



FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY

FESPB Newsletter

No. 02.11. September 2011

In this issue:

| | |
|--|----|
| - Message from the FESPB Secretary General | 2 |
| - Plant Biology Congress Freiburg 2012 | 2 |
| - Research news | 3 |
| 1. Flood-tolerant Rice Plants Can Also Survive Drought, Say UC Riverside Scientists Research could greatly benefit rice farmers and consumers worldwide | |
| 2. Production of Mustard Oils: On the Origin of an Enzyme | |
| 3. Male and female plant organs talk like brain cells | |
| 4. Taking Shape | |
| 5. EU 'failing to acknowledge benefits of GMs' | |
| 6. Starch-controlling gene fuels more protein in soybean plants | |
| 7. A new article in THE PLANT CELL sheds light on the formation of maize ears, which is a critical factor for the yield of the plant. | |
| 8. Decoding The Platypus Of The Plant Kingdom | |
| 9. It takes a community of soil microbes to protect plants from disease | |
| 10. Maintaining Receptor Balance | |
| 11. PP2A Phosphatases: The "On-Off" Regulatory Switches of Brassinosteroid Signaling | |
| 12. Transgenic Production of Arachidonic Acid in Oilseeds | |
| 13. Conducting Closure | |
| 14. Discovery of DNA Silencing Mechanism Reveals How Plants Protect Their Genome | |
| 15. Improving Photosynthesis? Solar Cells Beat Plants at Harvesting Sun's Energy, for Now | |
| 16. Genomes of Fungi That Threaten Wheat, Poplars Sequenced | |
| 17. Vitamins May One Day Hitch a Protected Ride on Corn Starch | |
| 18. Parental conflict in plants: Maternal factors silence paternal genes | |
| 19. Study Reveals Important Aspects of Signalling Across Cell Membranes in Plants | |
| 20. The First Plant Interactome | |
| | |
| - EU Framework Programme for Research and Innovation..... | 18 |
| - Forthcoming meetings | 19 |
| - Positions available | 20 |
| - New books | 22 |

Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

Message from the FESPB Secretary General

Dear FESPB Members,

As you know, the next FESPB Congress will be jointly organized by FESPB and EPSO (European Plant Science Organization) in Freiburg, from 29th of July to 3rd of August 2012.

For the best organization of the 2012 Congress, a meeting was held on 11th of July 2011 in Freiburg, which was attended by the members of the FESPB Executive Committee [Heinz Rennenberg, Bruce Osborne, Kalliopi A. Roubelakis-Angelakis, Christine Foyer, Karl-Josef Dietz, and Anna Rychter (Dolores Rodriguez could not attend)], and by the EPSO President, Heribert Hirt, ex-President, Wilhelm Whisslem and Karen Metzlaf. Also, from the Kongress & Kommunikation of the University of Freiburg, Dr Thomas Karsch and Mrs Katja Lemke were present.

During the meeting, all aspects of the organization of the FESPB/EPSO 2012 Congress were discussed. The 2012 Congress will be held at the premises of the University of Freiburg. The site is magnificent and the

green city of Freiburg is a relaxing place with all facilities at walking distance. Also, the scientific and the social programmes are very promising.

As in the previous FESPB Congresses, FESPB will sponsor approx 30 Travel Grants for Graduate students from ex Eastern European countries and 2 FESPB Awards to young European researchers, on the basis of excellence. Furthermore, EPSO will sponsor 20 Travel Grants for students from all European countries. Soon, the calls for submission of Applications will be available on our website (www.fespb.org) as well as on EPSO website (www.epsoweb.org).

All details on the 2012 Congress can be found at www.plant-biology-congress2012.de. On behalf of the members of the FESPB Executive Committee, I cordially invite all our Members as well as all Plant Scientists from the Globe to attend this great scientific event.

Popy A. Roubelakis-Angelakis
FESPB Secretary General

Plant Biology Congress Freiburg 2012

jointly organized by FESPB and EPSO



**The Federation
of European Societies
of Plant Biology**

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

Plant Scientists in Europe are represented by two independent organisations. The FESPB (Federation of European Societies of Plant Biologists) is the umbrella organisation of 27 national botanical societies in Europe, representing more than 24.000 individuals and has in addition several corporate

members from the European industry. The EPSO (European Plant Science Organisation) unites more than 220 research institutions and universities from 30 countries representing over 28.000 individuals and over 2.800 personal members. In addition EPSO cooperates with national learned societies, and it has NGOs and companies as observers. For the first time, both

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

Heinz Rennenberg and Ralf Reski

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

Research News



Flood-tolerant Rice Plants Can Also Survive Drought, Say UC Riverside Scientists **Research could greatly benefit rice farmers and consumers worldwide**

Source: University of California, Riverside. (March 2, 2011)

RIVERSIDE, Calif. – Rice, which is sensitive to drought due to its high water requirement, is particularly vulnerable to how global climate change is altering the frequency and magnitude of floods and droughts. If rice plants’ combined tolerance to flooding and drought could be improved, however, rice productivity could be protected and even substantially increased.

Now plant scientists at the University of California, Riverside have made a discovery that can greatly benefit rice growers and consumers everywhere. The researchers have demonstrated in the lab and greenhouse that rice that is flood tolerant is also better able to recover from a drought.

“Flood tolerance does not reduce drought tolerance in these rice plants, and appears to even benefit them when they encounter drought,” said Julia Bailey-Serres, a professor of genetics in the Department of Botany and Plant Sciences, who led the research project. Bailey-Serres and her team – Takeshi Fukao, a senior researcher, and Elaine Yeung, an undergraduate student – focused on Sub1A, a gene responsible for flood or “submergence” tolerance in rice and found only in some low-yielding rice varieties in India and Sri Lanka. Sub1A works by making the plant dormant during submergence, allowing it to conserve energy until the floodwaters recede. Rice with the Sub1A

gene can survive more than two weeks of complete submergence.

Plant breeders have already benefited farmers worldwide – especially in South Asia – by having transferred Sub1A into high-yielding rice varieties without compromising these varieties’ desirable traits—such as high yield, good grain quality, and pest and disease resistance.

Bailey-Serres’s lab found that in addition to providing robust submergence tolerance, Sub1A aids survival of drought. The researchers report that at the molecular level Sub1A serves as a convergence point between submergence and drought response pathways, allowing rice plants to survive and re-grow after both extremes of precipitation. Study results appear in the January issue of *The Plant Cell*. The journal has the highest impact factor of primary research journals in plant biology. The research paper also has been selected as a recommended read in the Faculty of 1000.

Bailey-Serres’s lab investigated the drought tolerance of flood-tolerant rice plants because her research team wanted to be sure that the flood tolerance trait, which the lab has studied for many years, did not reduce the ability of the plant to endure some of the other common stresses – such as drought.

“We found that Sub1A properly coordinates physiological and molecular responses to cellular water deficit when this deficit occurs independently, as in a time of drought, or following ‘desubmergence,’ which takes place when flood waters recede,” Bailey-Serres said.

She explained that after a flood, a period follows when the leaves that have been submerged lose water and become dehydrated. Moreover, because a period of dehydration is part of the natural progression of a flood, Sub1A also happens to have benefits after desubmergence and is therefore important for drought tolerance as well.

"Our finding suggests that the plant recovers well from drought by growing new shoots," Bailey-Serres said. "This is something that is also seen with flooding."

Next, colleagues of Bailey-Serres at the International Rice Research Institute in the Philippines will test the Sub1A rice for drought tolerance in the field.

Production of Mustard Oils: On the Origin of an Enzyme

Source: ScienceDaily (Mar. 17, 2011)

In the evolutionary arms race, small changes can be sufficient to gain advantage. Scientists found that the ancestor of a gene involved in making chemical defenses in plants of the mustard family, such as rapeseed, originally had a completely different function, playing a part in the formation of leucine, an amino acid. Small changes in the enzyme structure enabled it to take over new tasks that could increase the survival advantage of the plants. Plants are continually exposed to herbivore attack. To defend themselves, they have developed sophisticated chemical defense mechanisms. Plants of the mustard family, such as thale cress (*Arabidopsis thaliana*), produce glucosinolates (mustard oil glucosides) to protect themselves against herbivory. Scientists know many different kinds of these molecules; they have a similar structure, but different side chains. If insect larvae feed on mustard plants, glucosinolates are hydrolyzed to form toxic isothiocyanates. Chemists call this the "mustard oil bomb."

Special enzymes are responsible for catalyzing the synthesis of different side chains of the various glucosinolates. Scientists at the Max Planck Institute for Chemical Ecology in Jena have now isolated one of these enzymes from *Arabidopsis thaliana* and discovered a surprising new insight. Jan-Willem de Kraker and Jonathan Gershenzon reported that the enzyme

methylthioalkylmalate synthase (MAM), which catalyzes glucosinolate formation, strongly resembles another enzyme with a completely different function: The enzyme IPMS (isopropylmalate synthase) is involved in the synthesis of the amino acid leucine. However, the scientists found two major structural differences between IPMS and MAM: the last 120 amino acids are absent in MAM, and in the active site of the enzyme, where the substrates react, two amino acids had been exchanged.

IPMS encoding genes are present in eubacteria, archaeobacteria, algae and higher plants, but not in animals. Therefore, humans must ingest leucine as an essential amino acid with our food. In the model plant *Arabidopsis thaliana* IPMS consists of a chain of 631 amino acids. In actual enzymes, these amino acid chains, also called polypeptides, are not straight. Depending on the sequence of the respective amino acids, chains are folded into helices, sheets and other shapes necessary for the polypeptide to perform its biological function. Thus the function of IPMS is to bind 2-oxoisovalerate and acetyl-CoA and thereby produce leucine precursors.

To make sure that enzyme mediated catalysis does not happen uncontrolled in the cell, many enzymes are regulated by a feedback mechanism. In IPMS this mechanism is located in the last 120 amino acids of the polypeptide chain. Here, the enzyme receives a signal from the cell as soon as enough leucine is available and so stops producing leucine precursors. "We found that the missing 120 amino acids not only inactivate the regulation of enzyme activities, but also change the architecture of MAM completely," Jonathan Gershenzon says. The missing 120 amino acids cause a profound change in the active site: it expands and now is able to bind larger substrates, and can therefore produce completely new products. For this reason MAM synthesizes the precursors of glucosinolates, not leucine.

The Max Planck researchers came across IPMS when they were looking for genes involved in glucosinolate production. In the context of these studies they isolated and sequenced the IPMS gene. The scientists assume that after a duplication of the IPMS DNA sequence millions of years ago, the "twin DNA" lost the fragment encoding the

sequence of the last 120 amino acids. In the course of evolution this probably happened during the origin of the mustard family. The loss of the 120 amino acids turned out to be very advantageous for the plants: it enabled them to produce glucosinolates as a defense against herbivores. During further evolution, individual mutations in the active site of the emerging MAM enzyme occurred that accelerated the synthesis of glucosinolates by better binding of the substrates.

The assumptions could be confirmed by de Kraker and Gershenzon in extensive *in vitro* experiments. The way MAM emerged is probably typical for the way new phenotypes arise from the variety of genetic information encoded and stored in DNA. It is another example of how small changes can lead to the development of new weapons in the evolutionary arms race between plants and herbivores.

Journal Reference: J.-W. de Kraker, J. Gershenzon. From Amino Acid to Glucosinolate Biosynthesis: Protein Sequence Changes in the Evolution of Methylthioalkylmalate Synthase in *Arabidopsis*. *The Plant Cell*, 2011; 23 (1): 38 DOI: 10.1105/tpc.110.079269

Male and female plant organs talk like brain cells

Source: EC-CORDIS News. Date 2011-03-29

Male and female plant organs communicate in the same way as brain cells, according to research by scientists in Portugal. A study published in the journal *Science* shows how pollen, which contains the plant's male gametes, communicates with the plant's female organ using a mechanism commonly observed in the nervous system of animals. According to the researchers, the study reveals a new mechanism underlying reproduction in plants and opens an exciting new avenue in the study of how cell-cell communication is conserved between animals and plants.

Plant reproduction is a complex and highly coordinated process. Pollen grains, which contain the plants' male gametes (sperm cells), are carried from the male organ of the flower (the stamen) to the female organ (the pistil). Here the pollen germinates and grows a pollen tube, which extends and is guided to

the ovary, where it releases the sperm. The sperm fuse with the egg cells, giving rise to an embryo, part of the seed.

In this study, researchers from the Instituto Gulbenkian de Ciência (IGC) studied the development of the pollen tubes in the pistil. According to the researchers, while biologists have, for many years, observed regular oscillations in several parameters that control the growth of pollen tubes, the actual molecular channels that control these oscillations and their physiological output have remained elusive.

Dr José Feijó, group leader at the IGC and Professor at Lisbon University, and his colleagues have filled this knowledge gap with the discovery that in tobacco and the weed *Arabidopsis*, oscillations of calcium ions in the growing pollen tubes are facilitated by channels called Glutamate receptors-like (GLRs). Moreover, they found that these channels are opened by, amongst other components, a rare amino acid known as D-serine (D-Ser).

Both D-Ser and GLRs are not only found in plants; they are also key molecules in cell-cell communication in the animal central nervous systems. They play a central role in memory and learning processes in the brain, and have been implicated in a wide range of neurodegenerative diseases such as multiple sclerosis, Alzheimer's, Huntington's disease and others. 'And now, surprisingly, they also have a role in reproduction of plants,' noted the researchers.

The team used an extensive combination of genetic, pharmacological and electrophysiological techniques to reveal the role of glutamate receptor-like (GLRs) genes and D-serine in pollen grains, and their physiological impact on plant reproduction. In proving that GLRs are calcium channels, the team also solved two long-standing riddles in plant biology, namely the molecular nature of calcium channels in the outer membrane of plant cells. They also revealed the functions of GLRs genes in plants, a fact that has puzzled biologists ever since the first genome of the model plant *Arabidopsis* was sequenced.

The team's investigations revealed that impairing the GLR functions in male gametes leads to partial male sterility: fewer seeds are

produced by the plant, and the pollen tubes are abnormal.

Regarding D-serine, the team found that it activates the GLRs on the tips of pollen tubes, allowing calcium ions to flow into the tube. They took their research a step further by demonstrating that D-serine is indeed produced in the female sexual organs, and that the absence of D-serine in these organs also leads to deformed pollen tubes. Together, these findings strongly suggest that D-serine produced in the female sexual organs may have a role in guiding pollen tubes to their final target.

Dr José Feijó commented that 'pollen tubes are a model system for cellular tip-growth, a process common to fission yeast, filamentous fungi, the root hairs of plants and nerve cells'. He said that his group's work, 'implicating analogous genes in growth processes in both plants and animals, underscores how evolution re-uses successful mechanisms, over and over again'. Dr Feijó said the research 'performed in Arabidopsis and tobacco, now opens doors for the study of conserved cell-cell communication processes, across plant and animals species'.

For more information, please visit:

Instituto Gulbenkian de Ciência (IGC):
<http://www.igc.gulbenkian.pt/>

Science Express:

<http://www.sciencemag.org/content/early/2011/04/01>

Taking Shape

Source: The Scientist. Volume 25, Issue 4, Page 18. 2011-04-01

Floral bouquets are the most ephemeral of presents. The puzzle of how flowers get their shape, however, is more enduring. It's a question that has kept Enrico Coen, a plant biologist at the John Innes Centre in the United Kingdom, busy for more than twenty years. Now he thinks he may finally have a handle on the answer, thanks to a clever combination of detailed image analysis and computer modeling—an approach typically applied to engineering problems.

Although there have been sustained efforts to identify genes involved in organ growth and shape in *Drosophila*, how genetics translate into the final shape of a wing, for

example, is largely unknown. Coen and his colleagues used the flowers of *Antirrhinum majus*—better known as the snapdragon—to build a computational framework that would allow them to make experimentally testable predictions about shape generation (PLoS Biol, 8:e1000537, 2010).

Coen says that they asked a “very vague” question at the start of the project: “What would you need to do to grow from a simple starting shape to produce a final snapdragon flower?” He likens the problem to making the individual squares of a chessboard grow at different rates and in different directions: each square affects its neighbors, leading to puckering and rotation, all of which have to be modeled simultaneously. Engineers and physicists use a method called finite-element analysis for similar experiments, such as modeling how motor vehicles will deform in the event of a crash. But developing an analogous biological framework wasn't trivial and hadn't been done before, because, as Coen says, “most things in the world of physics don't grow.”

Coen and his team first modeled genes controlling different growth rates in different parts of the flower. “Most people would assume that's what genes do,” says Coen. But they soon ran into problems. “It wasn't easy to get a good snapdragon out of it,” he says, as the model led to swelling in the tubular part of the flower that they couldn't correct. So they tried a new model in which genes also controlled the orientation of growth.

Cells have different molecules at each end, which give them polarity. “It's not obvious,” Coen says, “but there's a little arrow in every cell.” So in a tissue, if you could see all these arrows it would look like a magnetic field. The researchers suspected that this field of orientations was controlled genetically, so they postulated the existence of tissue-polarity-organizing genes. Once they modeled these, they found that the computer could produce good-looking snapdragon flowers.

It took several years to get to that stage, though, as Coen and his team learned how to use the model and understand the results it gave them. Coen says that thinking of flower formation in terms of a two-dimensional, growing sheet was a new experience for

them all. Groping their way around this “very peculiar world” was a slow process, but “extremely satisfying,” he says. Only after mastering this could they experiment with the positions and effects of polarity-organizing genes.

F1000 Member Jan Traas, at École Normale Supérieure de Lyon, calls Coen’s findings a “quantitative framework to describe gene function in terms of geometry.” The framework can be used to make predictions about the functions of genes thought to be involved in the generation of flower shape, which can then be tested by making mutants and examining their effects in real plants. Traas notes that these models were not possible 20 years ago, because the computer power was not available.

Researchers at the Coen lab, in collaboration with the nearby Andrew Bangham lab, are developing finite-element methods for modeling the growth and development of curved, two-dimensional tissues such as leaves and petals.

Next, Coen wants to identify the molecular players behind the geometric organization he’s modeled, searching for genes and proteins in real flowers. He says that the genes involved are probably already described, but because the infrastructure to study their function didn’t exist before, other researchers hadn’t appreciated them for what they really were. “We’re looking through the literature and thinking, ‘Oh yes, that shows the right behavior: they just didn’t realize it.’” Coen and his colleagues are also extending the methodology to other tissues, including the leaf, before moving on to models of an entire plant.

EU ‘failing to acknowledge benefits of GMs’

By Caroline Stocks. 18 April 2011

Source: [Farmers Weekly Interactive](#)

The European Commission has slammed government across Europe for failing to acknowledge the benefits of allowing farmers to grow genetically modified crops.

In a report published on Friday (15 April), the commission criticised countries for not providing “objective analysis” of the positive impacts GM production could have.

Based on data from member states, including studies, opinion polls and field trials, the 10-

page report criticises the “lack of clarity” of analysis carried out by national government on GM technologies.

Talks on the issue must shift from “polarised perceptions to more tangible & objective results”, it says.

In its notes accompanying the report, the commission said the data from member states reflected the “polarised opinions built upon a limited fact-based background on the specific European context and preconceived ideas about GMO cultivation”.

It had been “difficult and often impossible to pinpoint clear positions or trends at national or European levels and to report them in a statistically relevant way”, it added.

While there were some gaps in the data, the commission said studies had shown yield increases for GM maize compared to maize grown by conventional farmers, as well as overall increased gross margins for farmers.

Among the seven member states which allow GM crop cultivation, yield increases of between 7% and 12.5% were reported in Portugal, Romania, the Czech Republic.

The results were mirrored by evidence from non-EU countries, with the benefits of GM crops for smallholders “equal or higher than those of large farmers”, the report says.

But Mute Schimpf, Friends of the Earth Europe food campaigner, criticised the study for failing to account for “the true environmental and economic costs of GM crops”, such as potential contamination damage.

EU farmers group DG SANCO said it regretted that the available information on impacts along the food chain was “rather limited, if not absent”.

The report marked a starting point for deeper and more focused discussion among EU institutions, it added.

Mark Buckingham, of the Agricultural Biotechnology Council, said it was essential farmers were given the opportunity to use GM technology so they could use resources more efficiently.

“This is all the more important with rising food prices and a growing population,” he said.

“This report demonstrates yet again the benefits associated with the use of GM technology - based on the experiences of its widespread use over the past 15 years.

"Not only does GM boost farm incomes, it can also play a significant role in reducing the environmental impact of farming, helping to meet emissions reductions targets."

Starch-controlling gene fuels more protein in soybean plants

Source: [Iowa State University](#)

A newly discovered gene introduced into soybean plants has increased the amount of protein in the plant's seed and could hold promise for helping meet nutritional needs of a hungry world.

Eve Wurtele, professor of genetics, development and cell biology; and Ling Li, an adjunct assistant professor and an associate scientist working in her laboratory, have placed a gene found only in Arabidopsis plants into soybean plants and increased the amount of protein in the soybean seeds by 30 to 60 percent.

The results were a pleasant surprise to the researchers as the function of the gene, known as QQS, in the Arabidopsis was previously unclear because its sequence is very dissimilar from all other plant genes.

Arabidopsis is a small, flowering plant in the mustard family that is often used in scientific research.

"Most genes contain clues in their DNA sequence as to their biological function," said Wurtele. "But this one has no sequence features that gave us any hint of what it's doing."

When the researchers neutralized the gene in Arabidopsis, they discovered the gene was involved in regulating starch accumulation, called deposition.

"Based on the changes in activities of other genes that occurred when we altered QQS, we conjectured that it wasn't directly involved in starch synthesis, but rather it may be involved in altering [the plant's] composition in general," said Wurtele. "We decided to test this concept by transferring the gene to an agronomically important plant species, soybean, which has a seed and is important as a source of vegetable protein and oil."

"We found that the QQS transgene increased protein production in the soybean seed," she added. "That was the best possible scenario."

In addition to having a DNA sequence that is not similar to any other gene in that or any other plant, the gene is also unusual because it has only 59 amino acids, Li said. The median size of a gene in Arabidopsis plants is 346 amino acids.

Li discovered the gene in 2004 and named it for her daughter.

"My daughter was a half-year old. This gene was so small and my daughter was so small," Li laughs. "QQ is my daughter's nickname in Chinese."

In addition to altering the protein-producing qualities of the gene, Wurtele hopes that the discovery may lead to greater understanding of other genes that don't have recognizable functionalities based on their sequences.

"This may give us an insight into the other genes with obscure features and provide us a window as to how they function," she said.

Wurtele hopes the discovery may help people in areas who survive on protein-deficient diets.

"We were so pleased [the gene] altered composition in soybean," she said. "What if this basic research discovery could lead to increased protein content in potatoes, cassava, or other crop species that are staples to people in developing nations?"

"That would be better than I imagined."

A new article in THE PLANT CELL sheds light on the formation of maize ears, which is a critical factor for the yield of the plant.

Source: *American Society of Plant Biologists (ASPB)*. 03/05/2011

Ears are the seed-bearing inflorescences of maize (*Zea mays*) plants and represent a crucial component of maize yield. The first step in the formation of ears is the initiation of axillary meristems in the axils of developing leaves. In the classic maize mutant barren stalk fastigate1 (*baf1*), first discovered in the 1950s, ears either do not form or, if they do, are partially fused to the main stalk. We positionally cloned *Baf1* and found that it encodes a transcriptional regulator containing an AT-hook DNA binding motif. Single orthologs of *Baf1* are found in syntenic regions of brachypodium (*Brachypodium distachyon*), rice (*Oryza sativa*), and sorghum (*Sorghum bicolor*), suggesting that the gene is likely present in

all cereal species. Protein–protein interaction assays suggest that BAF1 is capable of forming homodimers and heterodimers with other members of the AT-hook family. Another transcriptional regulator required for ear initiation is the basic helix-loop-helix protein BARREN STALK1 (BA1). Genetic and expression analyses suggest that Baf1 is required to reach a threshold level of Ba1 expression for the initiation of maize ears. We propose that Baf1 functions in the demarcation of a boundary region essential for the specification of a stem cell niche.

Reference: The Plant Cell Online May 2011, doi: 10.1105/tpc.111.084590

Decoding The Platypus Of The Plant Kingdom

by Joe Palca. Source: NPR. May 5, 2011.

If you like being alive, you might want to thank a plant. Plants and their microscopic relatives provide the oxygen we breathe. They're also the source of the energy for the modern industrial world. And we eat them, too.

Probing the secrets of plants at the genetic level is all the rage these days among scientists seeking to understand how plants evolved on Earth.

One of those plants is Selaginella, one of the first plant to develop a system of tubes that transport water and nutrients inside a plant.

"You can only reach a certain height before you have to have tubing to conduct the water from the ground to the top of the plant," says Jody Banks, a botanist at Purdue University.

Selaginella is a smallish plant, about 6 inches tall. It's found all over the world. Some varieties look a bit like a small Christmas tree. Selaginella turns out to be an important plant for modern civilization.

"When you burn coal today, actually the fossil fuel, the fossil is a fossil of the relatives of Selaginella," says Banks. How does she know Selaginella and its relatives became coal? "Because you can go into a coal mine and you can see it, the whole plant, fossilized."

Banks says Selaginella represents an important step in the evolution of plants. It was one of the first plants to develop a

system of tubing for transporting water and nutrients inside the plant.

In addition to tubing, Selaginella makes something called secondary metabolites. These are compounds that aren't absolutely essential for the plant's survival but are useful to have around. An example would be the compounds that make the scents of a flower, or a chemical the plant produces that keeps pests away. It turns out that these secondary metabolites have been useful in medicine — the anti-cancer drug Taxol is an example.

As Banks reports in the current issue of the journal Science, Selaginella is chock full of genes that make these secondary metabolites. "What that means is that Selaginella is likely to make many, many, many secondary compounds, and they're most likely going to be unique."

Another important plant undergoing genomic analysis is amborella. Victor Albert, a biologist at the University at Buffalo, says amborella doesn't look all that important. "It basically just looks like a small tree or shrub with fairly nondescript leaves and relatively nondescript flowers," says Albert.

But those nondescript flowers turn out to be from one of the first flowering plants that evolved on Earth. "Somewhere around maybe 130 or more million years ago, the flowering plant first emerged. And the flower was a great innovation," says Pam Soltis, a botanist at the University of Florida.

Flowering opened up all sorts of new ways for plants to change and disperse. Soltis says what makes amborella so interesting is that it turned out to be a genetic dead end, like the platypus — a relative of all mammals but ancestor of none. Amborella is the sibling of all flowering plants, but unlike the other early flowering plants, it has no direct descendants. That makes it useful to plant geneticists.

"It provides a reference point for orienting all of the other changes that have occurred within the flowering plants," says Soltis.

Understanding the evolution of flowering plants and their genes is important for modern agriculture. It helps crop breeders understand how to capture the taste of wild plants.

Jody Banks admits that the flowering plants, with their gaudy leaves and tasty fruit, are

more important to farmers and gardeners. But she intends to keep her research focused on Selaginella. "It's a survivor," she says. "It's been around hundreds of millions of years. And who knows, if there's another mass extinction, it may be what's left."

So if amborella is the platypus of the plant kingdom ... maybe that make Selaginella the cockroach. They're supposed to be survivors, too.

It takes a community of soil microbes to protect plants from disease

Source: e-Science News, Biology & Nature. May 5, 2011

Those vegetables you had for dinner may have once been protected by an immune system akin to the one that helps you fight disease. Scientists from the U.S. Department of Energy's Lawrence Berkeley National Laboratory (Berkeley Lab) and the Netherlands Wageningen University found that plants rely on a complex community of soil microbes to defend themselves against pathogens, much the way mammals harbor a raft of microbes to avoid infections. The scientists deciphered, for the first time, the group of microbes that enables a patch of soil to suppress a plant-killing pathogen. Previous research on the phenomenon of disease-suppressive soil had identified one or two pathogen-fighting microbes at work.

But the Berkeley Lab-led team found a complex microbial network. After analyzing soil from a sugar beet field that had become resistant to a pathogen that causes root fungus, the scientists found 17 soil microbes fighting to suppress the pathogen. They also determined that all of the microbes work together to reduce the incidence of fungal infection. Their discovery that plants use a tight-knit army of soil microbes for defense could help scientists develop ways to better protect the world's food crops from devastating diseases.

"Individual organisms have been associated with disease-suppressive soil before, but we demonstrated that many organisms in combination are associated with this phenomenon," says Gary Andersen of Berkeley Lab's Earth Sciences Division. He conducted the research with fellow Berkeley Lab scientists Todd DeSantis and Yvette

Piceno as well as several scientists from the Netherlands including Wageningen University's Jos Raaijmakers. Their research is published in the May 5 issue of Science Express.

The Berkeley Lab and Dutch scientists analyzed soil from a sugar beet field in the Netherlands. Something in the soil suppressed the presence of the pathogen *Rhizoctonia solani*, which causes root fungus in beets, potato, and rice.

The sugar beets' health followed the typical arc of plants in disease-suppressive soil: they enjoyed a few good years, then they succumbed to disease, followed by healthy beets again as pathogen-fighting microbes were activated and the soil became hostile to *R. solani*. To return the favor, the sugar beets funnel about a fifth of their photosynthetically captured carbon through their roots into the soil to fuel the microbes.

Disease-suppressive soils are quite common, and scientists have identified some of the microbes involved in this underground immune system. But they don't know all of the microbes that participate.

To find out, the scientists used the PhyloChip, which is a credit-card sized chip that can detect the presence of 59,000 species of bacteria and archaea in samples of air, water, and soil without the need of culturing. It was developed at Berkeley Lab to rapidly identify not only the most common and abundant organisms in an environmental sample, but also very rare types that are present in extremely small numbers. It does this by comparing a DNA sequences unique to each bacterial species with over one million reference DNA targets on the chip. The PhyloChip has shed light on many environmental mysteries, such as what's killing coral reefs near Puerto Rico and what degraded much of the oil from the Gulf of Mexico's Deepwater Horizon spill.

In this case, soil samples from the sugar beet field were modified to exhibit six levels of disease suppression. DNA was isolated from the samples and sent to Berkeley Lab for analysis. The PhyloChip detected more than 33,000 bacterial and archaeal species in the samples, with all six having more or less the same types of bacteria.

But when the scientists looked at the abundance of bacteria in each sample, they

found that each had a unique fingerprint. All of the samples in which disease was suppressed had a greater abundance of 17 unique types of bacteria. These included well-known fungal fighters such as *Pseudomonas*, *Burkholderia*, *Xanthomonas* and *Actinobacteria*. In addition, other types of bacteria that have no demonstrated ability to fight pathogens on their own were found to act synergistically to suppress plant disease.

Based on this, the scientists believe that an uptick in several bacterial types is a more important indicator of disease suppression than the presence of one or two bacteria that are especially good at killing pathogens.

"We now see that the complex phenomenon of disease suppression in soils cannot simply be attributed to a single bacterial group, but is most likely controlled by a community of organisms," says Andersen.

Their research will help scientists pursue unanswered questions about disease-suppressive soil: Do plants actively recruit beneficial soil microorganisms for protection against infection? And if so, how do they do it? It will also help scientists elucidate the mechanisms by which groups of soil microbes work together to reduce the incidence of plant disease.

Maintaining Receptor Balance

Source: Sci. Signal., 10 May 2011

Brassinosteroids control many aspects of plant development. Their receptors constitutively cycle between the cell surface and the internal membranes. Wu et al. now show that degradation of the brassinosteroid receptor BRI1 is stimulated by dephosphorylation of activated receptors and that the dephosphorylation is specified by methylation of a phosphatase, which causes the phosphatase to accumulate in membranes where it would encounter BRI1. These results provide insight into a regulatory mechanism controlling the abundance of receptors that constitutively cycle and suggest that cells can discriminate between unphosphorylated receptors that have not been activated (continue to cycle) and activated receptors that were subsequently dephosphorylated (become degraded).

Citation: G. Wu, X. Wang, X. Li, Y. Kamiya, M. S. Otegui, J. Chory, Methylation of a Phosphatase Specifies Dephosphorylation and Degradation of Activated Brassinosteroid Receptors. *Sci. Signal.* 4, ra29 (2011). [DOI: 10.1126/scisignal.2001258]

PP2A Phosphatases: The "On-Off" Regulatory Switches of Brassinosteroid Signaling

Source: Sci. Signal., 10 May 2011

Inactivation of ligand-bound plasma membrane receptors is crucial for the regulation of their signaling outputs. The internalization of activated receptors and their subsequent targeting for recycling or degradation is controlled by posttranslational modifications, of which phosphorylation and dephosphorylation play an important role. Recent work suggests that a similar mechanism acts on the brassinosteroid (BR) receptor BR INSENSITIVE 1 (BRI1) in *Arabidopsis thaliana* to switch off BR signaling. The degradation of BRI1 requires a protein phosphatase 2A (PP2A)-mediated dephosphorylation that is specified by methylation of the phosphatase by a leucine carboxylmethyltransferase on membranes. PP2A is also reported to act positively on BR signaling by targeting the transcription factor BRASSINAZOLE-RESISTANT 1 (BZR1), a component downstream of BRI1. Thus, PP2A proteins play a dual role in the regulation of the BR pathway to switch between inhibition and activation of the BR signaling, depending on their substrate specificity and localization. Citation: S. Di Rubbo, N. G. Irani,, E. Russinova, PP2A Phosphatases: The "On-Off" Regulatory Switches of Brassinosteroid Signaling. *Sci. Signal.* 4, pe25 (2011). [DOI: 10.1126/scisignal.2002046]

Transgenic Production of Arachidonic Acid in Oilseeds

Source: ISAAA. May 6, 2011

Long-chain polyunsaturated fatty acids such as arachidonic acid (ARA), eicosapentaenoic acid (EPA), and docosahexaenoic acid (DHA) are important to human health and development, especially on infant cognitive development. Deficiency in ARA may lead to hair loss, fatty liver degeneration, anemia,

and reduced fertility in adults. This led James Petrie of the CSIRO Plant Industry and other scientists to develop oilseeds *Brassica napus* and *Arabidopsis thaliana* that produce ARA. They induced seed-specific expression of a microalgal pathway (D9-elongase) into the genetic material of the oilseeds. Approximately 20% of the *A. thaliana* seed oil is ARA, while in *B. napus*, it comprised 10% of the total seed oil. Majority of ARA was located at the sn-2 position of triacylglycerol. Reference: Transgenic production of arachidonic acid in oilseeds. James R. Petrie, Pushkar Shrestha, Srinivas Belide, Maged P. Mansour, Qing Liu, James Horne, Peter D. Nichols and Surinder P. Singh. Transgenic Research, DOI: 10.1007/s11248-011-9517-7.

Conducting Closure

Source: *Sci. Signal.*, 17 May 2011

Stomata are pores in the plant epidermis that allow the movement of CO₂ into the plant concomitant with the loss of water. The opening and closing of these pores is mediated by the surrounding guard cells, which respond to drought, nutrient availability, and the plant stress hormone abscisic acid (ABA). Geiger et al. identified the anion channel SLAH3 as a player in the guard cell pathway downstream of ABA and defined its mode of regulation through an ABA receptor-phosphatase RCAR1-ABI complex and a calcium-dependent kinase, CPK21. Unlike previously characterized anion channels that are regulated by ABA and contribute to stomatal closure, activation of SLAH3 was promoted by nitrate and was 20 times as permeable to nitrate ions as to chloride ions. Thus, SLAH3 may integrate nitrate signaling and metabolism with signals initiated by drought conditions to control respiration and water loss.

Citation: D. Geiger, T. Maierhofer, K. A. S. Al-Rasheid, S. Scherzer, P. Mumm, A. Liese, P. Ache, C. Wellmann, I. Marten, E. Grill, T. Romeis, R. Hedrich, Stomatal Closure by Fast Abscisic Acid Signaling Is Mediated by the Guard Cell Anion Channel SLAH3 and the Receptor RCAR1. *Sci. Signal.* 4, ra32. [DOI: 10.1126/scisignal.2001346] (2011).

Discovery of DNA Silencing Mechanism Reveals How Plants Protect Their Genome

Source: *ScienceDaily* (May 13, 2011)

Researchers at the RIKEN Plant Science Center (PSC) have clarified a key epigenetic mechanism by which an enzyme in the model plant *Arabidopsis* protects cells from harmful DNA elements. Published in the online journal *PLoS Genetics*, the finding contributes to advancing our understanding of a broad range of biological processes in both plants and animals, opening the door to applications in cancer therapy and agriculture.

In everything from protein synthesis to gene expression to development, living cells depend critically for their survival on the successful functioning of their DNA. Certain DNA elements such as transposons, fragments of DNA that replicate within an organism's genome, can however disrupt this functioning and disable genes. To defend against such harmful elements, eukaryotic cells form inactive tightly-packed DNA called heterochromatin, whose dense structure serves to repress ("silence") the expression of nearby gene sequences and protect the genome.

Earlier research identified the enzyme HDA6 as playing a key role in such "heterochromatin silencing" in the model plant *Arabidopsis*, but the mechanism involved remained unclear. In order to clarify this mechanism, the research group investigated the involvement of HDA6 in two processes: DNA methylation, an epigenetic modification that changes the structure of DNA without altering its sequence, and the modification of histone, the main component of chromatin.

Through a genome-wide comparison, the researchers were able to show that plants with repressed HDA6 function are not able to silence harmful DNA elements, suggesting that the enzyme plays an important role in gene silencing. Further investigation revealed that HDA6 binds directly to transposons and silences their activity through specific histone modifications, and that another enzyme, the DNA methyltransferase MET1, cooperates with HDA6 in this gene silencing.

Together, the findings establish for the first time that MET1-mediated DNA methylation and HDA6-mediated histone modification

work together in repressing harmful DNA elements. By shedding light on the complex interplay between these two processes, the findings provide valuable insight on how plants and animals have evolved to protect their genome from harmful DNA, contributing to applications in areas such as cancer therapy and agriculture.

Reference: To et al. Arabidopsis HDA6 Regulates Locus-Directed Heterochromatin Silencing in Cooperation with MET1. *PLoS Genetics*, 2011; 7 (4): e1002055 DOI: 10.1371/journal.pgen.1002055

Improving Photosynthesis? Solar Cells Beat Plants at Harvesting Sun's Energy, for Now

Source: ScienceDaily (May 12, 2011)

In a head-to-head battle of harvesting the sun's energy, solar cells beat plants, according to a new paper in *Science*. But scientists think they can even up the playing field, says researcher David Kramer at Michigan State University.

Plants are less efficient at capturing the energy in sunlight than solar cells mostly because they have too much evolutionary baggage. Plants have to power a living thing, whereas solar cells only have to send electricity down a wire. This is a big difference because if photosynthesis makes a mistake, it makes toxic byproducts that kill the organism. Photosynthesis has to be conservative to avoid killing the organisms it powers.

"This is critical since it's the process that powers all of life in our ecosystem," said Kramer, a Hannah Distinguished Professor of Photosynthesis and Bioenergetics. "The efficiency of photosynthesis, and our ability to improve it, is critical to whether the entire biofuels industry is viable."

The annually averaged efficiency of photovoltaic electrolysis based on silicon semiconductors to produce fuel in the form of hydrogen is about 10 percent, while a plant's annually averaged efficiency using photosynthesis to form biomass for fuel is about 1 or 2 percent.

Plants, following the path of evolution, are primarily interested in reproducing and repairing themselves. The efficiency at which they produce stored solar energy in biomass is secondary.

Still, things can change.

Just as early Native Americans manipulated skinny, non-nutritious Teosinte into fat, juicy kernel corn, today's plants can be manipulated to become much better sources of energy.

Researcher Arthur J. Nozik, a NREL senior research fellow, and Senior Scientist Mark Hanna working at DOE's National Renewable Energy Laboratory (NREL), recently demonstrated how a multi-junction, tandem solar cell for water splitting to produce hydrogen can provide higher efficiency -- more than 40 percent -- by using multiple semiconductors and/or special photoactive organic molecules with different band gaps arranged in a tandem structure.

The coupling of different materials with different gaps means photons can be absorbed and converted to energy over a wider range of the solar spectrum.

"In photovoltaics, we know that to increase power conversion efficiency you have to have different band gaps (i.e., colors) in a tandem arrangement so they can more efficiently use different regions of the solar spectrum," Nozik said. "If you had the same gap, they would compete with each other and both would absorb the same photon energies and not enhance the solar conversion efficiency."

Photosynthesis does use two gaps based on chlorophyll molecules to provide enough energy to drive the photosynthesis reaction. But the two gaps have the same energy value, which means they don't help each other to produce energy over a wider stretch of the spectrum of solar light and enhance conversion efficiency.

Furthermore, most plants do use the full intensity of sunlight but divert some of it to protect the plant from damage. Whereas photovoltaics use the second material to gain that photoconversion edge, plants do not, Nozik noted.

One of NREL's roles at the DOE workshop was to help make it clear how the efficiency of photosynthesis could be improved by re-engineering the structure of plants through modern synthetic biology and genetic manipulation based on the principles of high efficiency photovoltaic cells, Nozik said. In synthetic biology plants can be built from scratch, starting with amino acid building

blocks, allowing the formation of optimum biological band gaps.

The newly engineered plants would be darker, incorporating some biological pigments in certain of nature's flora that would be able to absorb photons in the red and infrared regions of the solar spectrum.

As plants store more solar energy efficiently, they potentially could play a greater role as alternative renewable fuel sources. The food that plants provide also would get a boost. And that would mean less land would be required to grow an equivalent amount of food.

The new information in the Science manuscript will help direct the development of new plants that have a better propensity for reducing carbon dioxide to biomass. This could spur exploration of blue algae, which not only comprise about one quarter of all plant life, but are ideal candidates for being genetically engineered into feedstock, because they absorb light from an entirely different part of the spectrum compared to most other plants.

"It would be the biological equivalent of a tandem photovoltaic cell," said Robert Blankenship, one of the lead authors in the Science paper who studies photosynthesis at Washington University in St. Louis. "And those can have very high efficiencies."

Reference: Robert E. Blankenship et al. Comparing Photosynthetic and Photovoltaic Efficiencies and Recognizing the Potential for Improvement. Science, 13 May 2011: Vol. 332 no. 6031 pp. 805-809 DOI: 10.1126/science.1200165

Genomes of Fungi That Threaten Wheat, Poplars Sequenced

Source: ScienceDaily (May 11, 2011)

An international team of researchers co-led by a U.S. Department of Agriculture (USDA) scientist has sequenced the genomes of two fungal pathogens—one that threatens global wheat supplies and another that limits production of a tree crop valued as a future source for biofuel.

The sequencing of the genetic codes of wheat stem rust pathogen (*Puccinia graminis*) and poplar leaf rust pathogen (*Melampsora larici-populina*) is expected to help researchers develop control strategies

to address worldwide threats to wheat fields and tree plantations. The study, published in the Proceedings of the National Academy of Sciences, was a six-year collaborative effort of USDA's Agricultural Research Service (ARS), the U.S. Department of Energy Joint Genome Institute, the National Science Foundation, the Broad Institute of Harvard and the Massachusetts Institute of Technology, the University of Minnesota and the French National Institute for Agricultural Research.

"The threats these pathogens pose to two essential agricultural products are very real, and that makes it important to learn everything we can about them, from their molecular underpinnings to how they survive and spread infection," said Edward B. Knipping, administrator of ARS, USDA's principal intramural scientific research agency. The research supports the USDA priority of developing new sources of bioenergy and promoting international food security.

Wheat stem rust causes major epidemics of both barley and wheat worldwide. A strain known as Ug99 has spread across Africa and into Central Asia, and has been able to overcome most of the stem-rust-resistant wheat varieties developed over the past 50 years.

Poplar leaf rust can cause significant losses in poplar tree plantations. Poplar is an important crop for the wood industry and is becoming increasingly important to the biofuel industry in the United States and Europe because of its rapid and significant production of biomass.

The study represents the first genome-wide characterization of any rust fungus, a diverse group of more than 6,000 species, according to Les Szabo, a lead researcher on this project. Szabo works at the ARS Cereal Disease Laboratory in St. Paul, Minn.

Rust fungi depend on living tissue of their hosts for survival. The pathogens secrete proteins that enable them to block the host plant's defenses and steal nutrients. The research uncovered evidence that both pathogens have large numbers of such "effector" proteins, an indication that they likely co-evolved with their host plants, according to the study authors.

Because they need a plant host to survive, the pathogens can't be cultured in a laboratory and are notoriously hard to study. But the genetic sequencing opens a window into the never-ending arms race between these pathogens and their hosts, Szabo said. The team's sequence data has been released in GenBank, a genetic database administered by the National Center for Biotechnology Information at the National Institutes of Health.

Reference: S. Duplessis et al. Obligate biotrophy features unraveled by the genomic analysis of rust fungi. *Proceedings of the National Academy of Sciences*, 2011; DOI: 10.1073/pnas.1019315108

Vitamins May One Day Hitch a Protected Ride on Corn Starch

Source: ScienceDaily (May 15, 2011)

Vitamins and medications may one day take rides on starch compounds creating stable vitamin-enriched ingredients and cheaper controlled-release drugs, according to Penn State food scientists.

The technique may offer drug and food companies a less expensive, more environmentally friendly alternative in creating, among other products, medications and food supplements.

In a series of experiments, researchers formed pockets with corn starch and a fatty acid ester to carry oil soluble vitamins, such as vitamin A and vitamin C, into the body, according to Gregory Ziegler, professor, food sciences.

Heat and acids can harm or destroy vitamins. The starch molecule forms a protective pocket around the vitamins as they travel through the highly acidic stomach and into the small intestines, where they can be absorbed into the blood stream.

To form the pocket, the researchers, who released their findings in a recent issue of *Carbohydrate Polymers*, used a type of corn starch called high amylose maize starch. When amylose comes into contact with fatty acids esters of vitamin A, for example, it creates a coil with an internal wall that repels water -- hydrophobic -- and an exterior wall that attracts water -- hydrophilic. The oil-soluble molecules automatically move into

the coil that encapsulates the medication or vitamin.

"There's an ideal size and the real work is to get the right balance of the hydrophilic and hydrophobic properties," said Ziegler, who worked with Ursula V. Lay Ma, graduate student, and John D. Floros, professor, food sciences.

According to Ziegler, there are several benefits for using starches as hosts for delivering drugs and vitamins. Because starches are common, biodegradable and easily absorbed by the body, using corn starch could be inexpensive and better for the environment.

The pharmaceutical industry uses other ingredients and techniques to create inclusion complexes, said Ziegler. For example, cyclodextrin complexes -- donuts of sugar molecules -- form in a similar way to deliver controlled-release substances, such as Ibuprofen. Ziegler said that because the cavity in starch is a different size than that of cyclodextrin, it can increase the size range of molecules that can be encapsulated.

Corn starch could be used in a variety of other applications, including those outside the pharmaceutical and food industries, such as in make-up, containers and even optical and electronic devices, according to Ziegler. "We have more work and research to do," Ziegler said. "The trick is how can we set this up so we can do it simply."

Reference: Ursula V. Lay Ma, John D. Floros, Gregory R. Ziegler. Effect of starch fractions on spherulite formation and microstructure. *Carbohydrate Polymers*, 2011; 83 (4): 1757 DOI: 10.1016/j.carbpol.2010.10.041

Parental conflict in plants: Maternal factors silence paternal genes

Source: Science News, May 31, 2011

In flowering plants, the beginning of embryogenesis is almost exclusively governed by maternal gene activity. Maternal factors regulate the development of the embryo and silence paternal genes during early stages of development. This finding -- obtained using next generation sequencing technology -- was reported by an international team of researchers including plant geneticists from the University of Zurich. This newly uncovered mechanism

may be involved in the maintenance of species boundaries and could play an important role in the development of novel crop varieties. Mother and father each contribute one half of the genetic information to their offspring. Thus, it was thought that both parents contribute equally to the development of the next generation. Indeed, this holds true for late stages of embryo development in plants, but early on, things are quite different: during the earliest phase of embryo development - from the fertilized egg to the globular stage - predominantly the maternal genes are active. This phase of development is controlled largely by maternal factors, which actively repress or silence the genes inherited from the father. This surprising finding was recently published in the renowned American journal *Cell*, by an international team of scientists led by plant geneticists from the Universities of Zurich and Montpellier.

For their analysis, the Zürich scientists crossed two genetically distinguishable races of the model plant *Arabidopsis thaliana* (tale cress) and analyzed the relative contributions of the parental genomes shortly after the first division of the fertilized egg. Such molecular genetic analyses of plant embryos at very early stages are technically challenging, which explains why up to now researchers resorted to studying embryos at later stages. But Ueli Grossniklaus, Professor for Plant Developmental Genetics at University of Zurich, has a marked preference for tackling experimentally challenging problems, including the study of gametes and very young embryos that are hard to obtain. Using "Next Generation Sequencing", a novel and powerful technology, Grossniklaus and colleagues were able to show that in an early phase of plant embryo development, predominantly maternal genes are active. Via small ribonucleic acid molecules (siRNAs), the maternal genome controls paternal genes to ensure that, initially, most remain inactive. In the course of development, paternal genes are successively activated, which also requires the activity of maternal factors. This finding is surprising because it contradicts earlier findings, which suggested that these siRNAs have a specific role in preventing "jumping

genes" (transposons) to move within the genome.

According to Grossniklaus, the transient silencing of the paternal contribution during early development of the offspring is in the mother plant's best interest: the mother invests considerable resources into the formation of seeds. Before making this investment, the mother verifies the paternal contribution to the progeny for compatibility with her own genome. If the father's genome is too divergent from her own, e.g., originating from a different species, the embryo will die. In fact, the two parental plants have opposing interests with regard to their offspring. The pollen-donating father is interested in maximizing transfer of resources from the mother to the offspring. By contrast, the mother plant aims at optimizing the match with the fathers genome in order to prevent a waste of resources. „We are dealing with a classical parental conflict", Ueli Grossniklaus summarizes the opposing interests.

Maternally active genes direct and control early embryogenesis. Genetic incompatibility will cause embryos to abort, such that fertilization with pollen from other plant species is not successful. Therefore, the mechanism unraveled by Grossniklaus and colleagues may play an important role in the maintenance of species barriers. This may also explain why attempts to cross crop plants with their wild relatives, e.g., to transfer disease-resistance genes present in wild relatives to crops, often fail early in embryogenesis. A genetic divergence between the parents that is too large may be recognized by this novel mechanism, leading to embryo abortion. Commercial crop breeders will thus be interested in finding out how the maternal control of early plant embryo development can be circumvented in their breeding programs.

Study Reveals Important Aspects of Signalling Across Cell Membranes in Plants

Source: NSF. June 14, 2011

Every living plant cell and animal cell is surrounded by a membrane. These cellular membranes contain receptor molecules that serve as the cell's eyes and ears, and help it

communicate with other cells and with the outside world.

The receptor molecules accomplish three basic things in the communication process: 1) recognize an outside signal, 2) transport that signal across the cell's membrane and 3) initiate the reading of the signal inside the cell and then initiate the cell's response to that signal. These steps are collectively known as transmembrane signaling.

Transmembrane signaling in animal cells has been significantly more studied and observed than that in plant cells. But now, with support from the National Science Foundation, researchers from Joanne Chory's laboratory at the Salk Institute have published new observations about transmembrane signaling in plants; their paper appears in the June 12, 2011, advanced online edition of *Nature*.

According to the study, transmembrane signaling mechanisms used by plants differ from those used by animals. Specifically, Michael Hothorn of the Salk Institute reports that a small steroid molecule on the outside of the plant cell assists in the transmembrane signaling process. By contrast, this sort of molecule and its receptor is generally located inside the nuclei of animal cells.

While studying transmembrane signaling in plants, Hothorn and colleagues observed the steroid, shown in yellow, attach to a membrane-bound receptor, shown in blue. This attachment enabled the steroid's counterpart--a co-receptor protein, shown in orange--to bind to the blue receptor. Once bound, the orange co-receptor and the blue receptor become glued together by the yellow steroid, allowing their intracellular domains to touch and initiate communication.

In the case observed by Hothorn, transmembrane signaling initiated plant growth.

The First Plant Interactome

By Jessica P. Johnson

Source: *The Scientist*. July 28, 2011

Protein interaction networks in *Arabidopsis* give clues to plant evolution and immunity.

For the first time, a systematic protein interaction map—or interactome—has been constructed for a plant. In a pair of papers

published online today (July 28) in *Science*, researchers from the Arabidopsis Interactome Mapping Consortium (AIMC) present their data from an extensive effort to map the pairwise interactions of over 2,700 proteins expressed within the cells of *Arabidopsis thaliana*, and show that pathogens target the most active proteins during infection.

The map shows that “there are few proteins that are highly connected,” said Christian Landry, an assistant professor of Biology at Laval University, who did not participate in the research. “This kind of structure gives robustness to the network because if you target proteins randomly, you are more likely to hit peripheral proteins” and not significantly disrupt cell function.

The effort also serves to “put proteins that we don't know about into a molecular context,” added Pascal Braun, chair of AIMC and an author on both papers. While there has been much attention paid to sequencing projects, the genome tells researchers little about the functions of proteins that actually drive cellular processes, he said. “We need to know what the proteins do and how they interact. This is the first time we have done this at a systematic level for any plant.”

In the first study, Braun and colleagues expressed 8,000 *Arabidopsis* proteins—representing 30 percent of the plant's protein-coding genes—in yeast cells. The yeast cells were engineered to replicate when two isolated proteins came together, providing a visual cue for the protein interactions. The researchers tested all pairwise combinations of the 8,000 proteins, one couple at a time, and verified interactions among about 2,700 of them.

From the results, the team constructed a map of all the interactions, which revealed nodes of dense interconnectivity centered around a relatively small number of proteins. These highly connected proteins, known as hubs, “are important for keeping everything together,” Braun said. “The system collapses if you take down the hubs.” The vast majority of the proteins, however, had only a handful of connections. Removing any of these peripheral proteins from the cell would be unlikely to significantly disrupt any major cellular processes.

The researchers also looked at the impact of these networks on evolution. The protein products of duplicated genes, for example, might be expected to take on different functions, as one can maintain the original task while the other is free to accumulate mutations. But the researchers found that most gene duplicates in Arabidopsis tended to interact with many of the same proteins, even though those duplicates had originated more than 700 million years ago, suggesting that the interactome somehow reduces the freedom of duplicated proteins to diverge.

In the second study, Jeffrey Dangl of the University of North Carolina at Chapel Hill and his colleagues paired genes from the Arabidopsis interactome map and additional immune system proteins with effector proteins from known Arabidopsis pathogens—the bacteria *Pseudomonas syringae* and the fungus-like oomycete *Hyaloperonospora arabidopsidis*. Interestingly, rather than directly interacting with the immune system proteins, the effectors bound to Arabidopsis hub proteins, indicating that the pathogens induce immune responses indirectly.

Furthermore, despite the 2 billion years of evolution separating the two pathogens, they shared the strategy of targeting the hub proteins, and even interacted with 18 of the same major hubs. When the researchers knocked out those 18 genes individually in

Arabidopsis plants and exposed the plants to the effector proteins, 15 of the mutants had an altered immune response.

“This is an unheard-of validation rate,” said Braun. “Even though [the pathogens] have independently evolved and their mode of attack is different, they are still converging on the highly connected proteins.” This suggests that the pathogens have evolved to target proteins that participate in more than one immune response or pathogen recognition pathway.

The results point to ways researchers might protect plants from disease or engineer them to be better crops, for example, said Braun. “Plants play a fundamental role in food security, energy security, and climate change,” he said, and understanding how proteins interact in the cell could lead to the discovery of proteins with biotechnological applications.

But advancing plant disease resistance is not as simple as just removing these key proteins, because it not only alters the immune response, but would be detrimental to other plant cell processes. “The real challenge is to determine what the targeted plant proteins are doing in the innate immune response and how modifying the targets will modify the disease,” said Cyril Zipfel, group leader in molecular and microbe interactions at The Sainsbury Laboratory.

EU Framework Programme for Research and Innovation



We are pleased to inform you that Mrs. Máire Geoghegan-Quinn, European Commissioner for Research and Innovation, has announced on 21 June 2011 the new name for the future EU funding programme for research and innovation: "**Horizon 2020 - the Framework Programme for Research and Innovation**". It will enter into force on 1 January 2014, after the end of FP7 on 31 Dec 2013.

"**Horizon 2020 - the Framework Programme for Research and Innovation**" is not just a new name for the same Framework Programme. It is the name for the new, integrated funding system that will cover all

research and innovation funding currently provided through **the Framework Programme for Research and Technical Development, the Competitiveness and Innovation Framework Programme (CIP) and the European Institute of Innovation and Technology (EIT)**. These different types of funding will be brought together in a coherent and flexible manner. Research and innovation funding will focus clearly on addressing global challenges. Needless red tape will be cut out and access to programs and participation will be made easier and simpler.

More details can be found in the press release as well as the website of the European Commission:

<http://europa.eu/rapid/pressReleasesAction.do?reference=MEMO/11/435&format=HTML&aged=0&language=EN&quiLanguage=fr>.

Forthcoming meetings



The EMBO Meeting 2011

September 10 – 13, 2011. Vienna, Austria.

Deadline: 27 July 2011

Submit your abstract now!

More info: <http://www.the-embo-meeting.org/>

Applied Forestry Research in the 21st Century

September 13 – 15, 2011. Prague (Praha), Czech Republic

Forestry and Game Management Research Institute of Czech Republic

More info: <http://www.vulhm.cz/afr21/>

Plant Growth Biology and Modeling 2011

September 19 – 21, 2011. Elche, Spain.

More info: <http://pgbm2011.umh.es/>

Conference Molecular Basis of Plant Stress

September 21 – 23, 2011. Varna, Bulgaria.

Deadline for registration: 1 August 2011

Organizer: Dr. Tsanko Gechev, e-mail tsangech@uni-plovdiv.bg

More info: <http://cmbps.bio.uni-plovdiv.bg/>

1st BIONUT meeting " State of the art in Plant Nutrition Research"

September 27 – 29, 2011. Conegliano, Italy.

The deadline for early-bird registration is the 30 June.

Meeting website:

<http://www.jic.ac.uk/events/bionut/>

Lignofuels 2011

September 28 – 29, 2011. Copenhagen, Denmark.

More info:

<http://v11.vuturevx.com/exchange-sites/Whitmore%20Group/59/conferences/eu-eef2.asp>

International Symposium on Sunflower Genetic Resources

October 16 – 20, 2011. Kusadasi, Turkey.

More info:

<http://www.ttae.gov.tr/symposium/>

1st European Brachypodium Workshop

October 19 – 21, 2011. INRA Versailles, France.

More info:

https://colloque.inra.fr/1st_european_brachypodium_workshop

EWAC-EUCARPIA Cereals Section Conference

November 7 – 11, 2011. Novi Sad, Serbia.

EUCARPIA homepage:

<http://www.eucarpia.org>

19th International Symposium of CIEC (International Scientific Center of Fertilizers) Feeding Plants is Feeding People

November 7 – 11, 2011. Mexico City (Mexico)

The Symposium will address five central issues: I. Managing phosphorus scarcity. II. Standards for use of recycling products as fertilizers. III. Fertilizer strategies for moderating drought stress and salinity. IV: Fertilizers practices in Latin America. V. Fertilizer strategies for organic farming

Prof. Dr. habil. Dr. sc. agr. Dr. h.c. Ewald Schnug (President of CIEC)

Prof. Dr. Luc Dendooven (President of Symposium)

More info: <http://idw-online.de/pages/en/news388693>

SOL & ICuGI 2011 - 8th Solanaceae and 2nd Cucurbitaceae Joint Conference

November 28 – December 2, 2011. Kobe Convention Center, Kobe, Japan.

More info: <http://www.sol2011.jp/>

Positions available



Senior Lecturer - Plant Molecular Biology

University of Pretoria. Dept. of Plant Sci. and the Forestry and Agricultural Bio...

Pretoria, Gauteng. South Africa

<http://www.AcademicKeys.com/r?job=29758&o=777137&t=SC110419m-6e>

Two Group Leaders - Bio NMR

CEITEC - Central European Institute of Technology.

Structural Biology Research Program

Brno. Czech Republic

<http://www.AcademicKeys.com/r?job=29514&o=777137&t=SC110419m-6e>

Technical Officer -- Molecular Biology and Climate Control

University of Western Sydney

Hawkesbury Institute for the Environment

Sydney, Australia

<http://www.AcademicKeys.com/r?job=29019&o=777137&t=SC110419m-6e>

Full-time Faculty Position -- Biology

University of the Fraser Valley. Department of Biology

Abbotsford, BC, Canada

<http://www.AcademicKeys.com/r?job=29920&o=777137&t=SC110419m-6e>

Lecturer -- Biological Sciences

New Jersey Institute of Technology.

Department of Biological Sciences

Newark, NJ. USA

<http://www.AcademicKeys.com/r?job=29915&o=777137&t=SC110419m-6e>

Lecturer in Nutrition and Food Science

University of Western Sydney. School of Natural Sciences

Sydney, Australia

<http://www.AcademicKeys.com/r?job=29879&o=777137&t=SC110419m-4e>

Field Automation Applications Scientist

The Field Automation Applications Scientist is a primary technical contact for Diagenode's customers. As Field Applications Scientist, you will provide sales, technical, logistical, and troubleshooting support to all customers using Diagenode's automation product line as well as sonication, ChIP, DNA methylation related products. You will assist the company in developing excellent customer relationships and collaborations, and ensure customer success with our products.

The Field Applications Scientist should be based in the company's Head Office in Liège, Belgium.

Qualifications:

- . Ph.D. or equivalent in genomics, epigenetics or related field.
- . 3-5 years of biotech experience, preferably in life-sciences tools industry.
- . Demonstrated experience with epigenetics, ChIP, DNA methylation and/or high-throughput genomics methods.
- . Demonstrated understanding of commonly-used ChIP and/or DNA methylation sample prep, protocols, technologies and data analysis.
- . Demonstrated experience with instrumentation such as liquid handling robotics preferred.
- . Outstanding problem solving and interpersonal skills.
- . Demonstrated written and verbal communication and training skills.
- . Clear vision of and commitment to providing outstanding customer support.

Please contact us: job@diagenode.com

http://www.diagenode.com/en/company/ca_reers.php#automation

New books



AGRICULTURAL SCIENCES: TOPICS IN MODERN AGRICULTURE

Editors: Agustín González-Fontes, Agustín Gárate, Ildefonso Bonilla

Publisher: Studium Press LLC, Houston, TX, USA

Publication Date: Summer 2010

Binding: Hardback

ISBN 1-933699-48-5

More info:

<http://www.studiumpress.in/indetail.asp?id=12>

[1](#)

ANNUAL PLANT REVIEWS, VOLUME 41, PLANT POLYSACCHARIDES: BIOSYNTHESIS AND BIOENGINEERING

Peter Ulvskov

ISBN: 978-1-4051-8172-3

Hardcover

504 pages

December 2010, Wiley-Blackwell

<http://eu.wiley.com/WileyCDA/WileyTitle/productCd-1405181729.html>

ANNUAL PLANT REVIEWS, VOL 43. BIOLOGY OF PLANT METABOLOMICS

HALL, R.D.

ISBN 9781405199544

Wiley-Blackwell, 2011

Following a general introduction to the book, the first section of the book will include details of metabolomics of model species, including Arabidopsis, tomato and the legume Medicago. Chapters within the second section will consider the use and inter relationships of data integration, systems biology, genetics, genomics, metabolomics, chemometrics and biostatistics. The final section of the book will look at the use of metabolomics in food science, plant ecology, biodiversity and bioprocessing. Plant Metabolomics is an essential purchase for plant scientists, plant geneticists and physiologists.

BARLEY: PRODUCTION, IMPROVEMENT, AND USES

Steven E. Ullrich

2011, 640 pgs, tela.

Barley is one of the world's most important crops with uses ranging from food and feed

production, malting and brewing to its use as a model organism in molecular research. The demand and uses of barley continue to grow and there is a need for an up-to-date comprehensive reference that looks at all aspects of the barley crop from taxonomy and morphology through to end use. *Barley* will fill this increasing void. *Barley* will stand as a must have reference for anyone researching, growing, or utilizing this important crop.

CONTENTS: 1: Significance, Adaptation, Production, and Trade of Barley. 2: Barley Origin and Related Species. 3: Barley Genome Organization, Mapping, and Synteny. 4: Genome Analysis: The State of Knowledge of Barley Genes. 5: Cytogenetics and Molecular Cytogenetics of Barley: A Model Cereal Crop with a Large Genome. 6: Application of Molecular Genetics and Transformation to Barley Improvement. 7: Barley Germplasm Conservation and Resources. 8: Barley Breeding History, Progress, Objectives, and Technology. 9: Cultural Practices: Focus on Major Barley-Producing Regions. 10: Abiotic Stresses in Barley: Problems and Solutions. 11: Biotic Stress in Barley: Disease Problems and Solutions. 12: Biotic Stress in Barley: Insect Problems and Solutions. 13: The Development, Structure, and Composition of the Barley Grain. 14: Biochemistry, Physiology, and Genetics of Endosperm Mobilization in Germinated Barley Grain. 15: Malting and Brewing Uses of Barley. 16: Barley Feed Uses and Quality Improvement. 17: Food Uses of Barley. 18: Adapting Cereal Plants and Human Society to a Changing Climate and Economy Merged by the Concept of Self-Organization. Index. Color plate is located between pages 340 and 341.

BRASSINOSTEROIDS: A CLASS OF PLANT HORMONE

HAYAT, S.

ISBN 9789400701885

Springer, 2011

CONTENTS: Foreword.- Preface.- 1. Brassinosteroids-occurrence and chemical structures in plants, Andrzej Bajguz 2. Regulatory mechanism of brassinosteroid signaling in

plants; M.-C. Codreanu and E. Russinova 3. Regulation of brassinosteroid metabolism; L. Hategan, B. Godza and M. Szekeres 4. Brassinosteroid signaling in rice; H. Nakagawa, A. Tanaka and M. Mori 5. Brassinosteroids and light - regulatory factors of growth and development of plants; I. F. Golovatskaya 6. Brassinosteroids and photosynthesis; D. Holá 7. Physiological effects related to brassinosteroid application in plants; M.M.A. Gomes 8. Genomic and non-genomic events involved in the brassinosteroid promoted plant cell growth; A.B.Pereira-Netto 9. Role of brassinosteroids on horticultural crops; Y.Y.Kang and S.R.Guo 10. Brassinosteroid action and its relation with heat stress mechanisms in plants; L.M.Mazorra 11. Protective effects of brassinosteroids against herbicides; R. Piñol, E. Simón 12. Brassinosteroids: under biotic stress; Shamsul Hayat, Mohammad Irfan, Aqil Ahmad 13. The significance of ethanol as a hormone solvent in experiments on the physiological activity of Brassinosteroids; Anna Janeczko 14. Immunoassays of brassinosteroids; V.A. Khripach, V.N.Zhabinskii, R.P. Litvinovskaya 15. Transcriptomics and proteomics study in regulation of brassinosteroids; H. F. Juan 16. Brassinosteroids for phytoremediation application; M. Barbaferri, E. Tassi 17. Prospects of brassinosteroids in medicinal applications; R. Bhardwaj, N. Arora, P. Uppal, I. Sharma, M.K. Kanwar Index.

ECOLOGICAL ASPECTS OF NITROGEN METABOLISM IN PLANTS

Joe C. Polacco, Christopher D. Todd 2011, 448 pgs, tela.

Ecological Aspects of Nitrogen Acquisition covers how plants compete for nitrogen in complex ecological communities and the associations plants recruit with other organisms, ranging from soil microbes to arthropods. The book is divided into four sections, each addressing an important set of relationships of plants with the environment and how this impacts the plant's ability to compete successfully for nitrogen, often the most growth-limiting nutrient. *Ecological Aspects of Nitrogen Acquisition* provides thorough coverage of this important topic, and is a vitally important resource for plant scientists, agronomists, and ecologists.

ELEVATED CARBON DIOXIDE: IMPACTS ON SOIL AND PLANT WATER RELATIONS

M.B. Kirkham

2011, 416 pgs, tela.

Features

- Documents plant water relations under elevated CO₂
 - Draws on information from peer-reviewed scientific papers as well as pioneering studies previously unpublished
 - Includes over 200 high quality figures to illustrate the concepts discussed
 - Presents a humanistic side of science by providing biographies of key people in the area
- Summary

Between 1958 and 2008, the CO₂ concentration in the atmosphere increased from 316 to 385 ppm. Continued increases in CO₂ concentration will significantly affect long-term climate change, including variations in agricultural yields. Focusing on this critical issue, **Elevated Carbon Dioxide: Impacts on Soil and Plant Water Relations** presents research conducted on field-grown sorghum, winter wheat, and rangeland plants under elevated CO₂. It describes specific results from pioneering experiments performed over a seven-year period in the Evapotranspiration Laboratory at Kansas State University, along with experiments appearing in peer-reviewed journal articles.

Select articles from the literature serve as examples in the text. For each paper discussed, the author includes the common and scientific name of the plant under investigation. For each experiment, the author provides the type of soil used (if given in the original article) and general conditions of the experiment. All references are carefully documented so that readers can easily find the original source.

The first chapter of the book deals with drought, the three types of photosynthesis, and how water moves through the soil-plant-atmosphere continuum. With a focus on soil, the next several chapters discuss the composition of the soil atmosphere, the interaction of elevated CO₂ with physical factors that affect root growth, variable oxygen concentration of soil, and when the atmosphere above soil is elevated with CO₂. The author goes on to examine the use of carbon isotope ratios in plant science; the effects of elevated CO₂ on plant water, osmotic, and turgor potentials; and stomata under elevated CO₂, including stomatal conductance and density. The text also explains the effects of elevated CO₂ on transpiration and evapotranspiration, explores historical aspects of water use efficiency, compares C₃ and C₄

plants under elevated CO₂, and details the advantages of C₄ photosynthesis. The concluding chapters cover plant anatomy, the effects of elevated CO₂ on phenology, and measures of plant growth

GENETICS, GENOMICS, AND BREEDING OF SOYBEAN

Editor(s): Kristin Bilyeu, USDA-ARS, University of Missouri, Columbia, USA; Milind B. Ratnaparkhe, USDA-ARS, University of Missouri, Columbia, USA; Chittaranjan Kole, Clemson University, South Carolina, USA

Cat. #: N10274

ISBN: 9781578086818

ISBN 10: 1578086817

Publication Date: June 03, 2010

CRC Press

http://www.crcpress.com/product/isbn/9781578086818;jsessionid=X4-WQA-zfclExCcxYW73lw**

GENETICS, GENOMICS AND BREEDING OF VEGETABLE BRASSICAS

Jan Sadowski, *Adam Mickiewicz University, Poznan, Poland*; Chittaranjan Kole, *Clemson University, South Carolina, USA*

2011, 450 pgs, tela.

CONTENTS:

Basic Information on Vegetable Brassica Crops: *M. Cartea, M. Lema, M. Francisco, and P. Velasco*

Classical Breeding and Genetic Analysis of Vegetable Brassicas: *N. Ramchiary, S. Park, and Y.-P. Lim*

Diversity Analysis and Molecular Taxonomy of Brassica Vegetable Crops: *G. Bonnema, D. Pino, D. Carpio, and J. Zhao*

Molecular Linkage Maps: Strategies, Resources and Achievements: *D. Babula-Skowronska, A. Ciesla, and J. Sadowski*

Molecular Mapping of Complex Traits: *M. Kaczmarek, M. Nelson, and W. Cowling*

Cytogenetic Studies in Vegetable Brassicas: *P.A. Ziolkowski, M.A. Lysak and W.K. Heneen*

Brassica rapa Genome Sequencing Project: Strategies and Current Status: *J.-H. Mun, T.-J. Yang, S.-J. Kwon, and B.-S. Park*

Exploring the Paradoxes of the Brassica Genome Architecture: *I.A.P. Parkin and S.J. Robinson*

The Decoding of Gene Functions- Transcriptomics Tools Toward Molecular Physiology and Breeding: *A. Ludwikow, K. Krasowski, and L. Zeef*

GROWTH AND MINERAL NUTRITION OF FIELD CROPS, THIRD EDITION

Nand Kumar Fageria, EMBRAPA, San Antonio de Goias, GO, Brazil; Virupax C. Baligar, USDA/ARS SPCL, Beltsville, MD, USA; Charles Allan Jones, Texas A&M University, Dallas, USA

Price: \$149.95

Cat. #: K10875

ISBN: 9781439816950

Publication Date: October 19, 2010

Binding: Hardback

CRC Press

<http://www.crcpress.com/product/isbn/9781439816950>

HANDBOOK OF PLANT AND CROP STRESS, THIRD EDITION

Editor(s): Mohammad Pessaraki, University of Arizona, Tucson, USA; Mohammad Pessaraki, University of Arizona, Tucson, USA

Price: \$199.95

Cat. #: K10719

ISBN: 9781439813966

Publication Date: November 16, 2010

Binding: Hardback

CRC Press

<http://www.crcpress.com/product/isbn/9781439813966>

IMMUNOASSAYS IN AGRICULTURAL BIOTECHNOLOGY

Shan, G

2011, 368 pgs, tela.

A very broad range of professionals are using immunoassay technology daily to analyze genetically engineered (GE) crops and related areas, and many of these professionals are completely new to this technology. There is a great need for users to have a book containing technical and practical guidance, and describing limitations and pitfalls of applying immunoassay in agricultural biotechnology.

This book focuses on the application of immunoassays to GE plants and related areas. A group of international experts from government agencies, academics and industries, who have many years of related experience, contribute high quality chapters in their areas of expertise. This book covers topics including principles of immunoassay, antibody engineering in AgBiotech, current technologies (formats, kit development, manufacturing and quality control), method validation, applications in trait discovery and product development,

applications in grain products and food processing, applications in environmental monitoring, automation and high throughput, reference materials, data interpretation and source of error, and future perspectives and challenges. In addition, to meet the practical needs for a variety of readers from different backgrounds, methods and protocols are included as well.

PLANT CHROMOSOME ENGINEERING

Birchler, James A.

1st Edition., 2011, XI, 340 p. 44 illus., 16 in color., Hardcover.

With an increasing human population and a decreasing amount of arable land, creative improvements in agriculture will be a necessity in the coming decades to maintain or improve the standard of living. In *Plant Chromosome Engineering: Methods and Protocols*, expert researchers present techniques for the modification of crops and other plant species in order to achieve the goal of developing the much needed novel approaches to the production of food, feed, fuel, fiber, and pharmaceuticals. This volume examines vital topics such as transformation procedures, chromosome painting, production of engineered minichromosomes, gene targeting and mutagenesis, site specific integration, gene silencing, protein expression, chromosome sorting and analysis, protocols for generating chromosomal rearrangements, enhancer trapping, and means of studying chromosomes in vivo. As a part of the highly successful *Methods in Molecular Biology™* series, the methodological chapters include brief introductions to their respective topics, lists of the necessary materials and reagents, step-by-step, readily reproducible laboratory protocols, and professional tips on troubleshooting and avoiding known pitfalls. Authoritative and cutting-edge, *Plant Chromosome Engineering: Methods and Protocols* highlights the spectrum of tools currently available for modifying plant genomes and chromosomes and provides the foundation for crucial future developments.

PLANT METABOLISM AND BIOTECHNOLOGY

Hiroshi Ashihara (Editor), Alan Crozier (Co-Editor), Atsushi Komamine (Co-Editor)

2011, 400 pgs, tela

Various plant metabolites are useful for human life, and the induction and reduction of these

metabolites using modern biotechnical technique is of enormous potential important especially in the fields of agriculture and health.

Plant Metabolism and Biotechnology describes the biosynthetic pathways of plant metabolites, their function in plants, and some applications for biotechnology. Topics covered include:

Biosynthesis and metabolism of starch and sugars, lipid biosynthesis, symbiotic nitrogen fixation, sulfur metabolism, nucleotide metabolism, purine alkaloid metabolism, nicotine biosynthesis, terpenoid biosynthesis, benzylisoquinoline alkaloid biosynthesis, monoterpene indole alkaloid biosynthesis, flavonoid biosynthesis, pigment biosynthesis: anthocyanins, betacyanins and carotenoids, metabolomics in biotechnology

<http://eu.wiley.com/WileyCDA/WileyTitle/produ ctCd-047074703X.html>

PLANT MITOCHONDRIA

Kempken, Frank

1st Edition., 2011, XIII, 535 p., Hardcover.

Mitochondria are the product of a long evolutionary history. It is now a well established fact that mitochondria did evolve from free living bacteria being the common ancestor of both, eukaryotic mitochondria and α -proteobacteria. Advances in genome sequencing, the establishment of in organello and in vitro assays to name only a few, contributed significantly to advances in plant mitochondrial research. Second generation sequencing and the ability to directly sequence and analyse the whole plant transcriptome certainly will help to develop the research on plant mitochondria to another level in the future. In this book the current knowledge about plant mitochondria is presented in a series of detailed chapters, which have been organized in five main sections: (i) dynamics, genes and genomes; (ii) transcription and RNA processing; (iii) translation and import; (iv) biochemistry, regulation and function; and (v) mitochondrial dysfunction and repair. These sections consist of two to five chapters, each written by well-known specialists in the field. This book thus provides a comprehensive inside in the field of plant mitochondria for the specialist. The addition of a glossary and text boxes to each chapter provides easy access for readers from other subjects and hopefully will attract young scientist to the fascinating and exiting field of plant mitochondria. Frank Kempken graduated from

the Ruhr-University Bochum, Germany. He is professor for genetics and molecular biology in botany at the Christian-Albrechts-University at Kiel, Germany.

RECENT ADVANCES IN PLANT VIROLOGY

Edited by: Carole Caranta, Miguel A. Aranda, Mark

Tepfer and J.J. Lopez-Moya

ISBN: 978-1-904455-75-2

Publisher: Caister Academic Press

Publication Date: February 2011

Cover: Hardback

More info: <http://www.horizonpress.com/plant-virology>

ROOT GENOMICS

Costa de Oliveira, Antonio; Varshney, Rajeev K
1st Edition., 2011, XIV, 318 p., Hardcover.

With the predicted increase of the human population and the subsequent need for larger food supplies, root health in crop plants could play a major role in providing sustainable highly productive crops that can cope with global climate changes. While the essentiality of roots and their relation to plant performance is broadly recognized, less is known about the role of roots in plant growth and development. "Root Genomics" examines how various new genomic technologies are rapidly being applied to the study of roots, including high-throughput sequencing and genotyping, TILLING, transcription factor analysis, comparative genomics, gene discovery and transcriptional profiling, post-transcriptional events regulating microRNAs, proteome profiling and the use of molecular markers such as SSRs, DArTs, and SNPs for QTL analyses and the identification of superior genes/alleles. The book also covers topics such as the molecular breeding of crops in problematic soils and the responses of root systems to a variety of stresses.

THE RESTLESS PLANT

by Dov Koller,

edited by Elizabeth Van Volkenburgh
Harvard University Press (January 2011)

Plants, so predictable, stay where they are. And yet, like all living things, they also move: they grow, adapt, shed leaves and bark, spread roots and branches, snare pollinators, and reward cultivators. This book, the first to thoroughly explore the subject since Darwin's 1881 treatise on movements in plants, is a comprehensive, up-to-date account of the mechanisms and the adaptive values that move plants.

Drawing on examples across the spectrum of plant families-including mosses, ferns, conifers, and flowering plants-the author opens a window on how plants move: within cells, as individual cells, and via organs. Opening with an explanation of how cellular motors work and how cells manage to move organs, Dov Koller considers the movement of roots, tubers, rhizomes, and other plant parts underground, as well as the more familiar stems, leaves, and flowers.

Throughout, Koller presents information at the subcellular and cellular levels, including the roles of receptors, signaling pathways, hormones, and physiological responses in motor function. He also discusses the adaptive significance of movements. His book exposes the workings of a world little understood and often overlooked, the world of restless plants and the movements by which they accomplish the necessary functions of their lives.

WHAT'S NEW ABOUT CROP PLANTS: NOVEL DISCOVERIES OF THE 21ST CENTURY

U. S. Gupta, Retired Adj Professor, University of Georgia, Athens, USA

Price: \$179.95

Cat. #: N10329

ISBN: 9781578086993

Publication Date: February 03, 2011

Binding: Hardback

CRC Press

<http://www.crcpress.com/product/isbn/9781578086993>