FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY

FESPB Newsletter

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In this issue:

Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

FESPB 2010
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XVII Congress of the Federation of European Societies of Plant Biology (FESPB).
4-9 July 2010. Valencia, Spain.

The Congress web site has been updated.
Please, visit it for new information on the venue, preliminary programme and invited speakers at: http://www.geyseco.es/fespb/principal.php?seccion=welcome

Confirmed Invited Speakers:

Owen Kenneth Atkin (Functional Ecology Group, Research School of Biology. The Australian National University, Canberra, Australia)
Kirsten Bomblies (Organismic and Evolutionary Biology, Harvard University. Cambridge, USA)
Vincent Colot (Département de Biologie. Ecole Normale Supérieure, Paris, France)
José Antonio Feijó (Biologia Vegetal, Universidade de Lisboa. Lisboa, Portugal)
Niko Geldner (Department of Plant Molecular Biology. University of Lausanne, Lausanne, Switzerland)
Christophe Godin (INRA, Montpellier, France)
Ian Graham (Centre Novel Agricultural Products, University of York. York, UK)
Dirk Inzé (VIB Department of Plant Systems Biology, UGent. Ghent, Belgium)
Patrick Laufs (Cell Biology, INRA. Versailles, France)
Cathie Martin (Metabolic Biology, John Innes Centre. Norwich, UK)
David G. Robinson (Heildeberg Institute of Plant Sciences University of Heidelberg. Heidelberg, Germany)
Sabrina Sabatini (Genetica e Biologia Molecolare, Università di Roma La Sapienza. Rome, Italy)
David Salt (Horticulture and Landscape Architecture, Purdue University. West Lafayette, USA)
Paul Schulze-Lefert (Plant Microbe Interactions, Max Planck Institute for Plant. Breeding Research, Köeln, Germany)
Ramón Serrano (Instituto de Biología Molecular y Celular de Plantas (IBMCP). Universidad Politécnica de Valencia-C.S.I.C. Valencia, Spain)
Roberto Solano (Plant Molecular Genetics, CNB-CSIC. Madrid, Spain)
Fernando Valladares (Fisiología y Ecología Vegetal, Consejo Superior de Investigaciones Científicas (CSIC). Madrid, Spain)
Rens Voesenek (Biology, University Utrecht. Utrecht, The Netherlands)

FESPB new homepage
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The FESPB web site has been fully renewed thanks to the effort of the FESPB Secretary General **Prof. K.A. Roubelakis-Angelakis**.
Visit it at : http://www.fespb.org

Research News

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Stigolactones: a new hormone with a past

The recent discovery of an endogenous hormonal activity for strigolactones in shoot branching was surprising since these molecules were thought to mostly play roles as signaling molecules between organisms. Even in the context of plant hormones, strigolactones appear to be different in that their role in plant development is quite restricted. This most probably reflects early days and new hormonal functions will most probably be found for these compounds in the future. In this respect, the exogenous role of strigolactones in parasitic plant seed germination may hint to functions of this compound in seed development. However, showing new roles for strigolactones in the seed or any other aspect of plant development for that matter will require developing assays in model genetic systems such as Arabidopsis and rice where we can take full advantage of the experimental tools that are available.

Journal Reference: Yuichiro Tsuchiya and Peter McCourt. *Current Opinion in Plant Biology*, 2009 (In Press) *Available online 31 August 2009*.

Genomic imprinting and RNA silencing linked in plants

Small interfering (si) RNAs that are associated with gene silencing have been discovered in most eukaryotes. Here, in Arabidopsis, siRNAs are shown to be uniparentally expressed from the maternal genome, and their maximal expression is in the young developing seed. This unusual pattern of expression provides evidence for a link between genomic imprinting and RNA silencing in plants.

Journal Reference: Rebecca A. Mosher, Charles W. Melnyk, Krystyna A. Kelly, Ruth M. Dunn, David J. Studholme & David C. Baulcombe. Uniparental expression of PolIV-dependent siRNAs in developing endosperm of Arabidopsis. (*Nature*, 9 July 2009. Pg. 283).

Why so repressed? Turning off transcription during plant growth and development

To ensure correct patterns of gene expression, eukaryotes use a variety of strategies to repress transcription. The transcriptional regulators mediating this repression can be broadly categorized as either passive or active repressors. While passive repressors rely on mechanisms such as steric hindrance of transcriptional activators to repress gene expression, active repressors display inherent repressive abilities commonly conferred by discrete repression domains. Recent studies have indicated that both categories of regulators function in a variety of plant processes, including hormone signal transduction, developmental pathways, and response to biotic and abiotic stresses.

Journal Reference: Naden T Krogan, Jeff A Long. Current Opinion in Plant Biology 2009 (In Press) *Available online 21 August 2009.*

Getting Plants To Rid Themselves Of Pesticide Residues

Scientists in China are reporting the "intriguing" discovery that a natural plant hormone, applied to crops, can help plants eliminate residues of certain pesticides.

Jing Quan Yu and colleagues note that pesticides are essential for sustaining food production for the world's growing population. Farmers worldwide use about 2.5 million tons of pesticides each year. Scientists have been seeking new ways of minimizing pesticide residues that remain in food crops after harvest - with little success. Previous research suggested that plant hormones called brassinosteroids (BRs) might be an answer to the problem.

The scientists treated cucumber plants with one type of BR then treated the plants with various pesticides, including chloropyrifos (CPF), a broad-spectrum commercial insecticide. BR significantly reduced their toxicity and residues in the plants, they say. BRs may be "promising, environmentally friendly, natural substances suitable for wide application to reduce the risks of human and environmental exposure to pesticides," the scientists note. The substances do not appear to be harmful to people or other animals, they add.

Journal reference: Xia et al. Brassinosteroids Promote Metabolism of Pesticides in Cucumber. *Journal of Agricultural and Food Chemistry*, 2009; 090820125955050 DOI: 10.1021/jf901915a

Source: ScienceDaily (Sep. 15, 2009).

miR156-Regulated SPL Transcription Factors Define an Endogenous Flowering Pathway in *Arabidopsis thaliana*

There is more than one way to flower. In the thale cress, *Arabidopsis thaliana*, the well characterized *FT* gene encodes a pro-flowering protein that travels from leaf to shoot in response to changes in day length.

Now, Detlef Weigel and his colleagues at the Max Planck Institute for Developmental Biology in Tübingen, Germany, show that another pathway regulated by microRNAs molecules that prevent translation of messenger RNAs into proteins can stimulate flowering independently of daylight cues.

They find that levels of microRNA-156 decline as the plant ages, parallelling a rise in expression of the genes it seems to silence. The products of these genes, called SPLs, set off floral development.

Journal Reference: Jia-Wei Wang, Benjamin Czech and Detlef Weigel. *Cell*, 138, 4: 738-749, 2009. (*Nature* 460, 1061, 27 August 2009).

The jasmonate pathway: the ligand, the receptor and the core signalling module

Jasmonates regulate specific developmental processes and plant adaptation to environment by controlling responses to external biotic or abiotic stimuli. The core events of jasmonate signalling are now defined. After hormone perception by SCF^{COI1}, JAZ (JAsmonate ZIM domain) repressors are targeted for proteasome degradation, releasing MYC2 and de-repressing transcriptional activation. JAZs are homomeric and heteromeric proteins and have been instrumental in recent advances in the field, such as the identification of COI1 as a critical component of the jasmonate receptor and the discovery of the bioactive jasmonate in *Arabidopsis*, (+)-7-*iso*-JA–Ile. Small changes in jasmonate structure result in hormone inactivation and might be the key to switching-off signalling for specific responses to stimulus and for long-distance signalling events.

Journal Reference: Sandra Fonseca, Jose M Chico, Roberto Solano. *Current Opinion in Plant Biology* 2009 (In Press) *Available online 27 August 2009.*

Ethylene signaling and response: where different regulatory modules meet

The structural simplicity of the gaseous hormone ethylene stands in contrast with the complexity of the physiological processes ethylene regulates. Initial studies suggested a simple linear arrangement of signaling molecules leading from the ethylene receptors to the EIN3 family of transcription factors. Recent discoveries have substantially changed this view. Current models suggest existence of a complex signaling pathway composed of several phosphorylation cascades, feedback-regulated transcriptional networks, and protein and mRNA turnover regulatory modules. Interactions between ethylene and other signals determine which of the ethylene-mediated responses get activated in a particular cell at a particular time. Tissue-specific regulation of auxin biosynthesis, transport, and response by ethylene is emerging as a key element in this signal integration process.

Journal Reference: Anna N Stepanova, Jose M Alonso. *Current Opinion in Plant Biology* 2009 (In Press) *Available online 25 August 2009.*

First Evidence That Weed Killers Improve Nutritional Value Of A Key Food Crop

Scientists are reporting for the first time that the use of weed killers in farmers' fields boosts the nutritional value of an important food a crop. Application of two common herbicides to several varieties of sweet corn significantly increased the amount of key nutrients termed carotenoids in the corn kernels, according to a new study.

In the new study, Dean Kopsell and colleagues note that farmers grow about 240,000 acres of sweet corn in the United States each year, making it an important food crop. Corn is among only a few vegetable crops that are good sources of zeaxanthin carotenoids. Consuming carotenoid-rich vegetables may reduce the risk of age-related macular degeneration (a leading cause of vision loss among older people), heart disease, and cancer, the study notes.

The scientists exposed several varieties of sweet corn plants to the herbicide mesotrione or a combination of mesotrione and atrazine, another commonly used weed killer, and harvested mature corn 45 days later. Herbicide applications made the corn an even-better source of carotenoids, boosting levels in the mature kernels of some varieties by up to 15 percent. It specifically increased levels of lutein and zeaxanthin, the major carotenoids in sweet corn kernels, which studies have linked to a reduced risk of age-related macular degeneration.

Journal reference: Kopsell et al. Increase in Nutritionally Important Sweet Corn Kernel Carotenoids following Mesotrione and Atrazine Applications. *Journal of Agricultural and Food Chemistry*, 2009; 090619124509017 DOI: 10.1021/jf9013313
Source: ScienceDaily (July 9, 2009).

Database On Tiny Plant Will Help Scientists Create Better Crops, Biofuels and Medicines

A tiny plant with a long name (Arabidopsis thaliana) helps researchers from over 120 countries learn how to design new crops to help meet increasing demands for food, biofuels, industrial materials, and new medicines. The genes, proteins, and other traits of this fast-growing, tiny mustard plant reside in a vast database dubbed the Arabidopsis Information Resource (TAIR), which has over 1.6 million page hits each month.
The TAIR group, headed by Dr. Eva Huala at Carnegie's Department of Plant Biology, just released a new version of the genome sequence of this model plant, which includes an array of improvements and novel features that promise to accelerate this critical research.
The new TAIR9 genome release contains detailed information on all 33,518 genes that make up this tiny plant (including 114 newly discovered genes and 168 new pseudogenes), the proteins produced by these genes, and extensive new experimental and computationally predicted gene-function information.
Huala highlighted the advances: "We now have a ranking system that provides a measure of our confidence that the structure of a specific gene is correct; we've overhauled information on pseudogenes—the evolutionary remnants that start out as copies of conventional protein-coding genes and sometimes take on interesting new functions; and we've made extensive updates to the genome sequence based on new sequence data submitted to TAIR."
In 2000, Arabidopsis was the first plant genome to be sequenced. Partly due to the vast experimental data on gene function, which TAIR has painstakingly extracted from the literature and associated to the genes, and because of an extensive set of molecular tools developed for this plant, the Arabidopsis genome is the most advanced plant genome in the world and is the most commonly used experimental plant today. Its small size and fast growth allow large-scale experiments on drought and salt tolerance, resistance to plant diseases, and other topics with a direct impact on economic and food quality issues to be carried out quickly and economically, and the results applied to important crop species.
"TAIR is a crucial resource for plant sciences, but its impact goes far beyond," remarked Dr. Wolf Frommer, director of Carnegie's Department of Plant Biology. "TAIR9, as the 'green' reference database, is crucial for understanding the function and engineering of algae as well as crop plants. It is the basis for all improvement of crop plants to meet the challenges of a growing population as well as climate change."
The Arabidopsis Information Resource (TAIR) collects information and maintains a database of genetic and molecular biology data for Arabidopsis thaliana, a widely used model plant. TAIR is produced by the Carnegie Institution's Department of Plant Biology in Palo Alto, CA. Funding is provided by the National Science Foundation, (Grant No. DBI-9978564 and DBI-0417062).
Adapted from materials provided by Carnegie Institution.
Source: ScienceDaily. (July 12, 2009).

Scientists Closer To Developing Salt-tolerant Crops

An international team of scientists has developed salt-tolerant plants using a new type of genetic modification (GM), bringing salt-tolerant cereal crops a step closer to reality.
The research team – based at the University of Adelaide's Waite Campus in Australia – has used a new GM technique to contain salt in parts of the plant where it does less damage.
Salinity affects agriculture worldwide, which means the results of this research could impact on world food production and security.
The work has been led by researchers from the Australian Centre for Plant Functional Genomics and the University of Adelaide's School of Agriculture, Food and Wine, in collaboration with scientists from the Department of Plant Sciences at the University of Cambridge, UK.
The results of their work are published July 7 in the journal The Plant Cell.
"Salinity affects the growth of plants worldwide, particularly in irrigated land where one third of the world's food is produced. And it is a problem that is only going to get worse, as pressure to use less water increases and quality of water decreases," says the team's leader, Professor Mark Tester, from the School of Agriculture, Food and Wine at the University of Adelaide and the Australian Centre for Plant Functional Genomics (ACPFG).

"Helping plants to withstand this salty onslaught will have a significant impact on world food production."
Professor Tester says his team used the technique to keep salt – as sodium ions (Na+) – out of the leaves of a model plant species. The researchers modified genes specifically around the plant's water conducting pipes (xylem) so that salt is removed from the transpiration stream before it gets to the shoot.
"This reduces the amount of toxic Na+ building up in the shoot and so increases the plant's tolerance to salinity," Professor Tester says.
"In doing this, we've enhanced a process used naturally by plants to minimize the movement of Na+ to the shoot. We've used genetic modification to amplify the process, helping plants to do what they already do – but to do it much better."
The team is now in the process of transferring this technology to crops such as rice, wheat and barley.
"Our results in rice already look very promising," Professor Tester says.
Source: ScienceDaily (July 8, 2009).

Hormone Clue To Root Growth

Plant roots provide the crops we eat with water, nutrients and anchorage. Understanding how roots grow and how hormones control that growth is crucial to improving crop yields, which will be necessary to address food security and produce better biofuels.
Now an international group of scientists, led by the Centre for Plant Integrative Biology at The University of Nottingham, has shed light on how a plant hormone is crucial in controlling the growth of plant roots.
Plant growth is driven by an increase in two factors: the number of cells, and their size. It is already known that the plant hormone gibberellin controls how root cells elongate as the root grows in the model plant Arabidopsis thaliana. Now a paper appearing in Current Biology describes for first time how this hormone also regulates the number of cells in the root in order to control root growth.
Gibberellin normally acts by signaling the removal of proteins which repress growth, and so promotes root cell production. The new research shows that mutant plants that do not produce gibberellin are unable to increase their cell production rate and the size of the root meristem, the zone of cell proliferation.
Plants in which the cells in the meristem were made to express a mutant version of the growth-repressing protein GAI not degraded by gibberellin showed disrupted cell proliferation. Expressing this mutant form, gai, in only one tissue, the endodermis (the innermost layer of the root cortex of a plant), was sufficient to stop the meristem enlarging. In effect, the rate of expansion of dividing endodermal cells dictates the equivalent rate in other tissues.
This research was headed by Dr Susana Ubeda-Tomás and Professor Malcolm Bennett of the Centre for Plant Integrative Biology, in collaboration with scientists in Nottingham, Cambridge, Edinburgh, Spain, Belgium and Sweden.
Professor Malcolm Bennett, Biology Director for the Centre for Plant Integrative Biology and Professor of Plant Sciences in the Division of Plant and Crop Sciences, said: "We have shown that gibberellin plays a crucial role in controlling the size of the root meristem, and that it is the endodermis which sets the pace for expansion rates in the other tissues.
"Understanding precisely how hormones regulate plant growth is one of the key areas of fundamental plant biology which will underpin crop improvements in the future."
Source: ScienceDaily (July 7, 2009).

Novel mechanism revealed for increasing recombinant protein yield in tobacco

Elastin-like polypeptides (ELPs) cause plants to store GM proteins in special 'protein bodies,' insulating them from normal cellular degradation processes and increasing the overall protein yield. Researchers writing in the open access journal BMC Biology have visualised the mechanism by which the synthetic biopolymer increases the accumulation of recombinant proteins.
Rima Menassa worked with a team of researchers from Agriculture and Agri-Food Canada in London, Ontario, to develop and test the ELP tags by targeting an ELP-green fluorescent protein (GFP) fusion to various organelles in the leaves of the tobacco plant. Tobacco is well-suited as a production system for recombinant proteins but the mechanism by which ELP fusions increase production yields in transgenic tobacco leaves was previously unknown. Menassa said, 'ELP was shown to almost double the yield of GFP to 11% of total soluble protein when hyperexpressed in the endoplasmic reticulum (ER).'

Based on their confocal and electron microscopy analyses, the researchers suggest that ELP fusions targeted to the ER induce the formation of novel mobile protein body-like structures in leaves, which appear similar in size and morphology to the prolamin-based protein bodies naturally found in plant seeds. These bodies may be responsible for ELP's positive effect on recombinant protein accumulation by excluding the heterologous protein from normal physiological turnover.

The researchers targeted their ELP fusions to the cytoplasm, chloroplasts, apoplast and ER in Nicotiana benthamiana tobacco plants. They found that the ER was the only intracellular compartment in which the ELP significantly enhanced recombinant protein accumulation. They conclude, 'An ER-targeted ELP fusion approach provides an effective strategy for depositing large amounts of concentrated heterologous protein within the limited space of the cell.'

Source: BioMed Central. Science Centric, 7 August 2009.

Melons Sweetened With DNA Sequence

People smell them, thump them and eyeball their shape. But ultimately, it's sweetness and a sense of healthy eating that lands a melon in a shopper's cart.

Plant breeders now have a better chance to pinpoint such traits for new varieties, because the melon genome with hundreds of DNA markers has been mapped by scientists with Texas AgriLife Research. That means tastier and healthier melons are likely for future summer picnics.

"This will help us anchor down some of the desirable genes to develop better melon varieties," said Dr. Kevin Crosby, who completed the study with Drs. Soon O. Park and Hye Hwang. "We can identify specific genes for higher sugar content, disease resistance and even drought tolerance."

The results are reported in the Journal of the American Society of Horticultural Sciences.

Melons are fleshy, edible cucurbits grown worldwide in a multitude of varieties. Not only are they economically important, the scientists noted, but they are a favorite among consumers internationally.

The average person in the U.S. eats about 25 pounds of melon every year, according to the Agricultural Marketing Resource Center at Iowa State University.

Scientists from France and Spain already had completed partial maps of segments of the melon DNA sequence. The Texas researchers connected those segments with new findings in their study to complete the entire melon genome map.

For the study, the Deltex ananas melon was crossed with a wild melon called TGR 1551. More than 100 of the offspring from that cross were grown in the AgriLife Research greenhouses at Weslaco, Crosby noted.

DNA was extracted from leaf tissue collected 21 days after planting. Results from these tests were integrated into partial maps created by other researchers.

Previous knowledge of melon DNA was like two sets of directions - one from Miami to Houston and the other from El Paso to Los Angeles. That would make one wonder how to get from Houston to El Paso. The study by Crosby's group, in essence, devised the path from Miami to LA and all points between.

In addition to the complete map, the researchers located genetic markers linked to fruit sugars, ascorbic acid (vitamin C) and male sterility, which is useful for developing hybrid varieties.

The trio said the genetic map will be helpful for future studies in identifying fruit sweetness, quality, size, shape and resistance to disease.

Source: ScienceDaily (July 6, 2009).

Scientists devise efficient way of learning about complex corn traits

There's no 'silver bullet' gene or gene region that controls so-called complex traits in maize, commonly known as corn.

Instead, in two research papers published this week in the journal Science, North Carolina State University crop scientists and colleagues show that lots of small changes in a number of gene regions affect complex traits - like flowering time or reproductive ability - in corn.

Finding out more about the mechanisms behind complex traits like flowering time - as well as even more difficult-to-map traits like yield or drought tolerance, for example - has the potential to help plant breeders build the best traits into tomorrow's corn plants, says Dr Jim Holland, NC State professor of crop science, research geneticist for the U.S. Department of Agriculture-Agriculture Research Service (USDA-ARS) and one of the lead authors of the Science papers.

Holland and Dr Major Goodman, NC State professor of crop science, joined with researchers from Cornell University, the University of Missouri and other institutions to assemble a set of genetic maize varieties called the maize nested association mapping population. They found a number of chromosomal regions - called quantitative trait loci (QTL) - affecting flowering time in corn.
Identifying QTLs can help scientists get closer to figuring out the actual genes involved in certain traits. Holland likened it to looking for a specific house in a large city, with the QTL providing the correct street, but not necessarily the right house.
The scientists found that an average of 29 to 56 QTLs affected flowering time; the effects of these QTLs were small. That finding contrasts with studies of Arabidopsis, or mustard weed, the ubiquitous lab rat of the plant world. In that plant, small numbers of QTLs have large effects on genetic variance.
The scientists also studied more than 1,100 marker genes that characterise genetic inheritance. In other words, the researchers wanted to know if genes from one parent are inherited more frequently than genes from another parent.
While they predicted that more genes from one parent would be inherited, the study showed that, for the vast majority of the genome, each parent contributed about half. But subtle deviations from this were often observed, indicating that many genes had small effects on reproductive success.
Holland says that the nested association mapping population will be a resource for scientists to both build a better corn plant and to show how changes in the genome produce differences in individual plant families. That, in turn, will help scientists make more accurate predictions about complex traits.
'These findings will be a big help in the future,' Holland says. 'We can now take a complicated trait, identify gene regions involved in the trait, and then use that information in breeding to ensure the best combinations of genes from different sources or varieties.'
Journal reference: Buckler et al. *Science* 325 (5941), 714-718. McMullen et al. *Science* 325 (5941), 737-740.
Source: North Carolina State University. Science Centric, 7 August 2009.

Stressed crops emit more methane than thought

Scientists at the University of Calgary have found that methane emission by plants could be a bigger problem in global warming than previously thought.
A U of C study says that when crops are exposed to environmental factors that are part of climate change - increased temperature, drought and ultraviolet-B radiation - some plants show enhanced methane emissions. Methane is a very potent greenhouse gas; 23 times more effective in trapping heat than carbon dioxide.
'Most studies just look at one factor. We wanted to mix a few of the environmental factors that are part of the climate change scenario to study a more true-to-life impact climate change has on plants,' says David Reid, a professor in the Department of Biological Sciences who co-authored a paper with research associate Mirwais Qaderi in the advanced on-line edition of the journal Physiologia Plantarum.
Reid and Qaderi, who received funding from the University Research Grants Committee (URGC) and Natural Sciences and Engineering Research Council of Canada (NSERC), analysed methane emissions from six important Canadian crops - faba bean, sunflower, pea, canola, barley and wheat - that were exposed to combinations of three components of global climate change: temperature, ultraviolet-B radiation and water stress (drought). What they found they say is troubling. These stresses caused plants to emit more methane. In a warmer, drier world methane might be a bigger contributor in global warming than previously thought.
When it comes to the greenhouse effect, methane could be considered the misunderstood and often overlooked orphan greenhouse gas. Much of the attention has been focused on carbon dioxide but more recently it has been realised that methane should also be considered as a very significant greenhouse gas. Its concentrations have more than doubled since pre-industrial times. While the growth rate of methane concentrations has slowed since the early 1990s, some scientists say this is only a temporary pause.
'Our results are of importance in the whole climate warming discussion because methane is such a potent greenhouse warming gas, says Qaderi. 'It points to the possibility of yet another possible feedback phenomena which could add to global warming.'
Since elevated levels of carbon dioxide has been observed to counteract the negative effects of some environmental stresses, Qaderi and Reid are now studying the effect of increased carbon dioxide with factors such as drought, higher temperature and UVB on methane production in crops. (Source: University of Calgary. Science Centric, 6 August 2009).

Understanding how weeds are resistant to herbicides

In a little over seven hours, University of Illinois weed scientist Patrick Tranel got more genetic information about waterhemp than in two years time in a lab. The genetic information was obtained using pyrosequencing technology in the Keck Centre at the U of I. The genetic sequence will allow scientists to study herbicide resistance in waterhemp.

Ten years ago genomics was reserved for what Tranel refers to as 'important species' such as humans, cows, fruit flies, and mice. 'That's changed now that those species have been sequenced. Now we can start doing genomics on weeds to start understanding weeds better.

'With this type of technology, you can generate all of this genomic data relatively cheaply and quickly, so it's worthwhile doing in some of these non-model species like weeds. We're able to start generating data now that five years ago would have been cost-prohibitive.' Tranel believes waterhemp is the first weed to be partially sequenced using this technology.

The pyrosequencing machine emits a light signal that's captured every time a nucleotide is incorporated into a growing DNA strand. 'The reason it's so fast is that it's done in parallel,' said Tranel. 'The plate has thousands of tiny wells, and a sequencing reaction going on in every one of them simultaneously. There's a camera that monitors the light for each of these wells simultaneously and so in one seven and a half hour run you generate a million reads.'

Tranel explained that although more traditional herbicide resistance research takes years, it's more gene-specific. 'We sampled plants, brought them back to the green house, grew them up, confirmed that they were resistant and then we started crossing a resistant plant with a sensitive plant. We look at its progeny to see if the resistance is inherited to understand the genetics - if it's a dominant trait or a recessive trait.

'Pyrosequencing is more like just throwing out a fishing net - we know we're going to get continued resistance to other herbicides which can affect other genes. And we don't want to spend two years culling to find that gene every time. This is a way that we can get all of the genes at once.'

All of the data is publicly available. 'There's a website where you can go and get the 43 million base pairs of sequence. So anyone can get it and use that information.'

Tranel said that identifying weed resistance is an immediate outcome of having the genetic data. 'Once we obtain the sequence of a resistance gene, we can develop molecular tests that are specific for the resistance mutation. 'We can take a sample of waterhemp from a field that was sprayed and the waterhemp hasn't died and we can confirm whether it is resistant or not because we know the gene sequence and we know the mutation and the mechanism.'

Having the complete genomic data on waterhemp will help scientists not only to identify but also to understand resistance and how resistance evolves. 'If you understand how it evolves, that can help you devise strategies that cannot prevent it from evolving, but at least slow the rate at which it happens,' said Tranel.

'If you use the same herbicide year after year, you're exerting selection pressure - you're selecting for that rare plant or mutation that will survive. When you do that, and you kill all of the siblings that are weaker, the mutant survives and all of its progenies will survive and that's how resistance evolves. It's evolution in action,' said Tranel.

This genomic data will also help in answering broader questions about weeds such as: Why are some plants weeds? What makes a plant a weed? Is it certain genes? Is it the way the genes are expressed? 'These are questions that 10 years ago we couldn't address because we didn't know the genes. Now we're at the point where we can start doing that and on a broad scale. We can do this with waterhemp and we can do this with another weed and we can compare the two - are there things that these two weeds have in common that make it different from a corn plant or a soybean plant which explains why it's weedy? This is sort of a first step in that direction - starting to generate the type of information that will allow us to ask these sorts of questions.'

Waterhemp is a Midwestern problem, Tranel said, but it's a member of the genus Amaranthus which includes weeds that are a problem worldwide such as pigweeds. 'Because they all belong to the same genus, their genomes are very conserved. So if we have the sequence for the PPO gene in waterhemp you can use that information to get the PPO gene in redroot pigweed. It would be a similar sequence.'

Having this information is like building a tool kit, said Tranel. 'We're developing all of these resources and putting these resources in our freezer. When we have an interest in resistance to herbicide A which targets enzyme B, we can go to the freezer, or to the computer and get the sequence of the gene for that enzyme.'

Tranel said that because waterhemp is in the group of amaranthus weeds, it's a good model for weed genomics. 'A weed scientist in Georgia, where there's a lot of Palmer amaranth -

another pigweed evolving resistance, can go straight to that data base and get gene sequence data.'
Another outcome of having this genomic data is to be able to design markers - so you can fingerprint individual waterhemp plants and use that information to do population genetic studies.
'If you see herbicide resistance in northern Illinois and a year later you see the same resistance in a population in southern Illinois, one of the things you want to know in managing resistance is, did resistance evolve or occur here once and then a farmer moved a combine and that's how resistance got down here? Or did resistance occur here and independently down in southern Illinois?'
Understanding how the resistance occurred has implications for weed management. 'If it's evolving multiple times, you need to pay attention to what you're doing in your field whereas if it evolved once and is moving around then you've got to pay attention to what your neighbours are doing. It's important to know how it's evolving, how it's spreading.
'If you have these genetic fingerprinting tools, which we're able to do because of this research, you can go look at these populations and see, are these genetically similar, which would suggest that it was a movement event. If they're completely different, then that would suggest that it's evolving independently.'
Source: University of Illinois at Urbana-Champaign. Science Centric, 6 August .

Seeing The Tree From The Forest: Predicting The Future Of Plant Communities

The ability to envisage the future may be closer than you would think. A recent paper by Sean Hammond and Karl Niklas in the August 2009 issue of the American Journal of Botany presents an algorithm that may be used to predict the future dynamics of plant communities, an increasingly interesting area of study as significant environmental changes, such as global climate change and invasive species, are affecting current plant communities.
Similar ecological factors, such as nutrient availability and habitat stability, play a role in the growth and development of both an individual plant and a community of plants, like a forest; however, the length of time that these factors effect change differs between individual plants that may live for decades and plant communities that may exist for thousands of years. A goal of plant ecology has been to find ways to predict plant behavior in communities based on observed properties of a few representative members.
Hammond and Niklas have developed an algorithm-spatially explicit, reiterative algorithm, or SERA-that explores whether changes occurring in plant communities, such as self-thinning and the competitive displacement of one species by another, can be attributed to the characteristics of the individual plants that comprise the community. "Our model predicts how a plant population or community will behave when plant-plant interactions are predicated exclusively on the constraints imposed by a few physical principles and by competition for physical space and light," stated Dr. Niklas. Recent empirical studies have shown that a variety of plant communities in different environments exhibit some of the same size-dependent and age-dependent trends. One example is the relationship between the mass of tree canopies and the diameter of the tree trunks. In the simulations of plant growth within a community performed by SERA, various trends emerged as a result of competition for light and space among the individual plants, and these trends are in agreement with the trends found empirically in plant populations. Other results of SERA simulations were also found to be in agreement with empirical data. Although a few million years late, SERA predicted that angiosperms would outcompete gymnosperms as the dominant land plants, and it was able to accurately predict the age at which a variety of plant species would reach reproductive maturity.
"Remarkably, our model predicts the behavior of real plant populations, and thus suggests to us that many 'complex' ecological interactions emerge as a result of a few very 'simple' processes," commented Dr. Niklas. SERA may be very useful in predicting changes in community development and composition as environmental and climatic variability increases.
Journal reference: Hammond, Sean T., Niklas, Karl J. Emergent properties of plants competing in silico for space and light: Seeing the tree from the forest. *American Journal of Botany*, 2009; 96 (8): 1430 DOI: 10.3732/ajb.0900063. (Source: *ScienceDaily,* August 2009).

Restoring A Natural Root Signal Helps To Fight A Major Corn Pest

A longstanding and fruitful collaboration between researchers at the Max Planck Institute for Chemical Ecology and the University of Neuchâtel in Switzerland, together with contributions *from colleagues in Munich and the US, has produced another first: the successful manipulation of a crop plant to emit a signal that attracts beneficial organisms.*

Genetic transformation of maize plants resulted in the release of the naturally active substance (E)-beta-caryophyllene from their roots. The substance attracts nematodes that attack and kill larvae of the Western corn rootworm, a voracious root pest. In field tests, the enhanced nematode attraction resulted in reduced root damage and considerably fewer surviving rootworms. Further fine-tuning of this natural defense strategy will allow for an environmentally friendly growing of maize with minimized use of synthetic insecticides. The project was carried out within the framework of the Swiss National Centre of Competence in Research (NCCR Plant Survival).

The Western corn rootworm (*Diabrotica virgifera virgifera*) is the most damaging maize pest in the US and is responsible for enormous financial losses. Current methods to control the rootworm pest include insecticides, crop rotation and transgenic Bt maize lines that are not yet approved in Europe. After first invading the Balkans, the pest has since 2007 also been found in southern Germany.

The corn rootworm larvae feed on root hairs and bore themselves into the maize roots. The results are devastating: The plants take up less water and nutrients, and with the root mass severely reduced the plants lodge and collapse. In areas in Germany where the corn rootworm is a potential threat, the Federal Office of Consumer Protection and Food Safety (BVL) establishes safety zones and enacts the use of the insecticide chlothianidine. In spring 2008 this insecticide was directly applied on the seeds, but during sowing it was unintentionally emitted as dust from abraded seeds, contaminated flowers, and poisoned 330 million honey-bees.

"Instead of using insecticides, the use of natural enemies of the corn rootworm could be much more environmentally friendly," says Jörg Degenhardt, who was recently appointed professor at the University of Halle. While working in the group of Jonathan Gershenzon at the Max Planck Institute for Chemical Ecology in Jena he had already contributed to a key discovery four years ago by Sergio Rasmann in the group of Ted Turlings at the University of Neuchâtel. They found that maize roots attacked by rootworm attract nematodes by releasing (E)-beta-caryophyllene (E_C). One striking finding was that, after decades of breeding, most North American maize varieties no longer emitted E_C and had lost the ability to attract protective nematodes.

Therefore the research group in Jena and Neuchâtel teamed up again in an attempt to restore the E_C signal in a variety that normally does not emit the substance. Jörg Degenhardt, with the help of Monika Frey at the Technical University of Munich, transformed a non-emitting maize line with a gene that encodes an E_C generating enzyme, resulting in continuous emissions of E_C. Next, the Turlings group in Neuchâtel sent Ivan Hiltpold to Missouri, where, under the guidance of Bruce Hibbard of the United States Department of Agriculture, the transformed plants were tested in the field.

"Our study showed that the re-established natural E_C signal greatly enhanced the effectiveness of nematodes in controlling Western corn rootworm", Hiltpold reports. In rows with E_C-producing maize plants root damage was greatly reduced; 60% fewer Diabrotica beetles emerged as compared to rows with non-transformed maize plants. This control efficiency approaches that of conventional synthetic insecticides used to fight Diabrotica. Subsequent laboratory studies confirmed that transgenic plants attracted significantly more nematodes than the non-transformed equivalents.

"The use of this indirect defense is an attractive strategy to increase plant resistance against herbivores and to reduce the use of chemical pesticides," Degenhardt says. "The transgenic corn plants used in these experiments have no commercial value and the experiments simply served a 'proof of principle' that the E_C emission helps to protect the plants against underground infestation." The E_C trait is present in other, mainly European, corn varieties as well as in the maize ancestor species. The trait could be reintroduced into deficient plants by conventional breeding. On the other hand, generating E_C emitting maize varieties by means of gene technology may have advantages: it is faster and prevents the loss of other important traits.

In further experiments the researchers want to determine the most effective way the nematodes and their response to the E_C can be applied. Moreover, the diffusing properties of caryophyllene make it an ideal belowground signal that could also serve to protect other crop plants. A patent for this approach has been filed.

Journal reference: Jörg Degenhardt, Ivan Hiltpold, Tobias G. Köllner, Monika Frey, Alfons Gierl, Jonathan Gershenzon, Bruce E. Hibbard, Mark R. Ellersieck and Ted C. J. Turlings. Restoring a maize root signal that attracts insect-killing nematodes to control a major pest. *Proc. Natl. Acad. Sci. USA*, Early Edition, August 3, 2009 DOI: 0.1073/pnas.0906365106.

Source: ScienceDaily (Aug. 29, 2009).

Evolution Coup: Study Reveals How Plants Protect Their Genes

Unlike animals and humans, plants can't run and hide when exposed to stressful environmental conditions. So how do plants survive? A new Université de Montréal study, published in the journal Proceedings of the National Academy of Sciences, has found a key mechanism that enables plants to keep dangerous gene alterations in check to ensure their continued existence.

"We've discovered a new pathway that plants use to protect their genes against dangerous alterations that could also allow some useful mutations to occur," says Normand Brisson, a Université de Montréal biochemistry professor who made his discovery with graduate students Alexandre Maréchal and Jean-Sébastien Parent.

"Such mutations played an important role in the evolution of plants with high nutritional value, resistance to disease and harsh climate that are so important to modern agriculture," adds Dr. Brisson. "Our results open new research avenues for the study of similar mechanisms of gene repair in humans that might be important for human evolution, our responses to stress and the prevention of devastating diseases."

All living things are constantly exposed to stressors that can provoke gene mutations, yet if uncorrected such mutations can have disastrous consequences such as the development of cancers in humans or cell resistance to cancer-fighting drugs. Cells have evolved a battery of mechanisms to correct mutations, including recently discovered strategies that can also modify the number of copies of individual genes. These corrective mechanisms have attracted a lot of scientific interest since they could play a key role in species evolution. For example, while chimps and humans have almost identical genes, differences present in the number of copies of individual genes could account for distinctions between these species.

Dr Brisson suspected that a protein family he has studied for years, called the "Whirlies" (because of their peculiar structure similar to a whirligig) might be important to protect against mutations in plant cells - specifically in the chloroplast - the engine of photosynthesis that allows plants to transform carbon dioxide into sugar and expel the oxygen we breathe.

Working with his students and Biochemistry Professor Franz Lang, they showed that Whirlies are key to preventing major rearrangements of genes that could result in the creation of multiple gene copies. The discovery is important, since the number of copies of a gene must be kept scrupulously in balance with other genes so they can function correctly together. Even though gene multiplication can be thought of as detrimental, such multiplication can be an important adaptation to stressors and so keeping such mutations in check must be balanced against creating mutations that may actually help living things survive in changing conditions.

"As the effects of climate change and industrial pollution cause increasing concern for human health, we might overlook how increases in temperature and pollutants affect the plants we depend on for our survival,'' stresses Dr. Brisson. "These rapid changes in environmental conditions all cause great stress on crops, trees and wild plants and could have further unforeseen effects on their genes."

Journal reference**:** Alexandre Maréchal, Jean-Sébastien Parent, Félix Véronneau-Lafortune, Alexandre Joyeux, B. Franz Lang, and Normand Brisson. Whirly proteins maintain plastid genome stability in Arabidopsis**.** *Proc. Natl. Acad. Sci*. 2009; 106 (34): 14693 DOI: 10.1073/pnas.0901710106.

Source: ScienceDaily (Sep. 11, 2009).

Forthcoming meetings

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10th EMBO/EMBL Science & Society Conference 'Food, sustainability and plants science - A Global Challenge'

6-7 November 2009 - Heidelberg, Germany

http://www.embo.org/policy-and-society/science-society/conferences/2009.html

23rd New Phytologist Symposium: Carbon cycling in tropical ecosystems

17-20 November 2009 - Guangzhou, China

http://www.newphytologist.org/carbon/default.htm

International Conference on "Green Plant Breeding Technologies"
February 2-5, 2010. Vienna, Austria.
Invited speakers are internationally known names such as H. Geiger, J.B. Nasrallah, G. Pelletier, M. Koorneef, D.J. Mackill, P. Ozias-Akins, R.J. Nelson, R. Dirks, C.D. Chase, B. Stich, A.R. Fernie, P.C. Struik, R.A. van der Hoorn, J. Snape and others.
Conference webpage: http://www.univie.ac.at/greenbreeding/
For any questions please contact Mondial: gpbt2010@mondial-congress.com
or the conference organizers: greenbreeding.plantmolbio@univie.ac.at

III PanAmerican Plant Membrane Biology Workshop
February 13 – 16, 2010. Puebla, Mexico
http://sites.google.com/site/iiipanamericanplantmembrane/

Keystone Symposia: RNA Silencing Mechanisms in Plants
February 21 – 26. 2010. Hilton Santa Fe, New Mexico, USA.
Visit www.keystonesymposia.org/10B6 for more information.

International Conference on "Molecular Aspects of Plant Development"
February 23-26, 2010.Vienna, Austria.
Invited speakers: P.N. Benfey, U. Grossniklaus, M. Tsiantis, D.C. Bergmann, V. Sundaresan, L. Ostergaard, C.S. Gasser, T. Berleth, V. Walbot, K. Palme, S. De Vries, H. Ma, M.J. Holdsworth, A.J. Fleming, F. Hochholdinger and others.
Conference webpage http://www.univie.ac.at/mapd/.
For any questions please contact Mondial mailto: mapd2010@mondial-congress.com or the conference organizers mailto: mapd.plantmolbio@univie.ac.at

4th International Conference on Mechanisms of Growth, Competition and Stress Defence in Plants.
1-3 March 2010 - Munich, Germany.
http://www.wzw.tum.de/sfb607symposium2010/

IUFRO Kuala Lumpur 2010
March 7-12, 2010. Legend Hotel, Kuala Lumpur, Malaysia.
Conference website for on-line registration at: http://iufrokualalumpur2010.org/

Keystone Symposia
03/14/2010 - 03/19/2010. Granlibakken Resort, Tahoe City, California, USA.
Visit www.keystonesymposia.org/10C2 for more information.

24th New Phytologist Symposium: Plant Respiration and Climate Change
11-14 April 2010 - Oxford, United Kingdom.
http://www.newphytologist.org/respiration/default.htm

IX International Symposium on Plant Biotechnology
20-22 April, 2010 Villa Clara, Cuba
E.mail: simposio@ibp.co.cu
http://simposio.ibp.co.cu/

20th International Plant Growth Substances Association (IPGSA) Conference
06/28/2010 - 07/02/2010. Universitat Rovira i Virgili, Tarragona, Spain.
Information on the IPGSA website: http://www.ipgsa.org/meeting/index.htm
Contact: Valerie Sponsel (IPGSA Secretary) at http://www.ipgsa.org/contact.htm

12th World Congress of the International Association for Plant Biotechnology
06/06/2010 - 06/11/2010. America's Center in St. Louis, MO. USA.
http://www.iapb2010.org

21st International Conference on Arabidopsis Research
06/06/2010 - 06/10/2010. Yokohama, Japan.
http://arabidopsis2010.psc.riken.jp/

SEB Annual Main Meeting 2010
30th June - 3rd July 2010. Clarion Congress Hotel, Prague, Czech Republic
Enquiries: Kate Steel (k.steel@sebiology.org)
http://www.sebiology.org/meetings

4th International Conference "from Scientific Computing to Computational Engineering" (4th IC-SCCE)
7-10 July, 2010. Athens, Greece.
Organizer: Professor Demos T. Tsahalis, Director of Laboratory of Fluid Mechanics and Energy (LFME), University of Patras, Greece.
Conference's website: http://www.scce.gr/2010/

3rd Workshop on Molecular Aspects of Seed Dormancy and Germination
July 18-22nd 2010, York, UK.
Contact: Dr Steven Penfield, sdp5@york.ac.uk
http://www.york.ac.uk/org/cnap/meetings.html

Nitrogen2010: 1st International Symposium on the Nitrogen Nutrition of Plants
July 26th - 30th, 2010. Inuyama Int. Sightseeing Center "FREUDE", Aichi, Japan.
More information at:
http://www.agri.tohoku.ac.jp/cellbio/nitrogen2010/nitrogen2010.htm
http://www.agri.tohoku.ac.jp/cellbio/nitrogen2010/invitation.html

Plant Biology 2010
July 31st - August 4th. Montréal, Canada.
Joint Annual Meeting of the American Society of Plant Biologists and the Canadian Society of Plant Physiologists, Société Canadienne de Physiologie Végétale

Opinion
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Bring Back Reprint Requests
I miss the instant feedback from the larger scientific community on my papers.
By Steven Wiley
The Scientist. Volume 23, Issue 9, Page 29.

The Internet has changed scientific publishing in many ways, some good and some bad. No one would deny that it is easier to find papers on a particular subject than ever before. Looking up papers in *Index Medicus* or by browsing *Current Contents* has long been replaced by online searches on *Medline* or even *Google Scholar*. This has not necessarily improved our understanding of the literature, but it certainly provides a quick way to feel up to date.

In some ways, the Internet has even streamlined the submission of manuscripts, although formatting papers correctly still takes an enormous amount of time and the speed of paper review and acceptance doesn't seem to budge. I still find myself bugging editors after waiting 6–8 weeks with no response—about the same as 20 years ago. Still, overall, I think most scientists feel that the Internet has improved scientific publishing, especially by giving rise to open access journals.

One little-noted casualty of the transition to electronic publishing, however, is the reprint request. Although many authors might bid them good riddance, I sorely miss them because they provided me with one of the best sources of feedback on my scientific research.

For the younger readers, let me explain the concept of reprints and reprint requests. The scientific literature used to be accessed almost completely through journals delivered to libraries. If you found a paper you were interested in reading, usually by scanning article titles in *Current Contents* or by finding a reference within a paper, you looked it up in the library's journal collection and made a copy—a slow and cumbersome process. Alternately, you mailed the authors a card requesting a reprint. Indexing services, such as the Institute for Scientific Information, made this process very easy by providing reprint request cards, author addresses, and—eventually—software to print cards.

Requesting and sending reprints was extremely common. After your paper was accepted by a journal, you always ordered lots of reprints, not only to send to grant reviewers and promotion committees, but also to send to fellow scientists. And sending reprint requests to other scientists was a nice way to communicate that you liked their research. Although I usually retrieved papers from the library, I would still ask for reprints from the dozen or so scientists whose work I regularly followed. Although many of my fellow scientists considered reprint requests a big pain, I loved the instant feedback they provided on community interest in my research efforts.

I remember my delight at receiving hundreds of reprint requests for individual papers that I fought long and hard with reviewers to get published. However, I was also surprised to receive only a handful of requests for some papers that I thought were breakthroughs in their field. A quick reality check is always valuable, especially early in your career.

One of the best aspects of feedback from reprint requests was the detailed information it often provided. Requests showed which scientists were interested, their field of study (from their department affiliation), and whether they were following your work over time. Some scientists even included notes. It was also relatively fast. I found that in general, the number of reprint requests for a paper was correlated with eventual citation frequency, but the latter took years to assess. There were also other perks, such as the interesting stamps on requests from Africa, Eastern Europe, and Asia.

Nowadays, we don't bother with reprints—we just download PDFs. Although convenient, this discourages selective reading and almost completely removes the feedback step from the publication process. However, there really is no reason why online journals could not provide this information. Some journals do provide listings of "highly accessed" articles, but I want to consistently know the number of times that my articles are downloaded and the departments and institutions that download them.

Electronic publishing is rapidly becoming the dominant mode of scientific communication, but it is still a nascent medium with much room for improvement. The lack of a rapid feedback mechanism for our papers is still a significant problem. Fortunately, because of the flexibility and dynamic nature of the Internet, it should be relatively easy to fix this. Letting me know how often my articles are downloaded or accessed is one step, although it will not tell me who is doing the downloading. And I will still miss the neat postage stamps.

Steven Wiley is a Pacific Northwest National Laboratory Fellow and director of PNNL's Biomolecular Systems Initiative.

PNAS scraps special submission

By Bob Grant

The Scientist: NewsBlog. 10th September 2009.

A leading scientific journal has done away with a manuscript submission option that allowed members of the National Academy of Sciences to usher papers from non-members through the peer review process.

The *Proceedings of the National Academy of Sciences* (*PNAS*) offered the option, called "Track I," to members of the Academy as a way to bring papers written by non-members to the journal's attention. Members were allowed to "communicate" two Track I papers per year, and were responsible for procuring at least two reviews of the manuscript before submitting it to the *PNAS* editorial office.

Starting July 1, 2010, *PNAS* will require non-members to submit manuscripts to the journal via the normal route, "Track II," according to *ScienceInsider*. A paper submitted via this route is screened by a *PNAS* editorial board member, who decides whether the paper is scientifically sound and likely to represent the top 10% of its field. If the paper passes muster, the board member hands it off to an Academy member for editing.

"Since the introduction of Track II as the general route for submitted papers, many members will no longer communicate papers through Track I," wrote Alan Fersht, a *PNAS* associate editor, in a 2005 editorial in the journal. But in 2009 *PNAS* has published approximately 390 papers (about 12.5% of the total published) that were submitted using the Track I route, according to *ScienceInsider*.

Researchers submitting papers to *PNAS* will still be allowed to suggest referees and editors for their manuscripts.

Where's the Super Food?

By Bob Grant

The Scientist. Volume 23, Issue 9, Page 30

Scientists have genetically engineered several biofortified food plants to tackle a scourge of developing countries-micronutrient malnutrition. The crops have yet to be planted on a wide scale, but that may be about to change.

Right now, one billion people are starving. That's one in every six people on this planet. The number of these hungry people is roughly equivalent to the populations of the United States, Indonesia, Brazil, Pakistan, and Bangladesh combined.

The world reached this bleak milestone in the middle of June this year. With the global human population continuing to explode and resources being stripped at an increasing rate, the outlook is not good. More people will go hungry. Less will have access to the nutrients their bodies need. And more will succumb to the illnesses that take advantage of the malnourished body. More people will die.

But this is only half the story. The insidious corollary to the global hunger crisis is that even more people-at least half the world's population, according to a 2004 United Nations report-suffer from micronutrient malnutrition. People suffering from this “hidden hunger” may consume sufficient calories, but lack suitable amounts of essential nutrients, vitamins, and minerals. These legions of nutrient-starved people largely reside in developing countries. Their plight is dire. Even mild micronutrient deficiencies can increase infant mortality rates and lead to cognitive impairment and immune system problems in children, among other serious health issues.

In addressing global hunger and micronutrient malnourishment, biotechnology holds potential solutions: specifically, nutritionally enhanced, transgenic crops. The technology that makes these plants possible took center stage in January 2000 with the publication of a brief but high-impact Science paper on the creation of a prototype that would become known as “Golden Rice,” packed with beta-carotene (also called pro-vitamin A), the precursor to vitamin A and an essential component of healthy diets.1 Genetically modified (GM) crop plants were already becoming commonplace, but existing genetic changes mostly endowed plants with desirable producer traits, such as herbicide or pest resistance in soybeans or cotton plants. To create Golden Rice, European scientists, with funding from the Rockefeller Foundation, inserted bacterial transgenes into the latent pro-vitamin A biosynthesis molecular pathways in wild-type rice, which contains no pro-vitamin A. This modification transformed the normally nutrient-poor endosperm-or kernel-of milled rice into a source of beta-carotene.

Their work was trumpeted on the cover of TIME magazine with the headline: “This rice could save a million kids a year,” preventing night blindness and other disorders caused by low vitamin A, a nutrient often lacking in developing world diets. While it got people talking and thinking about the potential of genetic engineering to salve the world's hunger pangs, Golden Rice also set up a contentious debate that still rages today. “[Golden Rice] was something that attracted the attention of both opponents and proponents in the same way,” recalls Peter Beyer, a plant biochemist at the University of Freiburg in Germany and one of Golden Rice's inventors.

Nutritionists took Beyer and his co-inventor, now-retired biologist Ingo Potrykus, to task, pointing out that Golden Rice could do little to address vitamin A deficiencies in the developing world because its beta-carotene content was too low. Beyer says that anti-GM groups “hijacked” the issue and used Golden Rice as a springboard to rail against all GM crops. Largely due to this controversy, along with political and technological obstacles, nearly 10 years after it was unveiled, Golden Rice has yet to make its wide debut in the paddies of the developing (and vitamin A-deficient) world. “Once [the science] is there, your initial belief is that your work is done, but by far it is not,” says Beyer.

But Beyer, Potrykus, and several collaborators have continued to forge on, refining the technology that made Golden Rice possible and amassing a larger consortium to try to get the enhanced staple crop into the dinner bowls of the people who most need it. And the failure of Golden Rice to leap directly into the world's rice paddies has not dissuaded scientists from trying the same with other enhanced crops: carrots with twice the calcium, tomatoes with 20% more antioxidants, cassava boosted with additional iron, protein, and vitamins. There are dozens of reports in the scientific literature of common food plants that have been engineered to produce increased levels of one nutrient or another. One cannot yet find vast paddies of Golden Rice waving in the tropical sun or fields of super-cassava blanketing African farmland, but this may be about to change.

More than 250 million sub-Saharan Africans rely on the cassava, a starchy tuber native to South and Central America, as their staple food. Cassava supplies 38.6% of the caloric requirements in some parts of Africa, where hunger and nutrient deficiencies grip the populace and more than 40% of global cassava production takes place.

But cassava is not a particularly nutrient-rich food. It lacks much of the iron, zinc, and vitamins A and E that healthy bodies need to grow. University of Nebraska-Lincoln biochemist Ed Cahoon has worked for several years as part of the BioCassava Plus program, which aims to improve the nutritional profile of cassava through genetic engineering.

Launched in July 2005 with $7.5 million from the Bill and Melinda Gates Foundation's Grand Challenges in Global Health Initiative, the program's overarching goal is to develop what essentially amounts to a super-charged cassava plant variety-one with increased levels of iron, zinc, protein, vitamins, and resistance to the cassava mosaic and brown streak viruses plaguing African farmers.

The program has started by developing separate GM cassavas with each of these nutritional improvements one by one. Cahoon and his colleagues have produced a beta-carotene-enhanced cassava by inserting genes that impart higher levels of the pro-vitamin (and give an orangey glow to the normally pallid root). They inserted a gene called phytoene synthase (psy) originally derived from the soil bacterium Erwinia herbicola (and also used to develop Golden Rice), which codes for an enzyme that catalyzes a crucial step in the beta-carotene biosynthetic pathway.

The researchers packaged psy into the plasmid of a disarmed Agrobacterium-the workhorse of plant genetic engineering-together with a root-specific promoter derived from potatoes, a 5´ leader sequence consisting of plant DNA that shuttles the protein into root-bound plastids, and the standard 3´ untranslated region (UTR) from mRNA. Cahoon recalls the first time he saw the successfully engineered cassava root (the part of the plant that's eaten), in 2007. "It was a good day," Cahoon says. "[The cassava] was noticeably orange."

Meanwhile, Cahoon decided to try inserting the Arabidopsis gene, 1-deoxy-d-xylulose 5-phosphate synthase (dxs), which regulates the isoprenoid pathway, a set of biochemical reactions further upstream from the biosynthetic step in which psy is involved. Inserting dxs, which increases the amount of chemical precursors to beta-carotene, was "like turning up the whole isoprenoid pathway," Cahoon says. He found that inserting both the psy and dxs genes resulted in a cassava even more orange than the roots with only the psy modification-and with 30 times more beta-carotene than normal roots.

After running more greenhouse trials on plants with both the single and double genetic modifications and choosing the cassava with the most beta-carotene, Cahoon and his team sent tissue samples to Puerto Rico, where scientists propagated clonal offspring. Now, the cassava plants are growing in field trials, which Cahoon recently visited. "They're looking good," he says. "For the most part they look like the control plants," which contain normal levels of beta-carotene.

Eventually, the BioCassava Plus program hopes to move into its second phase-set to commence in 2010 with an additional infusion of funding-in which nutritional modifications to increase iron, zinc, protein, vitamins, and virus resistance will be combined into one cassava plant. "We would actually address all of the deficiencies in cassava in a single cultivar," says Richard Sayre, a molecular biologist at the Danforth Plant Science Center in St. Louis and director of the BioCassava Plus program. But, as he and Cahoon learned from Golden Rice, getting the science right is just the first step.

There are reasons Cahoon and his colleagues picked Puerto Rico as the site of field tests for the beta-carotene-boosted cassava. Puerto Rico enjoys a tropical climate like much of the core cassava growing areas of Africa but, equally important, the island territory operates under the laws and regulations of the United States, not Africa. "It's not Africa, but getting in the field in Puerto Rico is a much simpler process than getting through the regulatory processes in Africa," Cahoon says.

It's this regulatory tangle facing GM crops in much of the world, including Africa, that largely explains why many transgenic plants that could address widespread nutrient deficiencies are trapped in laboratories instead of growing in soil.

According to Val Giddings, president of Prometheus Agricultural Biotech, most of the restrictions stem from European politics, as influenced by vocal anti-GM groups. Giddings, who helped craft the US Department of Agriculture's GM crop regulations in the early 1990s as a geneticist at the agency's Animal and Plant Health Inspection Service (APHIS), says that European countries have effectively exported their restrictive regulations by "making their overseas development programs a slave to their domestic political policies." In 2004, American officials entreated EU officials to reassure three African nations-Zimbabwe, Zambia and Mozambique-that the hundreds of thousands of tons of GM food aid they had rejected was in fact safe; the EU refused. Add to this the influence that European importers and governments have over food producers in Asia and Africa, and the developing world's soil is rendered pretty infertile for GM crops. Robert Paarlberg, a Harvard political scientist and author of the book Starved for Science, concurs about the difficulties in getting biotech crops into developing nations. “It's an informal chain of influence,” he says, “that discourages African farmers from planting any GM crops at all.”

Even in the United States, GM regulations are cumbersome and require a team of people to navigate. Agricultural biotech entrepreneurs, like drug developers, often cite a 10-year time frame to go from initial discovery to saleable product. But compared to the European system, the US regulatory system is manageable. For the beta-carotene-fortified cassava to gain approval from the Department of Agriculture (USDA), for instance, the agency would require data indicating that the introduced genetic construct stably integrated, that the introduced gene does not cause plant disease or produce an infectious agent, and that the cassava was not modified using a gene derived from human or animal pathogens, among other criteria. “It may feel cumbersome to people, but I don't think [the regulations] are unreasonable,” says Mark Manary, a pediatrician at Washington University in St. Louis who collaborates on the BioCassava Plus program and spends more than half the year working with aid groups in the African nation of Malawi.

However, even if scientists get past the regulatory hurdles associated with any GM foods, there is another practical obstacle that stands in the way of fields full of nutrient-packed cassava or carrots: These foods will cost more than the non-modified versions, and the people who most need them are also the least able to afford them.

In a basement lab at a DuPont research facility, a technician loads bright green soybean tissue samples into a “gene gun,” an unassuming contraption that looks more like a toaster oven than a firearm, and shoots gold nanoparticles coated with DNA molecules into soybean cells at more than 1500 kilometers per hour. The machine makes a muffled pop and the deed is done. DNA will incorporate into the soybean genome and inhibit the activity of fatty acid saturase-2, an enzyme that normally catalyzes the biochemical conversion of oleic to linoleic acid in the soybean plant. Plant molecular biologist Ted Klein stands by, watching. “If we knock out the expression of that enzyme, specifically, in the seed at the right time, then there's no detrimental impact on the whole plant,” he says.

Elsewhere in DuPont's Wilmington, Del.-based experimental station, giant walk-in coolers feature lines of bright fluorescent bulbs glowing above rows of the modified soybean plants that grew from tissues earlier shot with the gene gun. While they may not address nutrient deficiencies in poverty-stricken corners of the globe, these plants may one day reduce the need to use hydrogenated oils-AKA the dreaded trans fats-in frying, for example. For now, the plants simply stretch to gather as much of the light as possible; eventually, they will produce oil that is more stable in storage and cooking conditions, with 20% less saturated fat and a higher proportion of oleic acid than normal soy oil. The company will screen these soybeans in the grow room looking for the best phenotypes, which develop after several semi-random gene gunshots. DuPont and Pioneer Hi-Bred, the DuPont company that managed the research and development of the technology behind the plants, known as Plenish, hopes to sell “high oleic oil” from the beans to food processing companies, restaurant chains, and other industrial customers around the world as early as the end of this year. With such a market, the company isn't too concerned about finding customers who can afford the technology.

The oil has already been approved by Mexican and Canadian regulatory agencies. “Now we're just waiting for the USDA,” says Susan Knowlton, a DuPont research manager.

Other scientists are also trying to tweak the nutritional content of common foods. Kendal Hirschi, a Baylor University pediatrician and geneticist, has genetically engineered a carrot that contains twice the calcium of normal carrots by upping the expression of a plant calcium transporter (sCAX1) in the roots with the addition of an Arabidopsis gene construct. He's even performed a pilot nutritional study, which was funded by the National Institutes of Health, where subjects absorbed about 40% more calcium from his carrots than they did from normal carrots.2 Feeding studies are essential if nutritionally enhanced GM foods are going to have a real-world impact, Hirschi says. “None of these improvements are any good until we actually show they're good in the food supply.”

In order to ensure that the technology has a buyer, that could perhaps compensate for the expense of distributing it free or below cost to the developing world, Hirschi is trying to attract attention from large food company General Mills, which has expressed some interest in his carrots as a way to make thicker canned soups. (Calcium chloride is often added to foods as a thickener.)

Cathie Martin, a geneticist at the John Innes Centre in Norwich, UK, has developed a tomato variety that may prove useful to consumers worldwide, not just the malnourished. Martin's deep purple tomato has 20% higher levels of anthocyanins, antioxidants that may guard the body against chronic diseases and cancer. She and colleagues recently showed that mice consuming a diet that includes her GM tomatoes, whose boosted antioxidant profile is thanks to two transcription factors from snapdragons, lived an average of 30% longer than mice that consumed regular tomatoes.3 Western countries-where people tend not to get the recommended 5 fruits and vegetables per day, and the giant food companies that operate therein-can play a role in moving these types of GM foods closer to a widespread reality, Martin says. "You've got to get the food companies interested in sowing better foods," she says. "If you can improve tomatoes, then you can get the good things in fruit and vegetables into something that people actually eat."

"We know how this story ends," says Val Giddings-nutritionally fortified, GM foods will get into the global marketplace and the mouths of the people who need them. "You can't stop the tide. Biotech will, in time, become the new conventional agriculture. The question is how long will it be until that happens, and what, if anything, can we do to accelerate the process."

There are hints now emerging that bear out Giddings' prediction. Since first introducing the world to Golden Rice in 2000, Beyer's collaborators have developed new versions of the beta-carotene-enhanced grain. Golden Rice 2, which Beyer says will be available on the market in the Philippines and in Bangladesh within the next 2 or 3 years, contains 30-35 micrograms of beta-carotene/gram-more than 30 times more beta-carotene than the original kernel introduced in 2000.4 Beyer and his colleagues accomplished this massive increase by tinkering with the promoter sequences used in the genetic modification, by changing the source of one of the gene inserts from daffodils to maize (which boosts beta-carotene production), and other subtle tweaks to the science behind Golden Rice. This new version recently completed feeding trials5 and is now growing in experimental plots in the Philippines and Bangladesh.

But the research was relatively easy-to create a GM product that regulators and citizens would accept, Beyer needed help. Funding came from philanthropic organizations, such as the Bill and Melinda Gates Foundation, the Rockefeller Foundation, and government aid agencies, such as the United States Agency for International Development. A private-public partnership between Golden Rice's inventors and the agrichemicals company Syngenta, along with several collaborations with research institutions throughout Asia, made the imminent market introduction of Golden Rice possible, Beyer says. The project is now conducting the social marketing research and local rice variety back-crosses, which will blend the beta-carotene trait into locally popular rice varieties-both necessary to successfully and safely introduce the crop and get farmers to grow the plants.

The BioCassava Plus program has also recently seen significant progress in its goal to introduce biofortified foods into the developing world. Director Richard Sayre says that the program's pro-vitamin A cassava plants have been approved for field trials in Nigeria, the world's number one consumer of the food. In July, the country planted between 4000 and 8000 m2 with Cahoon's two-gene GM cassava, the first GM product Nigeria has field tested. "We are quite proud of that," Sayre says. To advance the BioCassava Plus program to the next stage, Sayre says that more donor money will be needed. He says that the program is "planning on approaching other donors," but declined to name them.

Navigating through Nigeria's regulatory approval process was no small task, Sayre says, for which the BioCassava Plus program enlisted the help of Nigeria's National Root Crop Research Institute (NRCRI) and a Nigerian product developer who was a former member of the county's National Biosafety Committee. "We think that was an important part of our strategy," Sayre says, "because it meant that the government was buying into the process." The Nigerian regulations, for example, required experimenters to dig a fence around the experimental plots a meter deep into the soil to prevent burrowing animals from carrying off bits of the GM cassava. The Nigerian regulations were "redundancies upon redundancies of protection," according to Sayre.

To ensure the cassava gets where it needs to go, the project will again call upon the infrastructure and local knowledge of national agriculture research institutions such as the NRCRI and nongovernmental organizations to distribute the cassava plants to poor farmers for free or for a nominal fee. The BioCassava Plus project will utilize the traditional dissemination scheme-where farmers share cuttings of their successful plants with friends and neighbors-to further disseminate their enhanced cassava. (The Gates Foundation, in fact, requires that the technology come with royalty-free humanitarian license.) Poor farmers can get and share cuttings for free, while those who make more than $10,000 per year must pay a royalty fee to companies like Monsanto that donated enabling technologies (patented Agrobacterium transformation systems, and gene promotors, for example) to the project. Sayre also says that a "very critical" part of the BioCassava project is to eventually transfer research and production capabilities and responsibilities to African labs, scientists, and countries. "I put myself out of business in many ways," he says.

Other GM advocates say they hope cassava is not the only biofortified food to be planted in Nigeria. "What I'd like to see is hundreds of millions of very poor people improving their nutritional status and improving their health status," says Lawrence Kent, senior program officer of agricultural development at the Bill and Melinda Gates Foundation, which funds genetic research in biofortification, but also donates money to efforts aimed at conventional fortification, supplementation, and dietary diversification. "We're hoping some initial successes are going to trigger additional interest, especially from national governments. If we can help get more nutrients into these staple foods, we really can help millions of people improve their lives.

Positions available

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PhD fellowship

Instituto Valenciano de Investigaciones Agrarias (IVIA, 46113-Moncada, Valencia Spain).
Understanding of the better tolerance of polylpoid citrus rootstocks to abiotic stresses.
It is a joint project between IVIA and CIRD (A French agricultural research institution for developing countrie). The objective of the project is to enlighten the physiological and molecular determinants conferred by autotetraploid rootstocks to water deficit tolerance. Scion/rootstock interaction with different level of ploidy will be studied. Hormonal responses as well as detoxification processes will be investigated at the physiological and molecular levels. Applicants should have strong interest in plant physiology with excellent communication skills. Background in molecular biology is required. Interested candidates should send a CV to: Dr. Raphael Morillon, scientist at CIRAD, IVIA : morillon@cirad.fr; or Dr. Luis Navarro, Director del Centro de Proteccion Vegetal y Biotecnologia, IVIA : navarro@ivia.es.

PhD position in plant molecular cytogenetics/genome evolution

University of Vienna, Austria.
One full-time PhD position in plant molecular cytogenetics/genome evolution is available for 3 years in the Department of Systematic and Evolutionary Botany, University of Vienna, Austria starting November 2009.
The position is part of the FWF (Austrian Science Fund) project "Origin and genome evolution of chromosomal races in the polyploid complex of Prospero autumnale (Hyacinthaceae)". The project focuses on a chromosomally highly variable monocotyledonous plant complex which comprises diploids with different base chromosome numbers (x = 5, 6, 7), as well as numerous autoand allopolyploids. Essentially, every known form of chromosome mutation has been detected in this group. A thorough investigation of the cytological features of this remarkable group employing repetitive DNA analyses and the interpretation of changes in a sound phylogenetic context will allow addressing evolutionary questions concerning the origins, mechanisms, directions and frequencies of chromosomal changes. Ultimately it will allow establishment of the role of chromosome change in race formation and speciation.
The project is based on an integrative approach utilizing molecular cytogenetic and molecular biology techniques, bioinformatics (analyses of deep-sequencing data) and molecular phylogenetic approaches. Project will be performed in international collaboration with the groups in UK (Dr. A. Leitch, Dr. I. Leitch, Dr. J. Parker), and in Czech Republic (Dr. J. Macas).
The successful candidate will join a young and expanding research team.
She/he should hold a European or equivalent Master degree in biology/botany/molecular biology or related field. Prior practical experience in plant cytogenetics (chromosome preparation, FISH) and basic molecular biology techniques (PCR, DNA labeling, cloning) is preferred. The candidate should be motivated, good team player, and proficient in English (written and oral).
Please send an application including CV, a list of publications, a brief outline of research experience and scientific interests (max. one page), and two reference letters. Review of applications will begin immediately and continue until 1st of November 2009.
For further information or to apply for the position please contact: Dr. Hanna Schneeweiss. University of Vienna. Rennweg 14, A-1030, Vienna, Austria. hanna.schneeweiss@univie.ac.at

Job offer for a PhD student

Study of cell and tissue specificity of hormone responses in Arabidopsis

Profile:

· Master degree with good ranking, specialization in either biochemistry, biotechnology, biology, or bio-engineering
· Knowledge of molecular and microscopic techniques
· Strong interest in plant biology
· Be familiar with commonly used software packages (MS Office, Adobe Photoshop, Illustrator)
· Thorough knowledge of English (both spoken and written)
· Team player, but able to work independently

We offer:

· A challenging job in a dynamic research group
· An international surrounding
· Collaboration with several European laboratories
· 4 year contract

Interested send your CV by email to Prof. Van Der Straeten: Dominique.VanDerStraeten@ugent.be
with cc: to Dr. Vandenbussche filip.vandenbussche@ugent.be

PhD position

A PhD student position on environmentally triggered signalling events in Arabidopsis thaliana is available in the lab of Claudia Jonak (http://www.gmi.oeaw.ac.at/cjonak.htm) at the Gregor Mendel Institute of Molecular Plant Biology (GMI) in Vienna, Austria. Research in our group focuses on the mechanisms of how plants react and possibly adapt to adverse growth conditions.

The successful candidate should be highly motivated and have a solid background in biochemistry and/or molecular biology. He/she will investigate the fundamental role of glycogen synthase kinase 3 (GSK3)-directed signal transduction for adaptation to environmental stress. We offer cutting-edge technical equipment, service facilities and an international, intellectually stimulating environment at the Gregor Mendel Institute of Molecular Plant Biology (GMI) in Vienna, Austria.

Qualifications required: undergraduate degree in biological sciences

Employer: Gregor Mendel Institute of Molecular Plant Biology Vienna, Austria. www.gmi.oeaw.ac.at

For more information, please contact Claudia Jonak (claudia.jonak@gmi.oeaw.ac.at).

To apply, please send a letter of motivation, a curriculum vitae including a brief description of your research experience and interests, and contact information to claudia.jonak@gmi.oeaw.ac.at

Post-doctoral position

We are seeking a highly motivated post-doctoral fellow to study the regulation of cell proliferation in plants. The project will involve the use of high content screening technologies and an *in vitro* Arabidopsis cell system to identify genetic factors and small molecules that determine the proliferation potential of plant cells. The fellow will work and coordinate research with other scientists assigned to the project. He/she will be hired in the context of the AGRON-OMICS integrated project (www.agron- omics.eu), a large European consortium focusing on the global characterization of Arabidopsis leaf growth.

The candidate must hold a Ph.D. and have a strong interest in integrative biology. An excellent command of the English language is necessary.

The Department of Plant Systems Biology (VIB – Ghent University) is a leading institute that offers excellent opportunities to develop multidisciplinary projects combining molecular biology and genetics, functional genomics, bioinformatics and computational biology. Its campus is ideally positioned at the interface between academia and industry and is one of the largest biotechnology centres in Europe.

The position will be available as early as September 2009, for two years. To apply, send a letter of motivation, a curriculum vitae and the contact details of two references by email to:

Pierre Hilson
Functional Genomics Division
Department of Plant Systems Biology, VIB – Ghent University. B-9052 Ghent, Belgium
Phone: + 32 (0)9 331 38 30; Fax: + 32 (0)9 331 38 09; Email: pihil@psb.vib-ugent.be
http://www.psb.ugent.be/

Post-Doctoral Position

Dpt. Plant-Microbe-Environment. INRA/CNRS/Université de Bourgogne. Dijon. France.
A 2-year post-doctoral position is available from November 2009 to conduct research in the area of signal transduction in plant defence responses. The research will be focused on the analysis of the interaction between nitric oxide (NO) and reactive oxygen species (ROS) at the cellular and molecular level. The impact of their interplay in cell signaling as well as cell death will be particularly investigated. Applicants should have a real interest for signal transduction, a strong background in cellular imaging and protein biochemistry and be familiar with protein immunodetection and purification.
Salary will be approximately 2500 €/month.
Please send your curriculum vitae along with 3 letters of reference to:
Dr. Françoise Simon-Plas and/or Pr David Wendehenne
UMR 1088 INRA/5184 CNRS/Université de Bourgogne, plant-Microbe-Environment, 17 rue Sully, BP 86510, Dijon 21065 Cedex, France,
E-mails: simon@dijon.inra.fr; wendehen@dijon.inra.fr
Deadline : November 2009
For further information, please see the recent publications of the laboratory on relative subjects: Besson-Bard et al., Annu. Rev. Plant Biol. 59, 21-39, 2008; Besson-bard et al., Plant Physiol. 149, 1302-1315, 2009; Lherminier et al., Mol Plant Microbe Interact. 22, 868-878, 2009 ; Stanislas et al., Mol. Cell Proteomics, in press.
http://www.dijon.inra.fr/pme

Assistant Professorships

Three Positions, California State University, Northridge
Job Description:
California State University, Northridge invites applications for three tenure-track positions in the Department of Biology, starting August 2010.
Applicants must have a Ph.D. and postdoctoral experience.
Each successful candidate shall develop a vigorous research program involving undergraduate and M.S. students, seek extramural research funding and demonstrate teaching excellence.
1.) Microbiologist: Focusing on prokaryotic biology relating to any aspect of the health sciences.
Teaching options include Medical Microbiology, Principles of Microbiology, a specialty course and Introductory Biology.
2.) Evolutionary Biologist: Explaining patterns or processes of diversification among species or populations.
Teaching options include a course on the diversity of a group of terrestrial organisms, Molecular Systematics, Evolution and Introductory Biology.
3.) Molecular Geneticist: Emphasizing genomic or proteomic approaches to problems in eukaryotic genetics.
Teaching options include Molecular Genetics, Genetics, Introductory Biology and a specialized graduate course.
Applicants should submit a cover letter to the respective search committee, including a curriculum vitae, a summary of teaching experiences, statements of research interests and teaching philosophy and three publications.
Applicants should arrange to have three letters of recommendation sent to:
biology.dept@csun.edu
California State University, Department of Biology, 18111 Nordhoff Street, Northridge, CA 91330-8303
Screening shall begin on October 1, 2009.
For more information, visit:
http://www.csun.edu/facultyaffairs/openings/sm

Assitant Professorship in "Eukaryotic membrane biology

Interested contact:
Gunnar von Heijne
Center for Biomembrane Research. Dept of Biochemistry and Biophysics
Stockholm University
SE-10691 Stockholm, Sweden
e-mail: gunnar@dbb.su.se
phone: +46-8-162590, fax: +46-8-153679, mobile: +46-70-3941107

ERC Starting Independent Researcher Grant

(European Research Council)
Publication Date: 30 July 2009
OJ Reference: OJ C177 of 30 July 2009.
https://webmail.biology.uoc.gr/exchweb/bin/redir.asp?URL=
https://webmail.biology.uoc.gr/exchweb/bin/redir.asp?URL=
http://eur-lex.europa.eu/
ERC-2010-StG_20091118 for the domain Life Sciences (Panels: LS1 – LS9), with deadline 18 November 2009, 17.00.00 (Brussels local time).
Applicants must submit their proposals before the deadline applying to their respective domain.

New books

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Plant Stress Biology: From Genomics to Systems Biology

Heribert Hirt (Editor)
Wiley-Blackwell. October 2009. ISBN: 978-3-527-32290-9
This is the first book to present a comprehensive and advanced discussion on the latest insights into plant stress biology. Starting with general aspects of biotic as well as abiotic stresses, this handbook and ready reference moves on to focus on topics of stress hormones, technical approaches such as proteomics, transcriptomics and genomics, and their integration into systemic modeling. This book is a valuable resource for researchers as well as professionals not just in plant sciences but also in cell and molecular biology as well as biotechnology.

Nitric Oxide in Plant Physiology

Shamsul Hayat, Masaki Mori, John Pichtel, Aqil Ahmad (Eds.).
Wiley-Blackwell. October 2009. ISBN: 978-3-527-32519-1.
Written by a truly global team of researchers from Europe, Asia and the Americas with strong ties to agricultural research centers and the agrochemical industry, this ready reference and handbook focuses on the role of nitric oxide signaling in plant defense systems against pathogens, parasites and environmental stress response.
This is one of the first titles to provide a comprehensive overview of the physiological role of this ubiquitous signaling molecule in higher plants, making it an indispensable resource not only for academic institutions but also for those working in the agrochemical industry.

The Molecular Organography of Plants

Quentin Cronk .
Oxford University Press, 2009. ISBN: 978-0-19-955036-4
Written by a leading figure in the emerging discipline of plant "evo-devo" (evolutionary developmental genetics). Offers a unique synthesis of classical morphology and molecular developmental biology. Provides an authoritative overview of plant construction at the organ level, incorporating details of the molecular mechanisms responsible. Integrates pattern and process throughout.
From the cells of aquatic algae to the majestic redwoods towering 100 metres above the California coast, the history of plant evolution has been one of increasing complexity. The underlying rationale for this book is to answer the question: How, when land plant embryos at a few-celled stage are essentially comparable, do plants achieve such radically different adult phenotypes, from mosses to tree-ferns, and grasses to oak trees?
The Molecular Organography of Plants chronicles the origin, and importance, of the complex plant organs that have allowed plants to shape the earth's biosphere, and seeks to explain why and how the genetic mechanisms governing these developmental trajectories have diverged so much. It provides a detailed account of the organs produced by land plants (stems, roots, leaves, seeds, flowers) into which is incorporated what is rapidly becoming known of the molecular mechanisms responsible. Plant organs are therefore discussed in the context of the evolution of development ("evo-devo"), and their basis in molecular developmental genetics is described. The result is a novel synthesis of classical morphology and molecular developmental biology that takes a broad look at the evolution of plant form.

Photoperiodism. The Biological Calendar

Edited by Randy J. Nelson, David L. Denlinger, and David E. Somers
Oxford University Press USA, 2009. ISBN 978-0-19-533590-3.
This book examines the role of photoperiod (day length) in timing seasonal adaptations in plants, invertebrates, and vertebrates, and is the first to present such a broad perspective on the subject in quite some time. The current literature is distinctly separated among researchers working with these different taxa, resulting in inefficiency and redundancies. The field is poised to make rapid progress in the understanding of seasonal clocks at all levels of analysis, and *Photoperiodism* brings together experts working in disparate areas to stimulate conversation among investigators from all related disciplines. At the end of the book, the three editors analyze common themes in photoperiod time measurement across taxa, as well as common and dissimilar approaches to the study of photoperiodism, and propose future directions in research on photoperiodic time measurement.

Recent Advances in Plant Biotechnology

By Ara Kirakosyan and Peter B. Kaufman.
Springer, 2009. ISBN: 978-1-4419-0193-4
For this volume, we have brought together a group of contributors who address the most recent advances in plant biotechnology and what they mean for human progress and a more sustainable future.

Plant biotechnology, which is gaining in importance, applies in three major areas: the control of plant growth and development, the protection of plants against environmental and biotic stresses, and the expansion of ways by which specialty foods, biochemicals and pharmaceuticals are produced. Our lives are being affected in many ways, particularly in connection with sustainable food production and distribution systems, genetically modified organisms, integrative medicine strategies to treat human diseases, bioremediation of toxic waste sites, alternative energy production systems that utilize bioenergy sources, and both risks and benefits that fall within the rubric of plant biotechnology.

The topics covered in Recent Advances in Plant Biotechnology will be a valuable resource to plant biotechnologists, plant biologists, biochemists, molecular biologists, pharmacologists, and pharmacists; agronomists, plant breeders, and geneticists; ethnobotanists, ecologists, and conservationists; medical practitioners and nutritionists; research investigators in industry, federal laboratories, and universities; and students and teachers in the biological and biomedical sciences.

Introduction to Plant Biotechnology

Chawla, H.S.
Oxford & Ibh Publishing Co. Pvt Ltd. 2009. ISBN 978-1-57808-636-8.
This book has been written to meet the needs of students for biotechnology courses at various levels of undergraduate and graduate studies. This book covers all the important aspects of plant tissue culture viz. nutrition media, micropropagation, organ culture, cell suspension culture, haploid culture, protoplast isolation and fusion, secondary metabolite production, somaclonal variation and cryopreservation. For good understanding of recombinant DNA technology, chapters on genetic material, organization of DNA in the genome and basic techniques involved in recombinant DNA technology have been added. Different aspects on rDNA technology covered gene cloning, isolation of plant genes, transposons and gene tagging, in vitro mutagenesis, PCR, molecular markers and marker assisted selection, gene transfer methods, chloroplast and mitochondrion DNA transformation, genomics and bioinformatics. Genomics covers functional and structural genomics, proteomics, metabolomics, sequencing status of different organisms and DNA chip technology. Application of biotechnology has been discussed as transgenics in crop improvement and impact of recombinant DNA technology mainly in relation to biotech crops.

Signaling in Plants

Frantisek Baluska and Stefano Mancuso
Springer. 2009. Series: Signaling and Communication in Plants. ISBN: 978-3-540-89227-4
This book addresses diverse aspects of signaling at all levels of plant organization, starting from single molecules; through vesicle recycling and organelles, dynamic actin cytoskeletons, and plant organs bending in response to sensory stimuli induced by abiotic cues such as gravity and light; up to the whole organism as related to its circadian clock or pathogen defense. Emphasis is placed on the integrative aspects of signaling, which foster our understanding of sensory and communicative plants in all their complexity.

Reactive Oxygen Species in Plant Signaling

L. A. del Rio (CSIC, Granada, Spain), A. Puppo (INRA Sophia-Antipolis, Nice, France (Eds.)
Springer. Life Sciences. 2009. ISBN 978-3-642-00389-9.
Until recent years the production of reactive oxygen species (ROS) was generally considered to be a harmful process and a generator of oxidative stress. But more recently this concept has been re-evaluated and the term "oxidative signaling" was coined (Foyer and Noctor, 2005). This means that ROS generation is also an important component of the signaling network of plants. Results obtained during the last decade have highlighted that ROS are key regulators of plant metabolism, morphology and development which are also used by plants to respond to environmental challenges. The role of ROS as signals for gene expression has been established, and ROS also modulate the activity of key signaling compounds such as MAP kinases. The volume of research into the roles of ROS in plants is currently growing and the purpose of this book is to present recent advances in this field.

Abiotic Stress Adaptation in Plants: Physiological, Molecular and Genomic Foundation

Pareek, A.; Sopory, S.K.; Bohnert, H.J.; Govindjee (Eds.)
Springer. 2009. ISBN: 978-90-481-3111-2
Environmental insults such as extremes of temperature, extremes of water status as well as deteriorating soil conditions pose major threats to agriculture and food security. Employing contemporary tools and techniques from all branches of science, attempts are being made worldwide to understand how plants respond to abiotic stresses with the aim to help manipulate plant performance that will be better suited to withstand these stresses. The present book on abiotic stress is an attempt to search for possible answers to several basic questions related to plant responses towards abiotic stresses. This book presents a holistic view of the general principles of stress perception, signal transduction and regulation of gene expression. Further, chapters in this book analyze not only model systems but extrapolate interpretations obtained from models to crops. Lastly, we discuss how stress-tolerant crop or model plants have been or are being raised through plant breeding and genetic engineering approaches. Twenty three chapters, written by international authorities, integrate molecular details with overall plant structure and physiology, in a text-book style, including key references. This book serves as a complete package on the basics and applications for abiotic stress response sensing and genetic and metabolic response pathways in plants; it is designed for use by advanced undergraduate students, graduate students and beginning researchers in the area of stress biology, plant molecular biology, plant physiology, agriculture, biochemistry and environmental biology.

Grapevine Molecular Physiology & Biotechnology

By Kalliopi A. Roubelakis-Angelakis.
Springer. 2nd ed., 2009. ISBN: 978-90-481-2304-9
Grapevine is one of the most widely cultivated plant species worldwide. With the publication of the grapevine genome sequence in 2007, a new horizon in grapevine research has unfolded. Thus, we felt that a new edition of ‘Molecular Biology & Biotechnology of the Grapevine’ could expand on all the latest scientific developments. In this edition and with the aid of 73 scientists from 15 countries, ten chapters describe new aspects of Grapevine Molecular Physiology and Biotechnology and eleven chapters have been revised and updated. This book is intended to be a reference book for researchers, scientists and biotechnological companies, who want to be updated in viticultural research, but also it can be used as a textbook for graduate and undergraduate students, who are interested in the Molecular Biology and Biotechnology of Plants with an emphasis on the Grapevine

Chemical Elements in Plants and Soil: Parameters Controlling Essentiality

By Stefan Fränzle
Springer. 2009. Series: Tasks for Vegetation Science , Vol. 45. ISBN: 978-90-481-2751-1
Earlier works on plant essential elements have revealed a series of complicated, counter-intuitive relationships among various chemical elements in different plant species, due to both unlike usage of certain elements in plants and to different carriers effecting resorption and transport.
In an attempt to provide a more coherent theory behind plant mineral nutrition, this groundbreaking book adopts a very different approach from the existing literature, presenting an explanation of the essentiality of chemical elements in biological systems and the application of stoichiometric network analysis (SNA) to the biological system of elements. Starting with data from biochemical environmental analysis, and a discussion of the

phenomena involved in metal ion partition and autocatalytic behaviour, conditions and criteria controlling the partition of metals into biomass are investigated. Several rules are derived and investigated in terms of their interaction both in comparisons among contemporary organisms and in terms of evolution. This allows the construction, for example of a map which directly traces the biological feature of essentiality to parameters of coordination chemistry.
The book will have worldwide appeal for researchers interested in fields such as soil/plant interactions, bioinorganic chemistry, plant nutrition, phytomining, bioremediation, biogeochemistry, nutrient cycling, soil chemistry, and cellular physiology.

Signal Crosstalk in Plant Stress Responses

Keiko Yoshioka and Kazuo Shinozaki (Eds.)
Wiley-Blackwell, 2009. ISBN: 978-0-8138-1963-1
Signal Crosstalk in Plant Stress Responses focuses on current findings on signal crosstalk between abiotic and biotic stresses, including information on drought, cold, and salt stress and pathogen infection. Divided into seven chapters on critical topics in the field, the book is written by an international team of expert authors. The book is aimed at plant scientists, agronomists, and horticulturalists, as well as students.

Weedy and Invasive Plant Genomics

C. Neal Stewart, Jr.
Wiley-Blackwell 2009. ISBN: 978-0-8138-2288-4
Weedy and Invasive Plant Genomics offers a comprehensive, up-to-date reference on genetic and genomics research in weedy and invasive plants. Forward-looking in its approach, the work also assesses the areas of future research necessary to defeat these agricultural pests. This research-based, scholarly work engenders a further understanding of weeds and invasive plants, opening avenues for developing more effective methods of managing them. This volume will be a necessary reference for weed scientists, agrochemical industry researchers, conservation geneticist, and plant biologists.

Plant Metabolic Networks

J. Schwender, Brookhaven National Laboratory, Upton, NY, USA (Ed.)
Springer. Life Sciences. 2009. ISBN 978-0-387-78744.
Plants are the basis for human nutrition and of increasing interest for the chemical industry as a source of chemical feed stocks. Fuels derived from plant biomass will increasingly replace fossil fuels in the future. In order to increase crop productivity, design new plant products, and create new energy crops, there is need for methods of qualitative and quantitative analysis of metabolism which are able to guide the rational re-design of metabolic networks.
In this book, recent advances in qualitative and quantitative analysis of metabolism are summarized to give an overview of the current state of knowledge. Principles of the analysis of network structure, flux analysis, and kinetic modeling are described as are analytical methods necessary to produce the data needed for metabolic flux analysis and for kinetic modeling. The analysis of larger metabolic networks is only possible by using computer assistance. Therefore each chapter of the book shall also describe software available for this purpose.

The New Oxford Book of Food Plants (second edition)

by John G. Vaughan and Catherine A. Geissler.
Oxford University Press USA, 2009. 288 pp. ISBN: 978-0-199-54946-7.
This new edition of a classic book about the plants we eat provides accurate and attractive illustrations and exhaustive textual descriptions of the plants that serve the human race for food. The book also presents detailed nutritional information on food plants, as well as ancient and modern methods of preservation and preparation, including insight into hybridization and genetic modification.

In memoriam: Norman Borlaug

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Norman Borlaug dies
By Bob Grant
The Scientist: NewsBlog. 14th September 2009.

The Nobel Peace Prize-winning researcher who developed a high-yielding variety of disease resistant wheat and improved varieties of other crop plants that fed legions of starving people died September 12. Norman Borlaug won the 1970 peace prize for launching the green revolution -- which more than doubled world food production from the 1960s to the 1990s -- from his post at a research institute in Mexico. According to Texas A&M University, where Borlaug was a distinguished professor, the agronomist died from complications of cancer. He was 95 years old.

"[Borlaug] has been an inspirational and motivational reference point for the next generation of agricultural scientists, who have felt underappreciated and underfunded," Robert Paarlberg, a Harvard political scientist and author of the book *Starved for Science*, told *The Scientist*. "Every one of them would want to be the next Norman Borlaug," added Paarlberg, who served on the board of charitable non-profit Winrock International with Borlaug.

Kendal Hirschi, a Baylor University pediatrician and geneticist who studies ways to make more healthy vegetables using transgenic technologies, agreed with Paarlberg, but said that Borlaug was likely one of a kind. "We probably won't see someone like that again," Hirschi told *The Scientist*. "His capacity to affect change was so dramatic."

Borlaug's relationship with crops and farming started early. He was born in 1914 on a farm near Cresco, Iowa. After studying forestry at the University of Minnesota in the 1930s, Borlaug worked for the US Forestry Service in Massachusetts and Idaho. He later returned to the University of Minnesota to study plant pathology, earning his doctorate in 1942.

In the early 1940s, Borlaug worked as a microbiologist at the duPont de Nemours Foundation in Delaware, studying fungicides, bactericides, and preservatives. But in 1944, Borlaug was offered an opportunity that would change his life, and the lives of hundreds of millions of people around the world. That year, he accepted a post as a geneticist and plant pathologist at an institution called the Cooperative Wheat Research and Production Program in Mexico that was jointly supported by the Mexican government and the Rockefeller Foundation.

Within 20 years of working in Mexico, Borlaug had used breeding and selection to develop a stout variety of wheat that produced more grain and was more resistant to disease than conventional varieties. The immediate impact on the country's wheat production was dramatic. Mexico produced 250,000 tons of wheat in 1945, 1 million tons in 1956, and 2.5 million tons by 1965 -- a 10-fold, productivity-driven increase seen in the time Borlaug was working on the country's wheat crops.

The 1960s saw Borlaug exporting his expertise and his innovative crop varieties to other countries where people suffered under the oppression of hunger and food shortages. Borlaug helped to buoy agriculture in several countries in Latin America, throughout the Near and Middle East, and in Africa.

In 1984, Borlaug took a faculty position at Texas A&M, and continued to split his time between there and the Cooperative Wheat Research and Production Program in Mexico, where he mentored students and participated in research. In 1986, his years of lobbying the Nobel Foundation to create a new prize that specifically honored people who made improvements to the world's food supply paid off in the form of the World Food Prize, which is awarded annually. Still active late in life, Borlaug spoke at last year's ceremony, which is held in his home state of Iowa every year.

Borlaug seemed to focus his attentions on working with people and in farm fields rather than on amassing authorship credits on scientific manuscripts. In a speech presenting Borlaug with his Nobel Prize, Aase Lionaes, Chairman of the Nobel Committee, recounted one of the researcher's constant refrains. "Many people, we are told, who ask him to lecture or write a paper, get the following reply: 'What would you rather have - bread or paper?'"

Though Borlaug was working in agricultural science before the dawn of genetic engineering, he was an advocate of the techniques and their application to help lessen hunger and malnutrition. "I don't see any reason why [Borlaug] would have hesitated to put [transgenic technologies] to use" had they existed in the 1940s, 50s, or 60s, said Paarlberg. "He was a strong defender of the application of genetic engineering to agricultural science."

"He was always pushing the latest technology," Hirschi concurred. "Even as he got older, he was willing to pursue any technology to cure the world's hunger problems."

Borlaug won several prizes throughout his long career, including Iowa's highest honor, the Iowa Award, in 1978, the US Presidential Medal of Freedom, the National Service Medal of the National Academy of Science, and a Congressional Gold Medal. He held more than 55 honorary doctorate degrees from more than a dozen countries, and served on two US Presidential Commissions on World Hunger. Borlaug's memory lives on in several educational buildings -- Borlaug Hall at the University of Minnesota, the Norman E. Borlaug Center for Southern Crop Improvement at Texas A&M University, the Norman E. Borlaug Institute of Biotechnology at Leicester University in the United Kingdom, and even a grade school in Azcapotzalco, Mexico City -- that bear his name.
Despite the numerous kudos heaped upon Borlaug throughout his lifetime and his impact on salving world hunger, his name is not immediately recognizable to those outside the field of agricultural sciences. Hirschi likened Borlaug's impact and the amount of honors bestowed upon the researcher to the legacy of Martin Luther King, Jr. "He is the MLK in the field of agricultural sciences, but the lay people don't know him," he said. "And that's a sad thing. He did so much."