



**FEDERATION OF EUROPEAN SOCIETIES OF PLANT
BIOLOGY**

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FESPB Newsletter

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Editor: Prof. Dolores Rodriguez
**Chair of Publications
Committee**

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



Direct Transfer of Plant Genes from Chloroplasts Into the Cell Nucleus: Gene Function Preserved Despite Structural Differences in the DNA

Source: ScienceDaily (Apr. 13, 2012)

Chloroplasts, the plant cell's green solar power generators, were once living beings in their own right. This changed about one billion years ago, when they were swallowed up but not digested by larger cells. Since then, they have lost much of their autonomy. As time went on, most of their genetic information found its way into the

cell nucleus; today, chloroplasts would no longer be able to live outside their host cell. Scientists in Ralph Bock's team at the Max Planck Institute of Molecular Plant Physiology have discovered that chloroplast genes take a direct route to the cell nucleus, where they can be correctly read in spite of their architectural differences.

Cyanobacteria are among the oldest life forms, and appear to be the forerunners of green chloroplasts in plant cells. They do not possess a true cell nucleus, but their genetic substance is made up of the same four building blocks as that of humans, plants and animals. Therefore, the

genes encoded in the chloroplast DNA can also be read in the cell nucleus; indeed, many genes that were still found in the cell organelles during early evolution are now located exclusively in the genome of the nucleus. How they made their way there has previously been unclear. Two mechanisms appeared likely: either direct transport in the form of DNA fragments from the chloroplasts to the nucleus or transport in the form of mRNA, which is then transcribed back into DNA.

The direct transfer of DNA appears to predominate in the chloroplasts, but this pathway raises two problems. The first problem lies in the promoters, the DNA sequences which ensure that genes are recognised as such. They are located upstream of the genes and recruit proteins that are required for transcription of the genes. However, promoters from chloroplasts are not recognised as such by the proteins in the nucleus, so that the DNA reading machinery should overlook these incoming genes.

The second difficulty is in the correct processing of the gene sequence. Genes consist of several modules, separated by non-coding DNA regions (introns). Since the introns obstruct protein synthesis, they need to be removed from the mRNA, a procedure described as splicing. The whole process, ending in synthesis of the correct protein, can resume only once this has taken place. Once again, however, the mRNA is processed differently in the cell nucleus than in the chloroplasts, and for a long time, chloroplast introns seemed to have been an insurmountable hurdle for the correct reading of chloroplast genes in the nucleus.

"But they are actually nothing of the sort," stresses Ralph Bock, head of the research group. "Our trials have shown that the introns are recognised in the cell nucleus and spliced out, even if not always at exactly the same sites as might have been the case in the chloroplasts." Functional proteins are formed despite this. It is thought that the introns even help the splicing enzymes by folding themselves into stable RNA structures, thus directing the enzymes to the

right locations. At the same time, the RNA structure seems to help the ribosomes find the correct starting point for protein synthesis.

Since the transfer of genes into the cell nucleus is an extremely slow evolutionary process, which has taken nature millions of years, it has not been possible to investigate the underlying mechanism to date. However, researchers have now managed to fast-forward this gene transfer in the laboratory. Because the cells were subjected to high selection pressure, the transference of genes from the chloroplasts into the nucleus became essential for survival, so that it could be made readily visible. It was found that the transfer takes place without the involvement of RNA and that the DNA apparently jumps directly from the cell's chloroplasts into its nucleus.

Journal Reference: Ignacia Fuentes, Daniel Karcher, Ralph Bock. Experimental Reconstruction of the Functional Transfer of Intron-Containing Plastid Genes to the Nucleus. *Current Biology*, 2012; DOI: 10.1016/j.cub.2012.03.005

Mechanism That Gives Plants 'Balance' Discovered

Source: ScienceDaily (Apr. 23, 2012)

When a plant goes into defense mode in order to protect itself against harsh weather or disease, that's good for the plant, but bad for the farmer growing the plant. Bad because when a plant acts to defend itself, it turns off its growth mechanism.

But now researchers at Michigan State University, as part of an international collaboration, have figured out how plants can make the "decision" between growth and defense, a finding that could help them strike a balance -- keep safe from harm while continuing to grow.

Writing in the current issue of the *Proceedings of the National Academy of Sciences*, Sheng Yang He, an MSU professor of plant biology, and his team found that the two hormones that control growth (called gibberellins) and defense

(known as jasmonates) literally come together in a crisis and figure out what to do.

"What we've discovered is that some key components of growth and defense programs physically interact with each other," he said. "Communication between the two is how plants coordinate the two different situations.

We now know where one of the elusive molecular links is between growth and defense." This is important because now that scientists know that this happens, they can work to figure out how to "uncouple" the two, He added.

"Perhaps at some point we can genetically or chemically engineer the plants so they don't talk to each other that much," He said. "This way we may be able to increase yield and defense at the same time."

In this way, He said plants are a lot like humans. We only have a certain amount of energy to use, and we have to make wise choices on how to use it.

"Plants, like people, have to learn to prioritize," he said. "You can use your energy for growth, or use it for defense, but you can't do them both at maximum level at the same time."

The work was done on two different plants: rice, a narrow-leafed plant, and Arabidopsis, which has a broader leaf. This was significant because it demonstrated that this phenomenon occurs in a variety of plants.

He was one of the lead investigators on an international team of scientists that studied the issue. Other participating institutions included the Shanghai Institutes for Biological Sciences, Hunan Agricultural University, the University of Arkansas, Duke University, Yale University and Penn State University.

Journal Reference: Dong-Lei Yang et al. Plant hormone jasmonate prioritizes defense over growth by interfering with gibberellin signaling cascade. Proceedings of the National Academy of Sciences, 2012 DOI: 10.1073/pnas.1201616109

Ancient Plant-Fungal Partnerships Reveal How the World Became Green

Source: ScienceDaily (May 15, 2012)

Prehistoric plants grown in state-of-the-art growth chambers recreating environmental conditions from more than 400 million years ago have shown scientists from the University of Sheffield how soil dwelling fungi played a crucial role in the evolution of plants.

This ground breaking work provides fundamental knowledge of how plants colonised the land before roots evolved and the co-evolution of one of the most ancient relationships, between fungi and early plants that played a founding role in the evolution of Earth's ecosystems.

The research highlights the importance of mutually beneficial plant-fungal relationships prior to the evolution of roots, whereby plants gain growth-promoting soil phosphorus from the fungi in exchange for sugars fixed by the plant through photosynthesis.

The study compared the efficiencies of plant-fungal relationships in land plant species spanning more than 400 million years of evolution under both modern day atmospheric conditions and CO₂ concentrations on Earth at the time plants first emerged onto the land.

Lead author Dr Katie Field, of the University's Department of Animal and Plant Sciences, said: "Our research shows for the first time how Earth's terrestrial ecosystems were initiated in partnership with soil dwelling fungi nearly half a billion years ago and how these fungi played a crucial role in enabling plants to diversify into fantastically rich and biodiverse modern floras.

"The earliest land plants not only faced ever increasing competition for light with the evolution of new, taller species of plants, but also experienced reduced fungal symbiotic efficiency and subsequently lower total capture of phosphorus as global atmospheric carbon dioxide levels fell.

"In contrast, the fungal symbiotic efficiency of the more sophisticated, recently evolved land plants with complex organs such as leaves and

roots, increased as CO2 levels decreased. This would have given them a significant evolutionary advantage and has led to their dominance of world ecosystems today."

Dr Martin Bidartondo, of the Department of Life Sciences at Imperial College London, an expert in the ecology and evolution of mycorrhizas, one of the most widespread symbioses on Earth, was responsible for the molecular work carried out as part of the research.

Dr Bidartondo added: "We are finally starting to get information on which fungi allowed the colonisation of land by plants and about how they did it. This is because we can now discover which fungal lineages form intimate associations with the oldest groups of plants by using new molecular ecology and evolution approaches."

The scientists used liverworts as representatives of the earliest group of plants to leave the water. These plants have no roots or leaves, do not produce flowers or seeds, and are structurally very similar to fossilised remains of the very first land plants.

A fern was chosen to represent the earliest plants to have both roots and leaves. Finally, a common garden weed -- Ribwort Plantain -- was chosen as a typical example of the most recently evolved group of plants.

Dr Field said: "Our exciting findings clearly indicate that the co-evolution of complex plant rooting systems and fungal symbioses, against a background of falling atmospheric carbon dioxide, resulted in increased symbiotic efficiency and as such, ensured the success of plants in 'greening the Earth' and their ensuing diversification, creating the wonderfully varied terrestrial ecosystems that we are familiar with today."

The above story is reprinted from materials provided by University of Sheffield.

Tomato Genomes Sequenced: Both Domesticated Type and Wild Ancestor

Source: ScienceDaily (May 30, 2012)

The tomato genome sequence -- both the domesticated type and its wild ancestor,

Solanum pimpinellifolium -- has been sequenced for the first time by a large international team of scientists, including a researcher from the Hebrew University of Jerusalem.

The sequences provide the most detailed look yet at the tomato genome, revealing the order, orientation, types and relative positions of its 35,000 genes. The sequences will help researchers uncover the relationships between tomato genes and traits and broaden their understanding of how genetics and environmental factors interact to determine a field crop's health and viability.

The achievement -- an important tool for further development of better tomato production -- by the 300-plus-member Tomato Genome Consortium (TGC) is reported on in the May 31 issue of the journal *Nature*.

The consortium includes Prof. Dani Zamir of the Robert H. Smith Faculty of Agriculture, Food and Environment of the Hebrew University. Other scientists in the project are from Argentina, Belgium, China, France, Germany, India, Italy, Japan, South Korea, Spain, the Netherlands, the United Kingdom and the United States.

When Columbus brought tomato seed from America to the old world some 500 years ago, he probably never imagined that it would be such a major contributor to human nutrition, health, culinary pleasure and international cooperation. This latest quantum leap in knowledge of the tomato genetic code (35,000 genes) provides a means to match DNA sequences with specific traits that are important for human well being or taste, such as flavor, aroma, color and yield.

Tomato is a member of the Solanaceae or nightshade family, and the new sequences are expected to provide reference points helpful for identifying important genes in tomato's Solanaceae relatives. The group includes potato, pepper, eggplant and petunia and is among the world's most important vegetable plant families in terms of both economic value and production volume.

Beyond improvement of the tomato, the genome sequence also provides a framework for studying closely related plants, such as potato,

pepper, petunia and even coffee. These species all have very similar sets of genes, yet they look very different.

How can a similar set of "genetic blueprints" empower diverse plants with different adaptations, characteristics and economic products? This challenging question is being explored by comparing biodiversity and traits of tomato and its relatives.

The Tomato Genome Consortium started its work in 2003, when scientists analyzed the DNA sequence of tomato using the most modern equipment available at the time. Fortunately, with the recent introduction of so-called "next generation sequencing" technologies, the speed of data output increased 500-fold and enabled the project to move on efficiently to its conclusion.

Journal Reference: The Tomato Genome Consortium. The tomato genome sequence provides insights into fleshy fruit evolution. *Nature*, 2012; 485 (7400): 635 DOI: 10.1038/Nature11119

Scientists complete most comprehensive genetic analysis yet of corn

Source: e! Science News. June 3, 2012

An interdisciplinary team, led by researchers at Cornell University and the U.S. Department of Agriculture-Agricultural Research Service (USDA-ARS), have just published the most comprehensive analysis to date of the corn genome. The team expects the achievement to speed up development of improved varieties of one of the world's most important agricultural commodities. The results should boost international efforts to increase yields, expand areas where corn can be cultivated and produce varieties better equipped to resist pests and disease.

Funded in the United States by the National Science Foundation (NSF) and the USDA, the work was a collaborative effort by scientists at 17 U.S. and foreign institutions that include the University of Wisconsin-Madison; University of Missouri-Columbia; North Carolina State

University; Beijing Genome Institute; University of California, Davis and the International Maize and Wheat Improvement Center, Mexico City, Mexico.

The study appears in two corn genome projects published in separate reports in the June 3 online edition of the journal *Nature Genetics*.

"This work represents a major step forward and an important tool in the arsenal available to scientists and breeders for improving a vital source of nutrition," said Edward B. Knipling, administrator of USDA's Agricultural Research Service.

The analysis could also help those who develop corn yields as a source of fuel, who manage crops in the face of changing climates and who are concerned about the diminishing supply of arable land and growing populations, he said.

"This project is a stellar example of how collaborations of scientists, here and abroad, leverage resources across multiple agencies to enable transformational research with the potential to address urgent societal needs for a bio-based economy," said John Wingfield, assistant director for NSF's Biological Sciences Directorate.

It is anticipated that the tools and approaches generated in this project will enable scientists to look at genetic differences in other organisms as they respond to global climate change, human disturbance and invasive species, Wingfield explained.

The studies' collaborators shed light on corn's genetic diversity, detail how it evolved and outline how corn--known as maize among scientists--continues to diversify as it adapts to changing climates and habitats.

One study, published in the journal led by team member, USDA-ARS and Cold Spring Harbor Laboratory scientist Doreen Ware, examines the genetic structure and the relationships and sequential ordering of individual genes in more than 100 varieties of wild and domesticated corn.

Another study led by team member Jeff Ross-Ibarra from the University of California, Davis gives an extraordinary glimpse into how corn

evolved more than 8,700 years ago from a wild grass in the lowland areas of southwestern Mexico into today's ubiquitous international commodity.

The researchers compared wild varieties with traditional corn varieties from across the Americas and with modern improved breeding lines. They identified hundreds of genes that played a role in the transformation of corn from its wild origins to today's cultivated crop and show how that transition was largely achieved by ancient farmers who first domesticated it thousands of years ago.

Last year, the economic value of the U.S. corn crop was \$76 billion, with U.S. growers producing an estimated 12 billion bushels, more than a third of the world's supply. Corn is the largest production crop worldwide, providing food for billions of people and livestock and critical feedstock for production of biofuels.

Journal Reference: Xuehui Huang & Bin Han. A crop of maize variants. *Nature Genetics* 44, 734–735 (2012).

New insight gained into how plants may fight diseases

Source: BBSRC. 13 June 2012

A breakthrough discovery that has shown how plants may defend themselves in the face of pathogen attacks could hold the key to making crops more disease-resistant and to boosting food production to help global food security.

As part of a BBSRC-funded project led by Oxford Brookes University, STFC's Central Laser Facility has developed a unique technique that has answered a question which has puzzled scientists for many years - why certain proteins in plant cells don't move around as much as their counterparts in animal cells.

By enabling the movement of individual molecules in living plant cells to be observed in real time for the first time, the new technique has revealed that the cell wall plays a crucial role in limiting the mobility of proteins produced when a plant comes under attack. Specifically, it has shown that the cell wall allows these

proteins to stabilise in the plasma membrane (a 'skin' covering the inside of the cell wall). This restricts their ability to move around and fight invading pathogens and so increases the plant's vulnerability.

Dr Stan Botchway from the Lasers for Science division within the Central Laser Facility says: "The technique we've developed and deployed to solve this mystery has helped provide unprecedented insights into plants' defence mechanisms. As a result, we've plugged a major gap in scientists' understanding of how plants function at a microscopic level."

Dr John Runions of Oxford Brookes University, who has led the project, says: "This vital advance in our knowledge of the fundamental biological processes that take place in living plant cells will help us to improve crops' resilience and their ability to meet the challenges posed not just by diseases and pests but also by drought and a warming climate."

The breakthrough has been achieved using a single-molecule tracking technique specially developed at the OCTOPUS (Optics Clustered to OutPut Unique Solutions) imaging facilities, which form part of the world-leading Central Laser Facility's Lasers for Science division, located in the Research Complex at Harwell. This was complemented by the use of total internal reflection fluorescence (TIRF) microscopy - an established technique which, by eliminating background fluorescence, delivers extremely high-resolution images of samples under investigation.

The result was a clear demonstration that a plant's cell wall interacts with proteins produced in cell membranes and restricts their diffusion, possibly reducing their ability to ward off diseases.

As the world's population continues to grow, there is an urgent need to improve crop yields by enhancing the resilience of a range of crops to disease. This research project therefore represents a crucial stepping stone in bringing the sustainability of future food supplies within closer reach.

The research paper outlining this major discovery in plant biology has just been published in the Proceedings of the National Academy of Sciences (USA) at <http://www.pnas.org/content/early/recent>.

Link Between Vitamin C and Twin Seedlings Can Increase Seed Production in Crops

Source: ScienceDaily (June 18, 2012)

Biochemists at the University of California, Riverside report a new role for vitamin C in plants: promoting the production of twins and even triplets in plant seeds.

Daniel R. Gallie, a professor of biochemistry, and Zhong Chen, an associate research biochemist in the Department of Biochemistry, found that increasing the level of dehydroascorbate reductase (DHAR), a naturally occurring enzyme that recycles vitamin C in plants and animals, increases the level of the vitamin and results in the production of twin and triplet seedlings in a single seed.

The value of the discovery lies in the potential to produce genetically identical seedlings and increase production of high-value crops.

"The ability to increase fertility can be extremely useful when the inherent rate of fertility is low or the value of the crop is great, such as corn in which the production of multiple embryos would significantly boost its protein content," Gallie said. "The extra seedlings per seed may also enhance per-seed survival chances for some species."

Study results appear in the online journal PLoS ONE.

Just as in humans, twins in plants can be either genetically identical or fraternal. Gallie and Chen discovered that the twins and triplets produced in tobacco plants when vitamin C was increased were true twins or triplets as they were genetically identical.

In the lab, the researchers went on to show that injecting plant ovaries with vitamin C was sufficient to produce twins or triplets and that the vitamin causes the zygote, the fertilized egg, to divide into two or even three fertilized egg

cells before these cells proceed through subsequent stages of development to produce twins or triplets.

Although they used tobacco in their research, Gallie predicts vitamin C could generate twins and triplets in other plants as well.

"Because the early stages of embryo development are so conserved among plant species, we expect that vitamin C will have a similar effect in almost any plant," he said.

A question raised by the study is whether vitamin C might have a similar effect in humans. In contrast to most animals, humans cannot make vitamin C and it must, therefore, be obtained regularly from dietary sources.

"Although the development of plant and animal embryos differ in many respects, the manner in which the genetically identical twins were produced in our study is similar to that for identical human twins in that it is the very first division of the fertilized egg into two separate cells that produces the two separate embryos, resulting in two seedlings in plants or two fetuses in humans," Gallie said. "Despite the differences in the subsequent development of embryos in plants and humans, the critical effect of vitamin C is on this very first cell division."

To Gallie's knowledge, no study linking vitamin C to twins in humans has been carried out to date.

"Humans are mutants in that we lack the last enzyme in the pathway needed to produce vitamin C," he said.

Vitamin C is well known to prevent scurvy, a disease affecting collagen synthesis, iron utilization, and immune cell development. It also improves cardiovascular and immune cell function and is used to regenerate vitamin E. The vitamin is present at high levels in some fruits such as citrus and some green leafy vegetables, but present in low levels in those crops most important to humans such as grains. Vitamin C is as essential for plant health as it is for humans. It serves as an important antioxidant, destroying reactive oxygen species that can otherwise damage or even kill cells. In plants, vitamin C is important for photosynthetic function, in controlling water usage, in providing

protection against pollutants such as ozone, and promoting growth.

A grant from the University of California Agricultural Experiment Station supported the study.

Previously, Gallie and Chen, who helped develop technology to increase vitamin C in plants, showed that a boost of the vitamin can help plants defend themselves against the ravages of ozone -- smog's particularly nasty component. They also showed that reducing DHAR increases a plant's responsiveness to drought conditions.

Journal Reference: Zhong Chen, Daniel R. Gallie. Induction of Monozygotic Twinning by Ascorbic Acid in Tobacco. PLoS ONE, 2012; 7 (6): e39147 DOI: 10.1371/journal.pone.0039147

Key Part of Plants' Rapid Response System Revealed

ScienceDaily (June 18, 2012)

Science has known about plant hormones since Charles Darwin experimented with plant shoots and showed that the shoots bend toward the light as long as their tips, which are secreting a growth hormone, aren't cut off.

But it is only recently that scientists have begun to put a molecular face on the biochemical systems that modulate the levels of plant hormones to defend the plant from herbivore or pathogen attack or to allow it to adjust to changes in temperature, precipitation or soil nutrients.

Now, a cross-Atlantic collaboration between scientists at Washington University in St. Louis, and the European Synchrotron Radiation Facility and the European Molecular Biology Laboratory, both in Grenoble, France, has revealed the workings of a switch that activates plant hormones, tags them for storage or marks them for destruction.

The research appeared online in the May 24 issue of Science Express and will be published in a forthcoming issue of Science.

"The enzymes are cellular stop/go switches that turn hormone responses on and off," says Joseph Jez, PhD, associate professor of biology in

Arts & Sciences at WUSTL and senior author on the paper.

The research is relevant not just to design of herbicides -- some of which are synthetic plant hormones -- but also to the genetic modification of plants to suit more extreme growing conditions due to unchecked climate change.

Plants can seem pretty defenseless. After all, they can't run from the weed whacker or move to the shade when they're wilting, and they don't have teeth, claws, nervous systems, immune systems or most of the other protective equipment that comes standard with an animal chassis.

But they do make hormones. Or to be precise -- because hormones are often defined as chemicals secreted by glands and plants don't have glands -- they make chemicals that in very low concentrations dramatically alter their development, growth or metabolism. In the original sense of the word "hormone," which is Greek for impetus, they stir up the plant.

In plants as in animals, hormones control growth and development. For example, the auxins, one group of plant hormones, trigger cell division, stem elongation and differentiation into roots, shoots and leaves. The herbicide 2,4-D is a synthetic auxin that kills broadleaf plants, such as dandelions or pigweed, by forcing them to grow to the point of exhaustion.

Asked for his favorite example of a plant hormone, Corey S. Westfall brings up its chemical defense systems. Westfall, a graduate student in the Jez laboratory, who together with Chloe Zubieta, PhD, a staff scientist at the European Synchrotron Radiation Facility did most of the work on the research.

Walking through a public park in St. Louis near WUSTL, Westfall often sees oak leaves with brown spots on them. The spots are cells that have deliberately committed cell suicide to deny water and nutrients to a pathogen that landed in the center of the spot. This form of self-sterilization is triggered by the plant hormone salicylic acid.

Westfall also mentions the jasmonates, which cause plants to secrete compounds such as

tannins that discourage herbivores. Tannins are toxic to insects because they bind to salivary proteins and inactivate them. So insects that ingest lots of tannins fail to gain weight and may eventually die.

Hormones, in other words, allow plants to respond quickly and sometimes dramatically to developmental cues and environmental stresses. But in order to respond appropriately, plants have to be able to sensitively control the level and activity of the hormone molecules.

The Science paper reveals a key control mechanism: a family of enzymes that attach amino acids to hormone molecules to turn the hormones on or off. Depending on the hormone and the amino acid, the reaction can activate the hormone, put it in storage or mark it for destruction.

For example, in the model plant, thale cress, fewer than 5 percent of the auxins are found in the active free-form. Most are conjugated (attached) to amino acids and inactive, constituting a pool of molecules that can be quickly converted to the active free form.

The attachment of amino acids is catalyzed by a large family of enzymes (proteins) called the GH3s, which probably originated 400 million years ago, before the evolution of land plants. The genes diversified over time: there are only a few in mosses, but 19 in thale cress and more than 100 in total.

"Nature finds things that works and sticks with them," Jez says. The GH3s, he says, are a remarkable example of gene family expansion to suit multiple purposes.

The first GH3 gene -- from soybean -- was sequenced in 1984. But gene (or protein) sequences reveal little about what proteins do and how they do it. To understand function, the scientists had to figure out how these enzymes, which start out as long necklaces of amino acids, fold into knobby globules with protective indentations for chemical reactions.

Unfortunately, protein folding is a notoriously hard problem, one as yet beyond the reach of computer calculations at least as a matter of routine. So most protein structures are still

solved by the time-intensive process of crystallizing the protein and bombarding the crystal with X-rays to locate the atoms within it. Both the Jez lab and the Structural Biology Group at European Synchrotron Radiation Facility specialize in protein crystallization.

By good fortune, the scientists were able to freeze the enzymes in two different conformations. This information and that gleaned by mutating the amino acids lining the enzyme's active site let them piece together what the enzymes were doing.

It turned out that the GH3 enzymes, which fold into a shape called a hammer and anvil, catalyze a two-step chemical reaction. In the first step, the enzyme's active site is open allowing ATP (adenosine triphosphate, the cell's energy storage molecule) and the free acid form of the plant hormone to enter.

Once the molecules are bound, the enzyme strips phosphate groups off the ATP molecule to form AMP and sticks the AMP onto an "activated" form of the hormone, a reaction called adenylation.

Adenylation triggers part of the enzyme to rotate over the active site, preparing it to catalyze the second reaction, in which an amino acid is snapped onto the hormone molecule. This is called a transferase reaction.

"After you pop off the two phosphates," Jez says, "the top of the molecule ratchets in and sets up a completely different active site. We were lucky enough to capture that crystallographically because we caught the enzyme in both positions."

The same basic two-step reaction can either activate or inactivate a hormone molecule. Addition of the amino acid isoleucine to a jasmonate, for example, makes the jasmonate hormone bioactive. On the other hand addition of the amino acid aspartate to the auxin known as IAA marks it for destruction.

This is the first time any GH3 structure has been solved.

Understanding the powerful plant hormone systems will give scientists a much faster and more targeted way to breed and domesticate

plant species, speed that will be needed to keep up with the rapid shift of plant growing zones.

Plant hormones, like animal hormones, typically affect the transcription of many genes and so have multiple effects, some desirable and others undesirable. But GH3 mutants provide a tantalizing glimpse of what might be possible: some are resistant to bacterial pathogens, others to fungal pathogens and some are exceptionally drought tolerant.

Westfall mentions that in 2003, a scientist at Purdue University figured out that a corn strain that had a short stalk but normal ears and tassels had a mutation that interferes with the flow of the hormone auxin in the plant.

Because the plants are so much smaller, they are relatively drought resistant and might be able to grow in India, where North American corn varieties cannot survive. Similar high-yield dwarf varieties might prevent famine in areas of the world where many people are at risk of starvation.

Journal Reference: C. S. Westfall, C. Zubieta, J. Herrmann, U. Kapp, M. H. Nanao, J. M. Jez. Structural Basis for Preceptor Modulation of Plant Hormones by GH3 Proteins. *Science*, 2012; DOI: 10.1126/science.1221863

Rice Blast Infection Mechanism Uncovered

Source: ScienceDaily (June 21, 2012)

Scientists at the University of Exeter have made a new discovery that they hope might lead to effective control of rice blast disease.

Rice blast is the most serious disease of cultivated rice and affects all the rice-growing regions of the world, causing losses of up to 30% of the global rice harvest.

Yasin Dagdas and colleagues studied the rice blast fungus, which develops a pressurised infection cell, called an appressorium to rupture the rice leaf cuticle. The appressorium generates extreme pressure, estimated to be 40 times that of a car tyre. Dagdas and colleagues, who work under the supervision of Prof. Nick Talbot, have identified how the fungus channels its pressure to form a narrow infection peg that breaches the

rice leaf surface. Their work implicates a specialised group of proteins called septins in plant infection for the first time. These proteins may be important to allow the rigid, pressurised cell to focus force at the point of plant infection. Yasin Dagdas said: "This is another step in our journey to discover how this devastating fungus works and we hope, in the future, may help prevent the destruction of so much of the world's rice production."

Published June 21 2012 in the journal *Science*, the team came to its conclusion by analysing the septin gene family and its role in re-organisation of the infection cell, so that it grows an infection peg that extends through the rice cuticle and into rice tissue. The project used live-cell imaging, molecular genetics and genomic procedures and represents a significant breakthrough in our understanding of the plant infection process by cereal-infecting fungi. This could ultimately impact upon control of a range of rice, wheat and barley diseases.

Speaking about the discovery, Prof. Nick Talbot said "Rice blast is a terrible disease, affecting some of the poorest regions of the world. We hope that this discovery will allow us to understand plant infection in more detail and we can then apply the knowledge to provide better solutions to farmers in controlling blast outbreaks."

Journal Reference: Y. F. Dagdas, K. Yoshino, G. Dagdas, L. S. Ryder, E. Bielska, G. Steinberg, N. J. Talbot. Septin-Mediated Plant Cell Invasion by the Rice Blast Fungus, *Magnaporthe oryzae*. *Science*, 2012; 336 (6088): 1590 DOI: 10.1126/science.1222934

Is Your Leaf Left-Handed?

Source: ScienceDaily (June 23, 2012)

The front of a leaf is different from the back of a leaf and the tip is different from the base. However, a leaf from a tomato or an Arabidopsis plant superficially appears to be bilaterally symmetrical, or the same on the left and right sides. Don't let its appearance fool you; there is an underlying asymmetry between the left and

right sides of such leaves -- it just took a while for scientists to discover it. The story begins with the mechanism by which leaves form along a stem. In broad-leafed plants, dicots, leaves form from the meristem, an actively dividing tissue at the top of the plant, so that as you look down the stem, the oldest leaves are at the bottom.

Leaves don't just become arranged by random chance either -- phyllotaxis, the arrangement of leaves or flowers along a stem, affects key plant characteristics, such as how much light can filter through to lower leaves. Leaves can form opposite each other, or in alternation, or in whorls; often leaves form in spirals where the next leaf is offset by roughly 137 degrees, known as the "golden angle," which is related to the Fibonacci sequence.

Recent research has shown that leaf initiation in the meristem is specified by locally high concentrations of the plant hormone auxin. In a study published in *The Plant Cell*, an international group coordinated by Neelima R. Sinha, Ph.D., of the University of California at Davis, examined how the pattern of auxin concentrations might affect the symmetry of the leaf. She explains, "As leaves are initiated within a spiral context, we might expect that they would be asymmetric and exhibit the same handedness of the spiral, like propeller blades. Yet, superficially many leaves appear symmetrical." To examine whether the spiral pattern of leaves affected symmetry, her team first modeled the anatomy of the forming leaves and the location of the highest concentrations of auxin, finding that the two were not perfectly aligned. Following up, they found that this difference caused asymmetry at both the molecular level, altering gene expression, and the anatomical level, altering leaf shape, in tomato and *Arabidopsis thaliana* leaves. Indeed, the authors found measurable anatomical differences between the left and right sides of both young and mature leaves, identifying a previously overlooked axis of asymmetry.

Dr. Sinha summarizes: "Our results show that asymmetry is indeed very much present in the leaves around us and that the spiral, within

which they are initiated, influences their development from the earliest stages. Quite literally, the handedness of the spiral in plants transmits its asymmetry to leaves. By studying these asymmetries, we can begin to understand the mechanisms by which plants produce such a staggering array of leaf shapes in such regular arrangements."

Journal Reference: D. H. Chitwood, L. R. Headland, A. Ranjan, C. C. Martinez, S. A. Braybrook, D. P. Koenig, C. Kuhlemeier, R. S. Smith, N. R. Sinha. Leaf Asymmetry as a Developmental Constraint Imposed by Auxin-Dependent Phyllotactic Patterning. *The Plant Cell*, 2012; DOI: 10.1105/tpc.112.098798

How Sweet It Is: Tomato Researchers Discover Link Between Ripening, Color and Taste

Source: ScienceDaily (June 28, 2012)

For many grocery shoppers, those perfect, red tomatoes from the store just can't match the flavor from the home garden. Now, researchers at Boyce Thompson Institute for Plant Research at Cornell University, USDA and the University of California at Davis have decoded a gene that contributes to the level of sugar, carbohydrates and carotenoids in tomatoes.

Cuong Nguyen, a Cornell graduate student in plant breeding working at the Boyce Thompson Institute (BTI), along with colleagues at BTI, USDA, UC Davis, Universidad Politécnica de Valencia (Spain), Universidad de Málaga (Spain) and University of Suleyman Demiral (Turkey) revealed the gene that underlies the uniform ripening mutation.

This gene also influences how tomato fruits ripen and is used by commercial breeders to create tomatoes that develop into perfectly red, store-ready fruit. "Practically, it is a very important trait," says James Giovannoni, a plant molecular biologist with BTI and the U.S. Department of Agriculture, Agricultural Research Service, who is a senior author on the paper. "It's a gene that whether you realize it or not, most of your tomatoes have." However, this

same trait reduces sugars and nutrients in the fruit.

Naturally, tomatoes have uneven ripening, showing darker green patches when unripe and variable redness when ripe -- traits that still show up in garden-variety and heirloom breeds. However, in the late 1920s, commercial breeders stumbled across a natural mutation that caused tomatoes to ripen uniformly -- from an even shade of light green to an even shade of red. This mutation, known by plant biologists as 'uniform ripening', has become indispensable to the \$2 billion a year US commercial tomato market, showing up in almost all tomatoes produced for grocery stores. The uniform redness makes it ideal for the grocery sector, which has to appeal to customer expectations of evenly colored, red fruit.

Nguyen conducted positional cloning and, with access to solgenomics.net, an online, public database hosted at BTI, he determined that the uniform ripening gene was located at a specific location on chromosome 10. With this location now known, the team could decipher the gene coding for the protein that controls photosynthesis levels in tomato fruit. While leaves are the primary photosynthesis factories in a plant, developing tomato fruit can contribute up to 20 percent of their own photosynthesis, yielding high sugar and nutrient levels in fully ripe fruit. The uniform ripening mutation, which commercial breeders select for, eliminates this protein in the fruit, therefore reducing sugar levels. "This is an unintended consequence," says Giovannoni, explaining why commercial growers continued to select for the trait. "Producers currently don't get a penny more for [flavor] quality."

This discovery has practical applications. Commercial producers -- who wish to produce uniform red fruit over multi-colored, flavorful ones -- can now do an early test on seedling DNA for the uniform ripening mutation, rather than waiting to observe the mature fruit. Conversely, those who don't care about appearances can make sure of the opposite -- that their plants are

mutation free and thus may have better-tasting fruit.

Ann Powell, a research biochemist who led the UC Davis team's efforts on the research, says that the study "is a rare chance to translate scientific findings to the real world...it provides a strategy to re-capture quality characteristics that had been unknowingly bred out of modern cultivated tomatoes."

Journal Reference: A. L. T. Powell, C. V. Nguyen, T. Hill, K. L. Cheng, R. Figueroa-Balderas, H. Aktas, H. Ashrafi, C. Pons, R. Fernandez-Munoz, A. Vicente, J. Lopez-Baltazar, C. S. Barry, Y. Liu, R. Chetelat, A. Granell, A. Van Deynze, J. J. Giovannoni, A. B. Bennett. Uniform ripening Encodes a Golden 2-like Transcription Factor Regulating Tomato Fruit Chloroplast Development. *Science*, 2012; 336 (6089): 1711 DOI: 10.1126/science.1222218

Discovery May Lead to New Tomato Varieties With Vintage Flavor and Quality

Source: ScienceDaily (June 28, 2012)

A new discovery could make more tomatoes taste like heirlooms, reports an international research team headed by a University of California, Davis, plant scientist.

The finding, which will be reported in the June 29 issue of the journal *Science*, has significant implications for the U.S. tomato industry, which annually harvests more than 15 million tons of the fruit for processing and fresh-market sales.

"This information about the gene responsible for the trait in wild and traditional varieties provides a strategy to recapture quality characteristics that had been unknowingly bred out of modern cultivated tomatoes," said Ann Powell, a biochemist in UC Davis' Department of Plant Sciences and one of the lead authors of the study.

"Now that we know that some of the qualities that people value in heirloom tomatoes can be made available in other types of tomatoes, farmers can have access to more varieties of tomatoes that produce well and also have desirable color and flavor traits," she said.

For decades, plant breeders in the tomato industry have selected varieties that are uniformly light green before they ripen, in order to produce tomatoes that can be harvested at the same time.

However, this characteristic is accompanied by an unintended reduction in sugars that compromises the flavor of the fresh fruit and its desirability for processing.

Powell's UC Davis research team began studying the genes influencing tomato fruit development and ripening after spending two summers screening tomato plants for transcription factors that might play a role in both fruit color and quality. Transcription factors are proteins that regulate genes, or turn them on and off. These factors themselves are manufactured or expressed by genes.

The UC Davis researchers were particularly interested in tomatoes they observed in the field that were unusually dark green before they ripened.

Partnering with researchers at Cornell University and in Spain, who were mapping regions of the tomato genome, the scientists discovered two transcription factors, called GLK1 and GLK2, that control the development of chloroplasts. Chloroplasts are the structures in the plant cells that enable plants to photosynthesize, converting the energy of sunlight into sugars and other compounds that influence flavor and color.

The researchers scoured a collection of mutant and wild species of tomatoes at UC Davis established at UC Davis by the late Professor Charles Rick beginning in the 1950s. They discovered that dark green tomatoes that naturally express GLK2 produced ripe fruit with increased levels of sugars or soluble solids, important for processing tomatoes, as well as higher levels of the health-promoting compound lycopene.

"Nature presents numerous important genes and their variants, like uniform ripening, that breeders employ to facilitate the needs of growers, processors and consumers," said Jim Giovannoni, a USDA plant molecular biologist

with the Boyce Thompson Institute at Cornell University. "Understanding the genes responsible for these characteristics facilitates the challenging process of breeding crops that meet the needs of all components of the food-supply chain."

Cuong Nguyen, a Cornell graduate student in Giovannoni's laboratory co-authored the paper with Powell. Other members of the research team included: Theresa Hill, KaLai Lam Cheng, Rosa Figueroa-Balderas, Hakan Aktas, Hamid Ashrafi, Ariel Vicente, Javier Lopez-Baltazar, Roger Chetelat, Allen Van Deynze and Alan Bennett, all of UC Davis; Yongsheng Liu and Cornelius Barry of Cornell University and the Boyce Thompson Institute of the USDA; Clara Pons and Antonio Granell, of the Universidad Politécnica de Valencia, Spain; Rafael Fernández-Muñoz of the Universidad de Málaga, Spain.

Funding for the study was provided by The University of California Discovery program, the U.S. Department of Agriculture-Agricultural Research Service, the National Science Foundation, the Viet Nam Education Foundation, the Fundación Genoma España, and the Ministerio de Ciencia y Tecnología and the Instituto Tecnológico de Costa Rica.

Journal Reference: A. L. T. Powell, C. V. Nguyen, T. Hill, K. L. Cheng, R. Figueroa-Balderas, H. Aktas, H. Ashrafi, C. Pons, R. Fernandez-Munoz, A. Vicente, J. Lopez-Baltazar, C. S. Barry, Y. Liu, R. Chetelat, A. Granell, A. Van Deynze, J. J. Giovannoni, A. B. Bennett. Uniform ripening Encodes a Golden 2-like Transcription Factor Regulating Tomato Fruit Chloroplast Development. *Science*, 2012; 336 (6089): 1711 DOI: 10.1126/science.1222218

A New Source of Maize Hybrid Vigor

ScienceDaily (June 28, 2012)

Steve Moose, an associate professor of maize functional genomics at the University of Illinois and his graduate student Wes Barber think they may have discovered a new source of heterosis, or hybrid vigor, in maize. They have been looking at small RNAs (sRNAs), a class of double-

stranded RNA molecules that are 20 to 25 nucleotides in length.

"Hybrid vigor" refers to the increased vigor or general health, resistance to disease, and other superior qualities arising from the crossbreeding of genetically different plants. "We've always known that there's a genetic basis for this heterosis," said Moose. "Charles Darwin noticed it and commented that corn was particularly dramatic."

Scientists have been debating the sources of hybrid vigor since the early 1900s when Mendel's laws were rediscovered. Many of them disagreed with the model that prevailed from the 1920s to the 1950s, which linked heterosis to a single gene or to the interaction of several genes. "It seemed that the whole genome was involved," said Moose.

The discovery of DNA in 1953 eventually caused a paradigm shift in the way people looked at hybrid vigor but, Moose said, there was no unifying theory. Even as new genetic technologies were developed, the genes did not seem to explain everything.

"We thought that maybe it's the rest of the genome, the remaining 85 percent of the corn genome, that's important," said Moose.

sRNAs were originally found in 1998 in roundworms. Researchers studying virus resistance in plants then began to notice them and observed that the way that they function is very different from the functioning of protein-coding genes.

"Every time we have a breakthrough in our knowledge of genetics, people have looked to see if that breakthrough brings any insight into the mystery of the hybrid vigor," said Moose. "That's what we've done with the small RNAs."

"When you think about what small RNAs do, they participate in regulating growth and they tell other genes what to do," he continued. "So they have the two properties that we know fit what has been described (about heterosis) even though we do not have an explanation. We would argue that, while they are part of the explanation, they may not be the whole explanation."

Moose and Barber sampled small RNAs from the seedling shoot and the developing ear of maize hybrids, two tissues that grow rapidly and program growth, to investigate how the small RNA profiles of these hybrids differed from those of their parents. In collaboration with associate professor of crop sciences Matt Hudson, they analyzed what they described as a "deluge" of data.

"There were 50 million data points, but we whittled it down to the most important ones," said Barber.

They found that differences are due mainly to hybrids inheriting distinct small interfering RNAs (siRNAs), a subset of sRNAs, from each parent. The siRNAs interfere with gene expression. They also found that hybridization does not create new siRNAs, but hybrids have a more complex siRNA population than their parents because they inherit distinct siRNAs from both parents.

Moreover, the differences in parental siRNAs originated primarily from repeats, which are the result of retrotransposon activity. Retrotransposons are elements that move around and amplify themselves within a genome.

"This is a new source of genetic diversity that people had overlooked," said Barber.

"We are not saying that genes are not important," said Moose. "But probably the way corn properties are altered in the hybrid situation is mediated by the small RNAs in addition to the genes."

Moose and Barber hope that their work might provide more insight into how to decide which inbred maize lines to cross. "We don't want to alter how the plant grows, but if we can tweak it to do whatever it already does either faster or more, that could be an advantage," said Moose.

Journal Reference: W. T. Barber, W. Zhang, H. Win, K. K. Varala, J. E. Dorweiler, M. E. Hudson, S. P. Moose. Repeat associated small RNAs vary among parents and following hybridization in maize. *Proceedings of the National Academy of Sciences*, 2012; 109 (26): 10444 DOI: 10.1073/pnas.1202073109

Adoption of Advanced Techniques Could Propel Crop Improvement

Source: ScienceDaily (June 28, 2012)

Scientists could take greater strides toward crop improvement if there were wider adoption of advanced techniques used to understand the mechanisms that allow plants to adapt to their environments, current and former Purdue University researchers say.

A perspective for the journal *Science*, Brian Dilkes, a Purdue assistant professor of genetics, and Ivan Baxter, a research computational biologist for the U.S. Department of Agriculture's Agricultural Research Service, argue that today's technology could allow scientists to match physiological and genetic characteristics of plants with the soil characteristics that promote or inhibit their growth. Making those connections could reduce the time necessary to improve plants that are coping with changing environmental and climatic conditions.

"Evolution has solved the problems that we face in terms of adapting plants to grow in a multitude of environments," Dilkes said. "If we understand these processes, we'll be able to apply that knowledge to maintaining diversity in natural systems and improving and maintaining crop yield."

The majority of a plant's makeup, besides carbon dioxide, comes from elements and minerals absorbed from the soil as the plant grows. The physiological and genetic mechanisms that allow plants to obtain iron from the soil, for instance, can also cause the plant to accumulate other elements. Understanding how those changes interact is an important piece of improving plants, Baxter said. "This is just a hint of the complexity that's out there," said Baxter, a former post-doctoral researcher at Purdue who works for the USDA at the Donald Danforth Plant Science Center in St. Louis. "If we're going to make the necessary improvements in agricultural productivity, we will have to move forward with these techniques."

Much of the work done to understand how plants have adapted to their environments focuses on one gene and one element it controls at a time. Pinpointing one or more genes responsible for a particular trait can take years, even decades.

Dilkes and Baxter believe a wider adoption of molecular phenotyping techniques, such as ionomics and genome-wide association mapping, could allow scientists to work with multiple elements and genes at once.

"By focusing on one gene or one element at a time, you miss out on the other physiological mechanisms occurring in the plant," Dilkes said. "The potential to broaden our understanding of these complex interactions and have a dramatic effect on agriculture is there."

Genome-wide association mapping allows scientists to find genetic associations among multiple phenotypes, or physical traits. The process quickly shows which genes may be responsible for the physical characteristics.

Ionomics studies the elemental composition of plants and how those compositions change in response to environmental or genetic changes.

"Experiments with thousands of samples are now possible," Baxter said. "We've just started to put these things together."

Journal Reference: I. Baxter, B. P. Dilkes. Elemental Profiles Reflect Plant Adaptations to the Environment. *Science*, 2012; 336 (6089): 1661 DOI: 10.1126/science.1219992

Plain tomatoes taste... plain

Source: Nature Reviews blog. By Alice Lighton. 28 Jun 2012

Tomatoes bred to have a uniform colour are not as sweet as their more mottled counterparts. Decades of selecting fruit that begin life with pale green skin may have inadvertently contributed to the bland flavour of the modern supermarket tomato.

Uniform tomatoes are easier to harvest and preferred by consumers. Researchers have pinpointed the genes responsible for even-coloured fruit, and found an association with

photosynthesis in plants. Tomatoes with the mutation do not produce a protein responsible for chloroplast development in fruit, and pale unripe fruit produce less sugar while they develop, resulting in a less-sweet tomato. Their results are published today in Science.

But consumers cannot try before they buy, and they make choices based on looks. “The general perception is that consumers prefer uniformly coloured fruit,” says James Giovannoni, a molecular plant biologist at Cornell University in Ithaca, New York, and an author of the study. “They’ll pick up a fruit that’s more evenly coloured over one that’s splotchy.”

Farmers also prefer the pale, uniformly coloured fruit. Tomatoes destined for processing and tins are mechanically harvested, and colour is used to decide when to send in the machines.

Darker unripe fruits contain more chlorophyll and ripen into tastier red tomatoes, with more glucose, fructose and carotenoids. “The differences are not huge — around 10 to 20%,” says Giovannoni. But that is still enough to taste. Heritage varieties of tomato — which have never been bred commercially — contain the original version of the allele responsible for chloroplast development in fruit. The fruits often have a darker green top that ripens to a different colour from the bottom.

Low sugar content is not the only problem with the flavour of the commercial tomato. Last month, researchers in Florida reported that supermarket tomatoes lacked volatile organic compounds present in heritage varieties that make the fruit taste sweeter (see ‘It’s not sugar that makes heirloom tomatoes taste sweeter’).

At present, the tomato is the fleshy fruit of choice for plant geneticists: tomatoes grow quickly, have a relatively short genome and are easy to genetically modify. Giovannoni’s team contributed to the sequencing of the tomato genome, reported last month (see ‘Tomato genome sequence bears fruit’).

However, genetically modified crops are not popular among consumers, and a return to a patchy tomato may not be popular among farmers. Instead, breeders could try to produce

a fruit with a uniform dark green colour. Otherwise, consumers may have to resort to growing their own fruits in search of a delicious, if wonky-looking, tomato.

Reference: Powell et al. Uniform ripening Encodes a Golden 2-like Transcription Factor Regulating Tomato Fruit Chloroplast Development. Science 29 June 2012: Vol. 336 no. 6089 pp. 1711-1715. DOI: 10.1126/science.1222218



Scientists Obtain Complete Melon Genome

Source: redOrbit Staff & Wire Reports. July 4, 2012

Researchers in Spain report that they have obtained the melon genome. This is the first time that a Spanish initiative that unites private and state-run centers has gained the complete genome of a higher organism, a plant, which produces flowers and seeds. Also, it has been done by applying massive sequencing technologies.

Besides the complete melon genome, scientists have obtained the particular genomes of seven melon varieties.

The study is published in the magazine Proceedings of the National Academy of Sciences (PNAS).

The scientific project has been led by Pere Puigdomènech, at the Spanish National Research Council (CSIC), and Jordi Garcia Mas, at the

Institute for Research and Technology in Food and Agriculture (IRTA). Both scientists work at the Center for Research in Agricultural Genomics (CRAG), in Barcelona. Also, the team lead by Roderic Guigó, at the Genomic Regulation Center has made a huge contribution to the project.

The Melonomics project was launched by the Spanish Genome Foundation. Nine research centers have been involved, having the support of five companies and of five Spanish self-governing communities.

Results have shown that the melon genome has 450 millions of base pairs and 27.427 genes. It is much bigger than the genome of its nearest “relative,” the cucumber that has 360 million base pairs.

“This difference is due mainly to the amplification of transposable elements. We didn’t find recent duplications within the genome, which are very common in plant species”, highlights Puigdomènech.

“We have identified 411 genes that can be related in disease resistance. They are few but, nonetheless, the melon has a high capacity of adjustment to different environments”, explains the CSIC scientist. During the work, when comparing this genome with others that are near phylogenetically, they have observed how changes occur to the genome of this species, which is known for its high variability.

Another point of interest is related to the ripening of the fruit, a process which determines fruit characteristics such as taste and flavor. Scientists have identified up to 89 genes related with some aspects of this process: 26 genes related to the carotenoid accumulation – which gives the color to the melon flesh – and 63 related to the sugar accumulation and the taste of melon. 21 genes out of the last 63 had never been described before.

“Knowing the genome and the genes related to the characteristics of value for agriculture will allow us to improve this species for obtaining more disease resistant varieties and with better organoleptic properties”, points out the IRTA scientist Jordi Garcia Mas.

Melon belongs to the family of cucurbits that also includes species such as cucumbers, watermelons and squashes. Cucurbits have relatively small genomes. “These are species of high financial interest, especially in the Mediterranean, Asian and African countries. Diseases that affect them, such as the mosaic virus in the case of cucumber or fungi can cause high financial losses. Therefore, we hope the genome sequentiation will have an important impact on improving this crop”, says Pere Puigdomènech.

According to figures of 2009 from the Food and Agriculture Organizations (FAO) of the United Nations, the production of melon worldwide is 26 million tons every year. Spain is the fifth biggest producer in the world. About one third of the production is exported, which makes Spain the biggest exporter of melon.

The melon genome project has been led by CRAG, which is a consortium of different institutions and universities, where they have done the sequencing and assembling of the genome. The Center of Genomic Regulation has annotated the genome.

Also, the project has had teams working on it at different centers and universities: the Pompeu Fabra University (Barcelona), the CSIC’s Centro de Edafología y Biología Aplicada del Segura of the CSIC (Murcia), the Centro Nacional de Análisis Genómico (Barcelona), the Universidad Politécnica in Valencia and Wisconsin University (U.S.). Furthermore, the company Roche Diagnostics has facilitated technologies in order to help the genome assembling.

Salt Cress Genome Yields New Clues to Salt Tolerance

Source: ScienceDaily (July 13, 2012)

An international team, led by Institute of Genetics and Developmental Biology, Chinese Academy of Science, and BGI, the world's largest genomics organization, has completed the genomic sequence and analysis of salt cress (*Thellungiella salsuginea*), a wild salt-tolerant plant. The salt cress genome serves as a useful

tool for exploring mechanisms of adaptive evolution and sheds new lights on understanding the genetic characteristics underlying plant abiotic stress tolerance.

The study was published online in PNAS.

Salt Cress is a typical halophyte with high resistance to cold, drought, oxidative stresses and salinity. Due to its small plant size, short life cycle, copious seed production, small genome size, and an efficient transformation, salt cress could serve as an important genetic model system for botanist, geneticists, and breeders to better explore the genetic mechanisms of abiotic stress tolerance.

In the study, researchers sequenced the genome of salt cress (Shandong ecotype) using the paired-end Solexa sequencing technology. The genomic data yielded a draft sequence of salt cress with about 134-fold coverage.

The final length of the assembled sequences amounted to about 233.7 Mb, covering about 90% of the estimated size (~260 Mb). A total of 28,457 protein-coding regions were predicted in the sequenced salt cress genome.

Researchers found that the average exon length of salt cress and *A. thaliana* genes was similar, whereas the average intron length of salt cress was about 30% larger than that of *A. thaliana*.

The evolutionary analysis indicated that salt cress and its close relative- *Arabidopsis thaliana*-diverged from approximately 7 -12million years ago. When tracing the differences between salt cress and *A. thaliana*, researchers found salt cress was characterized by a dramatically different lifestyle, a unique gene complement, significant differences in the expression of orthologs, and a larger genome size. Noticeably, the salt cress genome showed a dramatically higher content of transposable elements (TEs)

than that of *A. thaliana*, which may be the reason for its enlarged genome size. In common with other higher plants, salt cress genome was consisted of abundance of long terminal repeat (LTR) retrotransposons.

Salt can have drastic effects on the growth and yield of agronomical crops. It is estimated that salinity renders about one-third of the world's irrigated land unsuitable for crop production. In this study, researchers identified many genes in salt cress that contribute to its success in high-salt environments, such as the genes related with cation transport, abscisic acid signaling, and wax production.

Junyi Wang, Director of Science & Technology, Research & Cooperation Center, BGI, said, "Salt cress provides an excellent model and opportunity for researchers to explore plant's mechanisms of abiotic stress tolerance.

The completed genomic sequence of salt cress will boost the advancement of stress tolerance research as well as provide a valuable theoretic instruct and technical support for researchers worldwide to better face the challenges of the soil salinization in irrigation area, the development and utilization of shallow offshore waters and beaches, and food security."

Journal Reference: H.-J. Wu, Z. Zhang, J.-Y. Wang, D.-H. Oh, M. Dassanayake, B. Liu, Q. Huang, H.-X. Sun, R. Xia, Y. Wu, Y.-N. Wang, Z. Yang, Y. Liu, W. Zhang, H. Zhang, J. Chu, C. Yan, S. Fang, J. Zhang, Y. Wang, F. Zhang, G. Wang, S. Y. Lee, J. M. Cheeseman, B. Yang, B. Li, J. Min, L. Yang, J. Wang, C. Chu, S.-Y. Chen, H. J. Bohnert, J.-K. Zhu, X.-J. Wang, Q. Xie. Insights into salt tolerance from the genome of *Thellungiella salsuginea*. Proceedings of the National Academy of Sciences, 2012; DOI: 10.1073/pnas.1209954109

Forthcoming meetings

9th International Conference "Plant Functioning in Stress Environment"

September 12 – 15, 2012. Cracow, Poland

<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

Root Systems Biology

September 19 – 21, 2012. Taipei, Taiwan

More info: <http://isrsb.sinica.edu.tw/index.html>

The 4th EMBO meeting NICE 2012 advancing the life sciences

September 22 – 25, 2012. Nice, France

Late abstracts: Missed the deadline? **Late**

abstracts now open. Deadline: 12 August 14.00h

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

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/>

The Future of Plant Genomes - Harvesting Genes for Agriculture

October 9 – 11, 2012. Barcelona, Spain

More info:

<http://www.bdebate.org/en/forum/future-plant-genomes-harvesting-genes-agriculture>

"The Future of Plant Genomes. Harvesting Genes for Agriculture" workshop will be held in Barcelona. It aims at bringing together around 60 experts in plant genomics, including 17 well-known invited speakers. You can apply to be selected as participant. Morning and afternoon sessions with a special interest in creating intense discussion among the participants are

scheduled.

Participants will discuss how the recent progress in plant genome sequence influences our understanding of plant genome architecture and evolution and how it creates new opportunities for crop improvement. Of special interest is the impact of next-generation sequencing technologies in sequencing and re-sequencing crop genomes and how these new data are currently being used by seed companies to provide consumers with improved products. Sessions will cover the following issues: the use of genome sequences to study natural variability and genome evolution; how genome information is translated to agricultural innovation by researchers of public and private organisations; genomes of monocot and dicot crop species; and the challenges faced by genome data processing and analysis in the field of bioinformatics.

Please visit the [CRAG webpage](#) for more details.

Contacts: Jordi Garcia-Mas (CRAG); Pere Arús (CRAG); [Pere Puigdomènech](#) (CRAG).

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

10th International Congress on Plant Molecular Biology

October 21 – 26, 2012. Jeju, South Korea

More info: <http://www.ipmb2012.org/>

Conference on Integrative Biology in Plants, Microorganisms and the Environment (SysBioLux).

November 6 – 9, 2012. Luxembourg

The current organization, an international discussion on fundamental and practical aspects of Systems Biology in studies related to plants, microorganisms and the environment, hosted by the Public Research Centre - Gabriel Lippmann is the first edition in this format. It is, however, a prolongation of a series of scientific conferences focused on proteomics applications in plants and microorganisms that started in 2002. The thematic broadening that resulted in the establishment of what will become a biennial event follows the current evolution in life sciences towards an increased multidisciplinary.

At the first [SysBioLux conference](#), participants will have the opportunity to present their recent research on the integrated use of high-throughput analytical techniques in the study of plants, microorganisms and the environment. The conference is organized in a relaxing setting thereby fostering interaction with colleagues to discuss recent advances, the opportunity for which is likewise offered in the social agenda of the organization. The seminar will include invited lectures and presentations selected based on submitted abstracts, intermixed with poster sessions.

Session 1: Plants for Food

Session 2: Plant for Bio-Based Products

Session 3: Plant-microbe interactions

Session 4: Plant and Environment

Session 5: Ecosystems Biology

Invited speakers:

Wilhelm GRUISSEM (ETH Zurich, Switzerland)

Kim HAMMOND KOSACK (Rothamsted Research, UK)

Dirk INZÉ (VIB - University of Gent, Belgium)

Rui MALHO (University of Lisbon, Portugal)

Hans-Peter MOCK (IPK Gatersleben, Germany)

Paul WILMES (University of Luxembourg, Luxembourg)

The general presentation, along with Registration as well as a Call for Abstracts and

more information can be found on the homepage of the conference (<http://sysbiolux.lippmann.lu>).

International Conference on Advances in Plant Sciences (ICAPS)

November 14 – 18, 2012. Chiang Mai, Thailand

More info: <http://plants2012.com/>

12th International Citrus Congress (ICC 2012). "Citrus and Health".

November 18 – 23, 2012. Valencia, Spain.

More info:

http://www.citruscongress2012.org/web/?page_id=5

International Conference on Agricultural and Food Engineering for Life 2012

November 26 – 29, 2012. Putrajaya, Malaysia

Website:

<http://www.eng.upm.edu.my/cafei2012>

Auxin 2012

December 9 – 14, 2012. The Big Island, Hawaii

More info: <http://auxin.hawaii-conference.com/>

2nd BIOTECHNOLOGY WORLD CONGRESS

February 18 – 21, 2013. Dubai, UAE

The conference offers the following sessions in biotechnology:

1. Pharmaceutical Biotechnology: biopharmaceuticals discovery (CNS, cancer, cardiovascular, endocrine, immune); vaccines; antibodies; protein engineering

2. Plant and Environmental: transgenic plants and crops; bioremediation; microbial diversity; bio-monitoring.

3. Industrial and manufacturing: bio-fuels; energy crops (cellulosic ethanol industry); industrial enzymes; bioprocess engineering and optimization.

4. Medical Biotechnology: stem cells; gene therapy; tissue engineering; biopharmaceutical manufacturing; cell based therapy; cell cultivation; diagnostics; imaging; pharmacogenomics (personalized medicine); microarray technology; biomarkers.

5. Business development: strategic alliances; partnering trends; product opportunities; growth; business models and strategies; licensing; merger and acquisitions; outsourcing; venture capital and financing; intellectual property.

6. Other areas: Food; Marine; Bio-safety; Systems Biology, Clinical Research/clinical trials; bioethics; nanobiotechnology.

Abstracts for consideration as Invited or Session Lectures, and Poster Presentations can be submitted at <http://eureka-mkt03.com/conference/bwc>. Alternatively, a maximum one-page length abstract written in English can be submitted to us by e-mail at info@dubaiconf11.com

DEADLINE FOR ABSTRACT SUBMISSION TO PRESENT LECTURE / POSTER: 1st DECEMBER, 2012

For more details and to register, please visit the conference Web site at <http://eureka-mkt03.com/conference/bwc> or alternatively you may contact info@dubaiconf11.com

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

9th European Conference on Precision Agriculture (ECPA)

July 7 – 11, 2013. Lleida, Spain

Abstract submission: June 1st to September 9th 2012

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

Forest Genetics 2013

July 22 – 25, 2013. Whistler, British Columbia, Canada.

More info: <http://www.forestgenetics2013.ca/>

Positions available



POSTDOC

2 Postdoctoral positions available in Plant Photoreceptor Signalling/Application

University of Glasgow, UK.

Contact: Prof. John Christie
(John.Christie@glasgow.ac.uk)

Closing date: 5th August 2012

A postdoctoral position in Czech Republic, University of South Bohemia.

Applications are invited for a 3 year postdoc position starting October or November 2012 to work on leaf-atmosphere interactions (stomata

development and function, mesophyll conductance, cuticle, hydraulic architecture). For detail see

<http://kebr.prf.jcu.cz/download/postdoc.pdf> or contact Dr. Jiri Santrucek (jsan@umbr.cas.cz) for further information.

Postdoctoral Position

We are interested in hosting Marie Curie IEF or IIF fellows, EMBO fellows or fellows from other similar programmes. Applications are invited to study the **environmental and genetic control of seed dormancy and germination** at the CBGP (<http://www.cbgp.upm.es>) under the supervision of Dr. Luis Oñate-Sánchez.

Complementary and novel approaches will be used to characterize key genes with profound effects on these processes when mutated and to identify new players involved in the regulation (<http://www.cbgp.upm.es/en/seedregulation.php>).

CBGP was created to carry out the most advanced research aimed at understanding plant function and to contribute to fulfil the needs of the economic agents within the agriculture, forestry and environment productive sectors that are potential users of this research. The CBGP has excellent infrastructures and resources and welcomes high quality researchers.

Requisites

Candidates should have a PhD degree and the ideal candidate will have a strong background in molecular biology and in plant science.

More info

For more information about the Marie Curie call or EMBO call, please visit:

<http://ec.europa.eu/research/participants/porta/page/people&state=open> (Calls: FP7-

PEOPLE-2012-IIF and FP7-PEOPLE-2012-IEF)

<http://www.embo.org/programmes/fellowships/long-term.html> (Call: EMBO Long-term fellowship)

Applicants should send a letter of interest and a CV to: luis.onate@upm.es (Deadline for CV submission: 29 July 2012)

PREDOC

PhD Position Function and regulation plant aquaporins

University of Louvain, Institute of Life Sciences, Louvain-la-Neuve, Belgium

Project

A PhD position is available in the laboratory of François Chaumont to investigate the function and regulation of plant aquaporins. The project will focus on the physiological role of maize

aquaporins and will combine the expertise of the host lab in molecular and cellular biology of membrane transport and plant cell hydraulics. Maize lines deregulated in the expression of specific aquaporin genes will be generated and characterized.

Place

The University of Louvain is the largest university of the French speaking part of Belgium. It is located in Louvain-la-Neuve, 30 km south of Brussels. One of the most recent towns in Europe, Louvain-la-Neuve is hailed as an achievement, combining modernity with tradition, inspired by the layout of mediaeval university towns. The host laboratory (<http://www.uclouvain.be/en-29178.html>)

belongs to the Institute of Life Sciences, which brings together more than 150 research staffs working in the field of biochemistry, molecular and cell biology and physiology. This Institute runs several technical platforms, such as confocal microscopy, proteomics and mass spectrometry.

Application

Applicants should hold a Master degree in biology/bio-engineering with some experience in plant molecular and cellular biology or physiology. The four year position is available October 1, 2012. The candidate will be evaluated after one year.

Applications have to be sent by e-mail to François Chaumont. Please include a statement describing your research interests, CV, and the names and contact information of two academic/professional referees. Closing date for application is July 22, 2012.

François Chaumont

Institut des Sciences de la Vie

Université catholique de Louvain

Croix du Sud 4-L7.07.14.

B-1348 Louvain-la-Neuve. Belgium

Email: francois.chaumont@uclouvain.be

New books



ABIOTIC STRESS RESPONSES IN PLANTS

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

ADVANCES IN AGRONOMY, VOLUME 116

Edited by Donald L. Sparks
This volume contains six reviews dealing with environmental sustainability and food security including one that addresses an important global factor affecting future food security, phosphorus utilization efficiency (PUE) by plants. And another is a stimulating review on the importance of computer simulation in plant breeding.

ADVANCES IN BOTANICAL RESEARCH, VOLUME 61

Edited by Lise Jouanin and Catherine Lapierre
Lignins are nature's aromatic polymers and are the second most abundant organic constituents of the biosphere, next to cellulose. This volume gives a special emphasis to the bioengineering of these enigmatic polymers. It is divided in nine chapters containing up-to-date reviews by expert groups in their field.

AGRICULTURAL BIOTECHNOLOGY AND GENETIC ENGINEERING

By Qurban Ali
Publisher: LAP LAMBERT Academic Publishing
(January 19, 2012)
Paperback: 488 pages
ISBN-10: 3847370359
ISBN-13: 978-3847370352
"Biotechnology," or "biotech" for short, refers to the application of biological research techniques to develop products and processes using biological systems, living organisms, or derivatives of organisms. Biotech processes have been used for thousands of years, yet the

industry we know today is scarcely more than a quarter century old. Bread, cheese and beer all products made from microorganisms have been part of the human diet for 6,000 years. But it was not until the 1970s that scientists began to apply components of these microorganisms at the molecular level to solve human problems in spheres ranging from medicine to agriculture and industry. Due to this breadth of applications, the term "biotechnology" gradually gave way to the more accurate "biotechnologies" or a collection of techniques that apply cellular and molecular characteristics and processes to solve human problems. Such techniques are applied at the molecular level and include genetic manipulation, gene transfer, DNA typing and cloning or microorganisms, plants and animals. Biotech products or "biologics" as they are sometimes called, thus originate from living organisms bacteria, cells or animals.

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

Ahmad, Parvaiz; Prasad, M.N.V. (Eds.)
2012, Springer New York. Hardcover
ISBN 978-1-4614-0814-7

FUNCTIONAL BIOLOGY OF PLANTS

by Martin J. Hodson (Oxford Brookes University, UK) and John A. Bryant (University of Exeter, UK)
Hardcover ISBN: 978-0-470-69940-9
Paperback ISBN: 978-0-470-69939-3
April 2012, ©2011, Wiley-Blackwell
Plant Science text book, taking you from cellular and molecular approaches through whole plant physiology to the environment. This beautifully illustrated book, presents a modern, applied integration of whole plant and molecular approaches to the study of plants.
It is divided into four parts: Part 1: Genes and Cells, looks at the origins of plants, cell structure, biochemical processes and genes and

development. Part 2: The Functioning Plant, describes the structure and function of roots, stems, leaves, flowers and seed and fruit development. Part 3: Interactions and Adaptations, examines environmental and biotic stresses and how plants adapt and acclimatise to these conditions. Part 4: Future Directions, illustrates the great importance of plant research by looking at some well chosen, topical examples such as GM crops, biomass and biofuels, loss of plant biodiversity and the question of how to feed the planet.

MOLECULAR BIOLOGY TECHNIQUES (Third Edition)

By Susan Carson, Heather Miller and D. Scott Witherow

Elsevier Inc. 2012

ISBN: 978-0-12-385544-2

With content already designed to prepare students for working in a molecular biology lab, the dynamic links into vetted and distilled reference source material greatly enhance the user experience of this book on ScienceDirect.

PLANT BIOTECHNOLOGY AND AGRICULTURE

Edited By Arie Altman and Paul Michael Hasegawa

Elsevier Inc. 2012

ISBN: 978-0-12-381466-1

This book lays the foundation for understanding the biotechnology interventions in plant and agricultural science rapidly developing over the past ten years and serves as a valuable cross-disciplinary reference source.

Obituary



Professor Alfonso Ros-Barceló (University of Murcia, Spain)

The sadness one feels when someone you know dies is doubly painful in the case of Professor Alfonso Ros-Barceló, who passed away on the 29th of January after long fight against cancer, because he was in the fullness of his personal life and his brilliant professional career. His absence is great loss to his family, friends and colleagues, but also to the international Plant Physiology community.



His academic activity was always linked with the University of Murcia, where he graduated in Chemistry in 1983. He was a brilliant

undergraduate, as many of his old teachers and later to be colleagues will testify: *both in his class work and examinations he showed a*

seriousness and rigour accompanied by a sharply critical faculty in the face of any information he was given. And it is this spirit that would underpin his exemplary professional career. He obtained his PhD in 1986 and the chair of Plant Physiology in 1998. Throughout his time at the University he worked at the Department of Plant Biology (Plant Physiology section), teaching and supervising the research of students at both the Chemistry and Biology Faculties.

Internationally recognised as one of the most active scientists of renown in the field of Plant Physiology, Professor Ros-Barceló stood out for the originality of his studies into cell wall lignification, the metabolism of active oxygen and nitric species in plants and the biosynthesis of alkaloids, among other topics. In what were to be the last years of his life, much of his work focused on the role of basic peroxidases in the process of lignification through the oxidation of hydroxycinnamyl alcohols by peroxidases and the regulation of xylogenesis by nitric oxide and hydrogen peroxide using the asteraceae *Zinnia elegans* as a model plant and the culture of

differentiating mesophyll cells to tracheid elements as a system model. The characterisation and regulation of a strongly basic peroxidase in this plant, the molecular cloning of the gene encoding for Zinnia's basic peroxidase, as well as the elucidation of the structural features that make it especially active in the oxidation of syringyl groups are among Professor Ros's most important milestones. At the same time, he carried out phylogenetic studies to localise proteins homologous to the above syringyl type peroxidases in different evolutive groups of plants, alongside the exhaustive study of the presence of S type lignins in the same. Professor Ros-Barceló was also a pioneer in the investigation on vacuolar class III peroxidases, including their role in hydrogen peroxide homeostasis and in important plant metabolic pathways such as the biosynthesis of the anticancer alkaloids of *Catharanthus roseus*. Moreover, he had set out a visionary proposal that peroxidases may be associated to plasma membrane or tonoplast microdomains where they interact with other proteins to fulfil their functions, leaving us a seed that may germinate to produce future breakthroughs in the field of plant biology.

During his time at the University of Murcia, Professor Ros-Barceló directed the doctoral thesis to a high number of students, some of whom have gone on to become distinguished scientists in their own right in Spain, Portugal and Italy. He also promoted the participation and cooperation of his research group (*Plant Peroxidases*) with other groups at national (Universities of *A Coruña*, *Alcalá de Henares* and *Cartagena*) and international (Universities of *Bari*, *Roma* and *Oporto*). He was a valuable member of several editorial committees and member of numerous scientific committees of International Symposia on Plant Peroxidases and Oxizymes and the 2nd Symposium of Science and Technology of Wood, (Brazil), reviewer of original scientific research studies in many

journals and of projects promoted by national and international agencies – in short, a scientist of international renown. The more than 200 articles published in scientific journals of quality corroborate his dynamism and enthusiasm as a researcher, a characteristic that was evident up to the end of his life despite his illness. His interest in science was also manifest in his capacity as principal investigator of national and international research projects and the contracts for innovation and research with different companies that he developed with a great successful. The same energy he showed towards research was also evident in his teaching, where he applied his scientific creativity to the conception and execution of new activities in an attempt to stimulate students' initiatives and awaken their interest in Plant Physiology.

However, these enormous professional qualities should not hide his tremendous human quality. Professor Ros-Barceló was generous with everyone, the door to his laboratory was always open and whatever equipment he possessed was for anyone to use.

His loss as a friend and colleague cannot be quantified. There are no words to describe the kindness shown to the people surrounding him or to express our gratitude for the comfort given to those of us who have suffered personal loss ourselves, for the encouragement given in both the highs and lows of academic life, for his advice always so accurate...

His absence is felt by the scientific community as a whole, proof of which are the numerous calls and electronic messages received from universities and research centres from all over the world – where he went and where he was known Professor Ros-Barceló sowed the seeds of friendship. It was a privilege to be counted as one of these friends.

Dr. M.A. Pedreño
Professor of Plant Phisyology
University of Murcia. Spain