



FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY



FESPB Newsletter



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Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

Letter from the FESPB Secretary General

Dear FESPB Members, dear colleagues,

Another year is over! The new year will be marked by the Plant Biology2012 Congress in Freiburg, jointly organized by FESPB & EPSO (www.plant-biology-congress2012.de).

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 (see attachments).

Furthermore, changes will take place in the FESPB Executive Committee. Next July, I intend to step down after having served for 11 years in various posts (President (2000-2002), Chair of Grants Committee (2002-2004) and Secretary General (2004-now). Also, the Treasurer, Prof. Karl-Josef Dietz will step down. Thus, new colleagues are invited to show their interest for these posts. More information will be sent to you in the near future.

On behalf of the FESPB Executive Committee, I wish to you and your families all the best for the Season, and a new year full of health, prosperity, hope and joy.

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



EPSO presents: Fascination of Plants Day *EPSO Newsletter. June 2011*

The European Plant Science Organisation (EPSO) will arrange a special attribute to plants with the *Fascination of Plants Day* that is scheduled for 18 May 2012. The event will be a Europe-wide initiative to bring back understanding and appreciation of plant science and plant research to the public. All participating plant science and research institutions - including plant breeding companies, farmers associations etc. - are invited to contribute with open lab days, public discussions or press conferences with

selected scientists, farmers, plant breeders, environmentalists, ecologists etc.

The many different approaches by which this can be achieved were then presented during the congress, both in detail and in a bigger perspective. Topics included photosynthesis,

large scale genomics and proteomics, cell and organelle biology, cell wall biosynthesis and degradation and pathogen defence. Taken together the data presented complemented each other well and pointed towards the power and possibilities of a better understanding of plant biology.

The event is open to all members of EPSO as well as non-members, but EPSO will make sure that the *Fascination of Plants Day* will be concertedly announced to the press and news media in the respective European countries.

Information about the events will be made available through press releases and press kits to both nation-wide and local newspapers and TV/radio stations, and even Facebook will be used to spread the message. In order to make the initiative as

appealing as possible, an entertainer who is very well known to the European public will become patron of the *Fascination of Plants Day*. Moreover, a professional designer will make a logo and a corporate design that will be consistently used by all participating institutions.

EPSO encourages everybody to participate in the preparation for the initiative by becoming members of the organizing working group. At present it consists of 9 members from 4 countries, but it is the intention to have at least one contact person from each European Country, Australia, New Zealand and possibly Japan. Their job will be to coordinate the events and to translate all information about the *Fascination of Plants Day* into the local language. If you are interested to become member of the working group or have any suggestions or questions, please do not hesitate to contact the coordinator of *Fascination of Plants Day 2012* Dr. Jan-Wolfhard Kellmann from Max Planck Institute for Chemical Ecology in Jena, Germany.

Scientists take a giant step for people -- with plants!

Source: *e! Science News*. July 29, 2011

Science usually progresses in small steps, but on rare occasions, a new combination of research expertise and cutting-edge technology produces a 'great leap forward.' An international team of scientists, whose senior investigators include Salk Institute plant

biologist Joseph Ecker, report one such leap in the July 29, 2011 issue of *Science*. They describe their mapping and early analyses of thousands of protein-to-protein interactions within the cells of *Arabidopsis thaliana* -a variety of mustard plant that is to plant biology what the lab mouse is to human biology. "With this one study we managed to double the plant protein-interaction data that are available to scientists," says Ecker, a professor in the Plant Molecular and Cellular Biology Laboratory. "These data along with data from future 'interactome' mapping studies like this one should enable biologists to make agricultural plants more resistant to drought and diseases, more nutritious, and generally more useful to mankind."

The four-year project was funded by an \$8 million National Science Foundation grant, and was headed by Marc Vidal, Pascal Braun, David Hill and colleagues at the Dana Farber Cancer Institute in Boston; and Ecker at the Salk Institute. "It was a natural collaboration," says Vidal, "because Joe and his colleagues at the Salk Institute had already sequenced the *Arabidopsis* genome and had cloned many of the protein-coding genes, whereas on our side at the Dana Farber Institute we had experience in making these protein interaction maps for other organisms such as yeast."

In the initial stages of the project, members of Ecker's lab led by research technician Mary Galli converted most of their accumulated library of *Arabidopsis* protein-coding gene clones into a form useful for protein-interaction tests. "For this project, over 10,000 'open reading frame' clones were converted and sequence verified in preparation for protein-interaction screening," says Galli. Vidal, Braun, Hill and their colleagues systematically ran these open reading frames through a high quality protein-interaction screening process, based on a test known as the yeast two-hybrid screen. Out of more than forty million possible pair combinations, they found a total of 6,205 *Arabidopsis* protein- protein interactions, involving 2,774 individual

proteins. The researchers confirmed the high quality of these data, for example by showing their overlap with protein interaction data from past studies.

The new map of 6,205 protein partnerships represents only about two percent of the full protein-protein "interactome" for Arabidopsis, since the screening test covered only a third of all Arabidopsis proteins, and wasn't sensitive enough to detect many weaker protein interactions. "There will be larger maps after this one," says Ecker.

Even as a preliminary step, though, the new map is clearly useful. The researchers were able to sort the protein interaction pairs they found into functional groups, revealing networks and "communities" of proteins that work together. "There had been very little information, for example, on how plant hormone signaling pathways communicate with one another," says Ecker. "But in this study we were able to find a number of intriguing links between these pathways."

A further analysis of their map provided new insight into plant evolution. Ecker and colleagues Arabidopsis genome data, reported a decade ago, had revealed that plants randomly duplicate their genes to a much greater extent than animals do. These gene duplication events apparently give plants some of the genetic versatility they need to stay adapted to shifting environments. In this study, the researchers found 1900 pairs of their mapped proteins that appeared to be the products of ancient gene-duplication events.

Using advanced genomic dating techniques, the researchers were able to gauge the span of time since each of these gene-duplication events - the longest span being 700 million years - and compare it with the changes in the two proteins' interaction partners. "This provides a measure of how evolution has rewired the functions of these proteins," says Vidal. "Our large, high-quality dataset and the naturally high frequency of these gene duplications in Arabidopsis allowed us to make such an analysis for the first time."

The researchers found evidence that the Arabidopsis protein partnerships tend to change quickly after the duplication event, then more slowly as the duplicated gene settles into its new function and is held there by evolutionary pressure. "Even though the divergence of these proteins' amino-acid sequences may continue, the divergence in terms of their respective partners slows drastically after a rapid initial change, which we hadn't expected to see," Vidal says.

In the July 29 issue of Science researchers from the Arabidopsis interactome mapping study reported yet another demonstration of the usefulness of their approach. Led by Jeffery L. Dangl of the University of North Carolina at Chapel Hill, they examined Arabidopsis protein interactions with the bacterium *Pseudomonas syringae* (Psy) and a fungus-like microbe called *Hyaloperonospora arabidopsidis* (Hpa). "Even though these two pathogens are separated by about a billion years of evolution, it turns out that the 'effector' proteins they use to subvert Arabidopsis cells during infection are both targeted against the same set of highly connected Arabidopsis proteins," says Ecker. "We looked at some of these targeted Arabidopsis proteins and found evidence that they serve as 'hubs' or control points for the plant immune system and related systems."

Ecker and his colleagues hope that these studies mark the start of a period of rapid advancement in understanding plant biology, and in putting that knowledge to use for human benefit. "This starts to give us a big, systems-level picture of how Arabidopsis works, and much of that systems-level picture is going to be relevant to - and guide further research on - other plant species, including those used in human agriculture and even pharmaceuticals," Ecker says.

1st large-scale map of a plant's protein network addresses evolution, disease process

Source: e! Science News. July 29, 2011

The eon-spanning clock of evolution – the millions of years that generally pass before organisms acquire new traits – belies a constant ferment in the chambers and channels of cells, as changes in genes and proteins have subtle ripple effects throughout an organism. In a study in the July 29 issue of *Science*, scientists at Dana-Farber Cancer Institute's Center for Cancer Systems Biology and an international team of colleagues capture the first evidence of the evolutionary process within networks of plant proteins. In a companion article, the investigators use their new map of these networks to uncover how microbes like bacteria and fungi undermine plants' defenses against disease. The microbes accomplish this by disrupting a relatively small set of "virtuoso" proteins that play a variety of different roles within the cell.

Together, these findings promise not only to propel crop-improvement and anti-blight efforts, but also – because human diseases involve disturbances in protein networks as well – increase the understanding of a variety of human health disorders, including cancer, the authors state.

"Although these papers focus on the interactions of proteins in plants, they have implications for what occurs in animal – and human – cells as well," says Dana-Farber's Pascal Braun, PhD, who had a leading role in both studies. "The central role of protein interactions in all of life suggests that our findings hold important lessons for the study of health and disease in humans."

The model for the two studies was *Arabidopsis thaliana*, a small, gangly plant with prim white flowers that would likely be considered a weed if it appeared in someone's front yard, but which is a favorite subject of plant biology because it germinates rapidly and has a relatively simple genome of 27,000 genes. Despite decades of research involving the plant, however, scientists have yet to determine the roles of more than 60 percent of those genes, Braun remarks.

To gain the first inklings of those roles, investigators used genetic blueprints to produce about 8,000 of the proteins normally made by the plant's cells. They then mixed each of those proteins with each of the approximately 7,999 others to see which interact. (When two proteins interact, they bind together or modify each other to carry out a specific biological function, such as sending signals from the exterior of the cell to the interior, or escorting other proteins through the cell.)

The experiment yielded a map of 6,200 interactions between 2,700 proteins – far more than had been shown in any previous map of the plant's interactome (its collection of protein-protein interactions). Graphing the interactions in network form revealed that some proteins interact with a large number of other proteins, while most interact with only a few. (Interestingly, the World Wide Web and social networks such as Facebook show the same type of network structure, in which a relatively small number of pages attract a disproportionately large number of visitors.)

The investigators used a newly developed mathematical algorithm to scour the map for "communities," clusters of densely interconnected proteins that are likely to function together. They identified 26 such communities, many of which correspond to known processes but contain new proteins, while the function of other communities will need to be investigated. Knowing which genes work together offers clues to their roles within the cell.

Lastly, the investigators explored whether the interactome map could be used to answer a basic question in biology: Does natural selection – the evolutionary process by which certain traits "win out" over others by increasing an organism's likelihood of survival – operate at the level of protein networks?

Evolution is thought to begin when cells duplicate their DNA prior to dividing. Imperfections in the newly copied genes give rise to slightly altered proteins which, in combination with other

proteins, gradually produce novel traits in an organism. If those traits – larger leaves, for example, or longer roots – give the organism an edge in the struggle for survival, its offspring are likely to inherit and retain those advantages. Because of the limited scope of most previous interactome maps, it has been difficult for scientists to trace the influence of gene duplication on protein-protein interactions.

"The proportion of near-duplicate genes is much higher in Arabidopsis than in many non-plant species, making it ideal for this kind of research," Braun remarks. "As novel proteins emerge as a result of gene alteration, those proteins produce a rewiring of the plant's protein networks," much as the arrival of a new tenant changes the lines of communication among residents of an apartment building.

When a novel protein first appears, the rewiring happens rapidly, as protein networks hasten to adapt to the new entrant. "Over time, these novel proteins assume new functions and become more critical for the plant's survival," Braun notes. "Evolutionary pressure tightens and the new proteins become fixed parts of the plant's operating machinery." The rewiring that occurred so quickly at first gradually tapers off as the interaction networks stabilize.

"In analyzing our interactome map of Arabidopsis, we found strong evidence of this rapid-then-slow process over the hundreds of millions of years of the plant's evolution," says Braun. "It provides the first-ever empirical evidence of evolution acting on protein networks."

For the second paper, researchers used the interactome map to explore how certain bacteria and fungi cause disease in plants by subverting their immune system. Plants respond to infection by directing specialized proteins at the causative agent, be it viral, fungal, or bacterial. The disease agents, known as pathogens, respond by releasing virulence effector proteins that subdue the plant's defenses.

To bring the details of this process to light, investigators mixed effector

proteins from a fungus and bacteria with thousands of proteins from Arabidopsis to see which would interact. Some of the Arabidopsis proteins are involved in the plant's immune system and some are not.

"We thought that mapping the interactions would enable us to identify the immune system proteins that are disabled by binding to the effector proteins," Braun recounts. "To our surprise, we found that the effectors bind to a small number of non-immune system proteins. These non-immune proteins tend to be highly connected; that is, they interact with a large number of other proteins and are therefore involved in a wide array of plant functions."

All of this points to the dexterity and sophistication of pathogens' attack on plants: instead of targeting proteins directly involved in the immune system, pathogens exploit other, highly linked proteins that control much of what happens within the cells of the organism.

"This suggests that the immune system is highly integrated with the rest of the plant cell – like having a guard at each point of activity within the cell," Braun remarks. "The system is much less compartmentalized than we'd thought."

"This work will help scientists derive general rules of how cells defend themselves from microbial infection, and how pathogens manipulate that system to their advantage. Ultimately, this may suggest new techniques for improving immune system functioning in plants."

Genomewide mapping reveals developmental and environmental impacts

Source: UC Davis. August 16, 2011

Complex traits that help plants adapt to environmental challenges are likely influenced by variations in thousands of genes that are affected by both the plant's growth and the external environment, reports a team of researchers at the University of California, Davis.

The findings were revealed by a genomewide association mapping of the defense metabolism in *Arabidopsis thaliana*, a common research plant. The researchers, led by UC Davis plant scientist Daniel Kliebenstein, report the study results today, Aug. 16, in the online journal PLoS Genetics.

In the study, Kliebenstein and colleagues measured glucosinolates (GSL), a key class of compounds that the plant produces to protect against insect attacks and disease-causing organisms. The researchers measured the compound in two developmental stages — at two days and 35 days after germination. They also sampled plant tissues that were either treated or not treated with silver nitrate, mimicking environmental damage caused by a pest.

"We showed that both external and internal environments altered the identified genes so significantly that using plant tissues from different developmental stages, or that were treated with the silver nitrate, led to the identification of very different gene sets for particular traits," Kliebenstein said.

The group noted that the developmental stage of the plant had three times as much influence as the environment on the genes they identified.

Because the genomewide association mapping identified so many different genes as potentially responsible for traits associated with GSL metabolism, the researchers developed a new process for winnowing candidate genes. The process analyzes overlapping datasets of genomic information to filter out true-positive gene identifications.

Genomewide association mapping involves rapidly scanning markers across entire genomes to find genetic variations associated with a particular trait, condition or disease. The approach has been used to study complex human diseases such as asthma and diabetes.

The researchers hope that the new two-pronged approach to genomewide association can be applied to any plant and animal species.

Plant proteins to help solve global challenges

Source: The University of Western Australia, 17 August 2011.

A protein database that will serve as a vital research tool for investigating how plants respond to environmental change is to be developed under a partnership between The University of Western Australia and Agilent Technologies.

The UWA-based Australian Research Centre (ARC) Centre of Excellence in Plant Energy Biology will use Agilent's informatics systems in its research to build a unique plant protein monitoring database.

The database will be shared with a global community of interested researchers and used to address future challenges such as how to feed an ever-increasing population, and how to get plants to grow in arid, cold or high salt environments.

Plant Energy Biology Chief Investigator, Winthrop Professor Harvey Millar, said the collaboration gave researchers access to technology that would allow them to revolutionise the way that scientists interrogate their data.

"We aim to produce an electronic notepad for lab results, where data are accessible for colleagues in the lab next door, and collaborators across the nation and around the world," he said. "Results are automatically updated into relevant databases and cross-matched to find previously unknown interactions. This will save time and also guarantee the integrity of data, so scientists can get on with the important tasks of discovery and innovation."

Mr Rod Minett, General Manager, Life Sciences South Asia Pacific and Korea, Agilent Technologies said: "Data mining and management are gaining importance in today's collaborative life science research environment.

"This announcement with UWA marks the first time a database for plant protein monitoring is created, and to have this creation using Agilent HPLC Chip-LC instrument along with our Electronic Lab

Notebook (ELN) software and our Enterprise Content Manager (ECM) is yet another novel approach to addressing a niche in the scientific community."

In this project, the UWA team will modify Agilent software (Agilent OpenLab ELN and ECM) workflows to develop a research lab-specific electronic environment.

The data will be used to search for unknown links between different plant species and their responses to drought, cold, salinity and low nutrition. It will also provide a pipeline for targeted analysis of defined sets of plant proteins to answer specific research questions.

"Gone are the days when protein analysis is all about 'shotgun searches' for whatever can be found in a sample. The future will see targeted analysis of defined proteins using the power of peptide mass spectrometry," said Plant Energy Biology Research Assistant Professor Nicolas Taylor.

Molecular Chaperones Traffic Signaling Proteins Between Cells in Plant Stem-Cell Maintenance Pathway

Source: ScienceDaily. Aug. 27, 2011.

Like all living things, plants depend for their growth and sustenance on elaborate signaling networks to maintain stem cells, cells that have an almost magical regenerative capacity. The signals sent through these networks convey an incredible diversity of instructions, which make it possible for plants to follow genetic and cellular programs regulating growth, shape, and energy production and consumption.

A team of plant biologists at Cold Spring Harbor Laboratory (CSHL) led by Professor David Jackson has pioneered the use of genetics to discover how plants cells communicate certain instructions from one to another via tiny channels called plasmodesmata (PD). Having previously demonstrated that a protein called KNOTTED1 (KN1) traffics selectively through these channels, the team has now discovered that proteins called chaperonins are an indispensable

factor in enabling this trafficking to occur.

The scientists have also demonstrated the importance of this specific signaling pathway, showing that it is needed to maintain stem cells, and suggest it is probably conserved broadly, in diverse species. The findings appear Aug. 26 in the journal *Science*.

Plasmodesmata are microscopic channels traversing plant cell walls that connect adjacent cells. This is where their resemblance to, say, pipes connecting your water tank to your shower ceases, however, because PDs are selective. Only certain signaling molecules, or molecular complexes, can enter these channels and emerge properly on the far side.

The discovery that trafficking cannot occur in a PD-mobile protein such as KN1 unless it is facilitated by chaperonins, opened the question of what the latter actually do in the process. Chaperonins are protein complexes well known to assist in the folding of newly manufactured amino-acid chains into proteins. Like intricate pieces of origami, nascent proteins become functional only if they are twisted and folded into very specific conformations. Since changes in protein function are related to changes in structure, it is not surprising that chaperonins, members of a larger class of folding machines called chaperones, are ubiquitous in living things.

Once Jackson's team had proven the necessity of chaperonins in KN1 trafficking, they set their sights on revealing the "how" and "why" of the relationship. In a series of experiments involving maize and *Arabidopsis*, a mustard plant used widely as a model for genetics research, they confirmed, first, that the entire chaperonin machinery -- a protein mega-complex consisting of eight segments, or subunits - is involved in cell-to-cell trafficking of KN1.

"We could then ask questions about the mechanism involved, and about the functional importance of this trafficking to the plants," says Jackson. Through an

ingenious process of elimination, he and his colleagues performed experiments showing that a portion of the chaperonin complex, called CCT8, had to be present in the "destination" cell if KN1 trafficking was to occur normally. "We inferred from our results that the chaperonin performs its role in the trafficking by refolding KN1 proteins in the destination cell. In other words, KN1 travels through the channel in a partly unfolded state."

Even more important, the team concluded that by selectively transporting KN1 and other "mobile signals" using this mechanism, plants are able to establish and maintain populations of stem cells. As Jackson's prior work has shown, this occurs, for instance, in meristems, the stem cell-rich tips of plants where new growth takes place.

Why do the signals that maintain stem cells need to be mobile? "Development is all about communication," Jackson explains. "Cells talk to each other, among other things, to influence one another. We hypothesize that the trafficking of signals like KN1 could serve to establish protein concentration gradients, an important part of the language plants use to develop and grow.

"You can think of molecules like KN1 as the 'words' in that language. The kind of information that is carried by concentrations and gradients are the rough equivalent of how the words are spoken, the intonation and emphasis."

Location-specific concentrations would correspond with specific developmental cues. Alternatively, Jackson speculates, "trafficking could be a backup mechanism to maintain the stem cell program, just as an extra hard drive backs up your computer programs and files." The team is already exploring these possibilities in its current work.

Arabidopsis: Thanks to Its Flexible Genome, the Plant Can Adapt to Various Environmental Conditions

Source: *ScienceDaily*. Aug. 28, 2011.

People can develop new technologies and animals may migrate to other regions. However, plants are tied to their location. Nevertheless, they have found ways to ensure their survival. This is the case for the plant *Arabidopsis thaliana*, which is found throughout the entire northern hemisphere. But how does this small, inconspicuous plant deal with all these different extremes?

In order to discover the whole-genome sequence variation, the 1001 Genomes Project was launched in 2008, with eleven research institutes participating worldwide. By investigating the genetic material of about one hundred strains of this plant from different geographical regions, researchers found a huge number of variations: in addition to millions of small differences that lead to a diversity of molecular gene products, they found hundreds of genes that are missing in some strains or have extra copies in others. It is probably this great flexibility within the genetic material that makes this plant particularly adaptable. In the medium term the complete catalog of the genome and gene product variation of a species can be applied to modern plant breeding.

Which genes and gene variants allow different individuals of one species to thrive under very different environmental conditions? The model plant for genetics, the thale cress, *Arabidopsis thaliana*, is especially well suited for the investigation of this question. It can deal with heat and drought in northern Africa as well as with cold in the central Asian highlands and temperate zones in Europe. Depending on the region it may display extensive foliage or appear small and fragile, yet it is always the same species. The answer lies without doubt in the diversity of its genetic material. Detlef Weigel and Karsten Borgwardt from the Max Planck Institute for Developmental Biology, Gunnar Rättsch from the Friedrich Miescher Laboratory in Tübingen, and Karl Schmid of the University of Hohenheim have, together with an international team, sequenced and analyzed the genome of different *Arabidopsis* strains from all over Europe

and Asia. To reveal the effect of geographic distance on the genes they selected plants from strains growing locally -- in the Swabian Neckar Valley -- as well as plants growing at opposite ends of the plant's distribution area, such as North Africa or Central Asia.

By sequencing nearly 100 genomes of different strains, the scientists hope to obtain a fundamental scientific understanding of evolution. The resulting information should pave the way for a new era of genetics in which alleles underpinning phenotypic diversity across the entire genome and the entire species can be identified. The scientists have found that thousands of proteins differ in their structure and function in the different Arabidopsis strains. In addition, they found several thousand cases of extra copies of genes, gene loss, as well as new genes that were previously only found in other plant species. "Our results show very impressively just how pronounced the genetic variability is," says Jun Cao from the Max Planck Institute for Developmental Biology and first author of one of the projects. Karl Schmid of the University of Hohenheim adds: "Adaptation through new mutations is very rare. More important is the recombination of already existing variants. With the information from more than a hundred genomes, not only can we make statements about these hundred individuals, but have thus laid the foundations to predict the genetic potential which could be realized by crossing particular individuals."

The geneticists working with Detlef Weigel, Karsten Borgwardt and Karl Schmid also found that the level of genetic variation differs widely between different regions. The researchers found the greatest genetic diversity in the Iberian Peninsula, where the plants have existed for a very long time. In Central Asia, which was only colonized after the last ice age, the Arabidopsis plants have relatively uniform genomes. Moreover, these populations have an above-average number of mutations that cause disadvantages for the plant, since protein functions are changed.

Normally, natural selection removes these mutations over time, but in young emigrant populations they are enriched through cases of random evolution. "Figuring out how the plants and their genomes adapt to their environment is like a puzzle," says Jun Cao. "We need to collect all the pieces, before we can fit them together." The scientists have managed to create a nearly complete catalog of the genome variation of a species.

But how do these variations interact at the molecular level and what changes do they cause in the gene products? The computational biologist Gunnar Rättsch from the Friedrich Miescher Laboratory examined these questions in detail in a second study together with his international colleagues. They analyzed 19 strains of Arabidopsis with a particularly large genetic variability. These 19 individuals formed the basis of an artificial population of several hundred strains, created through multiple crosses such that different genome segments were shuffled systematically. The resulting individuals are ideally suited for examining gene interactions.

The scientists studied the genome segments using novel analysis methods of analysis and discovered in detail how DNA is read in detail and how the intermediate stage of protein production, the RNA, is produced. The researchers obtained detailed insight into the altered gene products arising from the various genomic variants. Depending on the genomic context some gene segments were either shut down or reactivated. "We can find a surprising number of changes affecting a single gene. However, they are often compensated for and therefore often have no significant effect on the gene products," says Gunnar Rättsch about the new results. The concepts, methods and platforms developed based on the genomic variation of Arabidopsis thaliana can also be used to study crop plants and for fast and accurate mapping of desirable characteristics. In addition, researchers can transfer this

understanding about the influence of variation on gene products and their interactions to studies of the human genome.

These new projects should be viewed in the context of the 1001 Genomes Project, which was launched in 2008 at the Max Planck Institute for Developmental Biology and is being implemented through many individual projects in cooperation with ten other institutions worldwide. The aim is to analyze and compare the genes of 1001 different *Arabidopsis* strains. The goal of this large-scale project is to obtain fundamental insights into evolution, genetics and molecular mechanisms. Almost 500 different genomes have already been sequenced and analyzed at the different institutions. The data is being fed into a public database, which can be accessed not only by participants of the projects, but by all interested scientists.

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Organic food: Is it really good for you?

Gorm Palmgren. SPPS Newsletter. September 2011.

With an estimated global market of \$57 billion and a market share of approximately 4%, organic food is highly valued among consumers worldwide. Even facing a financial crisis and a price premium of 10-40%, consumption of organic food show an annual growth of 8%, which is about the double of conventionally produced food. The figures vary considerably between products and countries - e.g. the organic share of fruits and vegetables are almost an order of magnitude higher than on meats, and the same relative difference holds true between individual EU member states - but the general picture is clear: organic is hot!

The consumers' passion for organic food is reflected in a Belgian survey of consumer perception from 2009. It demonstrated that the vast majority of consumers believe that organic food is healthier, more nutritious and contains less harmful microbes and mycotoxins than conventional food - and this overall trend is independent of education, age, gender or how much organic food the responder actually bought.

Paradoxically, however, this unanimous praise of organic food is not based on scientific knowledge. Only limited research has been carried out in this area, but the results seem to indicate that while organically grown crops contain more secondary metabolites,

they might not always be to the benefit of consumers.

Unlike primary metabolites - e.g. amino acids and most carbohydrates and lipids - that are essential to life, plants contain huge amounts of secondary metabolites. As the name implies, they serve to meet the plant's secondary requirements and empower it to survive competition, provide defence and facilitate reproduction. Without them, the plant is not immediately threatened but in the long term it will eventually fare worse. At least 100,000 different secondary metabolites from plants have been identified to date and far more are believed to exist.

Ranging from disease preventing antioxidants like flavonoids over powerful narcotics like cocaine to lethal toxins like ricin from castor bean, the secondary metabolites come in many flavors - both good and bad. Their natural purpose can be to serve as chemical warfare against insects and other herbivores, as colorful shields that protect from sunlight or as irresistible scents that attract pollinators. In many cases they are extremely specialized in their action, and e.g. the powerful heart drug digitoxin from foxglove (*Digitalis*) is a highly specific sodium-potassium ATPase inhibitor.

Since many of the secondary metabolites are defense related chemicals induced by biotic and abiotic stress, their concentration in the plants depends on growing conditions. This has led several scientists to look for chemical differences between crops grown under conventional and organic regimes. The two crop management systems differ in terms of the fertilisers and plant protection methods used, and, generally speaking, the better the plant is taken care of, the less secondary metabolites it needs for its own protection. In a recent review, a meta-analysis of published comparisons suggests that organically grown crops have a 12% higher content of secondary metabolites. Most of the difference stems from a higher content of defence related chemicals (amounting to 16%), while antioxidants

like carotenoids and vitamin C only amount to a 6% increase.

It is, however, difficult to translate these chemical differences into health effects, since the secondary metabolites can have both beneficial and harmful effects. A few studies have compared the health effects of organic vs. conventional feed in laboratory animals. Though it is difficult to draw conclusions from the experiments, since they are not systematic and only look to short term effects, there seems to be some indication that organic feed activates the immune system and improves reproductive ability. One difference that seems to be consistently found in most analysis, however, is a lower protein content in organic food, and this can obviously have a negative nutritional effect.

The lower protein content in organic vs. conventional crops is believed to be the reason why a recent experiment found that birds prefer conventional wheat over its organic counterpart. Both wild garden birds and captive birds consumed more conventional than organic wheat when given free choice, but interestingly it took them about one week to distinguish between the two food types. The authors proposed that the birds need some time to 'learn' which is the better food, and this time lag might also explain why other studies have shown contradictory results.

The authors also tested for the presence of the mycotoxin DON in the two kinds of wheat. DON is a potent toxin produced by *Fusarium* spp. fungi, and it is known that both birds and mammals try to avoid food containing the mycotoxin. In this experiment, DON content varied considerably between samples (sometimes there was more mycotoxin in conventional than organic wheat and sometimes vice versa) and it did not correlate with consumption.

It has been suggested that since fungicides are not used in organic farming, the organic crops might be more heavily infested with mycotoxin producing fungi and this has prompted several researchers to look for the

presence of mycotoxins in crops grown under conventional and organic management. A Korean study from 2011 showed that among 5 mycotoxins only one, nivalenol, was present at significantly higher concentrations in organic vs. conventional rice. A similar Polish study from 2009 on wheat showed that the mycotoxins DON and T-2 was consistently present in 13 organically grown cultivars albeit in low concentrations, while the same cultivars grown by conventional means contained high levels of one of the mycotoxins in 4 of the cultivars and none or very little in the rest.

To sum up, it is assumed that organically grown crops contain higher concentrations of plant secondary metabolites that might be both more beneficial and harmful, but at the present time it can not be concluded what net effect this can have on human health. It should be kept in mind, however, that organic crops contain fewer residual amounts of pesticides and that they at least in this respect can be said to be more healthy than conventional crops.

DNA methylation is a marker of flowering

Reference: Meijon *et al.* *Physiologia Plantarum* 143: 82. 2011.

Induction of flowering in azalea (*Rhododendron* spp.) is associated with changes in DNA methylation levels and these epigenetic alterations seem to be markers of floral bud development. This was shown by Maria Jesus Canal from Universidad de Oviedo in Spain in an experiment where manipulations of photoperiod and temperature were used to promote flowering. Within days after the shift from long days to short days there was a substantial decrease in overall DNA methylation, eventually amounting to almost 50%. Subsequently, however, methylation increased sharply and climbed to a level approximately 25% above the initial value. This pattern of fluctuations in the DNA methylation level followed floral development and was consistent between different

cultivars and plants grown under various flower induction conditions. The authors suggest that measurements of DNA methylation can be used as a marker of flower development in commercial production of azalea and probably also other ornamentals.

A special pair of phytohormones controls excitability, slow closure, and external stomach formation in the Venus flytrap

Reference: Escalante-Pérez *et al.* *PNAS* September 13, 2011 vol. 108 no. 37 15492-15497

Venus flytrap's leaves can catch an insect in a fraction of a second. Since the time of Charles Darwin, scientists have struggled to understand the sensory biology and biomechanics of this plant, *Dionaea muscipula*. Here we show that insect-capture of *Dionaea* traps is modulated by the phytohormone abscisic acid (ABA) and jasmonates. Water-stressed *Dionaea*, as well as those exposed to the drought-stress hormone ABA, are less sensitive to mechanical stimulation. In contrast, application of 12-oxo-phytodienoic acid (OPDA), a precursor of the phytohormone jasmonic acid (JA), the methyl ester of JA (Me-JA), and coronatine (COR), the molecular mimic of the isoleucine conjugate of JA (JA-Ile), triggers secretion of digestive enzymes without any preceding mechanical stimulus. Such secretion is accompanied by slow trap closure. Under physiological conditions, insect-capture is associated with Ca²⁺ signaling and a rise in OPDA. Apparently, jasmonates bypass haptoelectric processes associated with trap closure. However, ABA does not affect OPDA-dependent gland activity. Therefore, signals for trap movement and secretion seem to involve separate pathways. Jasmonates are systemically active because application to a single trap induces secretion and slow closure not only in the given trap but also in all others. Furthermore, formerly touch-insensitive trap sectors are converted into mechanosensitive ones. These findings demonstrate that prey-catching

Dionaea combines plant-specific signaling pathways, involving OPDA and ABA with a rapidly acting trigger, which uses ion channels, action potentials, and Ca²⁺ signals.

**Plant RNAs Found in Mammals
MicroRNAs from plants accumulate in mammalian blood and tissues, where they can regulate gene expression.**

By Cristina Luiggi. September 20, 2011. The Scientist.

MicroRNAs from common plant crops such as rice and cabbage can be found in the blood and tissues of humans and other plant-eating mammals, according to a study published today in *Cell Research*. One microRNA in particular, MIR168a, which is highly enriched in rice, was found to inhibit a protein that helps remove low-density lipoprotein (LDL) from the blood, suggesting that microRNAs can influence gene expression across kingdoms.

"This is a very exciting piece of work that suggests that the food we eat may directly regulate gene expression in our bodies," said Clay Marsh, Director of the Center for Personalized Health Care at the Ohio State University College of Medicine who researches microRNA expression in human blood but who was not involved in the study.

MicroRNAs are, as the name implies, very short RNA sequences (approximately 22 nucleotides in length) discovered in the early 1990s. They are known to modulate gene expression by binding to mRNA, often resulting in inhibition. With the recent discovery that microRNAs circulate the blood by hitching a ride in small membrane-encased particles known as microvesicles (see our July 2011 feature on microvesicles, "Exosome Explosion"), there has been a surge of interest in microRNAs as a novel class of biomarkers for a variety of diseases.

Chen-Yu Zhang, a molecular biologist at Nanjing University in China, was studying the role of circulating microRNAs in health and disease when he discovered that microRNAs are present in other bodily fluids such as milk. This gave him

the "crazy idea" that exogenous microRNAs, such as those ingested through the consumption of milk, could also be found circulating in the serum of mammals, he recalled.

To test his hypothesis, Zhang and his team of researchers sequenced the blood microRNAs of 31 healthy Chinese subjects and searched for the presence of plant microRNAs. Because plant microRNAs are structurally different from those of mammals, they react differently to oxidizing agents, and the researchers were able to differentiate the two by treating them with sodium periodate, which oxidizes mammal but not plant microRNAs.

To their surprise, they found about 40 types of plant microRNAs circulating in the subjects' blood—some of which were found in concentrations that were comparable to major endogenous human microRNAs.

The plant microRNAs with the highest concentrations were MIR156a and MIR168a, both of which are known to be enriched in rice and cruciferous vegetables such as cauliflower, cabbage, and broccoli. Furthermore, the researchers detected the two microRNAs in the blood, lungs, small intestine, and livers of mice, in variable concentrations that significantly increased after the mice were fed raw rice (although cooked rice was also shown to contain intact MIR168a).

Next, the researchers scoured sequence databases for putative target genes of MIR156a and MIR168a and found that MIR168a shared sequence complementarity with approximately 50 mammalian genes. The most highly conserved of these sequences across the animal kingdom was the exon 4 of the low-density lipoprotein receptor adapter protein 1 gene (LDLRAP1).

LDLRAP1 is highly expressed in the liver, where it interacts with the low-density lipoprotein receptor to help remove low-density lipoprotein (LDL), aka "bad" cholesterol, from the blood.

The researchers hypothesized that MIR168a could be taken up by the epithelial cells lining the gastrointestinal

tract, packaged into microvesicles, and secreted into the blood stream, where they can make their way to target organs. Once in the liver, MIR168a binds to LDLRAP1 mRNA, reducing the protein levels and ultimately impairing the removal of LDL from the blood.

To test this hypothesis in vitro, the researchers transfected synthetic MIR168a into a human epithelial cell line and collected the secreted microvesicles. When they added these microvesicles to a liver cell line called HepG2, they found that while it did not change the levels of LDLRAP1 mRNA, it did decrease the levels of the actual LDLRAP1 protein.

Likewise, the LDLRAP1 protein level decreased in the livers of live mice 3 to 7 days after eating fresh rice or being injected with synthetic MIR168a—significantly increasing LDL in the blood. When the researchers injected the mice with an RNA sequence that bound to and neutralized MIR168a, the protein and LDL levels returned to normal.

“This microRNA inhibits this protein and increased the plasma LDL levels,” Zhang said. With higher levels of circulating cholesterol, “it can possibly increase the risk of metabolic syndrome,” he added. But more importantly, this research points to a “new therapeutic strategy for the treatment of diseases,” based on the enhancement or inhibition of exogenous microRNAs.

Although the team has still a long way to go in elucidating the mechanisms by which plant microRNAs can regulate gene expression in humans, these initial results promise to increase the understanding of how specific ingredients in food can mediate health and disease, Marsh said.

Indeed, Zhang suspects that this is just one example of many. With time, “I’m confident other people will find more exogenous plant microRNAs that can pass through the GI tract and also have effects on the host physiology,” Zhang said.

Reference: L. Zhang, et. al., “Exogenous plant MIR168a specifically targets mammalian LDLRAP1: evidence of cross-

kingdom regulation by microRNA,” *Cell Research*, doi:10.1038/cr.2011.158, 2011.

Evolution, Tout de Suite

Epigenetic perturbations could jump-start heritable variation.

By Richard P. Grant. The Scientist. October 1, 2011.

A central tenet of evolution is that small changes in an organism’s genome can be passed on to subsequent generations. Generally, we accept that this happens through the DNA sequences: small, random mutations are inherited by offspring. Indeed, many inherited characteristics, such as fruit color, flower shape, body size, or the direction a snail’s shell whorls are encoded in genes, but they do not always obey the simple laws of Mendelian inheritance. While transposable elements, extragenomic DNA, and—as was the case for the hawkweed that tormented Gregor Mendel himself—parthenogenesis can explain some of these anomalies, recently the spotlight has fallen on another type of inheritance altogether—epigenetic modifications.

Frank Johannes at the University of Groningen in The Netherlands has been trying to understand the intricacies of epigenetic inheritance—specifically, how methylation of DNA bases can contribute to the inheritance of particular characteristics in *Arabidopsis*. “People are beginning to speculate,” he says. “ ‘ Wait a minute. What’s going on in nature? Does this contribute significantly to adaptation?’ ”

But it’s hard to tell in most natural populations whether inheritance is due to DNA sequence variation or epigenetic changes. “We cannot delineate these two causes very well,” Johannes says. So with his collaborator, Fabrice Roux at the University of Science and Technology in Lille, France, he has been studying a large population of *Arabidopsis* plants with disrupted methylation patterns. The plants were derived from two *Arabidopsis* parents

with essentially identical genomes, but with one having a mutated DDM1 DNA methylation gene. DDM1 is required for normal methylation—the conversion of cytosine, in cytosine-guanine pairs in the DNA, into 5-methylcytosine—and its mutation reduces genomic methylation by 70 percent.

Roux's team backcrossed the first generation offspring and selected progeny that were homozygous for the wild type DDM1 gene; in other words, with fully functional methylation machinery. They propagated the plants through a further six rounds of inbreeding, creating "epigenetic recombinant inbred lines" (epiRILs), which carried a mosaic of the parental epigenome. When they grew them in a common garden in northern France to subject the almost 6,000 plants to "realistic" ecological selection, they found that the epiRILs yielded plants with distinctly different phenotypes despite being effectively genetically identical.

The segregation and heritability of these traits—which included flowering time and plant height—mirrored those found in naturally divergent *Arabidopsis* populations, in which phenotypic variation represents adaptations to different environmental conditions. But natural populations have had thousands of years to generate these variations: the epiRILs managed to do it in just eight generations. Andrew Hudson at the University of Edinburgh says there is a clear implication that "DNA methylation and epigenetic changes are important in evolution."

Johannes explains that there are at least two processes that can influence the epigenome: point mutations in genes that control methylation such as DDM1 that create an additional layer of variation; and environmental impacts that can influence the methylation state, which can then be inherited. New variations of plants, perhaps better adapted to a change in environment, could therefore arise much more quickly than previously thought. Research in this area is "still correlative but nevertheless very interesting," Hudson says.

But epigenetic changes are not typically as stable as changes in DNA sequence. Some stretches of DNA do remain unmethylated for at least ten generations, Johannes says, but other sequences revert to their "wild type" methylation state due to random fluctuations, or reversion brought about by small RNAs that try to correct the defects. It may be that epigenetic changes could be reinforced by mutations in the DNA, making them stable and heritable in the conventional way. Indeed, some of the sequences affected by the DDM1 mutation are likely to be associated with the mobilization of transposable elements, which would result in immediate—and heritable—DNA sequence changes.

Another complication arises because some traits, particularly those associated with seed production, don't seem to dabble in epigenetic inheritance. Johannes speculates that there might be an "obscure epigenetic editing process going on" that repairs disadvantageous epigenetic states for crucial genes. "You can imagine," he says, that there's "some sort of rescue mechanism," particularly for gene networks that control a process as important as seed production.

In collaboration with Vincent Colot at the École Normale Supérieure, Paris, Johannes hopes to answer such questions by performing genome-wide measurements to establish exactly which genetic elements in the genome are affected by epigenetic perturbation. He already has measurements of genome-wide methylation from more than a hundred individual plants, and is performing what he thinks is the first genome-wide epigenetic linkage study—the epigenetic equivalent of genome-wide association studies of human disease. In parallel, he wants to mathematically model the epigenetic effects and incorporate them into population genetics models, to understand dynamic inheritance patterns that cannot be explained by purely Mendelian genetics.

Plants May Have the Genetic Flexibility to Respond to Climate Change

Source: *ScienceDaily*. Oct. 6, 2011

Plants may have the genetic flexibility to respond to climate change. In experiments with the common European plant *Arabidopsis thaliana*, a team of researchers led by Brown University scientists learned that climate is the agent that determines the suite of genes that gives the plant the best chance of surviving and reproducing throughout its natural range. The finding may unlock the molecular basis for other plants' adaptability to climate change. Results appear in *Science*.

In the face of climate change, animals have an advantage over plants: They can move. But a new study led by Brown University researchers shows that plants may have some tricks of their own.

In a paper published in *Science*, the research team identifies the genetic signature in the common European plant *Arabidopsis thaliana* that governs the plant's fitness -- its ability to survive and reproduce -- in different climates. The researchers further find that climate in large measure influences the suite of genes passed on to *Arabidopsis* to optimize its survival and reproduction. The set of genes determining fitness varies, the team reports, depending on the climate conditions in the plant's region -- cold, warm, dry, wet, or otherwise.

"This is the first study to show evolutionary adaptation for *Arabidopsis thaliana* on a broad geographical scale and to link it to molecular underpinnings," said Johanna Schmitt, director of the Environmental Change Initiative at Brown and an author on the paper. "Climate is the selective agent."

The researchers believe that by identifying the genetic signatures that mark *Arabidopsis*' response to changing climate, scientists may understand how climate may cause the re-engineering of the genetic profiles of other plants. "There is still evolutionary flexibility to help plants take one direction or another," said Alexandre Fournier-Level, a

postdoctoral researcher at Brown and the paper's first author. "It gives us good hope to see, yes, it's adapting."

"This was a truly massive undertaking, tracking more than 75,000 plants in the field, from near the arctic circle to the Mediterranean coast," said Amity Wilczek, a former postdoctoral researcher in Schmitt's lab now on the faculty at Deep Springs College. "Arabidopsis is an annual plant, so we could measure total lifetime success of an individual within a single year. We gathered plants from a variety of native climates and grew some of each in our four widely distributed European garden sites. We shipped our harvested plants back to Brown and began the laborious task of counting fruits on these plants. In the end, we were able to assemble a very large and comprehensive dataset that gives us new insight into what it takes for a plant to be successful in nature under a broad range of climate conditions."

The team then burrowed into the *Arabidopsis* genome to find the molecular mechanisms that might give the plant genetic flexibility to roll with climate punches. To identify variations in the genome among the regional representatives, the researchers carried out a genome-wide association study for survival and fruiting comprising more than 213,000 single-nucleotide polymorphisms. These SNPs, Fournier-Level explained, are like signposts pointing to areas in the genome where survival and reproduction may be emphasized and areas that show variations in the regional representatives' genetic makeup.

From the experiments, the team discovered that the SNPs that determined fitness for *Arabidopsis* in one region are surprisingly different from those associated with the plant's fitness in another region. The team also learned from the experiments that SNP variants -- "alleles" -- associated with high fitness within each field site were locally abundant in that region, demonstrating a kind of home court advantage at the genomic level.

In addition, certain climate variables seemed to control the geographic distribution of fitness-associated SNPs. For example, fitness SNPs in Finland, at the northern range limit, were limited by temperature. In one example presented in the paper, the researchers identify a SNP allele in a water-stress tolerance gene, called SAG21. This allele was common in Arabidopsis's Spanish populations, but not in the cool climate of Finland where tests showed plants carrying that allele fared poorly.

"Climate explains the distribution of locally favorable alleles," Fournier-Level explained. "This helps explain how climate shapes distribution."

"We found that the genetic basis of survival and reproduction is almost entirely different in different regions, which suggests that evolutionary adaptation to one climate may not always result in a tradeoff of poor performance in another climate," said Schmitt, the Stephen T. Olney Professor of Natural History and professor of biology and environmental studies. "Thus, the Arabidopsis genome may contain evolutionary flexibility to respond to climate change."

Reference: A. Fournier-Level, A. Korte, M. D. Cooper, M. Nordborg, J. Schmitt, A. M. Wilczek. A Map of Local Adaptation in *Arabidopsis thaliana*. *Science*, 2011; 334 (6052): 86.

New Insight Into Plant Immune Defenses

Source: *Biotechnology and Biological Sciences Research Council*. Oct. 7, 2011

Researchers funded by the Biotechnology and Biological Sciences Research Council (BBSRC), among others, have identified an important cog in the molecular machinery of plant immunity -- a discovery that could help crop breeders produce disease-resistant varieties to help ensure future food security. There may also be implications for treating human immune-related disorders. The research, led by Professor Gary Loake at the University of Edinburgh with colleagues from

Syngenta is published this evening (02 October 2011) in the journal *Nature*.

Plants are under constant attack from disease-causing organisms and to protect themselves they have developed a simple immune system. One defence mechanism is to trigger threatened cells to die and so remove the food source from the invading pathogen. Professor Loake and his team have uncovered what is happening inside the cells to control this process and in doing so have put an enzyme called NADPH oxidase in the spotlight.

Professor Loake said "Plants generate a short, sharp shock that kills off the cells around where the pathogen is trying to invade and essentially starves it out. But we recognised that something must be going on to make sure that the plant doesn't go into complete meltdown."

When a plant is attacked by a bacterium or a fungus, for example, there are various ways in which they perceive this attack. One of the common responses is to trigger the production of a chemical called nitric oxide (NO) and a class of molecules known as 'reactive oxygen intermediates' (ROI's), which includes things like hydrogen peroxide and 'free radicals'. As well as being very toxic to the invading organism, NO and ROI's are key to encouraging cells to die if they are threatened. NADPH oxidase comes into the picture because it is critical for the production of ROI's.

The team has found that there is a feedback loop where as the levels of NO go up, NADPH oxidase is altered by the addition of an NO molecule to its structure so that it doesn't work so well. This causes the level of ROI's to drop and cell death tails off.

"This is really exciting!" said Professor Loake "We know that if a human being makes NADPH oxidase that doesn't work properly then they can suffer from an immune deficiency called chronic granulomatous disease or CGD. People with CGD have a particularly hard time fighting off bacterial and fungal infections and often suffer from pneumonia and abscesses.

"NADPH oxidase is really important in plant immunity as well, and we've been able to show how it is regulated in a normal immune response. We hope that plant breeders will be able to use this information to develop disease-resistant varieties. Our discovery might also open new opportunities to treat human immune disorders, such as CGD."

Professor Douglas Kell, Chief Executive, BBSRC said "If available nutrition cannot meet the rise in global population we will face a crisis. Anything that can be done to support the development of new disease-resistant crop varieties with excellent underpinning bioscience research is good news. We must find out as much as possible, through studies such as this one, about how plants deal with invading pathogens so that we can develop new strategies to reduce the impact of disease on yields."

The research is also funded by the Engineering and Physical Sciences Research Council (EPSRC), the Darwin Trust, the Ministry of Education Malaysia, and via a Torrance Scholarship.

Reference: Byung-Wook Yun, Angela Feechan, Minghui Yin, Noor B. B. Saidi, Thierry Le Bihan, Manda Yu, John W. Moore, Jeong-Gu Kang, Eunjung Kwon, Steven H. Spoel, Jacqueline A. Pallas, Gary J. Loake. S-nitrosylation of NADPH oxidase regulates cell death in plant immunity. *Nature*, 2011; DOI: 10.1038/nature10427

Maintaining Virulence

Source: *Science Signaling* - Editor's Summary. 18 October 2011

Agrobacterium tumefaciens is a bacterial pathogen that genetically transforms its hosts, which include several commercially important plants such as grapevines and roses, and induces neoplastic growths termed crown galls (tumors). *Agrobacterium*-induced genetic transformation and tumorigenesis require the integration of a bacterial DNA molecule into the host genome, a process that involves the virulence factor VirF, an F-box protein that is incorporated into the host cell

machinery that targets proteins for degradation. Many F-box proteins, including VirF, are themselves unstable and become degraded, leading Magori and Citovsky to investigate how *Agrobacterium* stabilizes VirF. They found that VirD5, another effector protein produced by *Agrobacterium*, associated with VirF and prevented its degradation. Indeed, a strain of *Agrobacterium* lacking VirD5 formed fewer tumors on tomato plants than did a wild-type strain with VirD5. These findings suggest a general strategy by which other pathogens may stabilize their F-box effector proteins in infected cells.

Citation: S. Magori, V. Citovsky, *Agrobacterium* Counteracts Host-Induced Degradation of Its Effector F-Box Protein. *Sci. Signal.* 4, ra69 (2011).

Plant Physiology paper describes resistance of Sitka spruce and plant defense mechanisms

By Adam Fagen, *ASPB*. 20/10/2011

Plants have a particular challenge in the ongoing arms race against insects in that they can't run away. As such, plants have developed a diverse array of defense compounds to counter rapidly evolving insect predators. Examples include the resins of coniferous trees, which are exuded when the tree is wounded as a result of insect attack or mechanical damage. The resins form a hardened barrier that can trap the insect invader; more than just a physical barrier, however, they also contain a complex array of chemical compounds that can inhibit the growth of microbes as well as deter or reduce insect feeding.

An article just published in *Plant Physiology* describes the role of an enzyme responsible for the wide array of compounds found in resin. A key product of this enzyme is known to play a role in the resistance of the Sitka spruce to spruce weevils, a major insect pest. The study by Hamberger et al. not only contributes to the understanding of defense compound metabolism in

general, but also opens a new avenue for developing markers for resistance to insect pests such as spruce weevils.

Citation: Bjoern Hamberger, Toshiyuki Ohnishi, Britta Hamberger, Armand Seguin, and Joerg Bohlmann. (2011) Evolution of diterpene metabolism: Sitka spruce CYP720B4 catalyses multiple oxidations in the biosynthesis of diterpene resin acids of conifer defense against insects. *Plant Physiology*, pp.111.185843; First Published on October 12, 2011; doi:10.1104/pp.111.185843

Blood proteins probably make you think of animals, not plants, but plant science has found a way to produce human serum albumin (HSA) in rice. A team lead by ASPB member Daichang Yang at Wuhan University in China has published their advance in the *Proceedings of the National Academy of Sciences* this week; the paper was also featured in a news article in *The Scientist*.

HSA is used in treating severe blood loss, burn injuries, and liver disease among other conditions as well as in commercial applications as an additive to cell culture media, a carrier for active compounds in medications, and in vaccine production. HSA is typically isolated from human plasma, the liquid portion of blood, where it is the most abundant protein. However, blood donors can be in short supply and there exists a theoretical risk of contracting bloodborne infectious diseases such as HIV/AIDS and hepatitis—a risk that can be eliminated by production of the protein in plants. Researchers are also able to circumvent several issues surrounding typical recombinant protein production schemes from microbial contamination to yield using rice to produce HSA in an economical manner. As the global demand for HSA exceeds 500 tons per year, an additional source of the pure protein would be welcomed. Yang He and colleagues utilized a natural protein storage organ, the endosperm located within the rice grain, where they obtained approximately 10% of total soluble protein as HSA. Important for the future commercialization of rice

HSA, the structure, function, and immunogenicity of the rice-produced protein are equivalent to plasma isolated HSA. While everything is on track for commercialization of rice HSA, several regulatory hurdles, from growing genetically engineered plants to clinical trials, must be cleared.

In the meantime, kudos to He and colleagues for blurring the boundaries between plant science and biomedical research.

Citation: Yang He, Tingting Ning, Tingting Xie, Qingchuan Qiu, Liping Zhang, Yunfang Sun, Daiming Jiang, Kai Fu, Fei Yin, Wenjing Zhang, Lang Shen, Hui Wang, Jianjun Li, Qishan Lin, Yunxia Sun, Hongzhen Li, Yingguo Zho, and Daichang Yang. (2011). Large-scale production of functional human serum albumin from transgenic rice seeds. *Proceedings of the National Academy of Sciences*, 10.1073/pnas.1109736108.

How parasites modify plants to attract insects

Source: John Innes Centre. November 7, 2011

Pathogens can alter their hosts, for example malaria parasites can make humans more attractive to mosquitoes, but how they do it has remained a mystery. Scientists from the John Innes Centre on Norwich Research Park have identified for the first time a specific molecule from a parasite that manipulates plant development to the advantage of the insect host.

“Our findings show how this pathogen molecule can reach beyond its host to alter a third organism,” said Dr Saskia Hogenhout from JIC.

Leaf hoppers are tiny sap-sucking, highly mobile and opportunistic agricultural pests. Certain species can acquire and transmit plant pathogens including viruses and phytoplasmas, which are small bacteria. Dr Hogenhout and her team focused on a phytoplasma strain called Aster Yellow's Witches' Broom, which causes deformity in a diverse range of plants.

"It is timely to better understand phytoplasmas as they are sensitive to cold and could spread to new areas as temperatures rise through climate change," said Dr Hogenhout.

Infected plants grow clusters of multiple stems which can look like a witches' broom or in trees like a bird's nest. The strain was originally isolated from infected lettuce fields in North America.

The phytoplasma depends on both the leafhopper and the plant host for survival, replication and dispersal. The new findings show how it manipulates the interaction of the plant host and insect vector to its advantage.

The scientists sequenced and examined the genome of the witches broom phytoplasma and identified 56 candidate molecules, called effector proteins, which could be key to this complex biological interaction.

They found that a protein effector SAP11 reduces the production of a defence hormone in the plant that is used against the leafhopper. As a consequence, leafhoppers reared on plants infected with witches broom laid more eggs and produced more offspring. The leafhoppers may also be attracted to lay eggs in the bunched branches and stems.

The higher fecundity rate is probably matched by a similar increased rate in transmission of the witches broom phytoplasma by leafhoppers to other plants.

"Phytoplasmas that can enhance egg-laying and offspring numbers in leafhoppers are likely to have a competitive advantage," said Dr Hogenhout.

Given their opportunistic nature, the leafhoppers are likely to migrate to uninfected plants and spread the pathogen.

"This is a vivid example of the extended phenotype, a concept put forward by Richard Dawkins, where an organism's phenotype is based not only on the biological processes within it but also on its impact on its environment," said Dr Hogenhout.

Reference: 'Phytoplasma protein effector SAP11 enhances insect vector reproduction by manipulating plant development and defense hormone biosynthesis'. November 2011, doi: pnas.1105664108.

BASF seeks EU approval for genetically engineered disease-resistant potato variety

By Kathy R. Munkvold. Source: ASPB, November 7, 2011.

The German chemicals giant, BASF, recently announced their application for European Union (EU) approval of a genetically engineered (GE) potato variety that resists late blight, one of the most devastating diseases in the potato growing industry. If granted, the permit would allow commercial cultivation for food and feed with an expected release date for the new variety, called Fortuna, by 2014 or 2015.

The late blight pathogen, *Phytophthora infestans*, is the same organism that caused the Irish potato famine of the 1800's. *Phytophthora infestans* is an oomycete that can produce an explosion of infectious spores during favorable cool, wet conditions. The spores can then travel through the air producing new infections distant from the inoculum source. Globally, late blight causes \$5.6 billion in losses per year while an estimated \$1 billion is spent on chemical applications to combat the disease.

In order to prevent late blight, BASF has armed its Fortuna variety with two resistance genes from a wild potato relative originating in South America. By engineering two resistance genes into a single variety, in a process known as pyramiding, plants often display enhanced resistance compared to the additive effects of each gene on its own and a slowing of the process by which a pathogen can overcome the resistance. If adopted, growing Fortuna would cut costs as well as environmental risks associated with chemical control of late blight.

The only other GE potato variety approved for commercial cultivation in the EU was also generated by BASF. Amflora, is approved for use in starch production for industrial uses, for instance in glossy printing paper. Similarly, the history of GE potato varieties in the United States is short. In the late 1990's Monsanto released several varieties engineered with resistance to various pests and diseases. However, refusal to use GE potatoes by some of the nation's largest potato purchasers—McDonalds, Wendy's, and Frito-Lay—led to their disappearance from the market. There are currently no GE potatoes grown in the United States, and while the potato growing industry would likely welcome the addition, the market may not.

Shoe Strings and Egg Openers: Scientists Discover Photosynthesis Helper Protein in Red Algae

Source: ScienceDaily. Nov. 8, 2011

Green plants, algae and plankton metabolize carbon dioxide (CO₂) and water into oxygen and sugar in the presence of light. Without this process called photosynthesis, today's life on Earth would not be possible. The key protein of this process, called Rubisco, is thus one of the most important proteins in nature. It bonds with carbon dioxide and starts its conversion into sugar and oxygen.

"Despite its fundamental importance, Rubisco is an enzyme fraught with shortcomings," says Manajit Hayer-Hartl, head of the Research Group "Chaperonin-assisted Protein Folding" at the MPIB.

One of the problems is that Rubisco binds to the wrong sugar molecules that inhibit its activity. The inhibitors have to be removed by a special helper protein, called Rubisco activase. The Max Planck scientists discovered that during evolution two different Rubisco activases developed in plants and in red algae. They differ in structure and in their working mechanism.

The newly discovered Rubisco activase in red algae repairs useless Rubisco proteins by pulling on one end of the protein, like someone who opens a shoe string. In doing so, the helper protein opens the active centre of Rubisco and releases the inhibitory sugar. The respective Rubisco activase in green plants works more like an egg opener, squeezing the inactive Rubisco protein and forcing it to let go of the sugar molecules.

"Understanding the structure and function of the two activase helper proteins should facilitate efforts in biotechnology to generate plants and microorganisms that are able to convert more CO₂ into valuable biomass than nature does," hopes Manajit Hayer-Hartl.

References: Oliver Mueller-Cajar, Mathias Stotz, Petra Wendler, F. Ulrich Hartl, Andreas Bracher, Manajit Hayer-Hartl. Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. *Nature*, 2011; 479 (7372): 194 DOI: 10.1038/nature10568. Mathias Stotz, Oliver Mueller-Cajar, Susanne Ciniawsky, Petra Wendler, F Ulrich Hartl, Andreas Bracher, Manajit Hayer-Hartl. Structure of green-type Rubisco activase from tobacco. *Nature Structural & Molecular Biology*, 2011; DOI: 10.1038/nsmb.2171.

Good Preparation Is Key, Even for Plant Cells and Symbiotic Fungi

ScienceDaily. Nov. 14, 2011.

Not only mineral oil and petroleum gas, phosphorus is also a scarce resource. According to scientists who gathered together for a conference in Cambridge this August, we will face significant problems relating to phosphorus deficiency in just 20 years. Many soils are already depleted for phosphorus today. Plants growing on these soils are only able to take up enough phosphorus by living in symbiosis with arbuscular mycorrhizal fungi (AM fungi). Arbuscular mycorrhizal symbiosis (AM symbiosis) can be found in almost all vascular plants and there is strong indication that plants have a special genetic programme for it. The goal of Franziska Krajinski and her

"Plant-Microbe Interactions" group from the Max Planck Institute of Molecular Plant Physiology is to understand which genes are involved in AM symbiosis. This symbiosis is a non-synchronous process, which means that different cells in the root can show different phases of symbiotic interaction with the fungus. For this reason, the scientists tried to analyse individual cells as opposed to whole roots. They managed to excise single root cells with the help of laser capture microdissection and deciphered these cells' specific gene activity.

When scientists are analysing the molecular composition of plant cells they usually assume that different cells from the same tissue are alike. In many cases, this assumption is true. The majority of cells from leaves, stems or roots show similar levels of gene expression and metabolic activity. It gets more complicated when plants undergo symbiosis, because interactions with the symbiotic partner may alter the cell's metabolism. And even cells adjacent to colonised cells that have not yet come into direct contact with the fungus can show drastic changes in their gene expression levels.

The most prevalent plant symbiosis is that between root cells and arbuscular mycorrhizal fungi, called AM fungi. AM fungi make sure that plants can grow on nutrient-depleted soil -- unnoticed by most people. These fungi outstretch their filamentary cells, called hyphae, far into the soil and are thereby able to take up more nutrients than plants can absorb with their roots. The fungus takes up mainly phosphate, but possibly also nitrate and metal ions like copper, zinc and iron and gives these willingly to the plant. In return, it is rewarded with sugars that plants produce via photosynthesis.

Interestingly, fungus and plant cell never really merge; they are constantly separated by membranes, the outer boundaries of the cells. To enable the relatively big sugar and phosphate molecules to pass through these membranes, the plant cells insert big protein complexes that resemble tunnels through which the molecules can freely

travel from one cell to another. This was already known, and it was not astounding that the scientists around Franziska Krajinski found genes that encode for such transport proteins to be highly expressed in cells that are already colonised by the fungus. A more surprising discovery was, however, that even cells that are in close vicinity of the colonised cells seemed to be already reprogrammed. More than 800 genes showed enhanced activity exclusively in these cells. "The higher transcription rate of genes that are responsible for transport proteins, lipid acid metabolism and gene regulation does not seem to be a result of the colonisation by the fungus," explains Nicole Gaude, first author of the study. "It is more likely that cells are preparing themselves for an imminent colonisation by the fungus."

These very precise and specific results were obtained with the help of laser capture microdissection. In this method, a laser beam is used to excise individual cells from a tissue. At least 5000 cells were cut out by Gaude and her team; a time-consuming manual labour that even Sisyphus would have been proud of. But the time and effort were worth it. "We now know which genes are activated even before a symbiosis is physically established," explains Gaude. Understanding the symbiotic programme of plants could enable the use of AM fungi in agriculture and reduce the application of expensive, artificial fertilizer in the future.

Reference: Nicole Gaude, Silvia Bortfeld, Nina Duensing, Marc Lohse, Franziska Krajinski. Arbuscule-containing and non-colonized cortical cells of mycorrhizal roots undergo a massive and specific reprogramming during arbuscular mycorrhizal development. *The Plant Journal*, 2011; DOI: 10.1111/j.1365-313X.2011.04810.x

Corn Gene Boosts Biofuels from Switchgrass

Source: ScienceDaily. Nov. 18, 2011.

Many experts believe that advanced biofuels made from cellulosic biomass

are the most promising alternative to petroleum-based liquid fuels for a renewable, clean, green, domestic source of transportation energy. Nature, however, does not make it easy. Unlike the starch sugars in grains, the complex polysaccharides in the cellulose of plant cell walls are locked within a tough woody material called lignin. For advanced biofuels to be economically competitive, scientists must find inexpensive ways to release these polysaccharides from their bindings and reduce them to fermentable sugars that can be synthesized into fuels.

An important step towards achieving this goal has been taken by researchers with the U.S. Department of Energy (DOE)'s Joint BioEnergy Institute (JBEI), a DOE Bioenergy Research Center led by the Lawrence Berkeley National Laboratory (Berkeley Lab).

A team of JBEI researchers, working with researchers at the U.S. Department of Agriculture's Agricultural Research Service (ARS), has demonstrated that introducing a maize (corn) gene into switchgrass, a highly touted potential feedstock for advanced biofuels, more than doubles (250 percent) the amount of starch in the plant's cell walls and makes it much easier to extract polysaccharides and convert them into fermentable sugars. The gene, a variant of the maize gene known as *Corngrass1* (*Cg1*), holds the switchgrass in the juvenile phase of development, preventing it from advancing to the adult phase.

"We show that *Cg1* switchgrass biomass is easier for enzymes to break down and also releases more glucose during saccharification," says Blake Simmons, a chemical engineer who heads JBEI's Deconstruction Division and was one of the principal investigators for this research. "*Cg1* switchgrass contains decreased amounts of lignin and increased levels of glucose and other sugars compared with wild switchgrass, which enhances the plant's potential as a feedstock for advanced biofuels."

The results of this research are described in a paper published in the Proceedings

of the National Academy of Sciences (PNAS) titled "Overexpression of the maize *Corngrass1* microRNA prevents flowering, improves digestibility, and increases starch content of switchgrass." Lignocellulosic biomass is the most abundant organic material on earth. Studies have consistently shown that biofuels derived from lignocellulosic biomass could be produced in the United States in a sustainable fashion and could replace today's gasoline, diesel and jet fuels on a gallon-for-gallon basis. Unlike ethanol made from grains, such fuels could be used in today's engines and infrastructures and would be carbon-neutral, meaning the use of these fuels would not exacerbate global climate change. Among potential crop feedstocks for advanced biofuels, switchgrass offers a number of advantages. As a perennial grass that is both salt- and drought-tolerant, switchgrass can flourish on marginal cropland, does not compete with food crops, and requires little fertilization. A key to its use in biofuels is making it more digestible to fermentation microbes.

"The original *Cg1* was isolated in maize about 80 years ago. We cloned the gene in 2007 and engineered it into other plants, including switchgrass, so that these plants would replicate what was found in maize," says George Chuck, lead author of the PNAS paper and a plant molecular geneticist who holds joint appointments at the Plant Gene Expression Center with ARS and the University of California (UC) Berkeley. "The natural function of *Cg1* is to hold plants in the juvenile phase of development for a short time to induce more branching. Our *Cg1* variant is special because it is always turned on, which means the plants always think they are juveniles."

Chuck and his colleague Sarah Hake, another co-author of the PNAS paper and director of the Plant Gene Expression Center, proposed that since juvenile biomass is less lignified, it should be easier to break down into fermentable sugars. Also, since juvenile plants don't make seed, more starch

should be available for making biofuels. To test this hypothesis, they collaborated with Simmons and his colleagues at JBEI to determine the impact of introducing the Cg1 gene into switchgrass.

In addition to reducing the lignin and boosting the amount of starch in the switchgrass, the introduction and overexpression of the maize Cg1 gene also prevented the switchgrass from flowering even after more than two years of growth, an unexpected but advantageous result.

"The lack of flowering limits the risk of the genetically modified switchgrass from spreading genes into the wild population," says Chuck.

The results of this research offer a promising new approach for the improvement of dedicated bioenergy crops, but there are questions to be answered. For example, the Cg1 switchgrass biomass still required a pre-treatment to efficiently liberate fermentable sugars.

"The alteration of the switchgrass does allow us to use less energy in our pre-treatments to achieve high sugar yields as compared to the energy required to convert the wild type plants," Simmons

says. "The results of this research set the stage for an expanded suite of pretreatment and saccharification approaches at JBEI and elsewhere that will be used to generate hydrolysates for characterization and fuel production."

Another question to be answered pertains to the mechanism by which Cg1 is able to keep switchgrass and other plants in the juvenile phase.

"We know that Cg1 is controlling an entire family of transcription factor genes," Chuck says, "but we have no idea how these genes function in the context of plant aging. It will probably take a few years to figure this out."

Reference: G. S. Chuck, C. Tobias, L. Sun, F. Kraemer, C. Li, D. Dibble, R. Arora, J. N. Bragg, J. P. Vogel, S. Singh, B. A. Simmons, M. Pauly, S. Hake. Overexpression of the maize *Corngrass1* microRNA prevents flowering, improves digestibility, and increases starch content of switchgrass. *Proceedings of the National Academy of Sciences*, 2011; 108 (42): 17550 DOI: 10.1073/pnas.1113971108

Forthcoming meetings



FESPB-EPSO 2012 CONGRESS

July 29 - August 3, 2012. Freiburg, Germany

The next FESPB Congress will be jointly organized with EPSO, and will be held in Freiburg, Germany from 29 of July to 3 of August 2012.

Attached please find the relevant Poster and take advantage of the early registration fee.

Also, attached are the Announcements for the **2012 FESPB Student Travel Grants** from ex-eastern european countries and the **FESPB Awards**.

Please notice that EPSO will also sponsor 20 Travel Grants for european students. Information will soon be available at the www.fespb.org and www.epsoweb.eu

Experimental Biology 2012

Apr 21 - Apr 25, 2012. San Diego, CA, USA

Experimental Biology is an annual meeting comprising of nearly 13,000 scientists and exhibitors representing six sponsoring societies and 18 guest societies. General fields of study include anatomy, pathology, biochemistry, molecular biology, investigative pathology, nutrition, pharmacology and

immunology. EB 2012 is open to all members of the sponsoring and guest societies and nonmembers with interest in research and life sciences. The majority of scientists represent university and academic institutions as well as government agencies, non-profit organizations and private corporations. <http://experimentalbiology.org/EB/pages/default.aspx?splashpage=1>

**Soil and irrigation sustainability practices
April 22 – 27, 2012. Vienna, Austria**

"Soil and irrigation sustainability practices" of the European Geosciences Union (EGU) General Assembly 2012 to be held in Vienna (Austria) April 22–27 (see program in <http://meetingorganizer.copernicus.org/EGU2012/session/9952>).

Participation to the meeting is very affordable. Posters and oral communications are available. Only the abstract is required to be sent before

January 17th and then, be ready to present your work the date specified at the final Programme. The deadline for the receipt of Abstracts is 15 Dec 2011 in case you would like to apply for support. If any doubt, please do not hesitate to contact to me (Tel: 913365675 FAX: 913365845.

leonor.rodriguez.sinobas@upm.es).

**28th New Phytologist Symposium:
Functions and Ecology of the Plant
Microbiome**

May 18 – 21, 2012. Rhodes, Greece

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

**EUCARPIA 19th General Congress: Plant
Breeding for future Generations**

May 21 – 24, 2012. Budapest, Hungary

<http://www.mgki.hu/index.php?conference=30>

6th Central European Congress on Food

**May 23 – 26, 2012. Novi Sad, Serbia,
Hotel Park**

<http://www.cefood2012.rs/>

ISTA Annual Meeting.

June 11 – 14, 2012. Venlo, The Netherlands.

The next ISTA Annual Meeting will be held at the venue of the World Horticultural Expo, Floriade 2012. The first day of the Annual meeting will be a seminar on 'New developments and technologies in seed testing' including sessions in which invited speakers will present papers on vision and image analysis, and on sensor applications and molecular technologies in seed testing. This will be followed by reports from ISTA's technical committees (12, 13 June) and the Ordinary Meeting (14 June).

Full details of the meeting can be found on ISTA's website

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

**Gordon Research Conference on: SALT &
WATER STRESS IN PLANTS**

June 24 – 29, 2012. Hong Kong, China

More info:

<http://www.grc.org/programs.aspx?year=2012&program=salt>

SEB Annual Main Meeting 2012

June 29, 2012. Salzburg, Austria

More info:

<http://www.sebiology.org/meetings/Salzburg2012/Salzburg.html>

Plant Vascular Development 2012

**July 1 – 2, 2012. Gregor Mendel Institute,
Vienna, Austria**

More info:

<http://www.icar2012.org/Satellite%20Meetings/plant-vascular-development-2012>

**2nd International Symposium on Woody
Ornamentals of the Temperate Zone**

July 1 – 4, 2012. Ghent, Belgium

Visit our **website** for more detailed information:

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

This symposium will cover all aspects of **woody plant production and management**: crop protection, cultural techniques, multiplication, breeding,

biodiversity, effects of climate change on plant physiology, and more. Join us for these **field trips**: a visit to woody ornamental research centres in Belgium and a post-congress tour of local growers to showcase Belgium's dynamic and innovative woody ornamental industry. We invite you to share your expertise with us at the symposium. We look forward to seeing you in Ghent in July 2012!

Fax: +32 9 272 29 01

E-mail:

woodyornamentals@ilvo.vlaanderen.be

Website:

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

23rd International Conference on Arabidopsis research

July 3 – 7, 2012. Vienna, Austria

More info: <http://www.icar2012.org/>

Malaysia International Biological Symposium: i -SIMBIOMAS 2012

July 11 – 12, 2012. Kajang, Malaysia

MALAYSIA INTERNATIONAL BIOLOGICAL SYMPOSIUM 2012 (i-SIMBIOMAS 2012) has catapulted into international status from the earlier biennial events of SIMBIOMAS 2009, and Kolokium Biologi 2007, 2005 and 2003 organized by the Department of Biology, Faculty of Science, UPM. The symposium is predominantly catered for informal exchange of research findings, ideas and views between postgraduates, researchers and collaborators from local and international. Year 2012 marks SIMBIOMAS goes international and henceforth will be continued biennially. The i-SIMBIOMAS 2012 aims to bridge researchers from various disciplines of Biology, and serves as a platform to foray fundamental biological sciences, applied biology and diversification of research into producing commercially viable knowledge, skill and bioproducts.

<http://www.science.upm.edu.my/biology/i-simbiomas2012/>

Plant Molecular Biology Gordon Conference Export to Your Calendar

July 15 – 20, 2012. New Hampshire, United States

More info:

<http://www.grc.org/programs.aspx?year=2012&program=plantmolec>

9th International Conference "Plant Functioning in Stress Environment" September 12 – 15, 2012. Cracow, Poland

[http://www.ifr-](http://www.ifr-pan.krakow.pl/main.php?lang=eng&page=akt)

[pan.krakow.pl/main.php?lang=eng&page=akt](http://www.ifr-pan.krakow.pl/main.php?lang=eng&page=akt)

Request the 2nd circular by email to:

Conf.krakow@gmail.com or

m.grzesiak@ifr-pan.krakow.pl

The EMBO Meeting 2012 - Advancing the life sciences

September 22 – 25, 2012. Nice, France

<http://2012.the-embo-meeting.org/>

17th Meeting of the International Council for Grapevine Viruses

October 8 – 12, 2012. Davis, California (USA)

More information can be found at

<http://ucanr.org/sites/ICVG/>

V INTERNATIONAL SYMPOSIUM ON BIOCHEMISTRY AND MOLECULAR BIOLOGY - V SIMPOSIO INTERNACIONAL DE BIOQUÍMICA Y BIOLOGÍA MOLECULAR October 9 – 12, 2012. Hotel Meliá Habana, Cuba

Genetics of Fagaceae

October 9 – 12, 2012. Agora - University of Bordeaux. Talence, France

Organized by The IUFRO working group "2.08.05 - Genetics of Quercus and Nothofagus"

Website:

<https://colloque.inra.fr/iufro2012>

Contacts: Alexis DUCOUSSO & Laëticia

PACALY: iufro2012@bordeaux.inra.fr

International Symposium of Plant Photobiology (ISPP)

June 3, 2013. Edinburgh, Scotland

More info:

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

Seed Ecology IV: 4th International Society for Seed Science Meeting on Seeds and the Environment.
June 22 – 26, 2013. Shenyang, China

More info Website:
<http://seed2013.csp.escience.cn/dct/page/1>
E-mail: seedecology4@iae.ac.cn

Positions available



PhD Research Opportunity

Newcastle University, Newcastle upon Tyne, United Kingdom

Establishing the functional role of vacuolar sugar transporters in plants under stress

Supervisor: Dr Anne M Borland

In many crop plants, the leaf vacuole is an important source of sugars that are used for growth and the production of secondary compounds (eg. osmoprotectants) under conditions of drought and/or salinity. It is hypothesised that sugar transporters located on the vacuolar membrane play a key role in regulating carbohydrate partitioning between growth and the production of osmoprotectants, thereby influencing plant resistance to stress. This hypothesis will be tested by examining responses to abiotic stressors in a number of recently identified mutants with impaired expression of different vacuolar sugar transporters. Approaches to be employed will include physiological measurements of leaf gas exchange and growth characteristics as well as real-time PCR (polymerase chain reaction) for monitoring gene expression and high-performance liquid chromatography for analyses of sugars.

<http://www.ncl.ac.uk/biology/postgrad/research/phds.htm>

Postdoctoral Research Job - Cellulose Biosynthesis

Pennsylvania State University, University Park, USA

A postdoctoral research position is available immediately in the Department of Biochemistry & Molecular Biology at Pennsylvania State University, Center for Lignocellulose Structure and Formation

(<http://www.lignocellulose.org>). We are

seeking highly motivated scientists to investigate the molecular and cellular mechanisms controlling cellulose biosynthesis in Arabidopsis. The project integrates molecular biology, genetics, and biochemistry to characterize novel components associated with cellulose synthase complexes (CSCs).

Applicants must have a Ph.D. in plant biology, genetics, or a related discipline. We seek applicants who have a strong background in cell biology and biochemistry. Excellent oral and written communication skills and the ability to work well in a collaborative research environment are essential.

Application Instructions: Applicants should provide their curriculum vitae, a brief description of research experience and long-term interests, and email address of three referees. Please include the following in the subject line: "Post Doctoral Application for cellulose biosynthesis" and send the above requested information to: Ying Gu by email: yug13@psu.edu. Screening of applications will begin immediately and will continue until the position is filled.

Postdoctoral Job - Plant Biotechnology

Delaware State University, Dover, USA

A Postdoctoral Fellow/Research Associate position sponsored by a NIFA-USDA grant is available immediately at the College of Agricultural and Related Sciences at Delaware State University, Delaware, USA. The project integrates molecular biology, genetics, and plant science, biochemistry to develop and characterize novel cassava tuberous roots with enhanced downstream bio-processing characteristics. The overall goal of the project is to make bio-ethanol production from cassava much cheaper hereby increasing its global

competitiveness as bio-energy feedstock.

-- Applicants must have a Ph.D. in plant biology, genetics, genomics, plant biotechnology or a related discipline

-- Highly motivated individuals with a strong background in molecular biology and recombinant DNA systems/or plant biology and genetics

Postdoctoral/Research Associate position is for one year with the possibility of extension for another two years based on strong performance. Salary is commensurate with experience. A full benefit package is provided with this position.

Applicants should provide their curriculum vitae, a brief description of research experience and long-term interests, list of publications and email address of three references. Send the above requested information to Dr. Bertrand Hankoua at bhankoua@desu.edu or Ms. Lisa Hopkins at lhopkins@desu.edu. Screening of applications will begin immediately and will continue until position is filled.

Postdoctoral Research Career Development Fellowship

University of Cambridge, United Kingdom
Sainsbury Laboratory, University of Cambridge (UK)

Applications are invited for Research Career Development Fellowships to be held in the Sainsbury Laboratory at the University of Cambridge. With the intention of nurturing the next generation of researchers in the field of plant science, the Fellowships provide an opportunity for talented junior investigators to develop their own research program and become creative leaders in the field. The positions are open to applicants of any nationality. Applicants should typically have between 3 and 6 years of postdoctoral experience in a field related to the overall scientific focus of the Laboratory in plant development and its computational modelling. Applicants should be able to provide strong evidence of their potential to

develop independent research programs.

Fellowships are for five years. Successful applicants will receive an initial three years of funding, with extension for a further two years contingent on a successful scientific review, and will hold an appointment with the University of Cambridge. Funds include full salary, benefits and £40,000 p.a. of unrestricted research support. As they develop into independent researchers, Fellows will be encouraged to apply for external funding. Fellows can apply for Research Group Leader positions within the Laboratory at any time.

Applications can be submitted electronically at any time as pdf files and include a full CV, a research proposal for three years, and the names of at least three referees. There is no fixed closing date- applications will be peer reviewed at least three times annually.

Further details about the posts and the Sainsbury Laboratory are available on the Sainsbury Laboratory web site: <http://www.slcu.cam.ac.uk/index.html>

Completed applications should be sent by e-mail to enquiry@slcu.cam.ac.uk.

* The funds for this post are available for 5 years in the first instance.

Quote Reference: PT08799

Closing Date: 15 October 2012

Postdoctoral Fellow - High Resolution Expression Analysis

GrassRoots Biotechnology, Durham, North Carolina, United States

A postdoctoral position is available immediately in the lab of Dr. Imara Perera, Department of Plant Biology at North Carolina State University. This position is funded by a collaborative NSF project involving Dr. Glenda Gillaspay at Virginia Tech and Dr. Victor Raboy at the USDA labs in Aberdeen, Idaho. The postdoctoral researcher will work as part of team to characterize novel inositol phosphate signaling molecules and associated regulatory genes/enzymes in Arabidopsis using a functional genomics approach. The project will require exchange and travel between the

institutions and provides a unique opportunity for a postdoc to receive training in both academia and government research labs.

Applicants must have a Ph.D. and proven experience in plant molecular biology, (particularly Arabidopsis genetics and transcript profiling), biochemistry and/or stress physiology. Excellent written and oral skills and the ability to work collaboratively with others are highly desirable qualifications. The position is available for one year, with renewal for a second year based on performance.

Please visit the NSF/ASEE website at <http://nsfsbir.asee.org/> for further details and to apply for this position. Please visit www.grassrootsbio.com for more information about our company.

Postdoctoral Position at Syracuse University

Regulation of pathogen defense by epigenetic mechanisms and by miRNAs
A postdoctoral position is immediately available in the laboratory of Dr. Ramesh Raina at Syracuse University to participate in one or more of the ongoing research projects focusing on understanding the molecular mechanisms regulating pathogen defense in Arabidopsis. The first project involves understanding epigenetic mechanisms regulating pathogen defenses. We have recently identified

and characterized an Arabidopsis histone demethylase that is required for defense against pathogens. This project will involve detailed characterization of this protein and identification of downstream

targets of this protein by ChIP analysis, and characterization of role of additional members of this family in pathogen defense and other stresses.

The second project involves understanding regulation of pathogen defense by miRNAs. We have recently identified a novel miRNA that is strongly induced in response to avirulent bacterial pathogens. This project involves detailed characterization of this miRNA including regulation of its expression, biogenesis and role in pathogen defense.

This position is available for 3 years. Candidate should have a Ph.D. in molecular biology, genetics, biochemistry or a related discipline.

Experience with ChIP analysis and/or next generation sequencing is desirable. The successful candidate must be able to independently design and conduct experiments, and willing to work collaboratively with other members of the laboratory.

Interested individuals should submit a CV, a statement of research experience and interests, and name and contact information of three referees as a SINGLE PDF file to raraina@syr.edu

New books



ABIOTIC STRESS RESPONSES IN PLANTS

Metabolism, Productivity and Sustainability

Ahmad, Parvaiz; Prasad, M.N.V. (Eds.).
Springer, 2012, 169,95 a
ISBN 978-1-4614-0633-4,
Hardcover Due: December 28, 2011

ENVIRONMENTAL ADAPTATIONS AND STRESS TOLERANCE OF PLANTS IN THE ERA OF CLIMATE CHANGE

Ahmad, Parvaiz; Prasad, M.N.V. (Eds.).
Springer, 2012, 169,95 a
ISBN 978-1-4614-0814-7,
Hardcover Due: December 28, 2011

MARSCHNER'S MINERAL NUTRITION OF HIGHER PLANTS (Third Edition)

Edited by **Petra Marschner**, Academic Press/Elsevier. 2012.

ISBN: 9780123849052

- A long awaited revision of the standard reference on plant mineral nutrition

- Features full coverage and new discussion of the latest molecular advances
- Contains new chapters on agro-ecosystems as well as nutrition and quality

PHOTOPERIODISM. THE BIOLOGICAL CALENDAR

Nelson R. J., Denlinger D. L., Somers D. E. eds. 2010.

Oxford University Press. £45 (hardback). pp. 596.

Photoperiodism -the biological calendar is a welcome contribution to the field of photoperiodic research because it brings together and summarises current understanding of the photoperiodic mechanisms present in all organisms, from animals and plants to invertebrates and fungi - something that has been needed for a long time. The book is appropriately divided into three sections, the first dealing with photoperiodism in plants and fungi, the second with photoperiodism in invertebrates, and the third with photoperiodism in vertebrates; at the start of each there is an overview written by one of the editors who are well known in those areas.

PHOTOSYNTHESIS

Plastid Biology, Energy Conversion and Carbon Assimilation

Series: Advances in Photosynthesis and Respiration, Vol. 34

Eaton-Rye, Julian J.; Tripathy, Baishnab C.; Sharkey, Thomas D. (Eds.), Springer, 2012. 199,95 €

ISBN 978-94-007-1578-3,

Hardcover, Due: December 31, 2011.

PLANTS AND ENVIRONMENT

Hemanth KN. Vasanthaiah and Devaiah Kambiranda (Ed.). InTech. Open Access Book

ISBN: 978-953-307-779-6

Available from:

<http://www.intechopen.com/books/show/title/plants-and-environment>

PLANT CYTOGENETICS

Genome Structure and Chromosome Function

Series: Plant Genetics and Genomics: Crops and Models, Vol. 4

Bass, Hank W.; Birchler, James A. (Eds.). Springer, 2012. 154,95 €

ISBN 978-0-387-70868-3,

Hardcover Due: December 28, 2011

RECEPTOR-LIKE KINASES IN PLANTS

From Development to Defense

Series: Signaling and Communication in Plants, Vol. 13

Tax, Frans; Kemmerling, Birgit (Eds.) 2012, 149,95 €

ISBN 978-3-642-23043-1, Hardcover Due: December 31, Springer, 2011.

TRANSPORTERS AND PUMPS IN PLANT SIGNALING

Edited by Markus Geisler and Kees Venema

Springer-Verlag Berlin Heidelberg 2011

386 p, ISBN 978-3-642-14368-7

BOOK OUTLINE

Terrestrial plants are unable to relocate when faced with biological, physical or chemical stress and have therefore developed efficient signaling mechanisms to respond to and ensure survival under adverse circumstances. The auxotrophic lifestyle obviously allows plants to fuel more primary active, ATP-dependent pumps than animals. Unlike bacteria that rely entirely on their cell walls, higher plants needed more secondary transport systems to control cell homeostasis and osmotic pressure. Moreover, plant-specific organelles and vacuoles provide storage pools for ions and catabolites that are filled by co-transporters. This correlates with an increased and more divergent number of transporter genes, mainly pumps and secondary active transporters, in higher plants compared with genomes from bacteria or animals. Although plant sensing and responding mechanisms might be considered as simple and even slow compared with nervous systems in animals, the basic mechanisms of signal transduction and sensing are very similar. At the same time, work in the recent years has identified novel, plant-specific signaling molecules and mechanisms. This volume focuses on the role of

transporters and pumps in regulation of movement, long-range transport and compartmentalization of water, solutes, nutrients and classical signaling molecules. Function, regulation and

membrane-transporter interaction of prominent transporters and pumps, and their individual roles in plant signaling controlling plant physiology and development is discussed.