the nucleus, but we will have to wait for further studies to see if those are involved in the regulation of transcript splicing too.

Chloroplasts have resided in cells with a nucleus for about a billion years now. That the chloroplasts have discovered ways of communicating to the nucleus is not entirely surprising. That they communicate using a mechanism that remains a mystery is fascinating. Learning the "words" of their language, such as the retrograde signal for splicing, will provide illuminating discoveries for the coming years. The Conversation

Reference: Science, 2014. DOI: 10.1126/science.1250322.

## Forthcoming meetings

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

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

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

**Description:** In this symposium, we will bring together a wide range of scientists from different disciplines working on mycorrhizal fungi and plant-microbe interactions. We aim to provide an overview of the advances in mycorrhizal ecology in the last decade. In addition to this, specific talks will highlight new research areas and address the big questions for future research.

**Website:**

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

### **Pan-American Congress on Plants and BioEnergy**

Ontario, Canada. June 4 – 7, 2014

More info:

<http://my.aspb.org/page/Bioenergy2014>

### **First conference of the International Society for Molecular Farming**

17-19 June 2014. Berlin-Dahlem, Germany

More info:

<http://societyformolecularfarming.org/>

### **The 4th International Conference on Algal Biomass, Biofuels and Bioproducts**

15 -18 June 2014. Santa Fe Convention Center, Santa Fe, New Mexico, USA

Más Info: <http://www.algalbbb.com/>

### **SEB Manchester 2014.**

**July 1 – 4, 2014. Manchester, UK.**

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

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

### **Plant Biology 2014**

Portland, Oregon (USA). 12-16 July 2014

More Info:

[http://my.aspb.org/?page=ME\\_Index](http://my.aspb.org/?page=ME_Index)

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

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

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

**Description:** We aim to promote basic research in crassulacean acid metabolism (CAM) by integrating functional genomics

with biochemistry, physiology, development, ecology, and evolutionary studies to gain new insights into the regulatory mechanisms and evolutionary origins of the pathway. We will highlight the potential of CAM research for tackling bioenergy and environmental challenges pertaining to water security and resource limitation and the maintenance of productivity and ecosystems services in a changing world. In addition to this, specific talks will look at new research areas and address the big questions for future research.

**Website:**

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

**2014 Plant Proteomics Workshop**

21- 25 July 2014. University of Wisconsin-Madison (USA)

More

info: <http://www.biotech.wisc.edu/ppw>

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

24-29 August 2014. Bischoffsheim, Strasbourg (France)

More

Info: <http://www.epsoweb.org/event/embo-workshop-intercellular-communication-plant-development-and-disease-24-29-august-2014-bisc>

**“Lignin 2014” Conference**

August 24-28, 2014. Umeå, Sweden.

<http://www.trippus.se/web/presentation/web.aspx?view=category&evid=6kky7MZwgcWizCbU2h6gVg%3D%3D&ecid=fPLUyuS6EJMCX3JRpr88gg%3D%3D&ln=eng&template=Desktop>

**6th International Conference on Silicon in Agriculture**

Stockholm, Sweden. 26-30 August 2014

<http://www.silicon2014.com/>

**11th Conference of the International Society for Seed Science (ISSS)**

15-19 September 2014. Changsha, China.

More Info:

[http://2014seed.doevent.com/?lang=en\\_us](http://2014seed.doevent.com/?lang=en_us)

**BIOSPAIN 2014. 7th International Meeting on Biotechnology.**

24-26 September. Santiago de Compostela. Spain.

BIOSPAIN is the largest biotech event organized by a national bioindustry association in Europe and one of the largest in the world by the number of one-to-one meetings (2.775) and companies participating (762).

More info: <http://www.biospain2014.org/>

**EMBO Workshop: Unravelling Biological Secrets by Single-Cell Expression Profiling**

Heidelberg, Germany. 25-26 September 2014

More info:

<http://www.embl.de/training/events/2014/SIC14-02/index.html>

**EMBO | EMBL Symposium: The Complex Life of mRNA**

5- 8 October 2014. EMBL Heidelberg (Germany)

More Info: [http://www.embo-embl-symposia.org/symposia/2014/EES14-05/index.html?\\_ga=1.246010372.1855902608.1390922562](http://www.embo-embl-symposia.org/symposia/2014/EES14-05/index.html?_ga=1.246010372.1855902608.1390922562)

**The 16th EMBL PhD Symposium: Inspired by Biology - Exploring Nature's Toolbox**

EMBL Heidelberg, Germany. October 23-25, 2014

More

info: [http://phdsymposium.embl.org/?\\_ga=1.2120246.747466003.1395777142#home](http://phdsymposium.embl.org/?_ga=1.2120246.747466003.1395777142#home)

**Agriculture and Climate Change. Adapting Crops to Increased Uncertainty**

15-17 February 2015. Amsterdam, The Netherlands

More Info:

<http://www.agricultureandclimatechange.com/index.html>

## Positions available



### PREDOC

#### **EMBL International PhD Programme**

You can submit your application irrespective of the fact if your referees have completed the online reference form or not, as the submission does not impede referees access to the application.

Referees must submit their online references by latest 25 June 2014, 23:59 CEST (GMT +2). We strongly suggest that you complete the 'general info' and 'references' part of the online application first in order to give your referees enough time to complete the reference online. Furthermore please make sure to contact your referees before completing this part in order to find out if they are available and willing to provide a reference. It is applicant's responsibility to ensure that references reach us on time.

More info:  
<http://www.embl.de/training/eipp/application/index.html>

#### **Two PhD student positions in Post-transcriptional control of gene expression: mechanisms and role in pathogenesis**

We offer two PhD student positions (Early Stage Researchers) for three years to undertake research in the field of gene expression regulation in plants and plant immunity. The projects are focused on the role of RNA binding proteins and small RNAs in bacterial pathogenicity (group of Ulla Bonas) and on the elucidation of the role of natural antisense long non-coding RNAs in *Arabidopsis thaliana* (group of Selma Gago-Zachert). This research is supported by a research training group (RTG1591) funded by the German Research foundation (Deutsche Forschungsgemeinschaft, ). The scientific goal of the RTG1591 is to investigate how gene expression is controlled at the post-transcriptional level and how this modulates cell fate, human diseases and

plant immunity. The RTG1591 provides a unique framework for interdisciplinary research in the field of RNA Biology in which 11 labs of the faculties of Natural Sciences and Medicine at the Martin-Luther-University Halle-Wittenberg join efforts. The training program of the RTG1591 provides a truly interdisciplinary structured workshop and seminar program supporting the education of early career researchers. For additional job details, entry requirements and the main activities of the project, please follow the link [www.medizin.uni-halle.de/grk1591](http://www.medizin.uni-halle.de/grk1591). Type of contract: Temporary stipend (limited to three years) Status: Full-time

Please apply online via our webpage on [www.medizin.uni-halle.de/grk1591](http://www.medizin.uni-halle.de/grk1591). The deadline for this round of recruitments is 31st of March 2014. The applications have to indicate that the applicant fulfills the entry requirements. The application should include a brief CV, diploma or master certificate(s), a letter of motivation and at least one letter of recommendation.

For further information contact: Mrs. Mechtild Wahle Email: [grk1591@medizin.uni-halle.de](mailto:grk1591@medizin.uni-halle.de)

### POSTDOC

#### **Postdoctoral position on nitrogen-fixation in cereals**

Place: University of Wisconsin – Madison. Wisconsin (U.S.A.)

Title: Postdoctoral Researcher

Salary: \$40,000 / year plus full-benefits

Percent Time: 100% (full-time position)

A postdoctoral position is available in the department of Agronomy at the University of Wisconsin – Madison. A Ph.D. in Plant Molecular and Cellular Biology, Molecular Microbiology, Plant Pathology, or related fields is required. An experienced postdoctoral scientist is needed to study interactions between nitrogen-fixing bacteria and cereals. The successful candidate will have co-authored one or



more peer-reviewed publications in reputable international journals in plant-microbe interactions, and will be familiar with plant molecular and cellular biology as well as microbial genetics. Candidates with prior experience in maize are especially encouraged to apply. Excellent oral and written communication skills in English, and the ability to work well in a collaborative environment are essential.

**Job Duties:** The postdoctoral researcher will study and engineer interactions between cereals and nitrogen-fixing bacteria. He/she will use a wide range of genomic, molecular and cellular and phylogenetic techniques to study and manipulate these associations. The postdoctoral researchers will be involved in interdisciplinary collaborations nationally and internationally.

**How to Apply:** Please send a cover letter, a CV and at least 3 references by email to Jean-Michel Ané (jane@wisc.edu).

**Contact Name Address:** Jean-Michel Ané, Department of Agronomy, University of Wisconsin - Madison, 348 Moore Hall, 1575 Linden Drive, Madison, WI 53726, USA

**Application Deadline:** Applications will be accepted until a suitable candidate is identified.

### **Senior Molecular Biologist (NGS Sample Preparation)**

Place: West London (England)

We are looking for a Senior Molecular Biologist with specialist knowledge and experience in Next Generation Sequencing (NGS) technology to be part of a growing development team and lead the technical development of the sample preparation platform of a NGS system.

From scalable semiconductor sequencing to rapid, portable molecular diagnostics, our client's mission is to enable and develop fast and user-friendly products with wide-reaching and high-impact applications in healthcare and beyond.

To be considered for these roles you must have the following skills and experience; Postgraduate degree (Molecular Biology, Biochemistry) with experience in the NGS industry leading the sample preparation for human, pathogen or plant nucleic acid.

Experience in a technical leadership role

developing sample handling, purification and next stage amplification tool within an integrated fluidic system.

Excellent problem solving, analytical, administrative, organisational, communication and interpersonal skills.

Excellent hands-on skills, understanding and proven expertise handling various forms of samples in the micro/macro fluidic environment.

Good all-round expertise in sample preparation, enriching the sample, isolation of inhibitors, handling of pathogens, plant tissues or various human samples.

Excellent experience and know how related to the various techniques of molecular biology systems, such as nucleic acid isolation, handling of pathogens, DNA, enzyme functionality

Strong analytical capability with the ability to be innovative/technically creative

The ability to work quickly, under pressure and to deadlines.

Excellent interpersonal skills and written / oral English

Highly motivated and results driven

More info: <http://jobs.newscientist.com/en-gb/job/1401503806/senior-molecular-biologist-ngs-sample-preparation/>

### **Two year post-doctoral in Plant Cell Biology**

Place: Umea Plant Science Center, Sweden

A two year post-doctoral position with the possibility for extension for additional year is available at Umeå Plant Science Center in the Bhalerao lab starting immediately to work on the role of secretion of auxin carriers and cell wall components in regulation of cell elongation in model plant *Arabidopsis thaliana*. The project builds on previous work in the lab: Gendre et al PNAS (2011), Boutte et al PNAS (2013) and Gendre et al Plant Cell (2013). We have isolated several cell elongation mutants in *Arabidopsis* in which components of vesicular trafficking machinery are defective and hormonal responses are altered. The project aims to characterise these mutants using cell biological and biochemical and genetical approaches. The applicant must have a strong background in use of confocal

microscopy and molecular biology and experience of working with Arabidopsis is essential.

The selected candidate will join a team using multidisciplinary approaches that range from cell biology, chemical genomics and modelling in the Wallenberg foundation funded project. The other members involved in the project are Prof. Markus Grebe, Prof. Karin Ljung, Prof. Henrik Jönsson, Dr. Stephanie Roberts, Dr. Daniel Simon and Prof. Magnus Berggren.

Umeå Plant Science Center ([www.upsc.se](http://www.upsc.se)) is one of the world leading centers for research in plant biology. UPSC has state of the art equipment in genomics, confocal microscopy, metabolomics and proteomics and excellent plant growth facilities. UPSC has 150 researchers including 50 post-doctoral fellows and equal number of Ph. D and Master students. UPSC has a very international environment with researchers from 37 countries. Umeå also provides close access to outdoor activities such skiing, hiking, kayaking, etc.

Interested applicants should send cv with statement of interest and description of prior research and names of 3 referees.

Please send your applications to Rishikesh P. Bhalerao. Email: [rishi.bhalerao@slu.se](mailto:rishi.bhalerao@slu.se)

### **Post Doctoral Fellow**

Place: J. Craig Venter Institute. Rockville. Maryland. U.S.A.

The J. Craig Venter Institute ("JCVI"), a not-for-profit research institute dedicated to the advancement of the science of genomics is seeking a Post Doctoral Fellow to join our Plant Genomics group and work on the Arabidopsis Information Portal (AIP). The successful candidate will work with an established team of bioinformaticians to develop and enhance the functionalities of the newly instantiated AIP. The post-doc will be the primary point of contact between the AIP staff and the user community. (S)he will help design and implement new functionalities for the site in response to user needs, including display and analysis tools, import of new data types and educational and other topical material. He/she will assist in

curation of the Arabidopsis Col-0 genome annotation. This position requires proven experience in plant molecular biology plus some familiarity with methods for next-generation data acquisition and analysis.

Successful candidates will have a Ph.D. in Plant Biology; familiarity with Arabidopsis thaliana as a model organism is preferred. JCVI offers an excellent working environment and a competitive benefits package. For more information and to apply to this position, please visit our website at <https://careers.jcvi.org/careers/>

### **Postdoc Research Genetics&Genomics of Flavor and Nutrition of Wheat Foods.**

Place: Heartland Plant Innovations. Manhattan. Kansas. U.S.A.

A position is available for an innovative Postdoctoral Research Fellow to join a multidisciplinary team focused on application of wheat genomics and genetics for discovery and development of novel genetic traits to improve the flavor and nutritional quality of whole wheat food products. The position is funded by a major US food company. It will be co-advised by Dr. Forrest Chumley of HPI and Dr. Eduard Akhunov of Kansas State University. Industry experts will also serve on the core project advisory team. Work locations will be in the Kansas Wheat Innovation Center, a new 35,000 sq ft research facility adjacent to KSU's main campus, and at KSU's Throckmorton Plant Sciences Center.

Minimum qualifications include a Ph.D. in plant sciences, with training and research experience in plant molecular biology, genetics and genomics. Experience in protein biochemistry is preferred. The successful candidate must have a good command of oral and written English and excellent research management skills. Recent graduates with the relevant research experience and an interest in working on projects of importance to industry are especially encouraged to apply. Preference will be shown to qualified applicants who are U.S. citizens or foreign nationals with authorization to work in the United States.

The successful candidate will be an employee of Heartland Plant Innovations, a public-private plant biotechnology

collaboration formed in 2009. HPI is majority-owned by Kansas wheat farmers and the Kansas Bioscience Authority. HPI works in close partnership with KSU and industry partners. HPI currently has 15 employees, including eight full-time, working to provide advanced plant breeding services and trait development research to customers across the USA, in Europe and South America.

Applicants should apply via email to:

[careers@heartlandinnovations.com](mailto:careers@heartlandinnovations.com).

Please submit a letter describing your interest in this position, together with your c.v. and the names of three professional references. For more information, contact Dr. Forrest Chumley ([fchumley@heartlandinnovations.com](mailto:fchumley@heartlandinnovations.com)).

#### **Postdoctoral Associate - Nusinow Lab**

Place: Donald Danforth Plant Science Center, St. Louis, MO, USA

We are currently looking to fill an opening beginning April 1st, 2014 for a motivated and enthusiastic scientist to work on uncovering the molecular mechanisms by which the circadian clock regulates growth and development in plants. We combine genetic, biochemical, molecular, proteomic, high throughput phenotyping and genomic methods in plants, such as Arabidopsis, Brachypodium and Setaria to gain deep understanding of the components that connect the circadian oscillator to specific output networks. Ideal candidates would be interested in circadian biology, plant physiology and development, possess a Ph.D. in either genetics, biochemistry, cell, developmental, molecular biology or plant physiology. Candidates with experience in any of the following techniques are encouraged to apply: qPCR, ChIP, protein expression and purification, mass spectrometry, genetic analysis, automated visual and bioluminescence imaging and analysis, bioinformatics, molecular biology, yeast-based interaction assays, and methods in plant physiology. Candidates with an interest in transitioning into plants are also encouraged to apply. Candidates should provide a current CV,

list of at least three contacts for recommendation, and a cover letter that includes a statement of past research experience and future interests.

The international and interdisciplinary research environment at the Danforth Center offers an excellent opportunity for career development. Salaries are competitive and commensurate with experience, and the Danforth Center offers an excellent benefits package including medical and 403B matching. The Danforth Center is currently ranked in the top ten of places to work in scientific research, and the St Louis region is a rich environment to work and live. To apply, send a cover letter, a detailed CV, and the names and contact information for three references to: [careers@danforthcenter.org](mailto:careers@danforthcenter.org) with Nusinow Post Doc in the subject line.

The Donald Danforth Plant Science Center is an equal opportunity/affirmative action employer and encourages applications from underrepresented groups, including minorities, women, and people with disabilities.

#### **Assistant Professor in Plant Physiology**

Place: Dept. of Agronomy and Plant Genetics, Univ. of Minnesota-Twin Cities. U.S.A.

This position would bridge plant stress physiology with molecular and breeding efforts and agronomic research associated with crop growth and development. Research will identify plant traits and mechanisms useful in minimizing stress responses to increase crop yields using molecular, transgenic, and traditional approaches. The successful candidate will regularly teach an undergraduate crop physiology course and develop a graduate level course that contributes to the Applied Plant Sciences graduate program. See U of M Human Resources for full description ([https://employment.umn.edu/applicants/js/p/shared/search/Search\\_css.jsp](https://employment.umn.edu/applicants/js/p/shared/search/Search_css.jsp) requisition #190092) or contact Seth Naeve, [naeve002@umn.edu](mailto:naeve002@umn.edu). Application review begins May 15, 2014