



**FEDERATION OF EUROPEAN
SOCIETIES OF PLANT BIOLOGY**



FESPB Newsletter



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Editor: Prof. Dolores Rodriguez
Chair of Publications Committee

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Letter from the last Secretary General

Dear FESPB Members, dear colleagues,

After 2 years as President (2000-2002), 2 years as Chair of Grants & Awards Committee (2002-2004) and 8 years as Secretary General (2004-2012), from now on I will serve FESPB from the backstage. From August 2012, new FESPB Secretary General is, the newly elected, Prof. Christine Foyer (C.Foyer@leeds.ac.uk).

During the first two years of the new millennium, the current infrastructure and spending patterns of FESPB were established, in collaboration with the Secretary General Prof. Michael Jackson. Our effort was focused on organizing world class FESPB Congresses, on supporting students from eastern Europe to attend congresses, on establishing a comprehensive web site, and on preparing a regular Newsletter. What I hope we now have is an effective system of administration accompanied by a degree of transparency achieved through the posting of committee records on the web site. Please keep in mind that all was done on a completely volunteer basis without spending the, anyway low, income of FESPB!

Our achievements include the holding of genuine world-class congresses (Heraklion 2002, Krakow 2004, Lyon 2006, Tampere 2008, Valencia 2010). Also, in 2012 the FESPB Congress was co-organized in Freiburg, in collaboration with EPSO. To continue this activity in the future, a committee from the FESPB E.C. and EPSO Board produced the Concept for joint FESPB/EPSO Congresses, which was approved by the FESPB E.C. and Council., and also by the EPSO Board. More info at: http://www.fespb.org/files/file/JOINT%20FESPBEP%20CONGRESS%20CONCEPT%2012_5_12.doc

Following the changes in the Statutes in 2010 for election of the FESPB E.C. members, and following the intention of FESPB E.C. members to step down, for first time open call for candidacies for the vacant positions was done. Unfortunately, for the positions of

Secretary General and Treasurer only one candidacy/each was submitted (Prof. Foyer and Renneberg, respectively), and two for the Chair of Grants & Awards Committee (Prof. Aliyev and DeGara). Following on-line voting, Prof. Christine Foyer was elected as the new Secretary General, Prof. Heinz Renneberg as Treasurer, and Prof. Laura De Gara as Chair of Grants & Awards Committee. You will undoubtedly be pleased to note that throughout this period there has been no increase in the membership fee.

I hope that after 8 years as Secretary General, I leave FESPB in reasonably good shape. I believe the framework is in place to allow FESPB to make a real difference to the scientific community it tries to serve, and can be a force for good as members pursue their scientific ambitions. Basically this is being achieved by promoting good Communications through electronic media and through the congresses. I have already expressed my concern that at present, this flow of information is mostly one-way with very little input from National Representatives. For example, the editor of FESPB Newsletter receives almost no news items from member societies about their activities, where and when its annual meetings are being held, who are the guest speakers, what its web site address is, if it has one, news of interesting books, monographs or other publications produced locally. I do urge you all to find a little more time for FESPB – it will be time well-spent.

I cannot end without saying a warm **THANK YOU ALL**, who have given me your personal support and encouragement during my time as FESPB E.C. Member, and especially the members of the Executive Committee and Council, with whom I have enjoyed working so much.

For the season, I wish you,

Happy Holidays and a very Happy, Healthy and Prosperous New Year.

Kalliopi (Popy) A. Roubelakis-Angelakis
Heraklion 12.12.12

Research News



Scientists uncover mechanism by which plants inherit epigenetic modifications

Source: Cold Spring Harbor, N.Y. 20 September 2012.

During embryonic development in humans and other mammals, sperm and egg cells are essentially wiped clean of chemical modifications to DNA called epigenetic marks. They are then held in reserve to await fertilization.

In flowering plants the scenario is dramatically different. Germ cells don't even appear until the post-embryonic period – sometimes not until many years later. When they do appear, only some epigenetic marks are wiped away; some remain, carried over from prior generations – although until now little was known about how or to what extent. “What we did know,” says Professor and HHMI-GBMF Investigator Rob Martienssen, Ph.D., of Cold Spring Harbor Laboratory (CSHL), “was that epigenetic inheritance – the inheritance by offspring of chemical “tags” present in parental DNA that modify the expression of genes – is much more widespread in plants than in animals.”

In new research published online in the journal *Cell*, Martienssen and colleagues show that genome reprogramming through these epigenetic mechanisms is guided by small RNAs and is passed on to the next generation.

It has long been known that in plants, as the male germline pollen grains develop, they give rise to two sperm cells, and a structure called the vegetative nucleus, which resembles “nurse cells” in animal germlines because it provides energy and nourishment to the sperm cells.

The DNA in germ cells can exist in two dramatically different states: in sperm cells, it is very densely packed and essentially

inaccessible to the cellular machinery that enables individual genes to be “expressed.” In the vegetative cell, in which the packing is much looser, genes can be expressed.

DNA and chromosomal proteins can also be modified by various chemical groups (two common ones are methyl and acetyl) which tend to attach to the DNA and proteins at specific locations. These chemical tags are called epigenetic marks. The attachment of, for instance, a methyl group to a particular stretch of DNA containing a gene tends to prevent that gene from being accessed by the gene-expression machinery, and thus prevents the gene from being expressed.

Previous work by the Martienssen lab and their collaborators, including a team of pollen specialists from the Instituto Gulbenkian de Ciencia in Lisbon, Portugal, has shown that these epigenetic mechanisms are important for keeping transposons in check. Also known as “jumping genes” for their ability to be expressed and then re-insert themselves at random into a different area of the genome, transposons are dangerous because they can cause damage to DNA and disrupt genetic function.

In the current study, probing further into the set of modifications on the DNA in plant pollen grains, Martienssen and colleagues decided to look at the particular set of chemical marks called methyl groups. When they separated out pollen grains in different stages of development they found distinct patterns of the attachment of methyl groups to DNA.

They also noticed the corresponding accumulation of small RNAs, including two classes of so-called short-interfering RNAs (siRNAs) – tiny RNA molecules, 21 or 24 nucleotides in length -- involved in silencing gene expression. These small siRNAs act as

guides to where methylation will occur, silencing gene expression.

Martienssen's team discovered that while in sperm, some areas of DNA containing transposons had "lost" methyl groups, and thus had the potential to be expressed, the same stretches of DNA were observed to be methylated in the seed embryo. This was associated with the accumulation of 21-nucleotide-long siRNA in the mature pollen and 24-nucleotide-long siRNA in the seed embryo. Martienssen speculates that the loss of methylation in the sperm and subsequent re-methylation during fertilization may reflect an ancient mechanism for transposon recognition and silencing.

A second important observation made by the team was of the loss of methylation in "nurse cells." Methylation at these same sites is retained in the associated sperm cells, and, too, is associated with accumulation of 24-nucleotide siRNA. This process results in areas of recurrent epigenetic marking that are pre-methylated in the germline sperm and carried on to the next generation.

"This is what, at least in part, enables plants to inherit acquired traits from prior generations – something that we mammals can rarely do," Martienssen observes.

Being able to trace the inheritance of traits – both wanted and unwanted -- in plants, and notably in agricultural crops, is important for farmers. Martienssen predicts that "defining inheritance through epigenetic modifications will influence the ways people think about cross-breeding to select for desired traits." Such traits as resistance to temperature variation in crops have important agricultural and economic implications.

"Reprogramming of DNA Methylation in Pollen Guides Epigenetic Inheritance via Small RNA" is published online in *Cell* on September 20, 2012. The authors are: Joseph P. Calarco, Filipe Borges, Mark T Donoghue, Frédéric Van Ex, Pauline E Jullien, Telma Lopes, Rui Gardner, Frédéric Berger, José A Feijó, Jörg D Becker, Robert A Martienssen. The paper can be obtained online at doi: 10.1016/j.cell.2012.09.001 via Cell press.

Demographic Miracle in the Deserts: Some Plants in Arid Regions Benefit from Climate Change

Source: ScienceDaily (Oct. 8, 2012)

Dryland ecosystems cover 41% of Earth's land surface. These ecosystems are highly vulnerable to global environmental change and desertification. But climate change seems to have a positive impact on some plants. A study involving the Max Planck Institute for Demographic Research in Rostock has come to this conclusion.

Using demographic methods, ecologist Roberto Salguero-Gómez investigates desert plants to find out how vulnerable they are to climate change. The results of his newest study are surprising: Climate change may have a positive impact on some plants.

Climate models used by scientists to forecast the effect of climate change on the various ecosystems predict a bleak future for these regions: temperatures will rise, there will be less rain, and it will rain more erratically -- all conditions seemingly unfavorable to plants.

To measure the impact of climate change on the dynamics of plant populations, researchers to date have mostly worked with average values, such as average temperature or average rainfall. "This is a method commonly used, but it cannot be applied to desert plants," says researcher Roberto Salguero-Gómez of the Max Planck Institute for Demographic Research.

Dryland plants cannot really be compared to plant species growing in other latitudes, where weather conditions are fluctuate less. Dryland plants have adapted to the extreme climatic conditions of arid regions in the course of evolution, even under conditions of no climate change, and they benefit from it.

Some plants produce dormant seeds in years of heavy rainfall. The seeds of other plant species have something like a sensor to detect the level of rainfall: not enough rain drops falling to secure their life until they reproduce and they will not germinate. A lot of rain after years of drought, and they start

to grow. The advantage is that many other plant species -- competitors for space -- have a low drought tolerance and this has thinned out the total population, freeing up space where individuals, who have waited for the big rain, can spread.

"Using average precipitation values to predict plant population dynamics does not correspond to the physiology of these plants, a physiology that is unique," sums up Roberto Salguero-Gómez.

It is for this reason that he, together with his colleagues Wolfgang Siewert and Katja Tielbörger (University of Tübingen) and Brenda Casper (University of Pennsylvania) have looked anew at two long-term studies that documented the population size of two desert plant species, one each in the USA and Israel, over a number of years.

Based on the data of these studies, a climate model and a demographic calculation method, the researchers have developed a new model that provides insights into the future dynamics of plant populations. The results, recently published in the scientific journal *Philosophical Transactions B* of the Royal Society of London, are astounding: Changing weather conditions do not seem to harm the population of these plants; quite to the contrary, they seem to benefit from it. "The plants adapt quite well," says Roberto Salguero-Gómez. They seem to have a sizeable buffer to adapt to climate change."

It is of great important to continue to observe and investigate these dynamics, he stresses, for example to assess which measures are best suited to alleviate poverty in the long run and where to apply them. Most dryland areas are located in the poorest regions of the world, i.e. Africa, Central Asia, and South America. Many people living there have to make a living from the scarce resources these barren regions offer. And there will be more of them as, undoubtedly, the share of dryland will increase due to climate change, desertification and other human-driven activities. It is thus all the more important to assess what impact climate change will truly

have on plants that serve as food for people and livestock in these areas.

Journal Reference: R. Salguero-Gomez, W. Siewert, B. B. Casper, K. Tielborger. A demographic approach to study effects of climate change in desert plants. *Philosophical Transactions of the Royal Society B: Biological Sciences*, 2012; 367 (1606): 3100 DOI: 10.1098/rstb.2012.0074

Computational Model Identifies Potential Pathways to Improve Plant Oil Production

Source: ScienceDaily (Oct. 8, 2012)

Using a computational model they designed to incorporate detailed information about plants' interconnected metabolic processes, scientists at the U.S. Department of Energy's Brookhaven National Laboratory have identified key pathways that appear to "favor" the production of either oils or proteins. The research, now published online in *Plant Physiology*, may point the way to new strategies to tip the balance and increase plant oil production.

The study focused on the metabolism of rapeseed, a crop grown primarily in temperate climates for the oil that accumulates in its seeds. Such plant oils are used worldwide for food, feed, and increasingly as a feedstock for the chemical industry and to produce biodiesel fuel.

"Increasing seed oil content is a major goal for the improvement of oil crops such as rapeseed," said Brookhaven biologist Jörg Schwender.

As a step toward that goal, Schwender and Brookhaven postdoctoral research associate Jordan Hay recently developed a detailed computational model incorporating 572 biochemical reactions that play a role in rapeseeds' central metabolism and/or seed oil production, as well as information on how those reactions are grouped together, are organized in subcellular compartments, and how they interact. They've now used the model to identify which metabolic pathways are likely to increase in activity -- and which have to decrease -- to convert a "low-oil" seed into a "high-oil" seed.

Such a switch would likely be a tradeoff between oil and protein production, Schwender explained, because with limited carbon and energy resources, "the plant would 'pay' for the increased cost of making more oil by reducing its investment into seed protein."

So far, efforts based on conventional plant breeding and genetics have had very limited success in changing the typical tradeoff of storage compounds in seeds.

"Behind the production of oil and protein in seeds is a complex network of hundreds of biochemical reactions, and it is hard to determine how this network is controlled and how it could be manipulated to change the tradeoff," Schwender said.

Schwender and Hay's computational model of 572 metabolic reactions turns the problem on its head to narrow the search. Instead of manipulating each pathway one by one to see which might tip the balance from protein toward oil, the model postulates the existence of seeds with different oil and protein content to see which of the many reactions are "responsive" to changes in the oil/protein tradeoff.

"This approach allowed us to narrow down the large list of enzyme reactions to the relatively few ones that might be good candidates to be manipulated in future experimental studies," Schwender said. "Our major goal is to computationally predict the least possible number of enzymes that have most control over the tradeoff between oil and protein production."

Of the 572 reactions included in the model, the scientists identified 149 reactions as "protein-responsive" and 116 as "oil-responsive."

"In addition, the model helps us evaluate how sensitive the reactions are in a quantitative way, so we can see which of these are the 'most sensitive' reactions," Schwender said. "This allows us to identify a relatively few possible targets for future genetic manipulation to tip the balance in favor of greater seed oil production."

Some of the reactions identified by the model confirm pathways pointed out in

previous research as important for oil synthesis. "But some of the reactions identified by our model have not really been implied so far to be important in the oil/protein tradeoff," Schwender said, suggesting that this could be new ground for discovery.

"These simulation tools may therefore point the way to new strategies for re-designing bioenergy crops for improved production," he concluded.

Journal Reference: J. Schwender, J. O. Hay. Predictive modeling of biomass component tradeoffs in *Brassica napus* developing oilseeds based on in silico manipulation of storage metabolism. *Plant Physiology*, 2012; DOI: 10.1104/pp.112.203927

Plant eating insects can drive the evolution of plants

Source: Rothamsted Research. 8 October 2012

In a paper published in the journal *Science*, scientists have discovered that plants naturally evolve to protect themselves from insect attack, for example from aphids (greenfly and blackfly), but do this as a trade-off with their ability to compete with other plants.

The scientists from the Universities of Zürich, Copenhagen, California (at Davis) and Cornell University worked with the Insect Survey team at the UK's Rothamsted Research, to examine natural populations of the plant *Arabidopsis thaliana* in Europe. They compared the geographic variation in the profiles of glucosinolates (a group of chemical compounds that plants can use to protect themselves) in the plants with the abundance of two specialist aphids from 39 years of field data collected through the BBSRC-funded Rothamsted Research Insect Survey.

They found that phytophagous (plant eating) insects may force the rapid evolution of plants through natural selection, with genes resistant to insect attack being favoured. But in areas where the probability of phytophagous insects damage is lower

these genes do not appear to be favoured. These authors argue that this finding “highlights the potency of natural enemies as selective forces”.

Dr Richard Harrington, Head on the Rothamsted Insect Survey, said “This study is one of a large range of applications to which Rothamsted's insect data are put and demonstrates the value and versatility of long-term, standardised datasets”

The Rothamsted Insect Survey is one of four National Capabilities which receives strategic funding through the Biotechnology and Biological Sciences Research Council (BBSRC). It operates two national networks for monitoring insect populations in the UK. It is accessed by large numbers of external partners and its data used in many publications. The data from both networks have a range of applications in fundamental and applied aspects of insect population dynamics and ecology.

These National Capabilities have national and international importance for the research underpinning sustainable agriculture and the BBSRC have placed a considerable emphasis in these capabilities to foster collaborative links with other researchers and share data collected for nearly 170 years to ensure that others can benefit from these publically supported resources.

Reference: Natural Enemies Drive Geographic Variation in Plant Defenses (10.1126/science.1226397)

Malaysian Researchers Create New Durable Wood-Plastic Composite Material Source: ScienceDaily (Oct. 9, 2012)

Researchers from the Universiti Teknologi MARA in Malaysia have created a new durable wood-plastic composite (WPC). Recent discoveries in the production of new materials have enabled researchers to develop new types of composite materials that perform better and are more durable.

Wood-plastic composites (WPCs) are one of the fastest growing construction components in the wood composites industry. Their popularity is due to low maintenance, high

durability, and resistance to termites and other insect attacks. However their widespread usage has been limited due to their high cost in production and in some instances low strength.

The present study focused on assessing the suitability of kenaf core fraction (about 65% of the whole stem of the plant) in powder form as filler material. Kenaf powder, processed from its core fibre, has been shown to offer one potential solution to the increasing scarcity of traditional filler materials. Kenaf stems contain two distinct fibre types, bast and core. Dosing with maleic-anhydride-modified polypropylene (MAPP) in the right amount displayed not only to bridge the interface between the ground kenaf core (GKC) and plastic in the present WPCs, improving stress transfer and increasing their strength and stiffness, but also allow a higher filler loading. Reducing the amount of plastic and increasing the amount of GKC, without sacrificing strength, stiffness or durability, would result in greener WPC products.

Researchers examined the possibility of replacing sawdust with GKC and measured the mechanical properties of the resulting composites. They also looked at the effect of increasing maleic-anhydride-modified polypropylene (MAPP) dosage. Material preparation included GKC drying followed by high intensity blending with polypropylene (PP), coupling agents (MAPP) pellets, and feeding this into a counter-rotating twin-screw extruder for compounding. Compounded blends were then fed to an injection-moulding machine to produce boards of dimensions 153mm x 153mm x 3mm. Specimens were cut from the boards for tensile and bending tests in five replicates. GKC formulation gave the highest average tensile strength, modulus of rupture and modulus of elasticity.

WPCs of polypropylene (PP) and ground kenaf core (GKC) fibre, dosed with maleic-anhydride-modified polypropylene (MAPP) in the right amount, was found not only to bridge the interface between the GKC and plastic, improving stress transfer and

increasing their strength and stiffness, but also allow a higher filler loading of 65%. Reducing the amount of plastic and increasing the amount of GKC, without sacrificing strength, stiffness or durability, would result in greener WPC products. The researchers recommend that additional testing and extended research is necessary to investigate the strength of WPC on mechanical properties of modulus of elasticity (MOE) and modulus of rupture (MOR) by carrying out impact test and compressive test which could reveal new discoveries about high filler loading WPCs.

Genetically Engineered Tomatoes Decrease Plaque Build-Up in Mice

Source: ScienceDaily (Nov. 5, 2012)

For the first time, genetically engineered tomato plants produced a peptide that mimics the actions of good cholesterol when eaten, researchers reported at the American Heart Association's Scientific Sessions 2012.

In the study, mice that ate the freeze-dried, ground tomatoes had less inflammation and reduced atherosclerosis (plaque build-up in the arteries).

"We have found a new and practical way to make a peptide that acts like the main protein in good cholesterol, but is many times more effective and can be delivered by eating the plant," said Alan M. Fogelman, M.D., senior author of the study and executive chair of the Department of Medicine and director of the Atherosclerosis Research Unit in the David Geffen School of Medicine at UCLA.

Researchers genetically engineered the tomatoes to produce 6F, a small peptide that mimics the action of ApoA-1, the chief protein in high density lipoprotein (HDL or "good" cholesterol). They fed the tomatoes to mice that lack the ability to remove low density lipoprotein (LDL or "bad" cholesterol) from their blood and readily develop inflammation and atherosclerosis when consuming a high-fat diet.

After the mice ate the tomatoes as 2.2 percent of their Western-style high-fat, calorie-packed diet, those given the peptide-enhanced tomatoes had significantly: lower blood levels of inflammation; higher paraoxonase activity, an anti-oxidant enzyme associated with good cholesterol and related to a lower risk of heart disease; higher levels of good cholesterol; decreased lysophosphatidic acid, a tumor promoter that accelerates plaque build-up in arteries in animal models; and less atherosclerotic plaque.

"To our knowledge this is the first example of a drug with these properties that has been produced in an edible plant and is biologically active when fed without any isolation or purification of the drug," Fogelman said.

New Way in Which Plants Control Flower Production

Source: ScienceDaily, 11 Nov. 2012.

Flowers don't just catch our eyes, they catch those of pollinators like bees as well. They have to, in order to reproduce. Because plants need to maximize the opportunity for pollinators to gain access to their seeds, variations in the timing of flowering can have profound effects on flower, fruit, and seed production, and consequently agricultural yields.

We know that the major driving forces of flowering are external factors such as light and temperature. However, new research from CSHL Assistant Professor Zach Lippman, Ph.D. and his collaborators, published online November 11 in *Nature Genetics*, shows there is a second, previously unknown mechanism controlling flowering.

Using the tomato plant as their model, Lippman and CSHL co-authors, Cora MacAlister, Soon Ju Park and Ke Jiang, show that loss of control of the timing of flowering, such that the flowering program turns on too fast, results in production of only a single flower on each branch, rather than the usual 7 to 10. Conversely, slowing down

the flowering program enables more flowering branches to grow, which means more fruit.

Such dissection of the timing mechanism of flowering in plants like tomato is leading to new strategies for increasing agricultural yield in important crops.

During the flowering process, plants form reproductive shoot structures called inflorescences. These structures derive from small stem cell populations buried inside the tiny growing tips of plants called meristems. As plants sense and respond to signals from light and/or temperature, it is at the meristems where plant organs -- leaves or flowers -- are formed.

Domesticated tomato plants, which we know and love for their shiny, tasty red fruit, typically grow several multi-flowered inflorescences on each shoot. Each inflorescence is arranged in a zigzag pattern of 7 to 10 flowers on a single branch. Curiously, many wild species of tomato produce multiple branches on each inflorescence, with each branch having many flowers, thereby increasing the reproductive potential of the plant. In rare cases, genetic mutants of domesticated tomatoes form broom-like inflorescences with dozens of branches like the wild species. Interestingly, there is another class of mutants that produce just a solitary, sometimes abnormal looking, flower.

In previous research Lippman and others reasoned that the timing of flowering would be important in determining whether an inflorescence was highly branched or not. By characterizing the activity of thousands of genes involved in the flowering process of tomato, Lippman and members of his laboratory revealed a "molecular clock" coordinating whether meristems give rise to branched or unbranched inflorescences.

In their newly published research, they reveal that one of those genes plays a critical role in keeping the clock from ticking too fast.

"In order for a plant to determine when and where to switch from making leaves to making flowers everything has to be timed

perfectly," says Lippman. "We know that the flowering process is regulated by temperature and day length; these control one aspect of the timing. But now we've found a new timing mechanism."

The moment of insight for Lippman and his team, including colleagues at the Unité de Recherche en Génomique Végétale in Evry, France and the Weizmann Institute of Science in Rehovot, Israel, came when studying mutant tomato plants. "We found a gene that when mutated converts the typical tomato multi-flowered inflorescence into one with a single flower," Lippman says. Interestingly, this caused the tomato plant to mimic other single-flowered plants of the same family, called Solanaceae, which includes the eggplant, tobacco, petunia, and pepper plants.

The gene Lippman's team found, called TERMINATING FLOWER (TMF), had not been previously known to have such a crucial role in plant growth. This was despite the fact the flowering process and the genes that control it have been studied in great depth over decades in many plant systems, including the model plant *Arabidopsis* as well rice and corn (maize).

"It seems TMF regulates a previously unknown pathway that is involved in the timing of flowering. The reason that mutations in TMF cause single-flower inflorescences is that the plant is tricked into thinking it is time to make a flower when it is still in the vegetative state -- the phase of growth that precedes flowering when leaves are still being made," explains Lippman.

Flowering is a tightly coordinated process, so when TMF function is lost the process becomes de-synchronized and uncoordinated. The external signals from light and temperature have not yet reached the critical threshold to tell the plant it is ready to make flowers, yet the program for making flowers starts anyway. Thus TMF acts as an internal check on the flowering transition. "Its normal function is to delay flowering, to gently slow it down, so that it doesn't happen too precociously," Lippman says.

If plants make flowers too quickly, there may not be enough energy from leaves to support those flowers and fruits. But Lippman suggests that some species of plants have taken advantage of this mechanism and evolved to make more or less flowers per inflorescence. It may be that in nature, some plants are more successful when making fewer flowers over a longer period of time, for example.

The Solanaceae species to which tomato belongs contains examples of all types of inflorescences, which is why Lippman finds the model is so fascinating to study. By learning about the genetic switches controlling flower production, the hope is that they can be manipulated in agricultural crops like tomato to improve yield.

Reference: Cora A MacAlister, Soon Ju Park, Ke Jiang, Fabien Marcel, Abdelhafid Bendahmane, Yinon Izkovich, Yuval Eshed, Zachary B Lippman. Synchronization of the flowering transition by the tomato TERMINATING FLOWER gene. *Nature Genetics*, 2012; DOI: 10.1038/ng.2465

Clocks Are Ticking and Climate Is Changing: Increasing Plant Productivity in a Changing Climate

Source: ScienceDaily (Nov. 16, 2012)

Dartmouth plant biologist C. Robertson (Rob) McClung is not your typical clock-watcher. His clocks are internal, biological, and operate in circadian rhythms -- cycles based on a 24-hour period. Living organisms depend upon these clocks to keep pace with Earth's daily rotation and the recurring changes it imposes on the environment. These clocks allow the plant or animal to anticipate the changes and adapt to them by modifying its biology, behavior, and biochemistry.

"If you know that the sun is going to go down, and if you are a photosynthetic plant, you have to readjust your metabolism in order to make it through the night," says McClung, the Patricia F. and Williams B. Hale 1944 Professor in the Arts and Sciences.

McClung uses the Arabidopsis plant in his research on the mechanisms that affect plant behavior and its genetics. He jokingly refers to it as "an inconsequential little weed," but holds it in high esteem as an experimental test bed.

According to the National Institutes of Health, this member of the mustard family is the model organism for studies of the cellular and molecular biology of flowering plants. "Because plants are closely related, it is quite likely that knowledge derived from Arabidopsis studies can be readily transferred to agronomically important species," says McClung.

McClung sees internal clocks as increasingly important in the face of global climate change, and to agricultural productivity in particular. "In the context of climate change and the need to exploit increasingly marginal habitats, fuller understanding of clock mechanisms may offer strategies to improve crop productivity," says McClung. "We need to know how an organism measures time and how it uses that information to coordinate its physiology and behavior."

Water is the landscape on which biological clocks and climate change intersect. Agriculture consumes the vast majority of our water, and warmer and dryer conditions are predicted for much of the agricultural land of the United States. This is based on our current understanding of the changes predicted to be associated with global warming, and in this scenario our aquatic resources will become increasingly scarce.

Water is lost during the gas exchange that takes place in photosynthesis -- carbon dioxide in, oxygen out -- through small pores in the surface of leaves that periodically open and close under the control of a biological clock. Exercising control over this clock could be a means of conserving water. "We know that these little cells on the surface of the leaf are controlled by the clock," says McClung. "It could be that different clocks regulate it slightly differently, and we would like to find the best clock, fine-tune it, and perhaps optimize the ability to get CO₂ in without losing water."

Water figures prominently in another aspect of plant physiology. Water moves up through the stem to the leaves, involving proteins called aquaporins. "There is a big family of genes that encode aquaporins, and in *Arabidopsis* the circadian clock governs the expression cycles of about a third of those genes," says McClung. "That suggests there is a mechanism to actually regulate this hydraulic conductivity over time, constituting another instance where the clock is involved in water use efficiency."

Together with colleagues in Wyoming, Wisconsin, and Missouri, McClung has been looking at another crop, *Brassica rapa*, a close relative of which is the source of canola oil. With a five-year National Science Foundation grant of more than \$5 million, the group is investigating *Brassica*'s circadian patterns, looking at inheritance and water use efficiency. "We have mapped 10 genetic regions that are associated with water use efficiency," says McClung. "We have also traced circadian parameters to most of those same areas, suggesting a link between the two. This association suggests that we could potentially use the clock to manipulate water use efficiency."

In a related project, McClung will be working with soybeans, attempting to correlate circadian period length with latitude. "If we can understand the clock, we might then manipulate the clock in ways to achieve desired goals, including water use efficiency and better yield."

McClung feels strongly that this sort of basic research has the potential to contribute in significant ways to food production increases. "Whether or not we achieve that increase or whether it allows us to fertilize a little less and so pollute a little less but maintain the same productivity level, anything in the net direction that is positive is going to help," he says. "We can't necessarily say exactly how it will help, but I think it's not unreasonable to think that this very basic research can have a real world impact, and one hopes it will."

"We will need to genetically modify our plants to control our circadian biological

clocks," says Professor Rob McClung. "Every domesticated plant and animal that we have today is already genetically modified. None of them are as they are found in nature. We have manipulated their genes by selective breeding and creating hybrids."

To produce the corn we eat today, prehistoric farmers first had to find some variant that had a desirable trait, keep its seeds and plant them, repeating the process for countless generations to bring out that trait. That is selective breeding and it produced a plant whose genome was modified.

To make a tomato plant resistant to a particular disease or pest, we might find some related pest-resistant species in the wild and cross it with our garden variety tomato to produce a hybrid. Successive crosses would preserve the "tomato-ness" while selectively retaining that little bit from the wild relative that resists tomato-eating bugs.

"Along with introducing the gene or set of genes encoding resistance, we may have also brought in a whole bunch of other ill-defined genes on either side," McClung says. "We don't know the extent of it. We don't know what else is in there. While some regard this as a 'natural' approach, the unknown genetic fellow travelers could be problematic or even dangerous."

For more than 20 years, we have possessed the technology to precisely insert a single gene, making one change and only one change, producing what is known as recombinant DNA. "We are modifying genes in a much more informed way and precise way, targeting specific genes and manipulating those," he says.

"Nevertheless, there is vocal opposition to this practice, in spite of the fact that we have been doing it for decades and there is yet to be a single example of anything bad happening from that," says McClung. "It is a philosophical standpoint based on a lack of understanding. People don't understand the science and they come up with a lot of arguments against it."

The dilemma rests on timing. Conventional breeding, though imprecise and unpredictable, is a workable but lengthy process. Recombinant DNA is fast. In a world beset by overpopulation, famine and global climate change, McClung questions whether we can really afford the time to wait.

Engineering Plants for Biofuels

Source: ScienceDaily (Nov. 26, 2012)

With increasing demands for sustainable energy, being able to cost-efficiently produce biofuels from plant biomass is more important than ever. However, lignin and hemicelluloses present in certain plants mean that they cannot be easily converted into biofuels. A study published in BioMed Central's open access journal *Biotechnology for Biofuels* appears to have solved this problem, using gene manipulation techniques to engineer plants that can be more easily broken down into biofuels.

Plants high in lignin and hemicelluloses -- lignocellulosic biomass -- have a high content of pentose sugars that are more difficult to ferment into fuels than plants with hexose sugars. In order to be useful for biofuel production, scientists need to be able to engineer plants with smaller amounts of xylan -- the major non-cellulosic polysaccharide -- present in secondary cell walls.

With this in mind, a research group from the Lawrence Berkeley National Laboratory, USA, used 3 mutant strains of *Arabidopsis* deficient in xylan -- irregular xylem (irx) mutants irx7, irx8 and irx9 -- in order to engineer plants with low xylan content and improved properties for easier breakdown of carbohydrate into simple sugars (saccharification). The irx mutants normally exhibit severe dwarf phenotypes that result from xylem vessel collapse and consequent impaired transport of water and nutrients. The team hypothesized that restoring xylan biosynthesis in the plants would complement the mutations.

To reintroduce xylan biosynthesis into the xylem of irx7, 8 and 9, Henrik Scheller and colleagues manipulated the promoter regions of vessel-specific VND6 and VND7 transcription factor genes. Significantly, they found that the ensuing phenotypes completely restored wild-type growth patterns in some cases, resulting in stronger plants with restored mechanical properties, whilst at the same time maintaining a low overall xylan content and improved saccharification properties that allowed for better breakdown into biofuels.

Plants with up to 23% reduction in xylose levels and 18% reduction in lignin content were obtained, whilst normal xylem function was restored. The plants also showed a 42% increase in saccharification yield after pretreatment.

Lead author Scheller said, "These results show that it is possible to obtain plants that have reduced amounts of xylan in their walls while still preserving the structural integrity of the xylem vessels. The xylan engineering system we present here is a great step towards tailored bioenergy crops that can be easily converted into biofuels. He continued, "This approach in *Arabidopsis* has the potential to be transferred to other biofuel crop species in the near future, in particular, the poplar species."

These results from this study provide hope that a viable alternative to fossil fuels may soon be available.

Journal Reference: Pia D Petersen, Jane Lau, Berit Ebert, Fan Yang, Yves Verherbruggen, Jin S Kim, Patanjali Varanasi, Anongpat Suttangkakul, Manfred Auer, Dominique Loque and Henrik V Scheller. Engineering of plants with improved properties as biofuels feedstocks by vessel-specific complementation of xylan biosynthesis mutants. *Biotechnology for Biofuels*, 2012.

From Mediterranean Coasts to Tatra Mountains and Beyond: Plant Chromosome Number Variation

Source: ScienceDaily (Nov. 27, 2012)

Chromosome number is the most basic feature concerning the genome of a species, and it is known for about one third of higher plant species. In particular, for plants of Italy, Slovakia, and Poland, online chromosome number databases have been developed: 'Chrobase.it -- Chromosome numbers for the Italian flora', 'Karyological database of ferns and flowering plants of Slovakia' and 'Chromosome number database -- PLANTS', respectively. The three datasets account for about 35%, 60% and 40% of the whole floras, respectively.

"We used these datasets to compare chromosome number variation among plants of the three countries, with the aim to verify whether the patterns of chromosome number variation parallel the differences in latitudinal ranges" said Dr Peruzzi, leading author of the article, published in the open access journal *Comparative Cytogenetics*.

A concept that the occurrence of multiple genome copies (polyploidy) in plants tend to increase with latitude had already been formed in the second half of twentieth century, but pioneer works in this field had not significant statistical coverage, due to the absence of large, readily accessible datasets.

In the study, significant differences among the three countries were evidenced, confirming that mean chromosome number increases with increasing latitude. Mean chromosome number was used as an objective proxy of polyploidy.

In perspective, it would be interesting to verify whether the same chromosome number evolution dynamics occurs in the Austral hemisphere as well. Unfortunately, as far as we are aware, large chromosome number databases of these territories with significant latitudinal variations are not available, at the moment.

Journal Reference: Lorenzo Peruzzi, Grzegorz Góralski, Andrzej Joachimiak, Gianni Bedini. Does actually mean chromosome number increase with latitude in vascular plants? An answer from the comparison of Italian, Slovak and Polish floras. *Comparative Cytogenetics*, 2012; 6

(4): 371 DOI:
10.3897/CompCytogen.v6i4.3955

The Hungry Caterpillar: Beware Your Enemy's Enemy's Enemy

Source: ScienceDaily (Nov. 27, 2012)

When herbivores such as caterpillars feed, plants may "call for help" by emitting volatiles, which can indirectly help defend the plants. The volatiles recruit parasitoids that infect, consume and kill the herbivores, to the benefit of the plant. However, such induced plant odours can also be detected by other organisms. A new study published Nov. 27 in the open access journal *PLOS Biology* shows how secondary parasitoids ('hyperparasitoids') can take advantage of these plant signals to identify parasitoid-infected caterpillars, and duly infect the primary parasitoid, to the detriment of the original plant.

Plant volatiles have long been considered to mediate this mutualistic relationship between plants and herbivores' natural enemies such as parasitoids. When a caterpillar feeds, the parasitoids are able to use the emitted volatiles to locate the otherwise inconspicuous caterpillar, releasing the plant from its attacker. This principle has made its way into sustainable agriculture by using natural enemies such as parasitoids to control herbivorous pests on agricultural crops. However, the largest group of enemies of parasitoids, hyperparasitoids, have so far been left out of studies in this area. This is because very little is known about the cues that hyperparasitoids use to locate their parasitoid hosts.

The new study, by a team of Dutch researchers led by Erik Poelman, shows that hyperparasitoids exploit the different plant odours that are released when a plant is fed upon by a parasitoid-infected caterpillar.

"In controlled laboratory assays as well as under field conditions, hyperparasitoids were offered plant odours coming from two types of plant: ones damaged by healthy caterpillars, and ones damaged by parasitoid-infected caterpillars. We found

that they preferentially detected odours of plants damaged by infected caterpillars," explained Dr Poelman. "We were excited by these results as they indicate that hyperparasitoids rely on a network of interactions among plant, herbivore and parasitoids to locate their host."

To show how this complex network of interactions can reliably provide hyperparasitoids with information on the presence of their parasitoid host, the researchers collected saliva of the caterpillars, as they noticed the colour of saliva in healthy, non-host caterpillars was different to that of caterpillars hosting a parasitoid. Factors in caterpillar saliva play an important role in provoking the release of odours from plants, and a change in saliva composition may then alter the cocktail of odours emitted by the plant.

Indeed, Dr Poelman's team found that plant odours induced by the saliva of parasitized caterpillars was more attractive to hyperparasitoids than plant odours induced by the saliva of healthy caterpillars. Consequently, plant odours may actually reduce the benefit of attracting parasitoids to a plant.

"Our results demonstrate that the effects of herbivore-induced plant volatiles should be placed in a community-wide perspective that includes species at the fourth trophic level, to improve our understanding of the ecological functions of volatile release by plants," said Dr Poelman. In addition to the ecological aspects of their work, the authors also stress that their findings are important for developing Integrated Pest Management strategies, in which crops are manipulated to control insect pests by using parasitoids.

Although parasitoids are effective biological control agents, this study suggests that using plant odours to optimize biological control of pests may have side effects that could actually reduce the benefit of pest control, said Dr Poelman.

Journal Reference: Erik H. Poelman, Maaïke Bruinsma, Feng Zhu, Berhane T. Weldegergis, Aline E. Boursault, Yde Jongema, Joop J. A. van Loon, Louise E. M.

Vet, Jeffrey A. Harvey, Marcel Dicke. Hyperparasitoids Use Herbivore-Induced Plant Volatiles to Locate Their Parasitoid Host. PLoS Biology, 2012; 10 (11): e1001435 DOI: 10.1371/journal.pbio.1001435

Taking a Slice at the Wheat Genome

Source: ScienceNOW, by Elizabeth Pennisi. 28 November 2012

Considered by some to be the Mount Everest of crop genomes, the challenging wheat genome is close to being scaled. An international team has produced a draft of wheat's DNA sequence, one that identifies many of its genes and has made possible the identification of thousands of potential genetic changes that could improve this key crop.

"A tremendous resource for wheat improvement and plant genetics has been developed," says Jeffrey Bennetzen, a plant geneticist at the University of Georgia, Athens, who was not involved with the work. Wheat is the world's most widely grown crop, and it feeds a substantial portion of the world's population. But scientists have struggled to get a grip on its complex genetics. One complication is that the two kinds of wheat—bread wheat and pasta wheat—have different DNA makeups. Pasta wheat (durum), which is a hybrid of two wild grasses, has two genomes, one from each of its ancestors.

Bread wheat is even more complex: It has three genomes, the result of pasta wheat hybridizing with a third grass species. The new study, published online today in Nature, focuses on the bread wheat genome.

The bread wheat has almost six times as much DNA as the human genome. Unlike corn, which melded two ancestral genomes into one, bread wheat passes each of its three genomes to the next generation intact. "Since wheat has three related genomes, a big problem has been to work out which gene comes from which genome," says Peter Langridge, a plant geneticist at the

University of Adelaide in Australia who is not involved with the study.

To begin to decipher the DNA, Michael Bevan, a plant geneticist at the John Innes Centre in Norwich, U.K., and his colleagues sequenced millions of DNA fragments from one variety of bread wheat; they then pieced together just the fragments containing genes. They also sequenced the genomes of two of wheat's ancestors and used them to assign two-thirds of the 95,000 genes they found to each of the three genomes. Genes are grouped into classes based on their similarity; in some cases, the classes expanded since hybridization, while in others, they shrank. As a result, bread wheat has more storage, defense response, and energy metabolism proteins than its ancestors.

As part of the project, the researchers also roughly sequenced several other bread wheat varieties and pinpointed the differences in their genes. Those differences represent potential sources of improved traits, such as drought resistance, that can be bred into new lines of wheat.

This draft genome didn't pin down the precise location of the genes or determine the identity of bases in between genes. "This is not a complete sequence," Langridge notes. "If the target genome sequence of wheat is Everest, then this very useful analysis is equivalent to a fly-by with a very good camera," Bennetzen says. "Nearly all the features can be seen, but understanding their connectedness will require a real effort to scale this genome by a [different] approach."

Carbon Dioxide Could Reduce Crop Yields

ScienceDaily (Nov. 30, 2012)

The carbon dioxide content of the atmosphere continues to climb and heat up the climate. The gas is, however, indispensable for plants, as they use the carbon it provides to form glucose and other important substances. Therefore, the more carbon dioxide the better? The equation is

unfortunately not as simple as that. The plants, which ensure our basic food supply today, have not been bred for vertical growth but for short stalks and high grain yields.

Scientists from the Max Planck Institute of Molecular Plant Physiology and the University of Potsdam have now discovered that an increase in carbon dioxide levels could cancel out the beneficial effects of dwarf varieties.

A variety of rice called IR8, which has now disappeared almost completely from the market, caused quite a stir in the 1960s. At the time, this dwarf variety of rice produced incredible yields and warded off the food shortages predicted at the time. While most other high-yielding varieties buckled under the weight of their grains, IR8's strong short stalks had no difficulty in supporting its high grain yields. In addition, the plant saved on nutrients and energy through the lack of vertical growth and was even more productive as a result. Everything that was not required to grow longer stalks was made available to the rice grains. Plants like IR8 succeeded in protecting humanity against global famine and were hailed as part of the "Green Revolution" in agriculture.

In the meantime, however, the yields from IR8 have declined by around 15 percent, and the cultivation of this previously very promising plant is no longer seen as worthwhile. To understand this development, it is necessary to know about the mechanism that lies behind dwarf growth in plants. The dwarf rice variety lacks an enzyme that is required for the production of the plant growth hormone gibberellic acid; without gibberellic acid, the rice plant remains short but strong and high-yielding. Although nothing has changed in the genetic makeup of the IR8 rice plant in the past 50 years, its yields have declined continuously. The researchers working with Bernd Müller-Röber from the Max Planck Institute of Molecular Plant Physiology and the University of Potsdam therefore wanted to find out whether this development was possibly linked with the global increase in atmospheric carbon dioxide levels. After all,

the current concentration of the greenhouse gas in the atmosphere is 25 percent higher than in the 1960s.

Using the model plant *Arabidopsis thaliana* (generally known as thale cress), the researchers were able to observe that a higher carbon dioxide concentration results in the unblocking of the capacity of dwarf plant to form gibberellic acid. The carbon dioxide appears to have the same growth-stimulating effect as that triggered by the gibberellic acid. Thus, in the experiment, the dwarf plants gradually lost their advantage and increasingly resembled the control plants.

"Breeders now face the challenge of developing new plants that can continue to provide good yields under the altered climatic conditions," says Jos Schippers, one of the authors of the study. The cultivation of dwarf varieties is not only common in the case of rice, farmers also prefer short-stalked varieties of wheat; both cereals are the staple food consumed by a majority of the global population. The researchers are now looking for the mechanism through which the gaseous carbon dioxide influences the growth of the plants.

Journal Reference: D. M. Ribeiro, W. L. Araujo, A. R. Fernie, J. Schippers, B. Mueller-Roeber. Action of gibberellins on growth and metabolism of *Arabidopsis thaliana* plants associated with high concentration of carbon dioxide. *PLANT PHYSIOLOGY*, 2012; DOI: 10.1104/pp.112.204842

Natural *Arabidopsis* brx loss-of-function alleles confer root adaptation to acidic soil

Source: <http://www.cnb.csic.es>. Nov. 2012.

Soil acidification is a major agricultural problem that negatively affects crop yield [1] and [2]]. Root systems counteract detrimental passive proton influx from acidic soil through increased proton pumping into the apoplast [3], which is presumably also required for cell elongation and stimulated by auxin [4] and [5]].

Here, we found an unexpected impact of extracellular pH on auxin activity and cell proliferation rate in the root meristem of two *Arabidopsis* mutants with impaired auxin perception, *axr3* and *brx* [6] and [7]]. Surprisingly, neutral to slightly alkaline media rescued their severely reduced root (meristem) growth by stimulating auxin signaling, independent of auxin uptake. The finding that proton pumps are hyperactive in *brx* roots could explain this phenomenon and is consistent with more robust growth and increased fitness of *brx* mutants on overly acidic media or soil. Interestingly, the original *brx* allele was isolated from a natural stock center accession collected from acidic soil [8].

Our discovery of a novel *brx* allele in accessions recently collected from another acidic sampling site demonstrates the existence of independently maintained *brx* loss-of-function alleles in nature and supports the notion that they are advantageous in acidic soil pH conditions, a finding that might be exploited for crop breeding.

Reference: Gujas B, Alonso-Blanco C, Hardtke CS. *Curr Biol*. 2012 Oct 23;22(20):1962-8

How Plants Feel

By Kerry Grens. Source: *The Scientist*. December 1, 2012

A hormone called jasmonate mediates plants' responses to touch and can boost defenses against pests.

Although it's known that plants can detect and respond to touch, how they relay information from physical contact has been less clear. Janet Braam's group at Rice University and other labs had previously shown that the expression levels of many genes are upregulated in response to touch and that plants develop stockier builds if they are routinely perturbed. In their latest work, Braam's team set out to identify how the physical perturbation was translated into growth changes. They found that a plant hormone called jasmonate is essential for

the developmental responses to touch in *Arabidopsis*, and that touch itself, via jasmonate, can boost pest resistance.

Given jasmonate's already-established roles in responding to light, injury, and pests, the addition of touch "means that what we're looking at is different ways that signal inputs are being integrated," says John Turner, a professor at the University of East Anglia, who was not involved in the study.

A member of Braam's team recognized that many of the genes upregulated in response to touch are also upregulated after wounding—a response known to be mediated by jasmonate signaling—leading the group to scrutinize the role of the hormone in touch as well. The researchers grew plants that were unable to produce jasmonate. After 4 weeks of gently bending the plants back and forth 10 times, twice a day, the researchers found that plants that didn't produce jasmonate continued to grow normally, while the plants that produced jasmonate when touched had delayed flowering, shorter flower stems, and smaller leaf clusters. Braam says her group is looking at how these responses might affect crop plants.

Knowing that jasmonate is also involved in plant defenses, Braam's group tested whether touching might also affect how well plants can ward off attackers. Indeed, plants that were touched had smaller wounds from a fungal infection, and moth larvae that fed on touched plants did not grow as large. When the researchers grew mutant plants that constantly produced jasmonate, the plants were more resistant to pests even if untouched.

Braam says the finding could have commercial applications, and her group is looking to see whether simple touch can enhance pest resistance in crops. However, it's still unclear whether pest protection comes at a price, since the jasmonate-producing plants were stunted in growth compared to those that were jasmonate-deficient.

Braam's findings also highlight that plants are more responsive to their environment

than had been expected. "They can perceive quite diverse stimuli and quite complex changes to the environment and can respond dynamically," she says. "This happens in a way that's pretty opaque unless you look at their molecular responses." There are two big questions that remain unanswered: How do plants actually perceive touch—what are the mechanosensors involved—and what signaling pathway leads to the accumulation of jasmonate in the first place? "That's where the black box is," says Turner.

Reference: E.W. Chehab et al., "Arabidopsis touch-induced morphogenesis is jasmonate mediated and protects against pests," *Cur Biol*, 22:701-06, 2012.

Evolving CO₂-Hungry Crops

By Lewis H. Ziska and Mark Howden.
Source: *The Scientist*. December 4, 2012

Breeding plants that can convert more carbon dioxide to food could help feed a growing population.

In 2007 and 2008, due in part to rapidly rising energy costs and climatic extremes, the world experienced a sweeping food crisis, with food riots observed in more than 30 countries. In 2010 and 2011, unprecedented drought in Russia reduced the global supply of wheat, with social and political ramifications for wheat importing countries around the globe. Last summer's extensive drought in the United States, the world's largest grain exporter, suggests that food supply will, once again, continue to be an immediate and global concern.

Since the "green revolution" of the 1960s increased crop production around the world, agricultural science has served as a bulwark against global hunger. But demands have been relentless, and there is a clear need for more. More food for a global population that, in 2011, exceeded 7 billion. More for the additional 2 billion people that will join the population by 2040. And more cereal crops for biofuels production, and more grain for livestock production.

The constraints to meeting such demands are many. Urbanization removes half a million hectares of arable land from global crop production each year; competition for water supplies between industry and agriculture leads to diminished availability for irrigating crops; and the cost of fossil fuels, necessary for growing, transporting, processing, and storing food, has staggered upwards. But topping all these challenges is the looming threat of climate change, which stems largely from an increase in greenhouse gas emissions and threatens to hinder crop production in many regions, as a result of severe droughts, heat waves and the spread of invasive species. In a recent issue of Proceedings of the Royal Society B (10.1098/rspb.2012.1005, 2012), we recognize that resources are likely to become constrained in the future; however we also recognize that one resource that plants need—carbon dioxide (CO₂)—is increasing.

Since Charles Keeling began monitoring atmospheric CO₂ at Mauna Loa in 1957, atmospheric CO₂ has increased by 25 percent, from 315 parts per million (ppm) to 394 ppm. However, no efforts have been made to actively select for crop varieties that are more efficient at converting additional atmospheric CO₂ into seed yield. In our paper we argue that there is increasing evidence that such an effort could boost yields significantly, particularly for cereal grains such as wheat and rice. This one strategy will not provide a complete solution to the emerging global food challenge, but it can serve as an example of the rapid innovation and adaptation measures possible to sustainably enhance food production. Other strategies could include selection and incorporation of genes from animals and plants that have evolved mechanisms to deal with hotter environments; new engineering techniques for more efficient water delivery; even new smartphone apps that could be used to determine, based on leaf color, when and how much nitrogen to apply.

Without question, the growing demand for crop production will provide challenges as substantial and long-term as anything faced through human history. Clearly, new scientific tools and their wise use will help ensure continued agricultural productivity in the face of global uncertainty.

Lewis H. Ziska is a Senior Plant Physiologist at the Crop Systems and Global Change Lab, of the US Department of Agriculture. Mark Howden is a Theme Leader in the Climate Adaptation Flagship of the Commonwealth Scientific and Industrial Research Organization (CSIRO).

Captured: the moment photosynthesis changed the world

Source: NewScientist. 07 December 2012 by Colin Barras

BILLIONS of years ago, a tiny cyanobacterium cracked open a water molecule - and let loose a poison that wrought death and destruction on an epic scale. The microbe had just perfected photosynthesis, a process that freed the oxygen trapped inside water and killed early Earth's anaerobic inhabitants.

Now, for the first time, geologists have found evidence of the crucial evolutionary stage just before cyanobacteria split water. The find offers a unique snapshot of the moment that made the modern world. With the advent of photosynthesis came an atmosphere dominated by oxygen and, ultimately, the diversity of life forms that we know today.

"This was the biggest change that ever occurred in the biosphere," says Kevin Redding at Arizona State University in Tempe. "The extinction caused by oxygen was probably the largest ever seen, but at the same time animal life wouldn't be possible without oxygen."

Photosynthesis uses light and a source of electrons to generate energy and power an organism. In the world as we know it, that source of electrons is water, with oxygen the waste product. But there are no signs that oxygen was being formed when

photosynthesis first appeared around 3.4 billion years ago, so early photosynthesisers probably scavenged electrons by splitting other molecules like hydrogen sulphide instead.

That had changed by about 2.4 billion years ago, when deposits of oxidised minerals tell us that oxygen was beginning to accumulate in the atmosphere. Photosynthesis as we know it had evolved.

To help work out how this happened, Woodward Fischer at the California Institute of Technology in Pasadena and his colleagues studied South African rocks that formed just before the 2.4-billion-year mark. Their analysis shows that although the rocks formed in the anoxic conditions that had prevailed since Earth's formation, all of the manganese in the rock was deposited in an oxidised form.

In the absence of atmospheric oxygen, manganese needs some sort of catalyst to help it oxidise - it won't react without a bit of help. The best explanation, say Fischer's team, is that a photosynthetic organism was using manganese as an electron source. That left unstable manganese ions behind, which reacted with water to form the oxides. Fischer presented the findings at the American Geophysical Union's conference in San Francisco on 6 December.

Every researcher contacted by New Scientist has hailed the significance of the study, in part because the evidence exactly matches what evolutionary theories have predicted.

A close look at today's plants and algae shows that manganese oxidation is still a vital part of photosynthesis. Within their photosynthetic structures are manganese-rich crystals that provide the electrons to drive photosynthesis. The crystals then snaffle electrons from passing water molecules to restore their deficit. It is this electron raid that cracks open water molecules and generates the oxygen we breathe.

This complicated process must have had simpler roots. In 2007, John Allen at Queen Mary, University of London, and William Martin at the University of Düsseldorf,

Germany, suggested one scenario (Nature, doi.org/bs65kb). They believe that modern photosynthesis was born when early cyanobacteria by chance floated into a watery environment rich in manganese, and quickly adapted to take advantage of the new source of electrons.

Later, because manganese is a relatively scarce resource that can't be tapped indefinitely, the cyanobacteria evolved a different strategy. They incorporated manganese directly into their photosynthetic structures and used it as a rechargeable battery: draining it of its electrons, but allowing its supplies to be replenished by stealing electrons from another, more plentiful source - water.

What Fischer's team has found is evidence of the initial step in this process: an anoxic environment rich in manganese that has been stripped of electrons and left in an oxidised state, almost certainly by primitive cyanobacteria. "There had to be some intermediate step in the evolutionary process," says Redding.

"This is big news," says Martin. He adds that we can expect publications in the near future that provide more evidence compatible with the theory. "But this somewhat more direct geochemical evidence is really exciting."

Plants ... in ... Space!

Source: ScienceNOW, by Sid Perkins on 6 December 2012

The lack of gravity in space doesn't seem to affect certain aspects of root growth in the botanical equivalent of lab rats, a new study suggests. In 2010, researchers sent petri dishes loaded with seeds of two particular strains of Arabidopsis to the International Space Station, where astronauts tended growth experiments on the plants—the first to monitor root development in great detail, the scientists say. Specifically, the researchers measured how roots "waved" (how the root tip wandered through a small circle over the course of a 24-hour period) and "skewed" (began growing at an angle when it touched a surface) every 6 hours during their first 15 days of growth. Previous

studies, all of them earthbound, have suggested that these traits are genetically determined but that gravity also plays a major role in waving and skewing, but the new findings reveal otherwise, the researchers report online today in BMC Plant Biology. In general, the seedlings grown in orbit were smaller but exhibited the same degree of waving seen in those strains grown on Earth. However, the root tips of space-grown plants (top) showed a tendency to skew a bit more than their earthbound counterparts (bottom) when they encountered an object, mostly due to their larger number of cells (edges of cells denoted by blue tick marks), the researchers say.

What happens to plant growth when you remove gravity?

Source: PHYS.org. December 7, 2012

It is well known that plant growth patterns are influenced by a variety of stimuli, gravity being one amongst many. On Earth plant roots exhibit characteristic behaviours called 'waving' and 'skewing', which were thought to be gravity-dependent events. However, Arabidopsis plants grown on the International Space Station (ISS) have proved this theory wrong, according to a study published in BioMed Central's open access journal BMC Plant Biology: root 'waving' and 'skewing' occur in spaceflight plants independently of gravity.

In plant roots, 'waving' consists of a series of regular, undulating changes in the direction of root tips during growth. It is thought to be associated with perception and avoidance of obstacles, and is dependent on gravity sensing and responsiveness. 'Skewing' is the slanted progression of roots growing along a near-vertical surface. It is thought to be a deviation of the roots from the direction of gravity and also subject to similar mechanisms that affect waving. Even though the precise basis of these growth patterns is not well understood, gravity is considered to be a major player in these processes. To test what happens to plant root growth when

you remove gravity entirely, a research team from the University of Florida, Gainesville, USA, grew two types of Arabidopsis thaliana cultivars - Wassilewskija (WS) and Columbia (Col-0) – on the ISS. The plants were grown in specialized growth units that combined a plant habitat with a camera system which captured images every six hours. Imaging hardware delivered the telemetric data in real-time from the ISS, and comparable ground controls were grown at the Kennedy Space Centre. The phenomenon of negative-phototropism in plant roots is well documented, but its role in orienting root growth is still being explored. The authors found that, in the absence of gravity, but in the presence of directional light, spaceflight roots remained strongly negatively phototropic and grew in the opposite direction of the shoot growth, as they do back on Earth. The path taken by the roots as they grew also retained the complex patterns of waving and skewing, characteristic of Earth-grown, gravity-influenced, roots. Furthermore, while in orbit, each cultivar retained its unique terrestrial skewing pattern. However, the team observed that the degree of waving exhibited by the plants in space did not match what would be predicted for roots showing an equivalent amount of skewing back on Earth. In space, waving was far more subtle. This result reinforces the idea that waving and skewing represent two separate phenomena, and that gravity is not a mechanistic part of the basic waving and skewing processes. Lead authors Anna-Lisa Paul and Robert Ferl commented "Although plants use gravity as an orientating tropism on the Earth's surface, it is clear that gravity is neither essential for root orientation, nor is it the only factor influencing the patterns of root growth. It seems that other features of the environment are also required to ensure that a root grows away from the seed, thereby enhancing its chances of finding sufficient water and nutrients to ensure its survival." Journal reference: BMC Plant Biology.

Cottoning on to genome duplications

Source: Double X Science, posted by Chris Gunter. December 19, 2012

Plants are hard. Not in the physical way, but in the genomics way: It's been estimated that 75% of domesticated plant genomes are polyploid, meaning they have up to 12 sets of each chromosome in every cell. This makes genome sequencing crazily difficult: Each gene segment is represented multiple times, and each one has changes between them, since these organisms multiplied their chromosomes millions of years ago.

Every genome sequence has errors produced along the way; it's just a factor of the technology and the scale involved. When you are trying to read the genome of a plant and you see a nucleotide position with multiple bases supposedly reported by the sequencer at that position, how do you know what's real and what's error?

Enter comparative genomics. Scientists around the world are attacking this problem by sequencing as many different plants as possible and comparing the genomes to each other across evolutionary time. This week, the plant in the spotlight is cotton, or the *Gossypium* genus. Scientists from 10 countries collaborated to produce a draft genome sequence for *Gossypium raimondii*, which produces a non-spinnable variety of cotton fiber.

The cotton genome produced is much larger than other plants that have been sequenced – poplar, rice, and grapevines – and in this case 61% of its genome size comes from repetitive elements, which are also quite hard to incorporate into a genome sequence. It's a little like putting together a multi-million piece jigsaw puzzle where over half the picture is blue sky. In the unique parts of the genome are over 37,000 genes, which is at least 10,000 more than humans.

By comparing this more complete genome sequence to other plants, the researchers can conclude that what we now know as cotton has gone through multiple transformations. At least 60 million years

ago, its ancestors diverged from other plants and went through an abrupt chromosome multiplication, to have the five or six sets of chromosomes we still see today.

Then, about 5-10 million years ago, fibers with a structure that allowed them to be spinnable into yarn evolved in some cotton subgroups and not others. To investigate what makes spinnable cotton, the researchers produced some genome sequence for a number of representatives of these subgroups. Intriguingly, they saw linkage between fiber quality and a block of mitochondrial genes that had transported to the nucleus of some cotton strains. Mitochondria are the structures in the cell that take nutrient energy and package it into molecules that cells can use as an energy source.

In the case of cotton, the co-opted mitochondrial genes relate to the way cells like ours and those of plants generate those energy-containing molecules, by transport of electrons through certain enzymes (like NADH dehydrogenase for you aficionados). There is no obvious connection between the observations about electrons and the spinnability of cotton, though, leaving open the question: Can this passage of electrons from protein to protein really be involved in allowing our own ancestors to start making clothes from cotton? Now that these genome data have been released, anyone can study them for an answer.

The paper is [freely available on the website of the journal *Nature*](#) and is entitled "Repeated polyploidization of *Gossypium* genomes and the evolution of spinnable cotton fibres."

Forthcoming meetings

International Conference on Plant Genetics and Breeding Technologies February 18 – 20, 2013. Vienna, Austria

This International Conference will provide leading academy and industry scientists a platform to communicate recent advances in Plant Genetics and Breeding Technologies and an opportunity to establish multilateral collaborations.

Amongst the **invited speakers** are internationally known names such as: Chen Z J (USA), Dunwell J (UK), Edwards D (Australia), Feuillet C (France), Graner A

(Germany), King G J (UK), Koorneef M (Germany-The Netherlands), Parry M A (UK), Rob Dirks (The Netherlands), Röder M S (Germany), Schreiber F (Germany), Tuberosa R (Italy), van Eeuwijk F (The Netherlands), Visser RG (The Netherlands), Wang J (China), Waugh R (Scotland, UK) etc.

Deadline for submission of abstracts:
December 20, 2012

Early bird registration deadline:
December 24, 2012

More info:
<http://vipca.at/conferences/active/conference3/index.php>

EGU 2013 - BG2.9 Ecological memory in terrestrial biogeosciences: How past conditions influence the present balances of carbon and water.

April 7 – 12, 2013. Viena, Austria

Abstract Submission (deadline: 9 January 2013)

One of the main assumptions underlying studies on plant, soil and ecosystem responses to environmental drivers is that an observed pattern is the response to concurrent conditions. However, increasing

evidence highlights that different processes associated with terrestrial carbon and water cycling actually respond to past events, and that variable temporal lags occur depending on the process and environmental driver of interest, a phenomenon we call 'ecological memory'. For instance, daily carbon assimilation in water-limited ecosystems often depends on precipitation that occurred in antecedent days, and annual transpiration or productivity has been reported to be affected by climatic conditions more than two years earlier. Similarly, soil microorganisms are affected by environmental conditions over different time scales, and this in turn implies different soil responses to a given environmental event (e.g. a water pulse) depending on preceding conditions. The implications of ecological memory are wide-ranging in scope –from the timing of the sampling scheme to our interpretation of the collected data - and in scale –different memory processes may imprint biological responses from molecular to global responses. This session aims to highlight and discuss recent advances on how ecological memory affects the terrestrial response of carbon and water cycling in leaves, whole plants, tree rings, soils and ecosystems. We anticipate ecological memory to be a key research area in years to come.

UK PlantSci 2013. Plant Science in a Changing World

April 16 – 17, 2013. Dundee, Scotland

The annual conference of the UK Plant Sciences Federation

<http://www.plantsci2013.org.uk>

8th International Symposium on In Vitro culture and Horticultural Breeding

Highlighting in vitro morphogenesis to improve plant breeding

June 2 – 7, 2013. Coimbra, Portugal

<http://www.uc.pt/en/congressos/IVCHB2013/>

The next IVCHB2013 will be held at the Department of Life Sciences, University of Coimbra, Portugal, from 2-7 June 2013. The main aim of the symposium is to bring together specialists and stakeholders interested in different areas of plant tissue culture to exchange ideas and information and to establish new lines of research for the future. Main topics of the symposium will be: plant cloning, plant conservation, somatic embryogenesis, rooting, haploid research, genetic transformation and physiological, biochemical and molecular aspects of in vitro culture. A technical tour and several cultural and social events (dinner and a serenade of Fado included!) will take place. The convener of this symposium (Prof. Jorge Canhoto) and his team have the pleasure to invite all the colleagues working in this field to join this meeting which will be held, for the first time, in Portugal.

For more information contact:
jorgecan@ci.uc.pt

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>

30th ISTA Congress Seed Symposium

June 12 - 14, 2013. Antalya, Turkey

Alison A. Powell

ISTA Executive Committee member; Chair, ISTA Seed Vigour Committee; Seed Symposium Convenor

Society for Experimental Biology (SEB) Annual Main Meeting 2013

July 3 – 6, 2013. Valencia, Spain

Abstract submission will open on the 1st of October 2012.

Registration will be available online from the 1st of November 2012.

More info:
<http://www.sebiology.org/meetings/Valencia/Valencia.html>

9th European Conference on Precision Agriculture (ECPA)

July 7th – 11th, 2013. Lleida, Spain

Extension of the Abstract Submission until September 30th.

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

4th Workshop on the Molecular Aspects of Seed Dormancy and Germination

July 9th -12th, 2013. Paris, France

University Pierre et Marie Curie, Paris, France.

<http://www.congres.upmc.fr/paris-iss2013/>

11th International Conference on Reactive Oxygen and Nitrogen Species in Plants

July 17 – 19, 2013. Warsaw, Poland

We are pleased to announce that many distinguished scientists confirmed their participation at the upcoming 11th POG meeting in Warsaw.

The list of Invited Speakers can be found at the conference website:

<http://www.pogwarsaw2013.org/>

XIII Portuguese-Spanish Congress of Plant Physiology (FV2013)

July 24 – 28, 2013. Lisbon, Portugal

The Portuguese Society of Plant Physiology (SPFV) in collaboration with its counterpart Spanish (SEFV) is organizing the "XIII Portuguese-Spanish Congress of Plant Physiology (FV2013)", <http://fisiologiavegetal2013.itqb.unl.pt> that will take place in Lisbon, Faculdade de Ciências da Universidade de Lisboa (Campo Grande), from 24 to 28 July 2013.

The SPFV invited world-renowned scientists from Portugal, Spain, USA, Chile, Germany and the UK, who will contribute to this conference with six plenary lectures. It will be a comprehensive and exciting program including ten sessions (each with a guest speaker) and 4-6 oral presentations of

selected abstracts, covering subjects ranging from "Cell biology and development" to "Biotechnology and innovation." Other sessions include "Plant-Microorganism Interactions and Plant-Environment", "Metabolism and Bioenergy", "Evolution and Biodiversity", "Applied Physiology", "Systems Biology and Omics", "Education and Training" and "Entrepreneurship / Opportunities Financing".

While aiming for a scientific meeting of high international level, we are also targeting high schools, promoting research in plants among young students and teachers and bringing some to participate in this conference (contest "**VIP - Vamos Investigar as Plantas** Let's Investigate Plants"). During this meeting we will promote high quality research and raise public awareness of the importance of plants and their research for global food security, renewable resources, bio-energy, environment and sustainability, health and wellbeing and for the global economy. We are offering special conditions to facilitate the participation of scientists from the Community of Portuguese Speaking Countries (CPLP) and the participation of students.

We would like to invite to participate in the FV2013 all those who are involved in research on plants or in the teaching of Plant Biology.

<http://fisiologiavegetal2013.itqb.unl.pt>

Third International Conference on Plant Vascular Biology

July 26 – 30, 2013. Helsinki, Finland.

<http://www.pvb2013.org>

7th EPSO Conference: Plants for a Greening Economy

September 1 – 4 , 2013. Porto Heli, Greece

<http://www.epsoweb.org/7th-epso-conference-1-4-september-2013-greece>.

ONLINE REGISTRATION STARTED!

AIM: The 7th EPSO Conference Plants for a Greening Economy will be held at the beautiful coast of Porto Heli, at the east side of the Peloponnese, in Greece, from 1 to 4 September 2013. The Conference will

address many of the challenges faced by the plant research community in an evolving world: basic research as well as applied research on climate change, preservation of the environment and of natural biodiversity, as well as the food and feed demands of a growing world population. Non-food crops for energy, biomaterials, biopharmaceuticals and other new products will also be an important focus of the conference.

TOPICS: Regulatory networks in plants
Plant response and adaptation to biotic stresses
Plant response and adaptation to abiotic stress
Plant response and adaptation to low resource availability
Climate change—the mitigating role of plants
Global food security—sufficiency and affordability
Global food security – nutritional quality and safety
Plant breeding and sustainability
Plant driven bioeconomy—bioenergy, biofuels, molecular farming, biomaterials
Plant evolution—biodiversity and ecosystems
Science policy – plant science and environment
Two dedicated poster sessions

LIST OF CONFIRMED SPEAKERS AND CHAIRS:

Eva-Mari Aro, David Beerling, Jose-Pio Beltran, Philip Benfey, Malcolm Bennett, Ton Bisseling, Marc de Block, Alain Charcosset, Jan Delcour, Xinnian Dong, Matthias Erb, Eckhard George, Jean-Christophe Glaszmann, Wilhelm Grissem, Jacek Hennig, Heribert Hirt, Jonathan Jones, Angela Karp, Sandy Knapp, Mauricio A. Lopes, Cathie Martin, Karin Metzloff, Maurice Moloney, John Mundy, Bruce Osborne, Javier Paz-Ares, Merja Penttilä, Christophe Plomion, Marcel Prins, Edward Rybicki, Uli Schurr, George Skaracis, Chiara Tonelli, Athanasios Tsaftaris, Rens Voeseneck, Olivier Voinnet, Tom Whitham, Dan Yakir, Kazuko Yamaguchi-Shinozaki and Jian-Kang Zhu.

CONTACT EPSO Conference officer at:
Katerina.Karkala@epsomail.org

Positions available



POSTDOC

Post doctoral position - structural basis of RNA silencing - University of Heidelberg, Germany

The Maizel and Russell groups are looking for a highly motivated post-doctoral scientist to study the structural determinant of small RNA biogenesis and action in *Arabidopsis thaliana*.

Our groups are using a variety of computational, genetics and biochemical approaches to address the structural basis of ARGONAUTE protein action. The candidate will be appointed in both groups. We seek a scientist able to work both independently and co-operatively with a team, and thrive in a competitive environment. An expertise in biochemistry, molecular biology and computational structural biology would be highly appreciated. He/she must have published articles in top ranking scientific journals.

The groups are part of the Center for Organismal Studies (Maizel) and Bioquant (Russell) of the University of Heidelberg which feature a truly multidisciplinary environment.

The position is available from January 2013 and funded for 2 years.

Applications will be done exclusively by email (alexis.maizel@cos.uni-heidelberg.de). Please enclose in a single PDF file: a CV, a list of publications, a brief summary of research experience, and names and e-mail of 2-3 referees.

Post-Doctoral Position in Biochemistry/Molecular Biology - University of Gothenburg, Sweden

Applications are invited for a two-year post-doctoral position available from February 2013 at the Department of Biology and Environmental Sciences, University of

Gothenburg. The successful applicant will join an active research group studying the Clp/HSP100 family of molecular chaperones and proteases in plants (*Arabidopsis*) and cyanobacteria (*Synechococcus elongatus*). The project will involve the bacterial over-expression and purification of selected cyanobacterial and chloroplast Clp proteins, followed by extensive biochemical and structural characterization. Applicants must have a PhD in biochemistry, molecular biology or related field. Experience with *Arabidopsis*, biochemistry, protein purification or enzymology would be an advantage.

Applications with *Curriculum vitae* should be sent by email before January 6 to: Adrian Clarke (adrian.clarke@bioenv.gu.se)

Postdoctoral position in plant genomics and bioinformatics

Max Planck Institute for Chemical Ecology, Jena, Germany

The Department of Molecular Ecology headed by Professor Ian Baldwin at the Max Planck Institute for Chemical Ecology is offering a postdoctoral position in plant genomics and bioinformatics.

The main tasks of the candidate will be to contribute to the analysis of *Nicotiana* genomes together with other researchers from the genomics team in the Department and help to build tools that will assist people in the group to optimally use the genome and transcriptome data.

The candidate should have strong background in bioinformatics, computational biology, and computational analysis of next-generation sequences (NGS). Experience in database design and construction is a plus.

The candidate should be experienced in at least one programming languages, such as Perl, Python or Java/C++. Experience in

Linux system administration and facilities operations is preferred.

The Max Planck Society offers a competitive fellowship, with a duration of 3 years starting May 2013. The opportunity for a German scale salary (TVL-D

13) will depend on the candidates' profile. The postdoctoral fellow will be part of the Max Planck Postdoctoral Network, which offers trainings and science communication opportunities.

Application review process will begin on the 10th January 2013 and continue until position is filled. In case of the (TVL-D 13) position the deadline for application is the 20th of January.

If you are interested in this position, please send a CV, a description of research interests and contact information of 2-3 referees to Prof. Ian Baldwin (baldwin@ice.mpg.de).

For further information, please contact Dr. Shuqing Xu (sxu@ice.mpg.de) or Dr. Aura Navarro (anavarro@ice.mpg.de)

PREDOC

2 PhD opportunities to study small RNA regulated root growth

University of Heidelberg, Germany

Starting in 2013 our laboratory is offering 2 PhD positions to study how small RNAs control root growth in *Arabidopsis thaliana*.

Requirements for the positions are: strong interest in plant developmental biology, cell biology and microscopy. We seek highly motivated and creative scientists. The students will be part of the HBIGS graduate school (<http://www.hbigs.uni-heidelberg.de>)

Our laboratory is part of the Center for Organismal Studies and of the Excellence Cluster CellNetworks of Heidelberg University. The campus is located downtown Heidelberg and host several other high profiles centres contributing to a lively, multi-disciplinary, and stimulating work environment.

For more informations on the positions see <http://www.maizel-lab.org>

New books



Plant Responses to Drought Stress. From Morphological to Molecular Features.

R. Aroca (ed). Springer-Verlag, Berlin, 2012. 466 pp. ISBN 978-3-642-32652-3. DOI 10.1007/978-3-642-32653-0.

Uno de los principales problemas a los que se enfrenta la agricultura moderna es la baja disponibilidad de agua de calidad adecuada para el riego. A su vez, los ecosistemas naturales también se enfrentan cada vez más a periodos de sequía más intensos y prolongados en el tiempo como consecuencia del cambio global que estamos experimentando. Las plantas, como organismos sésiles, se han visto forzados a desarrollar una serie de mecanismos

encaminados a resistir los episodios de sequía. En este libro se han compilado diecisiete revisiones sobre diferentes aspectos de las respuestas de las plantas a la sequía, desde aspectos morfológicos a moleculares, incluyendo aspectos de ecofisiología y respuestas en campo. En el primer capítulo del Dr. Farooq se sintetiza una visión general de la respuesta de las plantas a la sequía, sirviendo de introducción al libro y como revisión general para personas no iniciadas en la investigación en sequía. Los capítulos dos y tres están encuadrados dentro de la primera parte del libro (Respuestas morfológicas y anatómicas). Así, el capítulo 2 de la Dra. De

Micco se centra en respuestas anatómicas en general y el capítulo 3 del Dr. Vilagrosa específicamente en la problemática de la cavitación del xilema. La segunda parte del libro versa sobre las respuestas fisiológicas. En dicha parte se incluyen cuatro capítulos. El primero del Dr. Aroca trata sobre como la absorción de agua por la raíz se regula en condiciones de sequía. El segundo del Dr. Flexas resume la respuesta de la fotosíntesis a la escasez de agua. El tercero del Dr. Bacelar versa sobre las distintas estrategias que tienen las plantas para optimizar el uso del agua en condiciones de sequía. Por último, el cuarto del Dr. Colla compendia el efecto de la baja disponibilidad de agua sobre la nutrición vegetal. La tercera parte del libro se refiere a las respuestas bioquímicas y moleculares. De este modo, el capítulo 8 del Dr. Arndt resume todos los procesos implicados en el ajuste osmótico. El capítulo 9 del Dr. Munné-Bosch versa sobre la respuesta antioxidante de las plantas al estrés por sequía. El capítulo 10 del Dr. Davies evalúa la implicación de las hormonas vegetales en el crecimiento vegetal en condiciones de sequía. Finalmente, el capítulo 11 del Dr. Xiong resume la respuesta de la planta a la escasez de agua a nivel transcripcional. La cuarta parte del libro aborda la sequía desde un punto de vista ecofisiológico. Desde el capítulo del Dr. Aranda sobre los sistemas forestales al capítulo del Dr. Ryu sobre la influencia de los microorganismos del suelo para mejorar la tolerancia de las plantas a la sequía, pasando por los capítulos del Dr. Ruiz-Lozano y Dr. Erice sobre micorrizas arbusculares y fijación de nitrógeno, respectivamente. Finalmente, la última parte del libro contiene dos capítulos sobre ejemplos específicos en campo, como son el altramuz (capítulo del Dr. Palta) o frutales de hoja caduca (capítulo del Dr. López). Como se puede observar este libro cubre una gama amplia de aproximaciones al estudio del efecto de la sequía en las plantas, y aunque esté dividido en partes, en muchos de los capítulos se tocan varios aspectos de la respuesta de la planta y no

sólo los correspondientes al apartado en cuestión. De este modo, el presente libro es un compendio actualizado del conocimiento científico sobre como las plantas responden a la sequía, y por lo tanto sirve tanto para especialistas en sequía, como para aquellos que quieran iniciarse en este campo. Un valor añadido es la proximidad de los temas tratados. Puesto que ha sido escrito en gran medida por investigadores nacionales o de países próximos. Éstos han expuesto en gran medida sus experiencias y resultados de investigación con especies vegetales propias de nuestros cultivos y ecosistemas.

The Molecular Life of Plants

[Russell Jones](#) (University of California, Berkeley, USA), [Helen Ougham](#) (Aberystwyth University), [Howard Thomas](#) (Aberystwyth University), [Susan Waaland](#) (University of Washington, USA)

October 2012, Wiley-Blackwell. ISBN: 978-0-470-87012-9

The Molecular Life of Plants presents students with an innovative, integrated approach to plant science. It looks at the processes and mechanisms that underlie each stage of plant life and describes the intricate network of cellular, molecular, biochemical and physiological events through which plants make life on land possible. Richly illustrated, this book follows the life of the plant, starting with the seed, progressing through germination to the seedling and mature plant, and ending with reproduction and senescence. This "seed-to-seed" approach will provide students with a logical framework for acquiring the knowledge needed to fully understand plant growth and development.

Written by a highly respected and experienced author team *The Molecular Life of Plants* will prove invaluable to students needing a comprehensive, integrated introduction to the subject across a variety of disciplines including plant science, biological science, horticulture and agriculture.

Principles of Plant Genetics and Breeding, 2nd Edition

[George Acquaah](#)

September 2012, Wiley-Blackwell. ISBN: 978-0-470-66475-9

Description

To respond to the increasing need to feed the world's population as well as an ever greater demand for a balanced and healthy diet there is a continuing need to produce improved new cultivars or varieties of plants, particularly crop plants. The strategies used to produce these are increasingly based on our knowledge of relevant science, particularly genetics, but involves a multidisciplinary understanding that optimizes the approaches taken.

Principles of Plant Genetics and Breeding, 2nd Edition introduces both classical and molecular tools for plant breeding. Topics such as biotechnology in plant breeding, intellectual property, risks, emerging concepts (decentralized breeding, organic breeding), and more are addressed in the new, updated edition of this text. Industry highlight boxes are included throughout the text to contextualize the information given through the professional experiences of plant breeders. The final chapters provide a useful reference on breeding the largest and most common crops.

- Up-to-date edition of this bestselling book incorporating the most recent technologies in the field
- Combines both theory and practice in modern plant breeding
- Updated industry highlights help to illustrate the concepts outlined in the text
- Self assessment questions at the end of each chapter aid student learning
- Accompanying website with artwork from the book available to instructors

Functional Biology of Plants

by Martin Hodson (Oxford Brookes Univ.) and John Bryant (University of Exeter).

Ed. Wiley-Blackwell. 2012.

Hardcover ISBN: 978-0-470-69940-9;

Paperback ISBN: 978-0-470-69939-3

Functional Biology of Plants provides students and researchers with a clearly written, well structured whole plant physiology text. Early in the text, it provides essential information on molecular and cellular processes so that the reader can understand how they are integrated into the development and function of the plant at whole-plant level. Thus, this beautifully illustrated book, presents a modern, applied integration of whole plant and molecular approaches to the study of plants.

Web site: <http://www.hodsons.org/FBOP/>

Molecular biology techniques : a classroom laboratory manual

Susan Carson, Heather B. Miller, D. Scott Witherow, 3rd ed.

Elsevier, 2012

ISBN 978-0-12-385544-2

Texto ilustrado e interactivo de biología molecular e ingeniería genética : conceptos, técnicas y aplicaciones en ciencias de la salud

Ángel Herráez, 2a. ed.

Elsevier, D.L. 2012

ISBN 978-84-8086-647-7

Modeling Physiology of Crop Development, Growth and Yield

By A Soltany, Gorgan University of Agricultural Sciences and Natural Resources, Iran, T R Sinclair, University of Florida, USA

March 2012 / 336 pages / 9781845939700

Model studies focus experimental investigations to improve our understanding and performance of systems. Concentrating on crop modeling, this book provides an introduction to the concepts of crop development, growth, and yield, with step-by-step outlines to each topic, suggested exercises and simple equations. A valuable text for students and researchers of crop development alike, this book is written in five parts that allow the reader to develop a solid foundation and coverage of production models including water- and nitrogen-limited

systems. A valuable text for students and researchers of crop development alike.

Plant Sciences Reviews 2011

CAB Reviews

Edited by D Hemming, Commissioning Editor, CAB Reviews, CABI UK

April 2012 / 272 pages / 9781780640150

Plant Sciences Reviews 2011 provides scientists and students in the field with timely analysis on key topics in current research. Originally published online in CAB Reviews, this volume makes available in printed form the reviews in plant sciences published during 2011.

Molecular Plant Breeding

By Y Xu, Maize Molecular Breeder, International Maize and Wheat Improvement Centre (CIMMYT), Mexico

January 2012 / 752 Pages / 9781845939823

Now available in paperback, Molecular Plant Breeding provides an integrative overview of issues from basic theories to their applications to crop improvement. Chapters include discussions of breeding methodology, quantitative genetics, genomics and bioinformatics and present statistical issues related to gene mapping, marker-assisted selection and genotype by environment interactions in clear and concise language. Providing an integrated profile of molecular breeding in plants, this book will be an essential resource for researchers and students involved in plant biology and breeding, genetics and applied genomics.