



FEDERATION OF EUROPEAN SOCIETIES OF PLANT BIOLOGY



FESPB Newsletter



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Editor: Prof. Dolores Rodriguez

Plant Biology Congress Freiburg 2012 jointly organized by FESPB and EPSO



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

Plant Scientists in Europe are represented by two independent organisations. The FESPB (Federation of European Societies of Plant Biologists) is the umbrella organisation of 27 national botanical societies in Europe, representing more than 24,000 individuals and has in addition several corporate members from the European industry. The EPSO (European Plant Science Organisation) unites more than 200 research institutions and universities from 30 countries. To

date both organisations held strictly separate conferences.

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

Heinz Rennenberg and Ralf Reski

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

Research News



Getting to the root of nutrient sensing

Science Centric. 15 June 2010

New research published by Cell Press in the June 15th issue of the journal *Developmental Cell*, reveals how plants modify their root architecture based on nutrient availability in the soil.

Plants obtain most necessary nutrients by taking them up from the soil into their roots. Although plants cannot move to a new environment when nutrient availability is less than favourable, they can modify their development to favour root colonisation of soil areas where nutrients are abundant. Therefore, plants perceive the availability of external nutrients, like nitrogen, and couple this nutrient sensing to an appropriate adaptive response.

In *Arabidopsis*, the 'lab rat' of the plant world, lateral root growth is induced in nitrate-rich patches of soil. 'Nitrate is the main nitrogen source for these plants and a signalling molecule that regulates growth and metabolism,' explains senior study author Dr Alain Gojon from the Plant Biochemistry and Molecular Physiology Department in Montpellier, France. 'In *Arabidopsis*, the NRT1.1 nitrate transporter is crucial for nitrate signalling stimulating root growth.'

Dr Gojon's group was interested in investigating how NRT1.1-dependent stimulation of lateral root growth works. They discovered an unexpected connection between NRT1.1 and auxin, a plant hormone that plays a key role in root development. The researchers found that in addition to transporting nitrate, NRT1.1 also facilitates auxin transport. When external nitrate concentrations are low, NRT1.1 represses auxin accumulation in lateral roots and inhibits lateral root growth. A high nitrate concentration or disruption of the NRT1.1 gene suppresses NRT1.1-dependent auxin transport and auxin accumulates in lateral roots, which then grow out into the soil.

Taken together, the results indicate that NRT1.1 regulates root branching by exerting nitrate-dependent control of auxin accumulation in lateral roots. 'We propose that NRT1.1 represses lateral root growth at low nitrate availability by promoting auxin transport out of lateral root tips and towards the base of the root. Thus, high nitrate availability stimulates lateral root growth by inhibiting NRT1.1-dependent auxin transport and allowing auxin accumulation in root tips,' says Dr Gojon. 'This defines a mechanism

connecting nutrient and hormone signalling during organ development.'

Circadian clock components regulate entry and affect exit of seasonal dormancy as well as winter hardiness in Populus trees

The plant circadian clock is fairly well characterized, but understanding its 'purpose' is an ongoing endeavor; here, the authors show convincingly that circadian clock genes are critical to the seasonality traits of cold hardiness and bud dormancy in trees.

Starting from a targeted down-manipulation of candidate clock genes in poplar trees, and the technical advance of measuring molecular rhythms in living trees, the authors showed that so-called canonical clock genes participate in a tree circadian clock. From there, a phenotypic exploration of these genetically manipulated trees revealed an exciting finding that autumn-to-winter traits related to survival of winter cold in Northern climates require a functional clock. This 'hidden gem' of a paper is paradigm-driving in defining a tree's response to season, and the role of the circadian clock in said response.

Reference: Ibáñez et al. Circadian clock components regulate entry and affect exit of seasonal dormancy as well as winter hardiness in Populus trees. *Plant Physiol.* 2010 Jun 8.

Spanish scientists sequence the genome of *Pseudomonas savastanoi*, causal agent of the knot-disease of olive tree

Source: Universidad Politécnica de Madrid. July 2010.

The XXI century agriculture faces a number of pressing challenges related to the need to produce sufficient food for the growing world population and also to do it in a more

sustainable way, more respectful to the environment and with increased security. Plant diseases caused by pathogens not only reduce the overall production but also may alter the food quality and drastically reduce the commercial value of crops. The design of new strategies for disease control, indispensably required the management of the information contained in the genomes of pathogenic organisms. Similar to what has happened to the human genome, this technology is opening new doors for the identification, control, and development of novel disease resistant varieties of crops.

Pseudomonas savastanoi pv *savastanoi* is the causative agent of the knot-disease of the olive tree, an important disease in

olive production loss in Spain. The affected trees show tumors (known as warts) that can reach several centimeters in diameter on the trunks, branches, stems and buds. In general, infected trees show less vigor and reduced growth; when the attack is severe, the trees end up being unproductive. To date, due to the absence of effective methods of control, it is necessary to establish a preventive control strategy, reducing bacterial populations by pesticide treatments using variations of copper and insensitive.

The sequencing of the genome of this pathogen opens the door to the identification of genes responsible for virulence and bacterial survival on leaves, facilitating the design of specific strategies to combat this disease and the development of breeding programs of the olive. This project marks the first sequencing the genome of a plant pathogenic bacterium carried out in Spain, and provides the first known genome of a pathogenic *Pseudomonas* fruit tree, olive trees worldwide.

The work, included in the June issue of the journal *Environmental Microbiology*, has been developed by researchers at the Universidad Politécnica de Madrid (CBGP), Universidad de Málaga, Universidad Pública de Navarra, University of Wisconsin (USA) and IVIA (Valencia).

Plant 'breathing' mechanism discovered

Source: Science Centric (by way of Carnegie Institution). 13 July 2010

A tiny, little-understood plant pore has enormous implications for weather forecasting, climate change, agriculture, hydrology, and more. A study by scientists at the Carnegie Institution's Department of Global Ecology, with colleagues from the Research Centre Juelich in Germany, has now overturned the conventional belief about how these important structures called stomata regulate water vapour loss from the leaf - a process called transpiration. They found that radiation is the driving force of physical processes deep within the leaf. The research is published the week of July 12, 2010, in the on-line early edition of the Proceedings of the National Academy of Sciences.

Stomata are lip-shaped pores surrounded by a pair of guard cells that control the size of the opening. The size of the pores regulates the inflow of carbon dioxide (CO₂) needed for photosynthesis and the outflow of water vapour to the atmosphere - transpiration.

Transpiration cools and humidifies the atmosphere over vegetation, moderating the climate and increasing precipitation. Stomata influence the rate at which plants can absorb CO₂ from the atmosphere, which affects the productivity of plants and the concentration of atmospheric CO₂. Understanding stomata is important for climate change research.

Current climate change models use descriptions of stomatal response based on statistical analysis of studies conducted with a few plant species. This approach is not based on a solid understanding of the mechanism of stomatal regulation and provides a poor basis for extrapolating to environmental conditions.

'Scientists have been studying stomata for at least 300 years. It's amazing that we have not had good grasp about the regulatory mechanisms that control how much stomata open or close in response to a constantly changing environment,' remarked co-author Joseph Berry of Carnegie.

For the first time, these researchers looked at how the exchange of energy and water vapour at the outer surface of the leaf are linked to processes inside the leaf. They found that the energy from radiation absorbed by pigments and water inside the leaf influences how the stomata control water levels.

'In this study we illuminated a sunflower leaf with an incandescent light that was filtered to include or exclude near infrared light (NIR 700 nm),' remarked Berry. 'When the near infrared light was applied, the stomata responded by opening and indirectly stimulated photosynthesis. Light of different colours gave similar stomata opening at equal energy inputs - more evidence that heat is the driver.'

The scientists replicated the experiment with five other plant species and over a range of carbon dioxide levels and temperatures. The researchers also developed a model based on energy balance of the leaf system to simulate responses. Results from the model mimicked the results from the lab.

It has been assumed that the guard cells forming the pore have sophisticated sensory and information processing systems making use of light and other environmental cues to adjust the pores. The breakthrough of this research is that it is the first to demonstrate that regulation of the rate of water loss by stomata is linked to physical processes that occur deep within the leaf.

'This means that the current model for what drives stomata to change their size has to change,' remarked co-author

Roland Pieruschka, a Marie Curie Fellow from the European Union at the Carnegie Institution (currently at the Research Centre Juelich in Germany). 'For a long time researchers have thought that heat from the sun, which is absorbed by pigments, moves from cell to cell until it gets to the cavities beneath the stomata where evaporation has been thought to take place. This probably happens to some degree, but the results presented here are more consistent with our hypothesis that much of this heat is transferred through air spaces inside the leaf that are saturated with water vapour. This key difference is pivotal for understanding how Otto Lange's seminal work in the 1970s, on responses of stomata to humidity, can be fit into a leaf-scale concept of stomatal regulation.'

CSI at the Service of Cellulose Synthesis: Plant Researchers Identify Protein Involved in Formation of Cellulose

Source: ScienceDaily (July 21, 2010)

Grains, vegetables and fruit taste delicious and are important sources of energy. However, humans cannot digest the main component of plants -- the cellulose in the cell wall. Even in ruminants, animals that can metabolise cellulose, the digestibility of the cell wall plays a crucial role in feed utilisation. Scientists are therefore looking for ways of increasing the digestibility of animal feed, and of utilising plant cell walls to generate energy. To do this they must first understand how plant cells develop their cell walls from cellulose and identify the genes and proteins involved.

Scientists at the Max Planck Institute of Molecular Plant Physiology in Potsdam, working in collaboration with colleagues from the USA, have now discovered a hitherto unknown protein required for cellulose production. The research appears in the Proceedings of the National Academy of Sciences.

Unlike animal cells, plant cells have a cell wall made of various sugar polymers, the main component of which is cellulose. This gives the plant its stability, protects it against pathogens and is involved in seed germination and fruit maturity. Cellulose accounts for between 35% and 50% of the dry weight of plants, making it the most common biopolymer on earth.

Cellulose is synthesized directly at the plasma membrane by a protein complex. Up to now, cellulose synthase (CESA) was the only known component of this complex. This enzyme arises in plant cells in different forms that vary in structure. Genetic studies indicate that three of

these forms, CESA1, CESA3 and CESA6, are required for the synthesis of the primary cell wall, while CESA4, CESA7 and CESA8 are necessary for the synthesis of the secondary cell wall. The primary cell wall forms during cell growth and is particularly flexible and ductile. In contrast, the secondary cell wall forms when the cell is fully grown and is thicker and more rigid than the primary cell wall. It was not previously known how many forms of CESA exist in the protein complex and whether it contains other proteins. Scientists working with Staffan Persson at the Max Planck Institute of Molecular Plant Physiology and their colleagues in the USA have now identified the Cellulose Synthase-Interactive Protein -- CSI1 -- which is involved in cellulose synthesis. CSI1 appears to be associated with the CESA complex as it interacts with the cellulose synthases of the primary cell wall (CESA1, 3 and 6). The researchers succeeded in demonstrating that the protein plays an important role in the formation of cellulose. "Plants that cannot form any CSI1 due to a mutation demonstrably produce less cellulose. They have short and swollen roots, and their pollen grains collapse," explains Dr. Staffan Persson.

The scientists have yet to discover the precise role played by CSI1 in cellulose synthesis. They suspect that the protein influences the speed of cellulose production and the spatial orientation of the individual cellulose fibrils. The researchers would thus now like to examine the precise role of CSI1. The insights gained from these more detailed studies will contribute to a better understanding of the biosynthesis of cell walls. This knowledge could increase the chances of achieving better cell wall digestibility in animal feed, and enable the utilisation of cell walls to generate energy. Journal Reference: Y. Gu, N. Kaplinsky, M. Bringmann, A. Cobb, A. Carroll, A. Sampathkumar, T. I. Baskin, S. Persson, C. R. Somerville. Identification of a cellulose synthase-associated protein required for cellulose biosynthesis. Proceedings of the National Academy of Sciences, 2010; DOI: 10.1073/pnas.1007092107

Quantum entanglement in photosynthesis and evolution

Source: Science Centric. 22 July 2010
 Recently, academic debate has been swirling around the existence of unusual quantum mechanical effects in the most ubiquitous of phenomena, including photosynthesis, the process by which

organisms convert light into chemical energy. In particular, physicists have suggested that entanglement (the quantum interconnection of two or more objects like photons, electrons, or atoms that are separated in physical space) could be occurring in the photosynthetic complexes of plants, particularly in the pigment molecules, or chromophores. The quantum effects may explain why the structures are so efficient at converting light into energy - doing so at 95 percent or more.

In a paper in The Journal of Chemical Physics, which is published by the American Institute of Physics, these ideas are put to the test in a novel computer simulation of energy transport in a photosynthetic reaction centre. Using the simulation, professor Shaul Mukamel and senior research associate Darius Abramavicius at the University of California, Irvine show that long-lived quantum coherence is an 'essential ingredient for quantum information storage and manipulation,' according to Mukamel. It is possible between chromophores even at room temperature, he says, and it 'can strongly affect the light-harvesting efficiency.'

If the existence of such effects can be substantiated experimentally, he says, this understanding of quantum energy transfer and charge separation pathways may help the design of solar cells that take their inspiration from nature.

Cellulose: Hard to digest, but full of energy

Source: Science Centric. 21 July 2010
 Grains, vegetables and fruit taste delicious and are important sources of energy. However, humans cannot digest the main component of plants - the cellulose in the cell wall. Even in ruminants, animals that can metabolise cellulose, the digestibility of the cell wall plays a crucial role in feed utilisation. Scientists are therefore looking for ways of increasing the digestibility of animal feed, and of utilising plant cell walls to generate energy. To do this they must first understand how plant cells develop their cell walls from cellulose and identify the genes and proteins involved. Scientists at the Max Planck Institute of Molecular Plant Physiology in Potsdam, working in collaboration with colleagues from the USA, have now discovered a hitherto unknown protein required for cellulose production.

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against pathogens and is involved in seed germination and fruit maturity. Cellulose accounts for between 35% and 50% of the dry weight of plants, making it the most common biopolymer on earth.

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Plant–biotic interactions: advances on all fronts

Jane E [Parker](#) and Jeffrey G [Ellis](#)
Current Opinion in Plant Biology. Vol. 13,
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Plant–biotic interactions have positive and negative impacts on the health of natural and agricultural plant ecosystems. Positive interactions include symbioses where plant photosynthate is exchanged for scarce nutrients such as nitrogen and phosphorus provided by bacterial and fungal symbionts. Although most examples involve host–symbiont pairs, the situation can get more complex and involve three players, the so-called 'tri-trophic' interactions. De Vos and Jander (Volatile Communication in Plant–Aphid Interactions) provide an update of interactions, particularly those involving aphids, where insect pest-induced plant-derived molecules, sometimes antifeedants in their own right, can act as chemical attractants for predators and parasites of the pest. Here the advantage is to the host, but not in all cases of tri-trophic interactions it seems. Two recent reports are highlighted where plant virus infection of host plants can induce production of chemical attractants for the viruses' aphid vector and promote virus spread. Other recent advances highlighted in this review include the first aphid genome sequence and the use of host expressed RNAi to modify aphid gene expression.

In terms of beneficial interactions with plants Ivanov, Fedorova, and Bisseling (Intracellular plant microbe associations: secretory pathways and the formation of perimicrobial compartments) discuss advances in understanding the establishment and role of 'symbiosomes' which are organelle-like structures containing differentiated Rhizobium symbionts involved in N₂ fixation, surrounded by a host cell derived membrane. Similarities are drawn with arbuscules, the convoluted intracellular hyphae of mycorrhizal fungi, not only in the host membrane envelopment but also in the common use by Rhizobium bacteria and mycorrhizal fungi of host receptors to signal the initiation of symbiosis. The importance of host-derived secretion mechanisms in servicing the symbiosome membrane and its endosymbiont contents are highlighted, among others, in two recent advances showing duplication and specialization of a host signal peptidase devoted to secretion of small Medicago specific cysteine-rich proteins into this compartment.

The role of the host secretion machinery trafficking low and high molecular weight cargoes (such as antimicrobials, cell wall components, or cell membrane localized exporters), in defense against bacterial pathogens and penetration resistance

against nonadapted fungal pathogens, and maybe also in manipulating beneficial phyllosphere/rhizosphere communities, is outlined by Bednarek et al. (Not a peripheral issue: secretion in plant-microbe interactions). The effectiveness of the secretion-based defenses raises the question of how host-adapted pathogens overcome them. The answer probably is through 'effectors'-pathogen secreted molecules that interfere with various layers of host resistance to permit infection.

Two chapters in this issue are devoted to bacterial effector discovery and biology. Hahn and Rathjen (Bacterial virulence effectors and their activities) review recent achievements in understanding the roles of bacterial effectors delivered to host cells via the bacterial Type 3 Secretion System (T3SS). A common theme highlighted here is the recent demonstration by biochemical and protein structural studies that several different *Pseudomonad* effectors inhibit activities of receptor kinases involved in PAMP perception by the host and thus block PAMP induced defense.

Bogdanove, Schornack, and Lahaye (TAL effectors: finding plant genes for disease and defense) review some stunning advances with a completely different class of bacterial effectors, the transcription activator-like (hence TAL) class from *Xanthomonas* and *Ralstonia* spp. These effectors contain an N-terminal signal directing them through the T3SS, a region of polymorphic 34 amino acid repeats with specific DNA binding capacity and a domain that can initiate gene transcription. The effector function of these proteins is to activate expression of host genes that aid pathogenesis (disease susceptibility (S) genes). In some instances the host plant has co-opted the expression system to switch on defense. One significant advance from this research is the definition of host gene promoter DNA sequences targeted by the 34 aa repeat domain and decoding of the relationship between the repeat polymorphisms and single bases of the promoter target. The result is that designer transcription factors and target genes can be made to direct expression of any gene, including synthetic disease resistance genes.

Effector interference with host immunity also features in the chapter by Trujillo and Shirasu (Ubiquitination in plant immunity). Significant advances have been made in our understanding of the ubiquitination system as a regulator of plant signaling, especially in stress hormone responses.

Ubiquitin tagging of negative components leading to their destruction by the 26S proteasome emerges as an important means of pathway activation. The release of negative regulation on defense pathways places the ubiquitination system as a target for disruption by effectors. Discoveries of the bacterial effector AvrPtoB's activity as a ubiquitin E3 ligase disrupting plant defense to bacterial pathogens are especially revealing here.

The study of pathogenesis and effectors in eukaryotic pathogens, including filamentous fungi and oomycetes and nematodes, is making rapid progress due to high-throughput whole genome sequencing technologies. With reference to barley powdery mildew and maize smut fungi, Spanu, and Kämper (Genomics of biotrophy in fungi and oomycetes — emerging patterns) focus on the contribution of genome information to addressing the important question of how these strictly biotrophic fungi obtain nutrition from their hosts. In contrast to necrotrophs, the biotroph genomes contain far fewer genes involved in the degradation of complex plant structural components such as cellulose. Rather, they tend to more directly target photosynthates at the level of sucrose and/or hexoses. The authors highlight the fact that although the bean rust fungus has a hexose transporter in the haustorial membrane, suggesting that this pathogen could accumulate monosaccharides broken down by secreted invertases, invertase genes are rare or absent in mycorrhizal fungal and powdery mildew genomes. Indeed in the maize smut fungus, deletion of a single novel type of sucrose transporter expressed only during host plant infection has a major effect on virulence. Oliver and Solomon (New developments in pathogenicity and virulence of necrotrophs) focus on insights that genome sequence data are generating for the study of host species specific protein toxins that act as effectors. The genes for one of these, ToxA, has undergone horizontal gene transfer and whole genome sequencing of other pathogens is beginning to uncover more potential examples of gene transfers. Similarly, Rep and Kistler (The genomic organization of plant pathogenicity in *Fusarium* species) provide direct evidence for effector gene transfer between pathotypes of the wilt fungus *Fusarium oxysporum*. Whole genome sequencing of a tomato infecting pathovar identified strain specific genomic regions, in two instances whole chromosomes, in which effector genes are clustered. Direct

experimental evidence of interstrain transfer on effector gene-rich chromosomes has been obtained and this provides an explanation why different isolates of *F. oxysporum*, an asexual species, from a single host species (a pathovar), frequently have polyphyletic origins: isolates from the same host species in different environments may have diverse background genes providing environmental adaptation with the superimposition of the same effector genes on mobile chromosomes to determine host specificity.

Many effector proteins are proposed to have sites of action within host cells so the mode of delivery has become a focus particularly for fungi and oomycetes which have no known equivalent to the TTSS of bacterial pathogens. Thines and Kamoun (Oomycete-plant coevolution: recent advance and future prospects) provide insights into the diversity of oomycete plant pathogens and our current knowledge of effector genomics in the several sequenced *Phytophthora* genomes. Valent and Chang's review (Recent advances in rice blast effector research) provides some astonishing insights into effector delivery from *Magnapothe oryzae* to rice cells based on fungal transformants expressing effector-fluorescent protein fusions from effector promoters during invasion of rice. These effectors are secreted from discrete structures (Biotrophic interfacial complexes, BICs) localized on intracellular hyphae surrounded by host membrane and are translocated not only to the cytoplasm of infected cells but also to adjacent uninfected cells, apparently 'preparing the way' for the hyphal invasion of these cells (see cover picture). Like most fungal-oomycete effectors, effector protein sequences provide little information on biological function of the proteins. Bellafiore and Briggs' (Nematode effectors and plant responses to infection) overview of nematode genomics returns to the theme of genomics uncovering examples of horizontal gene transfer, in this case from host plant to nematode. They further highlight the use of the predicted secretome, coupled with direct protein detection using mass spectrometry, as a hunting ground for effectors. Here the problem of delivery of effectors to the host cell appears less of a mystery since nematodes are armed with an effective cell piercing stylet. However, establishing the function of many of the effectors is a challenge. Hence, identification of nematode effectors with sequence resemblance to the secreted

plant developmental regulatory protein Clavata 3 is intriguing. Effector function remains the underlying challenge in all of the plant-microbe interaction systems described in this volume. Blocking host immunity is an accepted phenomenon but altering host development and structure, for example tumors induced by maize smut (Spanu and Kamper) and morphological changes induced by oomycetes to improve host colonization and pathogen dissemination ('extended phenotypes', Thines and Kamoun), are other outcomes of effector activities. A novel proposal put forward by Wildermuth (Modulation of host nuclear ploidy: a common mechanism of obligate plant biotrophs) is that localized induction of host polyploid cells at the infection site, observed in *Arabidopsis*-powdery mildew interactions, may shift host metabolic balances in favor of the pathogen.

The ultimate outcome for pathogens is the evolution of host resistance. A current paradigm which is important for sustainable agriculture is that this resistance acts at two levels. Recognition of pathogen-specific molecular patterns (PAMPS) is particularly important in nonhost resistance but also has a measurable contribution to 'basal' resistance to adapted pathogens that are more effectively controlled by detection of specific effectors by plant Resistance proteins. Tsuda and Katagiri (Comparing signaling mechanisms engaged in pattern and effector-triggered immunity) explain how PAMP triggered immunity (PTI) and effector triggered immunity (ETI) utilize defense signaling components in different ways. Strong compensatory activities between individual defense pathways in ETI were deduced from transcriptome analysis of *Arabidopsis* pathway mutant combinations. This type of signaling network may help to create robustness against pathogen interference. Traw and Bergelson describe, from an evolutionary perspective, how crosstalk between individual plant stress signaling pathways and the environment can determine colonization by insect pests and pathogens in nature. They highlight a number of studies revealing the importance of temperature on stress hormone pathway interactions. This becomes particularly relevant in incompatible hybrids in which hormone pathway homeostasis has become disturbed. The authors argue that this, in turn, may have a profound effect on plant insect pest ecology in natural plant hybrid zones. Eitas and Dangl (NB-LRR proteins: pairs, pieces, perception, partners, and pathways) review the top

end of resistance pathway involving effector perception by the NB-LRR class of resistance proteins and, particularly, the recent flurry of papers revealing that in some cases R protein function relies on the activity of two distantly sequence-related NB-LRR proteins that are frequently tightly linked in the host genomes. Whether these proteins function as dimers or in relay awaits investigation. These chapters reveal the progress being made in fundamental science but what about the impact on agriculture? Oliver and Solomon show how genomics can be used to identify protein toxins in necrotrophic pathogens and how these toxins are being utilized in breeding programs to select insensitive host genotypes with increased disease resistance. Also, Yoder and Scholes (Host plant resistance to parasitic weeds: recent progress and bottlenecks) describe significant advances in analysis of host interactions with parasitic weeds that are among the most destructive agents in subsistence and developing agriculture. Genome analysis of hosts and parasites is beginning to identify key determinants of infection and resistance that provide new directions for crop improvement.

Engineered coral pigment helps scientists to observe protein movement

Source: *Science Centric*. 28 July 2010

Scientists in Southampton, UK, and Ulm and Karlsruhe in Germany have shown that a variant form of a fluorescent protein (FP) originally isolated from a reef coral has excellent properties as a marker protein for super-resolution microscopy in live cells. Their findings have been published online by Nature Methods and will appear in print in the upcoming August issue of that journal.

Fluorescent proteins produced by a range of marine animals glow with a rainbow of colours, adding to the visual spectacle of coral reefs. Over recent years, molecular biologists have isolated a number of FPs and their genes, and used them to create genetically engineered variant FPs with particular light-emission characteristics.

'Fluorescent pigments from corals and related animals have proved to be invaluable lead structures to produce advanced markers for biomedical research,' said Dr Joerg Wiedenmann of the University of Southampton's School of Ocean and Earth Science (SOES) based at the National Oceanography Centre, Southampton: 'They enable a plethora of exciting experiments, including non-invasive study of dynamical processes

within live cells,' Photoactivatable FPs (PA-FPs) can, as their name suggests, be switched on by light. When light of a particular wavelength is shone upon them they start to glow, emitting light of characteristic hue.

Wiedenmann and his collaborators previously described EosFP, a PA-FP from the reef-building coral *Lobophyllia*. Genetic engineering yielded the variant IrisFP with dual photoactivation capacity. In one mode it is irreversibly 'photo-converted' from a green- to a red-emitting form under violet light. In a second mode, these two light-emitting forms can be switched on and off more or less at will using light of different wavelengths ('photo-switching').

For use in cell biology experiments, PA-FPs are genetically fused to proteins of interest, and expressed in live cells. Small regions of the cell are then illuminated with laser light of specific wavelength, causing the marker proteins to emit light at another wavelength. This allows dynamical cell processes to be visualised and studied under the microscope.

In the native state, four molecules of IrisFP join together to form a tetramer, creating problems for fusion-protein applications. To get round this, the researchers have now modified the protein by introducing four mutations. This makes individual IrisFP molecules (monomers) more stable, reducing their tendency for form tetramers.

'The monomeric variant, mIrisFP, maintains dual photoactivation capacity and has excellent properties as a genetically encoded fluorescent marker protein,' explained Wiedenmann.

To test the usefulness of mIrisFP, the researchers genetically fused it with a number of other proteins within cultured cells. These included transcription factors, which regulate the expression of genes within the cell nucleus, and constituent proteins of the cell skeleton ('cytoskeleton'). In all cases, the fusion proteins functioned normally.

Further experiments demonstrated that mIrisFP fusion proteins could, as hoped, be used to study dynamical processes within live cells with a spatial resolution beyond the limits of conventional light microscopy. Specifically, the researchers successfully combined so-called pulse-chase experiments with photoactivation localisation microscopy (PALM) imaging to follow the movement of fluorescently marked fusion proteins over time and at very high spatial resolution.

'The dual photoactivation capability and the monomeric nature of mIrisFP should

allow cell biologists to perform a wider range of experiments than possible using only conventional PA-FPs,' said Wiedenmann.

'Marine animals such as corals and anemones are not only beautiful and important for ecosystem functioning, but also as source of fluorescent proteins of enormous value to biomedical research,' he added.

New Tool for Improving Switchgrass

Source: ScienceDaily (July 29, 2010)

Agricultural Research Service (ARS) scientists have developed a new tool for deciphering the genetics of a native prairie grass being widely studied for its potential as a biofuel. The genetic map of switchgrass, published by Christian Tobias, a molecular biologist at the ARS Western Regional Research Center in Albany, Calif., and his colleagues, is expected to speed up the search for genes that will make the perennial plant a more viable source of bioenergy.

Switchgrass is now grown as a cattle feed and to restore depleted soils. But interest in using it as a biofuel has intensified in recent years because it can be burned to produce electricity and, like corn stalks, can be converted to ethanol. It also grows on marginal lands, is adaptable to different regions, and -- as a perennial -- does not need to be replanted each year, which means lower energy costs and less runoff.

To assemble the genetic map, the team crossed a commercial variety of switchgrass known as Kanlow with an ARS-developed variety known as Alamo to produce 238 plants. They extracted DNA from that population and assembled a map based on more than 1,000 genetic markers that could each be attributed to one parent or the other.

The map divides the switchgrass genome into 18 distinct groups of genes linked together on the same strand of DNA. The results were recently published in the journal *Genetics*.

The work is funded by the U.S. Department of Energy and the U.S. Department of Agriculture (USDA) National Institute of Food and Agriculture, as part of the joint USDA-DOE Plant Feedstock Genomics for Bioenergy Program.

Understanding the genetic composition of switchgrass could produce big rewards. To make switchgrass more commercially viable as a biofuel, scientists are searching for ways to increase yields and make it easier to break down the plant cell walls,

an essential step in producing ethanol from cellulosic biomass.

The genetic map could lead to genes associated with cell wall composition, crop yields and other useful traits. Scientists will be able to use the genetic map to compare the genetic profile of switchgrass to that of rice, sorghum and other plants with better understood genomes and find analogues to genes linked to specific traits in those crops.

Journal Reference: Okada et al. Complete Switchgrass Genetic Maps Reveal Subgenome Collinearity, Preferential Pairing and Multilocus Interactions. *Genetics*, 2010; 185 (3): 745.

Flower Organ's Cells Make Random Decisions That Determine Size

Source: ScienceDaily (July 21, 2010)

The sepals of the plant *Arabidopsis thaliana* -- commonly known as the mouse-eared cress -- are characterized by an outer layer of cells that vary widely in their sizes, and are distributed in equally varied patterns and proportions.

Scientists have long wondered how the plant regulates cell division to create these patterns -- in other words, how it decides which and how many cells will be large, which slightly smaller, and which very small.

Melding time-lapse imaging and computer modeling, a team of scientists led by biologists from the California Institute of Technology (Caltech) has provided a somewhat unexpected answer to this question.

"We conclude that probabilistic decisions of individual cells -- rather than organ-wide mechanisms -- can produce a characteristic and robust cell-size pattern in development," says Elliot Meyerowitz, the George W. Beadle Professor of Biology and chair of the Division of Biology at Caltech.

These findings were published on May 11 in the online journal *PLoS Biology*.

A plant's sepals are the small green leaf-like organs that cup the petals of a flower, enclosing and protecting the flower before it blooms. The outer layer, or epidermis, of the *Arabidopsis* sepal consists of cells of widely varying sizes. These cells range in size from very small to very large; the largest cells are a type found only in the sepals and are dubbed, appropriately, "giant cells."

Each of the four sepals that cup an *Arabidopsis* flower has a unique pattern of cell sizes. What the Caltech-led team wanted to find out was what determines this pattern.

To gain insight into the process, Meyerowitz and Caltech postdoctoral scholar Adrienne Roeder imaged sepals during their early development. They tracked each round of cell divisions to determine how the different cell sizes were created, and what influences their distribution pattern. They then worked with senior postdoctoral scholar Vijay Chickarmane, who had designed a computer model to test the team's hypotheses about how the observed size-related patterning in the sepals comes to pass.

"We started using the live imaging of the sepals to gather data to make a hypothesis about the patterning," Roeder explains. "Then we ran that hypothesis as a model in the computer, to see whether it would give us the patterns we were seeing in the imaging."

At first, the computer model was unable to produce the patterns found in the actual sepals. So the team tweaked the model until it independently produced the range of cell sizes the team had seen in the living organ.

They found the sepal generates its epidermal cell-size pattern based not on an organ-wide control mechanism, but on when or whether each individual cell decides to divide and on the length of its cell cycle. This sort of random, probabilistic development process results in sepal patterns that not only differ from flower to flower, but from sepal to sepal within an individual flower.

"This is so contrary to our normal way of thinking," says Roeder, "in which we assume that there's always something dictating exactly what each cell is going to do."

Cells in the sepal can undergo one of two growth cycles. The first is normal cell division, in which the cell duplicates its chromosomes and then splits into two smaller cells. The other is a specialized type of cell cycle called endoreduplication, in which the cell duplicates its chromosomes but does not split in two; instead, it simply continues to grow ever larger.

The team's original hypothesis was that "the earlier a cell decides to endoreduplicate, the longer it will have to grow," says Roeder. "And the more endocycles it goes through, the bigger it will get."

For a cell to become a giant cell, she explains, it will generally need to endoreduplicate during its first cell cycle. If it waits a cycle or two to stop dividing, it will have less time to grow, and thus will be a slightly smaller cell. Cells that never

endoreduplicate -- i.e., cells that continue to divide with each cell cycle -- will be among the smallest cells in the sepal.

"Each cell starts out with a chance to become a giant cell," Roeder says. "It's a probabilistic thing; each cell has a certain probability of making that decision. Once it makes the decision, however, its fate is determined."

But endoreduplication isn't the only thing that decides the ultimate size of a sepal cell, the research team found. A cell that endoreduplicates early can grow to be an even larger giant if its cell cycles are longer than average, giving it plenty of growing time.

To prove their point, the team performed a series of experiments in which they altered the levels of cell-cycle inhibitors in the sepal cells. When they decreased the inhibitor -- increasing the frequency with which the cell divides, and thus reducing the length of the cell cycle -- the sepal cells were unable to grow into giant cells.

"These findings back up our hypothesis," says Roeder. "And when you change the parameters in the computer model, as if you were reducing the level of a cell-cycle inhibitor, the model shows the same pattern."

Understanding exactly how sepal cells decide whether to grow big or small could some day lead to practical applications, Roeder notes. For instance, the utility of various crops as biofuels depends on how much cellulose they contain. A sepal with a large number of giant cells has much less cell-wall surface area than a sepal with lots of smaller cells; since the cell wall is where cellulose is found, giant-cell-laden sepals would be less useful as biofuel.

"This work gives us ideas about how growth happens in these plants," says Roeder. "And once we better understand plant growth and cell division, we can better manipulate them."

In addition to Meyerowitz, Roeder, and Chickarmane, the other authors on the PLoS Biology paper, "Variability in the Control of Cell Division Underlies Sepal Epidermal Patterning in *Arabidopsis thaliana*," were Caltech computational scientist Alexandre Cunha; Boguslaw Obara, formerly at the University of California, Santa Barbara (UCSB), and now at the University of Oxford in the United Kingdom; and B.S. Manjunath from UCSB.

Their work was funded by a Helen Hay Whitney Foundation fellowship; the Gordon and Betty Moore Foundation Cell Center at Caltech; a grant from the Division of Chemical Sciences,

Geosciences, and Biosciences in the Department of Energy's Office of Basic Energy Sciences; and the National Science Foundation.

Why Some Plants Flower in Spring, Autumn and Some in Summer

ScienceDaily (July 20, 2010)

Scientists have uncovered a new piece in the puzzle about why some plants flower in spring/autumn and some in summer.

A team of researchers from Warwick have isolated a gene responsible for regulating the expression of CONSTANS, an important inducer of flowering, in Arabidopsis.

'Being able to understand and ultimately control seasonal flowering will enable more predictable flowering, better scheduling and reduced wastage of crops', explained Dr Jackson.

Whilst the relationship between CONSTANS and flowering time in response to day length is well established, the mechanism controlling the expression of CONSTANS is still not fully understood.

The scientists present their work at the Society for Experimental Biology Annual Meeting in Prague.

Many plants control when they flower to coincide with particular seasons by responding to the length of the day, a process known as photoperiodism. A flowering mutant of Arabidopsis, which had an altered response to photoperiod, was used in the study led by Dr Stephen Jackson.

In the study funded by the BBSRC, the team identified the defective gene in the mutant plant that caused its abnormal flowering time.

They then cloned a working version of the gene, known as DAY NEUTRAL FLOWERING (DNF), from a normal Arabidopsis plant and introduced it into the mutant plant to restore its normal flowering response to day length.

The role of DNF in normal plant flowering is to regulate the CONSTANS gene. CONSTANS is activated only in the light and the plant is triggered to flower when CONSTANS levels rise above a certain threshold level during the daytime.

In normal plants, DNF represses the levels of CONSTANS until the day length is long enough and conditions are favourable for the survival of their seedlings. In mutant plants without an active DNF gene, CONSTANS is not repressed and they are able to flower earlier in the year, when days are still short.

The presence of the DNF gene has not yet been identified in species other than Arabidopsis but the scientists believe their

on-going work may prove to have a wider significance for other species.

Scientists can override complex pathways that control flowering by artificially inducing or inhibiting key flowering genes such as DNF and CONSTANS. This can already be done in the laboratory by spraying an 'inducing agent' onto plants, stimulating them to flower early.

This could be used to extend the length of the harvesting season or to co-ordinate flowering or fruit production to a specific time. Growers already regulate the flowering of a few plants such as Chrysanthemum and Poinsettia, the latter specifically for Christmas and Easter.

Unravelling the complex pathways that control plant flowering will help scientists to understand and influence flowering patterns more effectively and in many different species.

UK researchers release draft sequence coverage of wheat genome

Source: *Science Centric*. 27 August 2010

A team of UK researchers, funded by the Biotechnology and Biological Sciences Research Council (BBSRC), has publicly released the first sequence coverage of the wheat genome. The release is a step towards a fully annotated genome and makes a significant contribution to efforts to support global food security and to increase the competitiveness of UK farming.

The genome sequences released comprise five read-throughs of a reference variety of wheat and give scientists and breeders access to 95% of all wheat genes. This is among the largest genome projects undertaken, and the rapid public release of the data is expected to accelerate significantly the use of the information by wheat breeding companies.

The team involved Prof Neil Hall and Dr Anthony Hall at the University of Liverpool, Prof Keith Edwards and Dr Gary Barker at the University of Bristol and Prof Mike Bevan at the John Innes Centre, a BBSRC-funded Institute.

Prof Edwards said: 'The wheat genome is five times larger than the human genome and presents a huge challenge for scientists. The genome sequences are an important tool for researchers and for plant breeders and by making the data publicly available we are ensuring this publicly funded research has the widest possible impact.'

Universities and Science Minister David Willetts said: 'This is an outstanding world class contribution by the UK to the global effort to completely map the wheat genome. By using gene sequencing

technology developed in the UK we now have the capability to improve the crops of the future by simply accelerating the natural breeding process to select varieties that can thrive in challenging conditions.'

The genome data released are in a 'raw' format, comprising sequence reads of the wheat genome in the form of letters representing the genetic 'code.' A complete copy of the genome requires further read-throughs, significant work on annotation and the assembly of the data into chromosomes. Large-scale, rapid sequencing programmes such as this have been made technically feasible by advanced technology genome sequencing platforms, including one based on BBSRC-funded research conducted in the UK in the 1990s. The majority of the sequencing work for this particular project was done using the 454 Life Science platform, developed in the US.

Prof Hall said: 'The genome sequence data of this reference variety, Chinese Spring wheat, will now allow us to probe differences between varieties with different characteristics. By understanding the genetic differences between varieties with different traits we can start to develop new types of wheat better able to cope with drought, salinity or able to deliver higher yields. This will help to protect our food security while giving UK plant breeders and farmers a competitive advantage.'

The sequence data can be used by scientists and plant breeders to develop new varieties through accelerated conventional breeding or other technologies.

Prof Bevan, a member of the Coordinating Committee of the International Wheat Genome Sequencing Consortium, said: 'The sequence coverage will provide an important foundation for international efforts aimed at generating a complete genome sequence of wheat in the next few years.'

Prof Doug Kell, BBSRC Chief Executive, said: 'Recent short-term price spikes in the wheat markets have shown how vulnerable our food system is to shocks and potential shortages. The best way to support our food security is by using modern research strategies to understand how we can deliver sustainable increases in crop yields, especially in the face of climate change. Genome sequencing of this type is an absolutely crucial strategy, building on previous BBSRC-funded work. Knowledge of these genome sequences will now allow plant breeders to identify the best genetic sequences to use as

markers in accelerated breeding programmes.'

Dr Jane Rogers, Member of the Coordinating Committee of the International Wheat Genome Sequencing Consortium and Director of BBSRC's The Genome Analysis Centre, said: 'The public release of the wheat genome data will be a useful resource for scientists and the plant breeding community and will provide a foundation to identify genetic differences between wheat varieties. In recent years genomics technology has advanced to a point that scientists can now produce sequence data for plants with genomes as large as wheat at a rate unimaginable a few years ago. This is an impressive achievement, notwithstanding the significant hurdles we still face to fully interpret and understand the data.'

A key feature of this research has been the quick release of the data into the public domain to allow other scientists and wheat breeding companies to rapidly employ it in practical applications. Richard Summers, Vice Chairman of the British Society of Plant Breeders, said: 'The wheat breeding community has been greatly impressed with the collaborative approach taken in this project. The team brought together world class skills in sequencing and wheat genetics to deal with a major barrier in wheat breeding. This is an excellent example of how to achieve technology transfer from research lab through to practical deployment.'

Decoding of wheat genome will aid global food shortage

Source: e! Science News. August 26, 2010
Wheat production world-wide is under threat from climate change and an increase in demand from a growing human population. Liverpool scientists, in collaboration with the University of Bristol and the John Innes Centre, have sequenced the entire wheat genome and will make the DNA data available to crop breeders to help them select key agricultural traits for breeding. Bread wheat, with an estimated world harvest of more than 550 million tonnes, is one of the most important food crops in the world and is worth more than £2 billion to the UK's agricultural industry. Wheat breeders, however, have few genetic tools to help them select key agricultural traits for breeding and do not always know the genes responsible for the trait they need. Scientists have analysed the wheat genome, which is five times larger than the human genome, to give breeders the tools required to select traits for a healthy yield.

Professor Neil Hall, from the Institute of Integrative Biology, explains: "Sequencing the human genome took 15 years to complete, but with huge advances in DNA technology, the wheat genome took only a year. The information we have collected will be invaluable in tackling the problem of global food shortage. We are now working to analyse the sequence to highlight natural genetic variation between wheat types, which will help significantly speed up current breeding programmes." The project, funded by the Biotechnology and Biological Sciences Research Council (BBSRC), was undertaken at the University's Centre for Genomic Research. The facility is home to five next generation genome analysers, which can read DNA hundreds of times faster than the systems that were used to sequence the human genome.

Dr Anthony Hall added: "Wheat production is already under pressure with failures in the Russian harvest driving up world wheat prices. It is predicted that within the next 40 years world food production will need to be increased by 50 per cent. Developing new, low input, high yielding varieties of wheat, will be fundamental to meeting these goals. Using this new DNA data we will identify variation in gene networks involved in important agricultural traits such as disease resistance, drought tolerance and yield."

Professor Keith Edwards, from the University of Bristol, said: "In a short space of time we have delivered most of the sequences necessary for plant breeders to identify genetic differences in wheat. The public release of the data will dramatically increase the efficiency of breeding new crop varieties."

Core knowledge of tree fruit expands with apple genome sequencing

Source: e! Science News. August 29, 2010
An international team of scientists from Italy, France, New Zealand, Belgium and the USA have published a draft sequence of the domestic apple genome in the current issue of Nature Genetics. The availability of a genome sequence for apple will allow scientists to more rapidly identify which genes provide desirable characteristics to the fruit and which genes and gene variants provide disease or drought resistance to the plant. This information can be used to rapidly improve the plants through more informed selective breeding.

An organism's genome is the total of all its genetic information, including genes. Genes carry information that determines, among other things, a plant's appearance,

health, productivity and color and taste of the fruit.

The domestic apple is the main fruit crop of the world's temperate regions. Apple is a member of the plant family Rosaceae which includes many other economically important species, including cherry, pear, peach, apricot, strawberry, and rose, to name just a few.

The state of Washington accounts for approximately 60 percent of total apple production in the U.S. and Rosaceae fruit production is a multi-billion dollar industry in the state. Washington state scientists played an important role in the project.

Led by Washington State University horticultural genomicist Amit Dhingra, the Washington-based team sequenced and analyzed a unique version of the genome of the golden delicious apple in which all duplicated chromosomes are genetically identical. This information was used to validate the sequence of the more complicated "heterozygous" golden delicious apple (in which duplicated chromosomes are not identical).

"Before genome sequencing, the best we could do was correlate traits with genes. Now we can point to a specific gene and say, 'This is the one; this gene is responsible for this trait'. That trait of interest might be, for instance, a disease, which is why sequencing the human genome was such an important milestone. Or the trait might be for something desirable, like flavor in a piece of fruit. We are already working on finding physiological solutions to issues like bitter pit in current apple varieties with the gene-based information available to us and lay a foundation for improved varieties in the future through generation of sports (mutations) and breeding," Dhingra said.

The Washington state contribution to the sequencing work was a unique collaboration between the cross-state Apple Cup rivals of WSU and the University of Washington.

Microbiologist Roger Bumgarner's lab at the University of Washington provided the initial sequencing expertise and capability to the project, which was later complemented and replaced by sequencing expertise in the Dhingra genomics lab, who obtained the same DNA sequencing instrument used in Dr. Bumgarner's lab.

"UW is a world leader in medical research and WSU is a world leader in agricultural research," said Bumgarner. "Technological advancements and techniques initially used to study medically important genomes and problems can be rapidly

applied to genomes and problems of agricultural importance. We both had something to contribute and to learn from one another. I think there are many more opportunities for such collaborations to develop in the coming years."

After the sequencing was completed, WSU computational biologist Ananth Kalyanaraman contributed to the analysis by comparing the apple genome with that of pear, peach and grape to identify the differences and commonalities that exist between these fruit crops.

While the apple genome provides a valuable resource for future research, one pressing question answered by the international team's paper in *Nature Genetics* was one of origin. Scientists have long wanted to know — and have for years argued vehemently about — the ancestor of the modern domesticated apple. The question is now settled: *Malus sieversii*, native to the mountains of southern Kazakhstan, is the apple's wild ancestor. Now that that question is settled, scientists will begin using the apple genome to help breed apples with desirable new traits, including disease resistance and, potentially, increased health-benefitting qualities.

"Having the apple genome sequence will greatly accelerate our ability to define the differences between apple cultivars at the genetic level," said Kate Evans, an apple breeder based at the WSU Tree Fruit Research and Extension Center. "This will allow us to exploit these differences and target areas of diversity to incorporate into the breeding program, resulting in improved cultivars for the consumers that are also better suited for long-term, sustainable production."

Dan Bernardo, dean of the WSU College of Agricultural, Human, and Natural Resource Sciences, said, "The Washington apple is an icon of quality around the globe. This is a natural home for the advanced science necessary to map the tree fruit genome and actively study how it functions."

Researchers discover novel mechanism protecting plants against freezing

Source: *Science Centric*. 27 August 2010
New ground broken by Michigan State University biochemists helps explain how plants protect themselves from freezing temperatures and could lead to discoveries related to plant tolerance for drought and other extreme conditions.

'This brings together two classic problems in plant biology,' said Christoph Benning, MSU professor of biochemistry and molecular biology. 'One is that plants

protect themselves against freezing and that scientists long thought it had something to do with cell membranes, but didn't know exactly how.

'The other is the search for the gene for an enigmatic enzyme of plant lipid metabolism in the chloroplasts,' in other words, how lipids, which are membrane building blocks, are made for the plant cell organelles responsible for converting solar energy into chemical energy by photosynthesis.

In an article published online this week by the journal *Science*, Benning and his then-doctoral degree candidate Eric Moellering and technical assistant Bagyalakshmi Muthan describe how a particular gene leads to the formation of a lipid that protects chloroplast and plant cell membranes from freeze damage by a novel mechanism in *Arabidopsis thaliana*, common mustard weed. Working on his dissertation project under Benning, Moellering identified a mutant strain of *Arabidopsis* that can't manufacture the lipid and linked this biochemical defect to work done by others who originally described the role of the gene in freeze tolerance, but did not find the mechanism. 'One of the big problems in freezing tolerance or general stress in plants is that some species are better at surviving stress than others,' Moellering said. 'We are only beginning to understand the mechanisms that allow some plants to survive while others are sensitive.'

There is no single mechanism involved in plant freezing tolerance, Moellering added, so he can't say that his findings will lead any time soon to genetic breakthroughs making citrus or other freezing-intolerant plants able to thrive in northern climates. But it does add to our understanding of how plants survive temperature extremes. Much plant damage in freezing temperatures is due to cell dehydration, in which water is drawn out as it crystallises and the organelle or cell membrane shrivels as liquid volume drops. Lipids in the membranes of tolerant plants are removed and converted to oil that accumulates in droplets, the researchers said, retaining membrane integrity, keeping membranes from fusing with one another and conserving the energy by storing oil droplets. With rising concern globally about water supplies and climate change, scientists see additional reasons to understand the ways hardy plants survive.

The research, funded by the U.S. Department of Energy Office of Science Basic Energy Sciences and the Michigan Agricultural Experiment Station, also leads

to speculation that freezing itself can prompt cell proteins directly to change the composition of the membrane, without activation by gradual acclimation. That has been a major focus in the plant freezing tolerance field, the researchers said.

'This opens a huge door now for people to do this kind of research, and to redirect researchers,' Benning said. 'There are lots of them out there trying to understand cold, salt and drought tolerance in plants, and we've given them a new idea about how they can approach this problem mechanistically.'

Journal Reference: Eric R. Moellering, Bagyalakshmi Muthan, and Christoph Benning. Freezing Tolerance in Plants Requires Lipid Remodeling at the Outer Chloroplast Membrane. *Science*, 2010; DOI: 10.1126/science.1191803

Plants give up some deep secrets of drought resistance

Source: *Science Centric*. 24 August 2010

In a study that promises to fill in the fine details of the plant world's blueprint for surviving drought, a team of Wisconsin researchers has identified in living plants the set of proteins that help them withstand water stress.

The new study, published 23 August in the *Proceedings of the National Academy of Sciences*, identifies the protein targets in cells of a key hormone that controls how plants respond to environmental stresses such as drought, excessive radiation and cold.

The work, which builds on decades of research with a key plant hormone known as abscisic acid, could help underpin the development of new crop plant strains capable of thriving in hotter, dryer climates. The work is considered important in light of the pressing need to expand and intensify agricultural production on marginal lands worldwide, and especially so in the context of global climate change.

'If we can figure out how this works with crops and make them able to resist drought, the benefits would be enormous,' notes Michael Sussman, a University of Wisconsin-Madison professor of biochemistry and the senior author of the new study. 'These are the first baby steps to understand the effects of dehydration in plants and it may give us the opportunity to develop crops that can withstand this kind of stress in the field.'

Working in the model laboratory plant *Arabidopsis*, the Wisconsin team explored the influence of abscisic acid, a long-studied hormone that, in addition to

influencing how plants respond to environmental stress, controls the naturally occurring processes of seed dormancy and germination.

The hormone has been known to science for 50 years, and was believed to influence certain proteins in cells in a complicated cascade of events that aided the ability of a plant to survive such stresses as dehydration, excessive radiation and cold temperatures. But any plant cell, Sussman explains, contains at least 30,000 different proteins, and the identity of the few proteins activated by the hormone was a deep mystery.

'Since they cannot walk or run, plants have developed an interesting and complicated system for sensing and responding very quickly to dehydration and other stresses,' says Sussman, noting that, on average, a plant is composed of 95 percent water. 'Most plants have what's called a permanent wilting point, where if water content goes below 90 percent or so, they don't just dehydrate and go dormant, they dehydrate and die.' Figuring out how to trigger a dormant state, such as exists naturally in seeds, which are 10 percent water and can in some cases remain viable for hundreds of years, could be key to creating plants that survive drought in the field, Sussman explains.

The team, which includes postdoctoral fellow Kelli G. Kline and scientist Gregory Barrett-Wilt, utilised a new stable isotope technology and mass spectrometry to comb 5,000 candidate proteins in the cells of living plants and found 50 that were influenced by the abscisic acid hormone. The survey is the first of its kind in a living plant and many of the proteins identified were previously not known to be influenced at all by abscisic acid.

Surprisingly, the hormone was found to regulate some of the plant proteins in a completely different way than was known before, by inhibiting their ability to have a phosphate moiety removed from an amino acid, by a type of enzyme called a protein phosphatase. Protein phosphatases are the opposite side of the coin that catalytic enzymes known as protein kinases occupy. In many important biological processes, such as cancer, it is the protein kinases that are the dominant actors.

The finding that phosphatases play a more critical role in a hormonally regulated system is a new idea in biology discovered through work with plants. Sussman's group's findings indicate that the dynamic interplay between the hormone and the proteins it affects is a more complicated process than previously suspected. 'The

story is far from complete,' says the Wisconsin biochemist. 'There is something very interesting, and complicated, going on.'

Journal Reference: K. G. Kline, G. A. Barrett-Wilt, M. R. Sussman. In planta changes in protein phosphorylation induced by the plant hormone abscisic acid. *Proceedings of the National Academy of Sciences*, 2010; DOI: 10.1073/pnas.1007879107

Growing Drought-Tolerant Crops Inching Forward

ScienceDaily, Aug. 25, 2010.

A collaborative team of scientists led by researchers at The Medical College of Wisconsin, in Milwaukee, has used the tools of structural biology to understand how a synthetic chemical mimics abscisic acid (ABA), a key stress hormone that helps plants cope with adverse environmental conditions such as drought. The results are published online in *Nature Structural & Molecular Biology* in advance of print publication later.

For years scientists have searched for practical ways to use ABA signaling to improve drought tolerance in agriculture. Unfortunately, the synthetic form of ABA used commercially is light sensitive and expensive. The new study builds on the earlier discovery by scientists at University of California, Riverside of pyrabactin, a synthetic chemical that mimics ABA. However, unlike ABA, pyrabactin activates only a few of the 14 ABA receptors in the plant needed for effective drought tolerance.

"By better understanding how pyrabactin works, we can develop new chemicals to enable plants to resist drought. These same chemicals that signal the response to drought may also contribute to increasing crop yields," says Francis Peterson, Ph.D., lead author and assistant professor of biochemistry at the Medical College.

An ABA receptor is a protein that functions as a molecular switch inside the cell. When an ABA molecule inserts into a cavity within the receptor, it sends a signal by changing the protein structure in a way that resembles the closing of a gate. To identify the specific atoms required for gate closure by ABA or pyrabactin, Dr. Peterson used X-ray diffraction to solve the three-dimensional structures of multiple receptor proteins. From the changes in position of only a few atoms, the research team discovered why pyrabactin can close the gate on some receptors but not others.

"These insights suggest new strategies for modifying pyrabactin and related compounds so that they can mimic the signaling process of the naturally occurring ABA. This work has paved the way for manufacturing new molecules that activate or turn on receptors" said Sean Cutler, Ph.D., associate professor of plant cell biology at UC Riverside.

"The current research is an important step on the way to what is likely to be the next big result: an ABA-mimicking chemical that can be applied to corn, soy bean and other crops," explained Dr. Peterson.

In addition to Drs. Peterson and Cutler, research collaborators included Brian Volkman, Ph.D., Davin R. Jensen and Joshua J. Weiner of the Medical College of Wisconsin; as well as Sethe Burgie, Craig A. Bingman and George N. Phillips, Jr. of the University of Wisconsin-Madison; and Sang-Youl Park and Chia-An Chang of UC Riverside.

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Researchers discover how the storehouses of plant cells are formed

Source: *Science Centric*. 20 August 2010

Bite into a sour apple and you destroy them - plant cell vacuoles. Even though these vacuoles make up the largest volume of plant cells, only little was known about how these cellular storehouses form and how the substances stored in them find their way there. Scientists at the Technische Universitaet Muenchen (TUM) have now discovered a new protein essential to the formation of vacuoles. In the process they uncovered new clues that may help demystify the vacuole formation mechanism. They now hope to unravel the process completely.

Cells - whether plant, animal or human - comprise a variety of organelles, delineated structures that assume different roles within the cells. In plant

cells, the largest organelle by far is the so-called vacuole. Enveloped by a membrane, it stores substances vital for the plant cell - for example, proteins essential for our nutrition found in peas, beans and lentils, the pigments of blossoms, the bitter substances in tea, or the fruity acids of sour apples. How these vacuoles are formed inside plant cells and how the substances stored in them get there are only vaguely understood. A research team from the TUM Centre of Life and Food Sciences Weihenstephan has now discovered a new protein that is indispensable in the formation of vacuoles. Prof. Claus Schwechheimer and his team of scientists from the Department of Plant Systems Biology used *Arabidopsis thaliana* as the model plant for their investigations. 'Using comparisons of the wild-type variant with a mutant, we were able to demonstrate that a very specific protein substance was all-important in the formation of functional vacuoles,' says Schwechheimer. Two things occur when this protein is missing: First, instead of one large vacuole, many small, partially functional ones are produced in the cell. Second, the transport of substances within the plant cells falls into disarray. Instead of finding their way into the vacuoles, the important substances are discharged from the cells - the plant ceases to grow and withers.

The protein the researchers identified functions as a 'splitting protein': It can split off a small protein called ubiquitin, found almost everywhere in cells, from other proteins. Appending and removing ubiquitin is a mechanism that cells generally use to initiate and terminate metabolic processes and to assign specific tasks to the proteins involved. The research team used wilted control plants to show that functioning storage organs cannot be produced in cells without the investigated splitting protein. The reason: In absence of the discovered protein, a certain ubiquitin-marked protein substance accumulates - and prevents the cell from forming a normal vacuole. Worldwide, this is the first time ever that researchers have observed that ubiquitin-marked proteins might play a role in the formation of these cellular storage organs. In a second step, the research team is now searching for the particular ubiquitin-marked protein that blocks the formation of vacuoles. 'This will be a tough nut to crack,' says Dr Erika Isono, who is coordinating these studies in the Department of Plant Systems Biology. 'For one, it is known that ubiquitin-marked proteins are generally rather unstable and

as such difficult to confirm. On the other hand, cells contain myriad ubiquitin-marked proteins with very different tasks.' In short: The hunt for this protein, so important in the formation of vacuoles, is not unlike the proverbial search for the needle in a haystack.

The TUM researchers have nonetheless taken up the challenge. Very useful for the pending investigations into this cellular process will be the three new fluorescence microscopes, together worth 500,000 euros, put into operation with financial support from the Deutsche Forschungsgemeinschaft (German Research Foundation), the Technische Universität München, and the state of Bavaria. Once the systems biologists have completely deciphered the vacuole formation process, their work may help to alter the contents of these storage organs in a targeted way in the future. This could lead to improved quality of vegetable food products, for example, by making sour apples sweeter or increasing the protein content of beans, lentils and peas.

Plants' Modified SOS Call

Laura M. Zahn

Science, AAAS, Washington, DC 20005, USA

Plants have several ways of defending themselves against insect attack. The release of distinctive volatile chemicals betrays the location of herbivores to their predators, but volatile production can be slow and the pests may escape. Compounds known as green leaf volatiles are released immediately after damage, and Allmann and Baldwin have found that, when attacked by tobacco hornworm (*Manduca sexta*) caterpillars, *Nicotiana attenuata* plants emit a compound that, when combined with an oral secretion from the caterpillar, is transformed into an attractant for the generalist hemipteran predator *Geocoris pallidus*, which preys on the hornworm eggs and young larvae. Thus, insect feeding activity can begin the process of plant defense before other protective volatiles are synthesized and emitted.

Reference: S. Allmann, I. T. Baldwin, Insects betray themselves in nature to predators by rapid isomerization of green leaf volatiles. *Science* 329, 1075–1078 (2010).

Source: *Sci. Signal.*, 31 August 2010. Vol. 3, Issue 137, p. ec265.

Making Roots

Pamela J. Hines

Science, AAAS, Washington, DC 20005, USA

A tiny bunch of stem cells generates the bulk and diversity of plant roots. These cells are found at the root meristem and are themselves regulated by signaling inputs from a variety of sources. In *Arabidopsis*, Matsuzaki et al. have identified a family of peptide factors that regulate these root stem cells. These peptides, known as root meristem growth factors, carry the posttranslational modification tyrosine sulfation and are essential for maintaining the root stem cell niche.

Reference: Y. Matsuzaki, M. Ogawa-Ohnishi, A. Mori, Y. Matsubayashi, Secreted peptide signals required for maintenance of root stem cell niche in *Arabidopsis*. *Science* 329, 1065–1067 (2010).

Source: *Sci. Signal.*, 31 August 2010. Vol. 3, Issue 137, p. ec267

Black Rice Rivals Pricey Blueberries as Source of Healthful Antioxidants

ScienceDaily, Aug. 27, 2010.

Health conscious consumers who hesitate at the price of fresh blueberries and blackberries, fruits renowned for high levels of healthful antioxidants, now have an economical alternative, scientists reported at the 240th National Meeting of the American Chemical Society (ACS). It is black rice, one variety of which got the moniker "Forbidden Rice" in ancient China because nobles commandeered every grain for themselves and forbade the common people from eating it.

"Just a spoonful of black rice bran contains more health promoting anthocyanin antioxidants than are found in a spoonful of blueberries, but with less sugar and more fiber and vitamin E antioxidants," said Zhimin Xu, Associate Professor at the Department of Food Science at Louisiana State University Agricultural Center in Baton Rouge, La., who reported on the research. "If berries are used to boost health, why not black rice and black rice bran? Especially, black rice bran would be a unique and economical material to increase consumption of health promoting antioxidants."

Like fruits, "black rice" is rich in anthocyanin antioxidants, substances that show promise for fighting heart disease, cancer, and other diseases. Food manufacturers could potentially use black rice bran or the bran extracts to boost the health value of breakfast cereals, beverages, cakes, cookies, and other foods, Xu and colleagues suggested.

Brown rice is the most widely produced rice variety worldwide. Rice millers remove only the outer husks, or "chaff,"

from each rice grain to produce brown rice. If they process the rice further, removing the underlying nutrient rich "bran," it becomes white rice. Xu noted that many consumers have heard that brown rice is more nutritious than white rice. The reason is that the bran of brown rice contains higher levels of gamma-tocotrienol, one of the vitamin E compounds, and gamma-oryzanol antioxidants, which are lipid-soluble antioxidants. Numerous studies showed that these antioxidants can reduce blood levels of low-density lipoprotein cholesterol (LDL) -- so called "bad" cholesterol -- and may help fight heart disease. Xu and colleagues analyzed samples of black rice bran from rice grown in the southern United States. In addition, the lipid soluble antioxidants they found in black rice bran possess higher level of anthocyanins antioxidants, which are water-soluble antioxidants. Thus, black rice bran may be even healthier than brown rice bran, suggested Dr. Xu.

The scientists also showed that pigments in black rice bran extracts can produce a variety of different colors, ranging from pink to black, and may provide a healthier alternative to artificial food colorants that manufacturers now add to some foods and beverages. Several studies have linked some artificial colorants to cancer, behavioral problems in children, and other health problems.

Black rice is used mainly in Asia for food decoration, noodles, sushi, and pudding. Dr. Xu said that farmers are interested in growing black rice in Louisiana and that he would like to see people in the country embrace its use.

Relief for parched plants

By Carrie Arnold

The Scientist. 14th October 2010

Heat and drought are wreaking havoc on the world's crops, but scientists are engineering plants that may be able to survive such harsh conditions.

Blazing heat and drought across Russia have withered much of the country's wheat crop, triggering a dramatic rise in food prices worldwide. But what if plants could survive long periods without water?

Groups of scientists around the world are working on engineering crops that can do just that. And with temperatures and drought frequency expected to continue to climb, and an increasing demand on dwindling fresh water supplies, the need for drought-resistant plants is more pressing than ever.

"The number one limiting factor on [crop] yield in the world is available water," said Mark Lawson, an agricultural scientist at Monsanto, in St. Louis, Mo. And in many countries around the world, "drought is essentially an annual occurrence."

But scientists are looking for ways to tweak plant physiology to enable crops to feed the world using significantly less water. Many research groups have focused on improving root systems, which function like miniature straws to slurp water. Healthier, more abundant roots mean a plant can take up water from the soil more efficiently. Other scientists have begun to identify the subtle genetic differences between domesticated crops and their more drought-resistant wild relatives in search of water-saving tricks.

Plant biologist Sean Cutler of the University of California, Riverside, for example, has focused on the plant hormone abscisic acid (ABA). When a plant's roots sense a shortage of water in the surrounding soil, they synthesize ABA, which tells the plant to close microscopic pores on their leaves through which moisture can escape. Although closing these microscopic pores, known as stomata, prevents water loss, it also blocks the entry of carbon dioxide, a critical component of photosynthesis. Without sufficient CO₂, plants can't photosynthesize and crop yield drops.

By studying how ABA triggers stomata closing, Cutler hopes to harness the plant's ability to conserve water without negatively affecting photosynthesis. His goal is to create a molecule that selectively activates certain ABA pathways under drought conditions to maximize water conservation, as well as photosynthesis. Crop plants don't respond well to a lack of water, he said. "What we want to do is tinker with the physiology a bit so that we can get better yields when conditions aren't ideal."

Paleobotanist Robin Allaby, at the University of Warwick in the UK, thinks that looking at the wild ancestors of current crops may be one of the keys to creating more drought-resistant plants. Domesticated barley (*Hordeum vulgare*) produces six smaller grains on each stalk, compared to two slightly larger grains on the wild variety. The greater number of grains and their higher protein content give them tremendous advantage as a food source, but previous research has shown that six-grain barley plants need more water than two-grain domestic barley.

In Qasr Ibrim, an archaeological site in southern Egypt, Allaby found evidence

that the domestic barley grown there reverted to the wild-type two grain, and he suspects the barley may have evolved rapidly in response to drought conditions. "When plants need to change," he said, "they can change very, very quickly. They're very evolvable." This swift evolutionary response to drought may give scientists genetic clues about how crops can better survive water stress.

One such drought-resistant technique comes in the form of an enzyme known as proton pyrophosphatase in *Arabidopsis*. Proton pyrophosphatases reside in plant organelle membranes and maintain the proper electrical charge in the organelle by moving protons across the membrane. In *Arabidopsis*, this enzyme helps the plant survive stress from drought and salty soil by sequestering toxic sodium ions accumulated from the water the plants drink and storing them in the vacuole, a plant cell's storage tank, where they cannot harm the cell.

Furthermore, Roberto Gaxiola of Arizona State University recently found that the enzyme also enlarges the root system, which aids in water absorption under drought conditions. Gaxiola suspects the enzyme may increase the plant's sensitivity to growth hormones known as auxins, leading to greater root growth. "[*Arabidopsis*] can get water more efficiently because they have an enhanced root system." These plants still can experience drought, he added -- they just experience it later.

Genetically modified corn that carries a single bacterial gene has also shown increased drought resistance. The agricultural giant Monsanto has focused on a type of transgenic corn carrying the cold shock protein B (CSPB) gene from *Bacillus subtilis*, a common soil bacterium. Plants under stress often have misfolded RNA and proteins. Lawson and his colleagues believe that the CSPB gene may mitigate some of that misfolding and help the plant cell run more efficiently, just as it does in *Bacillus*. This improves RNA translation and photosynthesis capability, which ultimately increases yield.

The impact of the CSPB transgenic corn, or any other drought-resistant crop, is hard to calculate, Lawson said. Still, "being able to mitigate the effects that drought has on crops would be an extremely important characteristic to get into farmers' hands."

Although their approaches may differ, these scientists believe that more than one pathway exists towards the final goal of improving drought tolerance in crops.

Even seemingly small improvements may have large effects.

"If it's a severe drought, like what they have in Russia right now, and we could boost yields by 20 percent in [those] bad years," Cutler said, "that would be huge."

Nightshades' mating habits strike uneasy evolutionary balance

Source: Science Centric. 23 October 2010
Most flowering plants, equipped with both male and female sex organs, can fertilise themselves and procreate without the aid of a mate. But this may only present a short-term adaptive benefit, according to a team of researchers led by two University of Illinois at Chicago biologists, who report that long-term evolutionary survival of a species favours flowers that welcome pollen from another plant.

'We've shown that a strong, short-term advantage experienced by individuals that have sex with themselves can be offset by long-term advantages to plant species that strictly avoid self-fertilisation,' says Boris Igic, UIC assistant professor of biological sciences. The result is 'an apparently unending competition between these two reproductive strategies,' he said, 'contributing to disparities in species diversity observed among different groups of plants.'

The findings are reported in the Oct. 22 issue of *Science* by Igic and lead author Emma Goldberg, postdoctoral research associate in biological sciences.

Their study focused on Solanaceae, the large and diverse plant family commonly known as nightshades. It includes such important crop plants as potatoes, tomatoes and tobacco. Just under half of the known nightshade species cannot self-fertilise.

Goldberg and Igic measured the long-term effects of self-fertilisation, which is caused by frequent mutations and is difficult to lose once a plant acquires it. The researchers applied a mathematical model to calculate the rate of accumulation of species, also called the diversification rate. 'We found those species that avoid self-fertilisation diversify faster, giving them a long-term advantage,' Goldberg said.

'It's a trade-off,' Igic added. 'The short-term benefits of mating assurance and ability to invade a new environment are pitted against long-term advantages of greater genetic diversity, allowing plants that avoid self-fertilisation to have more offspring during unpredictable environmental changes.'

Avoiding self-fertilisation also allows plants to more easily keep beneficial mutations and provides a degree of

protection against some harmful mutations, Igic said.

The findings underscore that both individual and species characteristics can strongly shape how a group of plants evolves and diversifies.

'The ability or inability to self-fertilise is subject to forces that act strongly, and in opposite directions,' Goldberg said. 'The balance between these opposing forces helps explain the diversity of plants within the nightshade family, and potentially many other plant groups.'

Mutation Over 100 Million Years Ago Led Flowers to Make Male and Female Parts Differently

Source: ScienceDaily. Oct. 19, 2010

Research by University of Leeds plant scientists has uncovered a snapshot of evolution in progress, by tracing how a gene mutation over 100 million years ago led flowers to make male and female parts in different ways.

The findings -- published in the *Proceedings of the National Academy of Sciences (PNAS) Online Early Edition* -- provide a perfect example of how diversity stems from such genetic 'mistakes'. The research also opens the door to further investigation into how plants make flowers -- the origins of the seeds and fruits that we eat.

In a number of plants, the gene involved in making male and female organs has duplicated to create two, very similar, copies. In rockcress (*Arabidopsis*), one copy still makes male and female parts, but the other copy has taken on a completely new role: it makes seed pods shatter open. In snapdragons (*Antirrhinum*), both genes are still linked to sex organs, but one copy makes mainly female parts, while still retaining a small role in male organs -- but the other copy can only make male.

"Snapdragons are on the cusp of splitting the job of making male and female organs between these two genes, a key moment in the evolutionary process," says lead researcher Professor of Plant Development, Brendan Davies, from Leeds' Faculty of Biological Sciences. "More genes with different roles gives an organism added complexity and opens the door to diversification and the creation of new species."

By tracing back through the evolutionary 'tree' for flowering plants, the researchers calculate the gene duplication took place around 120 million years ago. But the mutation which separates how snapdragons and rock cress use this extra

gene happened around 20 million years later.

The researchers have discovered that the different behaviour of the gene in each plant is linked to one amino acid. Although the genes look very similar, the proteins they encode don't always have this amino acid. When it is present, the activity of the protein is limited to making only male parts. When the amino acid isn't there, the protein is able to interact with a range of other proteins involved in flower production, enabling it to make both male and female parts.

"A small mutation in the gene fools the plant's machinery to insert an extra amino acid and this tiny change has created a dramatic difference in how these plants control making their reproductive organs," says Professor Davies. "This is evolution in action, although we don't know yet whether this mutation will turn out to be a dead end and go no further or whether it might lead to further complexities.

"Our research is an excellent example of how a chance imperfection sparks

evolutionary change. If we lived in a perfect world, it would be a much less interesting one, with no diversity and no chance for new species to develop."

The researchers now plan to study the protein interactions which enable the production of both male and female parts as part of further investigation into the genetic basis by which plants produce flowers.

The research was supported by funding from the European Union Marie Curie Research Training Program and the Biotechnology and Biological Sciences Research Council.

Journal Reference: Chiara A. Airoidi, Sara Bergonzi, Brendan Davies. Single amino acid change alters the ability to specify male or female organ identity. *Proceedings of the National Academy of Sciences*, 2010; DOI: 10.1073/pnas.1009050107

Opinion



Avoid the career virus!

By Morgan Giddings

The Scientist. 19 October 2010.

When we come down with flu, we do everything we can to get rid of the virus and get better. But when we come down with mind viruses—or ideas that harm us rather than help us—we often just accept them as “how things are,” doing nothing to counter their damaging effects.

There's one mind virus, particularly acute these days, we should all pay attention to: *“Science is a real struggle. It is a dog eat dog endeavor, and if you aren't hyper competitive, super smart, and working 80 hours a week, you won't succeed”*.

This mind virus was highlighted by the recent case of the postdoc poisoning his colleague's cell cultures, because he was afraid she might be getting ahead. Not only was the act itself borne of this mind virus, but so were many of the comments following it. “That's just the way it is in science these days,” was a common refrain in the blogosphere.

Realize that holding onto that particular mind virus will do far more harm to you than good.

The question we should always be asking ourselves is: “what viewpoint can I hold that will do me the most good in my life?”

Let's consider the effect of this mind virus on the postdoc. He paid big fines, lost his job, and then was let go from his subsequent job. This virus caused him a lot of harm, as well as also those around him.

I've seen the effect of this on others. I know of one fellow who regularly worked 80 hour weeks, often staying up all night, trying to “get things done.” He was one of the more ineffective people I know, because he was too stressed out from the lack of sleep to think straight. He really struggled to get his PhD. A person with a fresh and clear mind, working only 25 hours per week, could have accomplished just as much (if not more).

Getting ahead isn't about just “getting lots of stuff done.” It is about getting the right things done at the right time. To do that, you need to be relaxed and confident, not stressed-out and fearful. And the key is to realize that we can choose to hold whatever mental model of the world we want.

By default, we often hold onto mental models given to us by others, accepting them without asking, “does this serve me?” We accept them because we haven’t learned that we have the power to rewrite the program. We haven’t learned to question the motivations of the people telling us these things. Additionally, many of these ideas are based on fear, coming from all around us—from the media, news, and water cooler conversations—and these are highly infectious.

Once I realized—relatively late in life—that I have the ability to rewrite my own programming and fight off the fear infection, I’ve been doing it a lot. It has benefitted me hugely. I have tried to lose “dog-eat-dog” mentality, and instead to focus on the joy of doing science. And I get more of it done, I’m more creative, and I have more fun doing it.

So I ask you, dear reader, if you hold some variant of this particular fear-based thought virus, to contemplate whether it serves you or not. If you decide that it doesn’t, I can suggest a few things that might help you.

1. Learn to live “in the moment” and enjoy every moment. If you’re in the moment, then you’ll realize that you have great power to make things happen. Some people refer to this as “mindfulness.” It works.

2. Don’t focus on what success others are having, or what you haven’t achieved yet. Focus only on your own success and what you want to achieve.

3. Help other people rather than being afraid of them. The more you help others, the more it will come back to help you. This doesn’t mean giving away your results to a competitor—but it does mean helping a lab-mate or a colleague whenever you have the chance.

4. Get enough sleep. Many of us academics think that the only way to get ahead is to spend long hours working, while depriving ourselves of sleep. That’s like driving your car without enough engine oil. You can get away with it for a while, but eventually the engine blows out.

5. Realize that the only thing you can control in your life is what’s in front you, here and now. You can’t control the competition. You can’t control whether your experiments will have the outcome you want. Make the most of what you can control, by doing the right work at the right time—and ignore the rest.

If you do these five things, you will permanently eliminate the thought virus, and see a marked improvement in your productivity and quality of life.

* Morgan Giddings is a tenured Associate Professor of Microbiology & Immunology, Biomedical Engineering, and Computer Science at UNC Chapel Hill, and also a serial entrepreneur who has been involved in six business ventures. She loves to study personal productivity and to share what she learns with others.

Redesigning Scientific Reputation

By Bo Adler, Luca de Alfaro, and Ian Pye. *The Scientist* Volume 24, Issue 9. 2010-09-01

Rewards and incentives for online collaboration can make better science. The current system of peer-reviewing scientific publications has the momentum of centuries, and is still ruled by a rigid cycle based on its original print medium. The review phase must be complete before publication takes place; once the work is published, it cannot be updated. While insightful comments may have been made during the review process, or afterward by readers, these comments are not distributed together with the published work, so that crucial context may not be passed on to readers. What if we could redesign the process of scientific review to take advantage of modern technologies? People are experimenting with new ideas. Archival sites are available that allow scientists to post their work without delay: the most prominent is Cornell’s arXiv.org, and other institutions such as the California Digital Library are following suit. Many researchers are interested in developing review systems around these repositories that may augment, and eventually supplant, the traditional process of journal and conference reviews. Several scientific publishers and Web platforms—e.g., PLoS, BioMedCentral, AcaWiki, Faculty of 1000, and the recently announced LiquidPublications—are using article metrics, comments and other post-publication rating systems to identify important research. These systems are interesting, but they can be subject to the same drawbacks of the current peer review system, where social or academic obligation and coercion can skew the results. Peter Frishauf, founder of Medscape, has proposed that quantifiable “reputation systems” would reflect the depth of review a paper has undergone, and could serve as a reward system for those scientists who contribute to enhancing or judging a paper’s value. He draws his ideas from a 2003 paper by Jeff Ubois, published in Esther Dyson’s Release 1.0 newsletter, titled “Online Reputation

Systems." From this early work he expands on research by us and others who have proposed quantification schemes based on longevity and impact of text passages in articles and review comments. Thus, one's reputation is not measured by credentials, but by one's contribution both to expanding knowledge and to the community.

If an online reputation system is to replace the traditional process of review, several technical obstacles must be overcome. How to prevent the site from being swamped by second- or third-rate submissions, if not outright spam? How to ensure that all promising papers, including those by novices, receive their due share of insightful comments? And that the most qualified reviewers distribute their attention impartially, rather than flocking to authors they know already? How to ensure that comments actually add value, and how to prevent or eliminate reviews that are wide of the mark?

Our work in building large-scale reputation systems suggests that it may be possible to build such a system on two pillars: a system of incentives for authors of papers and reviews alike, and a content-driven way of measuring merit and attributing rewards. The reputation of people as authors would depend, as usual, on their publishing works of high measured value. And crucially, the reputation of people as reviewers would depend on their ability to be early reliable predictors of the future value of a work. Thus, two skills would be required of a successful reviewer: the ability to produce reviews that are later deemed by the community to be accurate, and the ability to do so early, anticipating the consensus. This is the main factor that would drive well-respected people to act as talent scouts, and to review freshly published papers, rather than piling up on works by famous authors. Reviews would be ranked by reputation, thus diminishing irrelevant comments, as Amazon has shown it is possible to do.

Using reputation scores to help search, to guide which reviews emerge, and to promote one's academic standing would provide strong incentives to researchers to interact productively with their colleagues and to spotlight great science.

Bo Adler and Ian Pye are PhD students of Luca de Alfaro at UC Santa Cruz, who is currently on leave at Google Inc. They are working on the WikiTrust project to provide reputation analysis for Wikipedia and other open collaboration systems (e.g., Web forums, Google Maps, and DNS). They recently created a Wikipedia vandalism detection tool based on

reputation analysis. Opinions expressed do not necessarily reflect those of their employers.

Billion-euro boost to EU science

by Bob Grant

Source: The Scientist, 20th July 2010

European science is set for a serious shot in the arm, after the European Union's commissioner for research and innovation announced yesterday (19th July) that the EU will invest approximately €6.4 billion in research and development on the continent through 2011.

The investment package, the largest ever infusion of funding into research activities across Europe, will create more than 165,000 jobs and help save struggling economies, said Ireland's Máire Geoghegan-Quinn in a statement. "Investment in research and innovation is the only smart and lasting way out of crisis and towards sustainable and socially equitable growth," she added. "This European package will contribute to new and better products and services, a more competitive and greener Europe, and a better society with a higher quality of life." Health researchers can expect €600 million of the total funding, with a third of that going towards clinical trials designed to speed important new drugs to market, according to Geoghegan-Quinn. An additional €1.3 billion will go to scientists hand-picked by the European Research Council, and small and medium-sized enterprises in the EU will vie for about €800 million. Another €772 million is slated to go to 7,000 researchers through the Marie Curie Actions, a fellowship program designed to encourage cross-border collaboration.

The funding is part of the EU's new project, dubbed "Innovation Union Flagship," which gets underway in earnest this autumn.

Publish or post?

Posted by Jef Akst

The Scientist, 9th August 2010

A new European-funded initiative is advocating an entirely new system of science publishing, in which scientists avoid the hassles of traditional peer review by taking a quietly radical step: post their results on their websites.

As the news release for LiquidPublication simply states: "Don't print it; post it." To

disseminate the information, the program has a software platform that lets other scientists search for what's been posted, leave comments, link related works, and gather papers and information into their own personalized online journals -- all for free.

"I think it's exactly what is needed -- a paradigm shift," said peer-review critic David Kaplan of Case Western Reserve University in Ohio. "This is a different system that utilizes the unique characteristics of the web [to provide] a different way of looking at manuscripts [and] a different way of evaluating them." The downfalls of the current scientific publishing scheme are no secret, and while many journals are aiming to better it (see The Scientist's feature in this month's issue), their efforts are relatively minor alterations to what many consider a fundamentally flawed system. Now, information engineer Fabio Casati of the University of Trento in Italy and his collaborators are suggesting science publishing try something entirely new, taking full advantage of the rapidly evolving Web 2.0 technology.

They suggest making research -- including formal manuscripts, datasets, presentation slides, and other presentations -- available through the web without any sort of traditional peer-review process. That research would then be searchable and citable by the rest of the scientific community at no cost.

"In this way -- by looking at what people do in terms of reading, sharing, or connecting scientific knowledge -- we can have a way of finding out which scientific resources are considered good and interesting by the scientific community," Casati said.

Specifically, he and his team envision a new age of scientific journals, created by the users themselves -- the scientists. "I [could] have my own journal, which I maintain on peer review, for example," he explains. "[When I find an interesting paper], I drag and drop the pdf file [in] the journal" using the platform provided by LiquidPublication, which recognizes the file, obtains the url, and retrieves the metadata, etc. "I do this because I want to keep track of it for myself [and alert] all my team, [but] by doing this, we also share [our thoughts on the research] with the world."

The LiquidPublication site, which already has a prototype up and running, will then collect basic metrics (for example, the number of people who include a contribution in their journals, the number of subscribers to a particular journal, or

the number of times someone links to a scientific resource) by which users can judge the reputability of different pieces of knowledge -- or the merit of its authors. "In essence, what we want to do is to allow scientists to easily build this web of scientific resources," Casati said.

"I think it's really interesting, and I think it could make a lot of difference," said Richard Smith, former editor of the British Medical Journal, who has written extensively about peer review. It takes advantage of "the whole idea of the invisible college," he said.

Of course, this system is not without its drawbacks, most agree. "My fear is that people would put out garbage," Kaplan said. "Who's going to wade through all of that?" The solution to this, however, would be to employ gatekeepers of the content, "and the more you gatekeep, the more you're back to the system we have now."

But under the system Casati has in mind, gatekeepers wouldn't be necessary. The research, he said, will be vetted by those who understand it best -- those scientists working on closely related subjects. For instance, scientists can follow "how frequently reputable people, who are respected in science, put [them] into their journals."

In his opinion, there's no reason such a system can't coexist with many of today's journals, with or without peer review. "We're not saying you should use this system religiously and not use peer review," he said. "You can have a journal with this model, but still have peer review behind it."

Indeed, the project has attracted interest from the scientific branch of Springer Publishing. While the publisher is currently not contributing any funds to the project, "Springer was brought in because of their knowledge in the field," Casati said. "I think it's clear to them that the world is going to change. In the past, [journals have been] used to provide the value of printing and distinction, [but in the future] it will be radically different." Springer was not able to comment by deadline.

In addition to making scientific publishing much more efficient, Casati and his collaborators hope that LiquidPublication will encourage quality over quantity, and "discourage the attitude of trying to publish as many papers as possible as opposed to trying to do as much research as possible," he said. The way the platform will link papers, for example, will be able to show when one publication is merely an incremental addition to a previous one. The world "will know

whether your 14 papers you've published are minor variations or are actually 14 new and different scientific contributions." Unfortunately, Smith said, the scientific community has so long been stuck in its ways, that such a dramatic change will be difficult for many to accept. "I would be surprised if this is the sort of the breach of

the dikes that really causes things to change in a real way," Smith said, "but let's hope it might be."

The LiquidPublication project is funded by the FET-Open strand of the European Commission's Seventh Framework Programme for research.

Forthcoming meetings



Frontiers of NMR in Biology January 8 – 13, 2011, Big Sky, Montana (USA)

Organizers: Michael F. Summers,
Dorothee Kern and David E. Wemmer
More info:

<http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1126&subTab=program>

Plant Abiotic Stress Tolerance Mechanisms, Water and Global Agriculture January 17 – 22, 2011, Keystone, Colorado (USA)

Sponsored by Monsanto Company
Organizers: Julian I. Schroeder and
Jacqueline E. Heard
More info:

http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1124#utm_source=StandardEmail737&utm_medium=email&utm_campaign=StandardEmail737&utm_content=11A7

50th Vegetable & Flower Seed Conference January 22 – 25, 2011, California (USA)

More info:
http://www.amseed.com/mtg_vegflo11_intro.asp

The Evolution of Protein Phosphorylation January 23 – 28, 2011, Keystone, Colorado (USA)

Organizers: Tony Hunter and Tony Pawson
More info:

http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1088#utm_source=StandardEmail740&utm_medium=email&utm_campaign=StandardEmail740&utm_content=11F1

Genomic Instability and DNA Repair

January 30 – February 4, 2011, Keystone, Colorado (USA)

Organizers: Junjie Chen, Karlene A.
Cimprich and Michael B. Yaffe
More info:

http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1097#utm_source=StandardEmail740&utm_medium=email&utm_campaign=StandardEmail740&utm_content=11B4

International Conference on Solanaceae Resistance Breeding February 17 – 19, 2011, Chiang Mai (Northern Thailand)

The conference program includes oral presentations from leading scientists in Solanaceae Genetics and Genomics and will cover all aspects of conventional and modern resistance breeding. The conference creates a forum for exchange of scientific ideas and knowledge between plant breeders, geneticists, molecular biologists and plant pathologists to which is expect to contribute to development of new tools and technologies for plant breeders. We expect this conference will also contribute to stronger ties between researchers and plant breeders in the public and private sector, and create a better awareness of the exciting career opportunities for graduate students in plant breeding, genetics, and related disciplines.

More info:
<http://www.sol-symposium2011.com/>

Plant Transformation Technologies II February 19 – 22, 2011, Vienna (Austria)

Plant Transformation Technologies II will cover the following topics: -Agrobacterium Mediated Plant Transformation -Particle Bombardment and Other Transformation Methods -Explants Used for Plant Transformation -Transformation of Important Crops -Plant Transformation

Tools: Genes, Vectors, Promoters etc - Selectable and Screenable Markers - Molecular Analysis of Transgenic Events and Transformants - Expression of Transgenes in Transgenic Plants (Integration, Stability) - Marker Excision and Marker Free Trans technologies - Plastid Transformation and Biotechnology - Transgenic Plants as Bio Factories - Transgenic Plants and Public - Intellectual Property in Plant Transformation - Emerging Plant Trans-Technologies

Amongst the invited speakers are internationally known names such as M. Van Montagu, C.N. Stewart, Jr., V. Citovsky, S.B. Gelvin, H.D. Jones, H. Kobayashi, D.W. Ow, R. Bock, M. Boutry, L.-Y. Lee, A. Trewavas, G. Lomonosoff, G. Corrado, S.-S. Kwak, G. Angenon, H. Daniell and others. For any questions please contact Mondial ptt2011@mondial-congress.com or the conference organizers ptt2011@vipca.at

More info: <http://www.vipca.at/ptt2011/>

BioSystematics Berlin 2011
February 21 – 27, 2011, Berlin
(Germany)

7th International Congress of Systematic and Evolutionary Biology (ICSEB VII), 12th Annual Meeting of the Society of Biological Systematics (Gesellschaft für Biologische Systematik, GfBS), and 20th International Symposium "Biodiversity and Evolutionary Biology" of the German Botanical Society (DBG). The congress will be held at the "Seminaris Campus Hotel, Science & Conference Center", located at the campus of the Freie Universität in Berlin-Dahlem in February 2011. It combines excellent and modern meeting equipment and vicinity to the Botanic Garden and the Botanical Museum as well as the Ethnological Museum. The venue is easily accessible by public transport from the airport and the city center's railway station.

More info: www.biosyst-berlin-2011.de

Plant Gene Discovery Technologies
February 23 – 26, 2011, Vienna
(Austria)

Plant Gene Discovery Technologies will cover the following topics: - Reverse Genetics & Mutants Technologies - Gene Discovery by TILLING - DNA Sequencing Technologies - Protein Sequencing & Protein Discovery - Microarrays - Protein Microarrays - Gene Discovery using "OMICS" - Bioinformatics - Evaluation and Application of Sequencing - System Biology & Gene Network Discovery

Amongst the invited speakers are internationally known names such as G.W.

Haughn, J.-K. Zhu, B.J. Till, S.B. Gelvin, P. Ronald, L.O. Lomas, C.J. Mann, R.L. Last, K. Shinozaki, B.C. Meyers, C. N. Stewart, Jr., J.-F. Gibrat, K. Mitchelson, M. Matsui, V. Bafna, B. Ülker and others. For any questions please contact Mondial pgdt2011@mondial-congress.com or the conference organizers pgdt2011@vipca.at

More info: <http://www.vipca.at/pgdt2011/>

Keystone Symposia: Evolutionary Developmental Biology
Feb 27 – Mar 3, 2011, Tahoe City,
California (USA)

More info:
<http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1092&subTab=program>

Meeting Summary:
 One major goal of evolutionary biology is to understand how morphological variation arises within populations and how species diverge. Four major challenges in understanding the genetic and molecular basis of morphological evolution are the identification of loci underlying trait divergence, the elucidation of functional changes within these loci, tracing the origin of functional variation and adaptations in populations, and reconstruction of how major innovations have been assembled over time. Current research in evolutionary developmental biology is addressing these challenges in a variety of model animals, plants, and microbes. The pace of progress is such that it is now possible to pose general questions about the process of morphological evolution, such as: are there any general themes underlying the genetic and developmental basis of variation and divergence? And, are the phenomena and mechanisms observable over short time scales sufficient to explain processes that have unfolded over much longer time scales in the fossil record? The purpose of this Keystone meeting on evolutionary developmental biology is to gather the leading researchers across the discipline to share emerging information and to address these general questions. The prospective speakers include the most notable contributors to the field and emerging young investigators who together constitute an exceptionally broad representation of this highly interdisciplinary research field.

DNA Replication and Recombination
February 27 – March 4, 2011,
Keystone, Colorado (USA)

Organizers: Peter M. Burgers, Lorraine S.

Symington and Johannes Walter

More info:

http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1117#utm_source=StandardEmail740&utm_medium=email&utm_campaign=StandardEmail740&utm_content=11C2

Biofuels

March 1 – 6, 2011, Singapore

Organized in Collaboration with Agency for Science, Technology and Research

Organizers: Stephen P. Mayfield, Martin Keller and Jeffrey P. Obbard

More info:

http://www.keystonesymposia.org/meetings/viewMeetings.cfm?MeetingID=1125#utm_source=StandardEmail740&utm_medium=email&utm_campaign=StandardEmail740&utm_content=11C3

EUCARPIA Genetic Resources section meeting "To Serve and Conserve"

April 5 – 7, 2011, Wageningen (The Netherlands)

More info: <http://www.epgrc2011.nl>

Proteases2011 Plant Protease Conference

April 10 – 14, 2011, Hemavan (Sweden)

Take a look at the plant protease website at <http://www.plantproteases.se/> for further details about the meeting and program updates as they occur. The conference will deal with the biology, biochemistry and molecular biology of plant proteases collecting together the foremost scientists in the field. The approach of the conference is broad, but a special emphasis is paid on a few topics listed: Organellar proteases, Metacaspases, Subtilases, Proteases in senescence and cell death, Novel methods, such as proteomics and degradomics, Proteases in xylem tissues and cell wall formation. In addition, a one-day mini-symposium will be organised on xylem development and wood formation. Instructions for registration and Abstract submission can be found at the website (<http://www.plantproteases.se/>). When submitting your abstract please indicate in your message in which session your abstract should be placed and if you would like to give an oral or poster presentation; although please note that we will not necessarily be able to accommodate all the oral presentations in the time available for the meeting. Deadline for registration is February, 10,

2011. (Observe that registration can close even earlier if we exceed the maximum number of participants, which is 103).

10th Conference of the International Society for Seed Science

April 10 – 15, 2011, Bahia (Brazil)

More info:

<http://www.seedscience2011.com.br/>

Molecular Bioenergetics of Cyanobacteria: From Cell to Community

April 10 – 15, 2011, Sant Feliu de Guixols (Spain)

The European Science Foundation (ESF) – in partnership with EMBO – is organising a conference on 'Molecular Bioenergetics of Cyanobacteria: From Cell to Community' which will be held next April in Spain. The closing date for applications is the 27th of January, 2011.

More info:

www.esf.org/conferences/11351/

Plant Neurobiology 2011

May 15 – 19, 2011, Kitakyushu (Japan)

In May 2011 (15th-19th), Plant Neurobiology 2011 (PNB 2011: 6th International Symposium on Plant Neurobiology) will be held in Kitakyushu, Japan, under auspices of the Society for Plant Signaling and Behavior. Hot discussions on the emerging topics in plant signaling studies, plant membrane biology, plant-microbe interactions, chemical plant ecology, and plant actions and behaviors in responses to changing Environmental Factors are expected.

For more information please visit

<http://www.dd-plus.net/pnb2011/>

11th World Congress on Parasitic Plants

June 7 – 12, 2011, Martina Franca (Italy)

Parasitic plants - both the weedy species that severely constrain agriculture and the many other non-weedy species - present unanswered questions with regard to their origin and evolution from non parasitic plants, population structures and dynamics, evolutionary pathways towards crop parasitism, ecology, physiology, molecular biology, and the structure, function and development of their haustoria. The Congress will include presentations at the cutting edge of parasitic plant research and management of parasitic weeds. For any information please visit <http://ipps2011.ba.cnr.it> or contact Maurizio Vurro, at maurizio.vurro@ispa.cnr.it

9th International Symposium of Oenology OENO 2011
June 15 – 17, 2011, Bordeaux (France)
Faculty of Oenology, Victor Segalen 2 University, ISVV
More info: www.oeno2011.u-bordeaux2.fr

International Rubus and Ribes Symposium
June 22 – 26, 2011, Zlatibor (Serbia)
On behalf of the International Society for Horticultural Science (ISHS)
Symposium website: <http://www.x-rubusribes.agrif.bg.ac.rs/>
E-mail symposium: x.rubusribes@agrif.bg.ac.rs

5th European Symposium on Plant Lipids
July 10 – 13, 2011, Gdansk (Poland)
Web site:
<http://www.eurofedlipid.org/meetings/gdansk2011/index.htm>

IBC2011 XVIII International Botanical Congress
July 23 – 30, 2011, Melbourne (Australia)
Registration now open
More info: <http://www.ibc2011.com/>

12th International Symposium on Pre-Harvest Sprouting in Cereals (12TH ISPHSC)
July 24 – 27, 2011, Alberta (Canada)
For those who are planning to attend the 12TH ISPHSC to present a paper/poster you can send the **title** of your paper to: Fran Teitge frances.teitge@gov.ab.ca
More details will follow and keep watching new information at our website:
[http://www1.agric.gov.ab.ca/\\$department/EFE.nsf/all/efe2613](http://www1.agric.gov.ab.ca/$department/EFE.nsf/all/efe2613)
Joseph M. Nyachiro
e-mail: joseph.nyachiro@gov.ab.ca
[http://www1.agric.gov.ab.ca/\\$department/deptdocs.nsf/all/fcd5615](http://www1.agric.gov.ab.ca/$department/deptdocs.nsf/all/fcd5615)

Plant Genome Evolution
September 4 – 6, 2011, Amsterdam (The Netherlands)
www.PlantGenomeEvolution.com

VII International Symposium on In Vitro Culture and Horticultural Breeding: IVCHB

September 18 - 22, 2011, Ghent (Belgium)
More info: www.ivchb2011.ugent.be

23rd Asian-Pacific Weed Science Society Conference
September 25 – 30, 2011, Queensland (Australia)

The theme for APWSS 2011 is "*Weed management in a changing world*". We invite you to submit an abstract on one or more of the following sub-themes:
Threats and risks in the Asian-Pacific region.
Sustainable weed management in the Asian-Pacific region.
Weed solutions for the Asian-Pacific region.
Economics of weed control in the Asian-Pacific region.
For further information on submitting your abstract, download the **Abstract Instructions** (http://dynamail.entegy.com.au/download/files/01693/1255945/APW11_Abtract%20Instructions.pdf), **Submit your abstract now** (https://www.eventcorp.com.au/ei/cm.esp?id=451&pageid=_3160U1JD3), **Conference updates** (<http://dynamail.entegy.com.au/forms/s/999a827/1693/283177.html>), and **Conference website** (<http://www.apwss2011.com/>).

3rd International Rhizosphere Conference RHIZOSPHERE 3
September 25 – 30, 2011, Perth (Western Australia)
For further information regarding the sponsorship packages visit the conference website <http://rhizosphere3.com> or contact the Conference Organisers, International Conferences & Events on +61 8 9381 9281 or via email to rhizosphere3@iceaustralia.com.

17th Meeting of the International Council for Grapevine Viruses
October 8 – 12, 2012, Davis, California (USA)
More information can be found at <http://ucanr.org/sites/ICVG/>

Positions available

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Laurent.Farinelli@fasteris.com Tel. +41 22
794 22 23

PhD student (Basel, Switzerland).

We are looking for a PhD student to work on a project "Next generation sequencing for studying viruses and RNA silencing-based antiviral defense in model and crop plants"

We shall apply the Illumina deep-sequencing technology and develop bioinformatic tools to study the viral genome, transcriptome and small RNA populations in experimentally infected Arabidopsis plants and naturally-infected crop plants with the ultimate goal to obtain knowledge for designing an effective RNA-based antiviral vaccine.

Virus-infected crop plants including rice, cassava, blackgram, cotton, banana and tomato, collected in fields worldwide, will be investigated by deep-sequencing of fractionated nucleic acids in order to (i) identify and de novo assemble complete genomes of newly emerging and resistance-breaking viruses, viral strains and viral satellites; (ii) determine the nucleotide polymorphism in virus populations; (ii) de novo assemble the viral transcriptome and (ii) create genome-wide maps of virus-derived siRNAs.

The project is part of a large COST action network with more than 20 member-countries (<http://costfa0806.aua.gr/>).

A successful candidate should have a master/diploma degree in molecular biology and a background and/or a strong interest in bioinformatics.

The position is available from the 1st of January 2011; earlier or later starting dates will also be considered.

The working places will be:

- 1) Institute of Botany, University of Basel, Basel, Switzerland
- 2) Fasteris AG, Geneva, Switzerland (www.fasteris.com)

The PhD project will be co-supervised by PD Dr. Mikhail Pooggin (University of Basel) and Dr. Laurent Farinelli (Fasteris AG).

Contact info:

Mikhail.Pooggin@unibas.ch Tel +41 61
267 27 29 or

Postdoctoral position in Lisbon, Portugal

One post-doctoral position is immediately available in the Plant Stress Signaling group at the Instituto Gulbenkian de Ciencia located near Lisbon, Portugal (<http://www.igc.gulbenkian.pt>). The position is initially for one year but renewable up to two.

Research in the lab focuses on energy signaling and its connection to environmental changes and growth. The Arabidopsis SnRK1 protein kinases play a central role during the stress response and are required for the proper integration of environmental cues into growth and development.

Sensing and signaling stress-associated energy deprivation, SnRK1s trigger global gene expression reprogramming, enabling the adjustment of energy homeostasis necessary for coping with stress.

The present project aims at further dissecting and understanding SnRK1-mediated signaling through the elucidation of the regulatory mechanisms associated with SnRK1 nuclear localization, post-translational modifications, and modulation by upstream phosphatases. Applicants should have a PhD in genetics, biochemistry or molecular biology, with excellent communication skills and a strong background in molecular biology and biochemistry. Experience in Arabidopsis signaling and traditional biochemistry techniques (recombinant protein production, immunoprecipitation, protein complex isolation and/or cell fractionation) is a plus.

Interested candidates should send CV, a letter of motivation with a brief description of previous research, and three letters of reference to ebaena@igc.gulbenkian.pt
References:

Baena-Gonzalez E (2010) Mol. Plant 3:300-313

Baena-Gonzalez E and Sheen J (2008) Trends Plant Sci. 3: 474-482

Baena-Gonzalez E, Rolland F, Thevelein J, and Sheen J (2007) Nature 448: 938-942

Postdoctoral position. University of California, Berkeley

A postdoctoral fellow position is available in the Department of Plant and Microbial biology, University of California, Berkeley, to study epigenetic regulation of gene expression, specifically on genes regulated by the Polycomb Group proteins. Applicants should have a PhD in Genetics, Biochemistry or Molecular Biology with excellent communication skills. Experience in Arabidopsis growth and development, genomics and biochemical skills in immunoprecipitation, protein complex isolation are desirable. Interested candidates should send CV, 2 letters of recommendation with a brief description of long term research interest and career goal to Dr. Z. Renee Sung at sungr@berkeley.edu

Post Doctoral Research Associate position available

The United States Department of Agriculture, Agricultural Research Service's Weed Biology Research Unit, of the Red River Valley Research Center, Fargo, ND, USA.

The United States Department of Agriculture, Agricultural Research Service's Weed Biology Research Unit, of the Red River Valley Research Center, in Fargo, ND, has a Research Molecular Biologist (Plants), Post Doctoral Research Associate position available. Research is focused on proving the concept that growth and development of underground adventitious bud can be manipulated by growth regulators. The incumbent will evaluate the effect of glyphosate and other compounds on the growth and viability of leafy spurge (*Euphorbia esula*) shoots derived from vegetative crown and root buds, and investigate transcriptome changes in relation to glyphosate induced witches' brooming (i.e., uncontrolled outgrowth of shoots). Citizenship restrictions apply and a recent Ph.D. is required.

Interested applicants should go to

<http://www.afm.ars.usda.gov/divisions/hrd/hrdhomepage/vacancy/pd962.html>

Send application materials and references to Dr. Michael E. Foley, USDA-ARS-BRL, 1605 Albrecht

Blvd., Fargo, ND 58102-2765 or e-mail michael.foley@ars.usda.gov.

Postdoctoral Position in Wheat Genetics

Department of Plant and Soil Sciences at Oklahoma State University, USA.

Cereal aphids such as greenbug and Russian wheat aphid are the two major pests of wheat worldwide, and they cause millions of dollars of losses to this important food crop each year. We have been identifying sources of aphid resistance and developing high-performance wheat germplasm/cultivars with genetic resistance to the aphid pests. It is important to develop a better understanding of host-plant resistance.

Thus, a postdoctoral position is available immediately in the Department of Plant and Soil Sciences at Oklahoma State University. This postdoctoral research fellow will join a cooperative research project under Dr. Brett Carver of Oklahoma State University in collaboration with Dr. Yinghua Huang of the USDA-ARS. The incumbent will design and implement research experiments to identify resistance gene(s) and characterize genetic mechanisms of aphid resistance in winter wheat through genetic and genomic approaches. Research will also involve developing molecular markers and using genetic and breeding methodologies to identify genes controlling aphid resistance and to incorporate them into advanced breeding lines.

Candidates should have a strong background in genetics, molecular biology, plant breeding, or related discipline. Experience in genomic technology, molecular mapping and QTL analysis, marker-assisted breeding, and statistical/bioinformatic methods are desirable. Documented ability to communicate effectively in English both writing research publication and spoken language. Review of applications will begin December 1, 2010, and continue until the position is filled. Please send a letter of research interest and professional goals, curriculum vitae, and contact information for three references by email to:

yinghua.huang@ars.usda.gov or
brett.carver@okstate.edu.

For additional information, please contact:
Dr. Yinghua Huang, USDA-ARS Plant
Science Research Lab, 1301 N. Western
Road, Stillwater, OK 74075, (405) 624-
4141.

Postdoctoral Researcher Position Available

The Epigenetic Regulation of Transposable Elements

The Ohio State University. Columbus, OH, USA

A post-doctoral researcher position is available at The Ohio State University in the Department of Molecular Genetics. The position will be part of a new plant molecular genetics laboratory studying the epigenetic regulation of transposable elements in *Arabidopsis thaliana*. The position will use fluorescence microscopy, molecular genetics and genome-wide approaches to explore the epigenetic regulation of the plant genome. For research details, please see:

http://www.biosci.ohio-state.edu/pcmb/osu_pcmb/people_faculty_slotkinRKeith.php

The position will both conduct research with the goal of publication, as well as mentor and advise students in the laboratory. This is a basic science project, and the applicants should have a strong background in plant cellular and molecular biology. A Ph.D. in molecular biology or related field and previous work in plant biology is required. Good oral and written skills and a strong publication record in refereed journals are also required, as well as a strong understanding of genetics and experience in greenhouse protocols. Experience with fluorescent microscopy, epigenetic regulation, or transposable elements are desired.

Additional opportunities for teaching and professional development are available if desired. The position is located in a modern, well-equipped facility at The Ohio State University in Columbus, Ohio and offers competitive salary and benefits with the opportunity for professional growth and advancement. The successful candidate is expected to demonstrate independence and creativity. Good oral and written skills and a strong publication record in refereed journals are required. We seek highly motivated researchers

with demonstrated outstanding ability and accomplishment. Salary will be commensurate with qualifications.

Please apply to R. Keith Slotkin (Slotkin.2@osu.edu) and/or use the following link to apply to the above position: <http://jobs.osu.edu>, using the requisition number 353809. To build a diverse workforce Ohio State encourages applications from minorities, veterans, women and individuals with disabilities. Flexible work options available. EEO/AA Employer.

Assistant Professor in the area of Experimental Climate Change Research.

**The University of Western Ontario
London, Ontario, Canada.**

Applications are invited for a probationary (tenure track) faculty position at the rank of Assistant Professor in the area of **Experimental Climate Change Research** in the Department of Biology, Faculty of Science, at The University of Western Ontario (www.uwo.ca/biology) starting July 1, 2011. Candidates must have a Ph.D. in Biology or a related field, and postdoctoral experience (or equivalent). The successful candidate will be expected to develop an independent, externally-funded research program in Experimental Climate Change Research. Priority will be given to applicants with expertise in the areas of community ecology, plant stress biology or invertebrate neurobiology. The successful candidate is expected to contribute to the graduate and undergraduate degree programs in Biology. Experimental Climate Change Research represents an emerging area of interest in the Department of Biology, and bridges existing research strengths in stress biology and ecosystem function, and the successful candidate will complement these. The successful candidate will be housed in, and is expected to be a primary user of, the Biotron, a state-of-the-art research facility purpose built for climate change research (<http://www.thebiotron.ca/>).

Consideration of applications will begin February 01, 2011 and continue until the position is filled. Applications must include a curriculum vita, a statement of research interests, a statement on teaching philosophy, and the names of three references. Applications, submitted electronically as a single pdf file to expccres@uwo.ca should be addressed to the attention of

Dr. Mark Bernards, Chair Department of Biology The University of Western Ontario
This position is subject to budgetary

approval. Applicants should have fluent written and oral communication skills in English. All qualified candidates are encouraged to apply; however, Canadians and permanent residents will be given priority. The University of Western Ontario is committed to employment equity and

welcomes applications from all qualified women and men including visible minorities, aboriginal people and persons with disabilities.

Courses



International Graduate Course on Forest Ecophysiology

January 6 – 14, 2011, Parque Katalapi (Chile)

More info: www.parquekatalapi.cl

Seed Biology, Production and Quality

February 16 – 17, 2011, Seed Biotechnology Center. University of California, Davis (USA).

This unique two-day course is designed for professionals in the seed industry, crop consultants and growers to update and expand their current knowledge. Participants will learn fundamental and specialized information on topics including seed development, production, harvesting, testing, conditioning, enhancement, storage, pathology and quality assessment. The

course content has been updated with the latest information and instructors include: Dr. Derek Bewley (University of Guelph, Canada), Dr. Henk Hilhorst (Wageningen University, The Netherlands), Dr. Hiro Nanogaki (Oregon State University, Corvallis), Dr. Robert Gilbertson (University of California, Davis), Deborah Meyer (California State Seed Laboratory) and Dr. Kent Bradford (University of California, Davis).

More info:

http://sbc.ucdavis.edu/education/Courses/Seed_Biology_Production_and_Quality_-_2011.html

New books



PLANT BIOCHEMISTRY (4th Edition)

Hans-Walter Heldt and Birgit Piechulla

ISBN: 9780123849861

Publisher: Academic Press

Published: October 2010

Illustrated with two-color diagrams and well designed metabolic schemes, this book presents plant metabolism in the context of the structure and function of the plant. Many examples of commercial applications for the protection and quality improvement of harvest crops, plant breeding, and the production of raw materials for industrial use are also covered.

AUTOMATION IN PROTEOMICS AND GENOMICS: AN ENGINEERING CASE-BASED APPROACH

Gil Alterovitz, Roseann Benson, Marco Ramoni

ISBN: 0470727233

Publisher: Wiley

Published: 1 de mayo de 2009

Book Description:

* is based on the course material from two popular MIT and Harvard interdisciplinary special studies courses, which have an engineering-based, problem-solving approach.

* describes current automation technology in areas of analysis, design, and integration, as well as providing basic biology concepts behind proteomics and genomics.

* identifies development opportunities that could inspire the next incremental improvement or disruptive technology to change the research landscape dramatically.

Edited by the team responsible for Systems Bioinformatics: An Engineering Case-Based Approach, this book is ranked number one in current sales for bioinformatics on Amazon.

ADVANCES IN PLANT CYTOGENETICS

Reprint of: Cytogenetic and Genome Research 2010, Vol. 129, No. 1-3
Karger Publications
Editors: Birchler, J.A.; Pires, J.C. (Columbia, Mo.)
264 p., 96 fig., 80 in color, 38 tab., hard cover, 2010
CHF 179.- / EUR 132.50 / USD 179.00
ISBN: 978-3-8055-9494-3
e-ISBN: 978-3-8055-8495-0

ADVANCES IN BOTANICAL RESEARCH VOLUME 53

Edited by Jean-Claude Kader and Michel Delseny

Academic Press. ISBN: 978-0-12-380872-1. Copyright 2010.

Contents:

1. Advances In Coffea Genomics
Alexandre de Kochko, Sélastique Akaffou, Alan Andrade, Claudine Campa, Dominique Cruzillat, Romain Guyot, Perla Hamon, Ray Ming, Lukas A. Mueller, Valérie Poncet, Christine Tranchant-Dubreuil, Serge Hamon
2. Arabidopsis Histone Lysine Methyltransferases
Frédéric Pontvianne, Todd Blevins and Craig S. Pikaard
3. Plant nematode interaction: a sophisticated dialogue
Pierre ABAD and Valerie M. WILLIAMSON
4. Regulatory components of shade avoidance
Jaime F Martínez-García, Anahit Galstyan, Mercè Salla-Martret, Nicolás Cifuentes-Esquivel, Marçal Gallemí and Jordi Bou-Torrent

ADVANCES IN BOTANICAL RESEARCH VOLUME 54

Kader Jean-Claude, Laboratoire Physiologie Cellulaire et Moléculaire des Plantes, CNRS, Université de Paris, France; Michel Delseny, Laboratoire Génome et Développement des Plantes, CNRS IRD UP, Université de Perpignan, France.
2010, ISBN: 978-0-12-380870-7.

Advances in Botanical Research publishes in-depth and up-to-date reviews on a wide range of topics in plant sciences. Currently in its 54th volume, the series features a wide range of reviews by recognized experts on all aspects of plant genetics, biochemistry, cell biology, molecular biology, physiology and ecology. This

eclectic volume features reviews on cutting-edge topics of interest to postgraduates and researchers alike.

PLANT TISSUE CULTURE, DEVELOPMENT, AND BIOTECHNOLOGY

Robert N. Trigiano. 2010

Summary:

Addressing several specialized areas generically termed biotechnology, Plant Tissue Culture, Development and Biotechnology uses a broad range of species that are studied via laboratory exercises. Based on the editors' previous textbooks *Plant Development and Biotechnology* and *Plant Tissue Culture Concepts and Laboratory Exercises - Second Edition*, the book provides detailed perspectives and hands-on training in this rather diverse field. It concentrates on plant development and its application in biotechnology, while maintaining as broad of a base as possible. Supporting laboratory exercises are provided.

ESSENTIAL PLANT PATHOLOGY

New Second Edition includes new DVD that works on PC or Mac

Gail L. Schumann and Cleora J. D'Arcy
2010; 8½" x 11" hardcover; 384 pages; 290 color images; DVD .

The first edition of this best selling textbook was carefully reviewed by subject matter specialists and plant pathology course instructors to help update the content, especially some of the quickly changing molecular aspects of host-parasite interactions. This new edition includes an important new section to teach students about gene silencing using RNA interference.

This inviting new edition is written specifically to the introductory plant pathology course level by award-winning educators, Gail Schumann and Cleo D'Arcy. The book is reader-friendly with important terms and concepts clearly identified. Special "Did you know?" boxes will spark student interest by providing cultural and historical facts about plant diseases and every chapter will guide students to recommended resources, study questions, "Words to Know," Internet research exercises, and DVD exercises. This DVD contains many important supplementary materials that can be used without internet access, including: expanded and revised identification exercises, new APSnet Education Center peer-reviewed instructional materials, and new web links for each chapter.

HARTMANN & KESTER'S PLANT PROPAGATION: Principles and Practices

Hudson Hartmann, Dale Kester, Fred Davies, Robert Geneve
8a edic. 2010, 912 pgs. Rust.

CONTENTS: 1. How Plant Propagation Evolved In Human Society 2. Biology of Plant Propagation 3. The Propagation Environment **PART II. SEED PROPAGATION** 4. Seed Development 5. Principles and Practices of Seed Selection 6. Techniques of Seed Production and Handling 7. Principles of Propagation from Seeds 8. Techniques of Propagation by Seed **PART III. VEGETATIVE PROPAGATION** 9. Principles of Propagation by Cuttings 10. Techniques of Propagation by Cuttings 11. Principles of Grafting and Budding 12. Techniques of Grafting 13. Techniques of Budding 14. Layering and Its Natural Modifications 15. Propagation by Specialized Stems and Roots 16. Principles and Practices of Clonal Selection **PART IV. CELL AND TISSUE CULTURE PROPAGATION** 17. Principles of Tissue Culture and Micropropagation 18. Techniques for Micropropagation **PART V. PROPAGATION OF SELECTED PLANT SPECIES** 19. Propagation Methods and Rootstocks for Fruit and Nut Species 20. Propagation of Ornamental Trees, Shrubs, and Woody Vines 21. Propagation of Selected Annuals and Herbaceous Perennials Used As Ornamentals Subject Index Plant Index, Scientific Names Plant Index, Common Names.

RECENT ADVANCES IN PLANT VIROLOGY

Carole Caranta, Miguel A. Aranda, Mark Tepfer and J.J. Lopez-Moya
2010, 470 pgs, tela.

Viruses that infect plants are responsible for reduction in both yield and quality of crops around the world, and are thus of great economic importance. This has provided the impetus for the extensive research into the molecular and cellular biology of these pathogens and into their interaction with their plant hosts and their vectors. However interest in plant viruses extends beyond their ability to damage crops. Many plant viruses, for example tobacco mosaic virus, have been used as model systems to provide basic understanding of how viruses express genes and replicate. Others permitted the elucidation of the processes underlying RNA silencing, now recognised as a core epigenetic mechanism underpinning numerous areas of biology. This book

attests to the huge diversity of research in plant molecular virology. Written by world authorities in the field, the book opens with two chapters on the translation and replication of viral RNA. Following chapters cover topics such as viral movement within and between plants, plant responses to viral infection, antiviral control measures, virus evolution, and newly emerging plant viruses. To close there are two chapters on biotechnological applications of plant viruses. Throughout the book the focus is on the most recent, cutting-edge research, making this book essential reading for everyone, from researchers and scholars to students, working with plant viruses.

PLANT CYTOGENETICS: Genome Structure and Chromosome Function

Bass, Hank W.; Birchler, James A. (Eds.)
2010, 400 pgs, tela.

CONTENTS: Polyploidy and aneuploidy.- Chromosomal rearrangements, Inversions and translocations.- Chromosome additions, substitutions, and deletion lines.- B chromosomes.- Karyotypes.- Molecular cytology, tools for the 21st century.- Cytogenetic FISH mapping.- High-resolution cytogenetics.- Defining centromeres; location, function, and dynamics.- Heterochromatin.- Integrating cytogenetic data into genome databases.- Functional architecture of the plant nucleus.- Cytology of meiotic chromosome behavior.- Evolutionary comparative cytogenetics.- Cytology of chromatin modifications and epigenetics.- Cytogenomics of plant organelles.- Glossary.- Index.

PLANT MITOCHONDRIA

Kempken, Frank
2010, 400 pgs, tela.

In this book the current knowledge about plant mitochondria is presented in a series of detailed chapters, which have been organized in five main sections: (i) dynamics, genes and genomes; (ii) transcription and RNA processing; (iii) translation and import; (iv) biochemistry, regulation and function; and (v) mitochondrial dysfunction and repair. These sections consist of two to five chapters, each written by well-known specialists in the field. This book thus provides a comprehensive inside in the field of plant mitochondria for the specialist. The addition of a glossary and text boxes to each chapter provides easy access for readers from other subjects and hopefully will attract young scientist to the fascinating and exiting field of plant mitochondria.

MYCORRHIZAL BIOTECHNOLOGY

Devarajan Thangadurai, Karnatak University, India; Carlos Alberto Busso, Universidad Nacional del Sur, Argentina; Mohamed Hijri, Universite de Montreal, Canada

2010, 226 pgs, tela.

CONTENTS: Arbuscular Mycorrhiza and Soil Microbes, *M. Miransari*. Ectomycorrhizae and Forest Plants Fitness, *L. Montecchio and L. Scattolin*. Role of VAM in Nutrient Uptake of Crop Plants, *V. Davamani, A.C. Lourduraj, R.P. Yogalakshmi, and M. Velmurugan*. Advances in Mass Production Technology of Arbuscular Mycorrhiza, *A. Khaliq, D.J. Bagyaraj and M. Alam*. Biomass Production, Arbuscular Mycorrhizae, and Soil Plant-Available P under Water Stress in Native Perennial Grasses, *C.A. Busso and A.I. Bolletta*. Induced Resistance in Plants and the Role of Arbuscular Mycorrhizal Fungi, *Y. Ismail and M. Hijri*. Influence of VAM in Bioremediation of Environmental Pollutants, *V. Davamani, A.C. Lourduraj, and M. Velmurugan*. Rhizosphere Management Practices in Sustaining Mycorrhizae, *C. Harisudan, M. Velmurugan, and P. Hemalatha*. Importance of Mycorrhizae for Horticultural Crops, *P. Hemalatha, M. Velmurugan, C. Harisudan, and V. Davamani*. Mycobization as a Biotechnological Tool: A Challenge, *M.S. Velázquez and M.N. Cabello*. Phytoremediation: Biotechnological Procedures Involving Plants and Arbuscular Mycorrhizal Fungi, *S.E. Hassan, M. St-Arnaud, M. Labreque, and M. Hijri*. Molecular Characterization of Genetic Diversity among Arbuscular Mycorrhizal Fungi, *M. Velmurugan, P. Hemalatha, C. Harisudan, and D. Thangadurai*. Molecular Tools for Biodiversity and Phylogenetic Studies in Mycorrhizas: The Use of Primers to Detect Arbuscular Mycorrhizal Fungi, *F. Covacevich*. The Impact of Climate Changes on Belowground: How the CO₂ Increment Affects Arbuscular Mycorrhiza, *F. Covacevich and Ricardo Luis Louro Berbara*.

PLANT VIRUS, VECTOR

S. Mukhopadhyay, B C Agricultural University, Nadia, India; R. T. Plumb, Rothamsted, UK

2010, 520 pgs, tela.

Stressing the key role vectors play spread of virus diseases, this volume represents the priorities in practical plant virus research and ways in which their control or management should be sought through an understanding of the practical and

environmental aspects of the interactions of viruses with their vectors and their environment. It provides an in-depth understanding of the vectors, their biology, dispersal, movement and migration, contemporary canvases of epidemiology, and the management of virus diseases keeping in view the globalization of agriculture as also the viruses and their quarantine requirements.

PRINCIPLES AND PRACTICES OF PLANT GENOMICS, VOLUME 3: Advanced Genomics

Chittaranjan Kole, Clemson University, South Carolina, USA; Albert G. Abbott, Clemson University, South Carolina, USA
2010, 370 pgs, tela.

This book presents the basic and applied aspects of sequencing of genes and genomes and their implication in the fine-scale elucidation of the plant genomes. The third volume presents an overview on the advances of plant genomics made in the past century; deliberations on the genomics resources; concepts, tools, strategies, and achievements of comparative, evolutionary, and functional genomics and whole-genome sequencing. It also presents critical reviews on the already completed genome initiatives and glimpses on the currently progressing genome initiatives. This volume is an ideal reference book for students, scholars and scientists in academia, industry, and government.

THE CHLOROPLAST: Basics and Applications

Rebeiz, C.A.; Benning, C.; Bohnert, H.J.; Daniell, H.; Hooper, J.K.; Lichtenthaler, H.K.; Portis, A.R.; Tripathy, B.C. (Eds.)
1st Edition., 2010, 500 p., Hardcover.

This book is designed for graduate students and researchers in chlorophyll metabolism, integrative plant biology, plant physiology, plant biochemistry, plant molecular biology, biotechnology, bioenergy and biofuels.

PLANT DEVELOPMENTAL BIOLOGY: Methods and Protocols

Hennig, Lars; Köhler, Claudia
1st Edition., 2010, XI, 448 p. 142 illus., 71 in color

In Plant Developmental Biology: Methods and Protocols, expert researchers provide a collection of protocols for many of the common experimental approaches in plant developmental biology, including diverse methods that range from grafting over bimolecular fluorescence complementation to chromatin immunoprecipitation. Comprehensive and revolutionary, Plant

Developmental Biology: Methods and Protocols is an essential guide for all plant developmental geneticists, biochemists, and researchers in stress physiology and plant nutrition.

HERBICIDES AND PLANT PHYSIOLOGY

Andrew Cobb, John Reade
2010, 296 pgs, rust.

This expanded and fully revised second edition of *Herbicides and Plant Physiology* provides a comprehensive and up-to-date account of how modern herbicides interact with target plants, and how they are used to manage crop production. This second edition of *Herbicides and Plant Physiology* is a valuable reference for students and researchers in plant physiology, crop production/protection, plant biochemistry, biotechnology and agriculture. All libraries in universities, agricultural colleges and research establishments where these subjects are studied and taught will need copies of this excellent book on their shelves.

LABORATORY MANUAL TO ACCOMPANY STERN'S INTRODUCTORY PLANT BIOLOGY

James Bidlack
12a edic. 2010, 256 pgs, rust.

This laboratory manual assumes no previous knowledge of the biological sciences on the part of the student. It is designed for use in a one-semester or one-quarter introductory course in plant biology and shorter introductory botany courses open to both nonmajors and majors. Both the principles of biology and the scientific method are introduced, using plants as illustrations. The exercises demonstrate the underlying unity of all living organisms at the cellular level. The manual is designed so that students can work independently. Instructors are free to require different drawings or other assignments and may also omit some of those suggested within each exercise. Students are encouraged to read the laboratory exercise before coming to class. Laboratory preparation quizzes are provided at the end of each exercise. Answers to the laboratory preparation quizzes are discernible within the particular exercises and should not require checking other sources. Each exercise includes suggested learning goals and exercise review questions.

GENETICALLY MODIFIED PLANTS: Assessing Safety and Managing Risk

Authors: Roger Hull, G. Tzotzos, Graham Head.

Published: 2009. ACADEMIC PRESS
ISBN 10: 0-12-374106-8. ISBN 13: 978-0-12-374106-6

A transgenic organism is a plant, animal, bacterium, or other living organism that has had a foreign gene added to it by means of genetic engineering. Transgenic plants can arise by natural movement of genes between species, by cross-pollination based hybridization between different plant species (which is a common event in flowering plant evolution), or by laboratory manipulations by artificial insertion of genes from another species. Methods used in traditional breeding that generate transgenic plants by non-recombinant methods are widely familiar to professional plant scientists, and serve important roles in securing a sustainable future for agriculture by protecting crops from pest and helping land and water to be used more efficiently. There is worldwide interest in the biosafety issues related to transgenic crops because of issues such as increased pesticide use, increased crop and weed resistance to pesticides, gene flow to related plant species, negative effects on nontarget organisms, and reduced crop and ecosystem diversity. This book is intended to provide the basic information for a wide range of people involved in the release of transgenic crops. These will include scientists and researchers in the initial stage of developing transgenic products, industrialists, and decision makers. It will be of particular interest to plant scientists taking up biotechnological approaches to agricultural improvement for developing nations.

Audience: plant scientists studying genetically modified crops; agricultural engineers; agronomists; researchers; industrialists; lawyers; students; regulators

PLANT CELL BIOLOGY

Randy Wayne.
Published: 2009. ACADEMIC PRESS
ISBN 13: 978-0-12-374233-9

Plant Cell Biology is a semester long course for undergraduates and graduate students which integrates mathematics and physics, two years of chemistry, genetics, biochemistry and evolution disciplines. Having taught this course for over ten years, the author uses his expertise to relate the background established in plant anatomy, plant physiology, plant growth and development, plant taxonomy, plant biochemistry, and plant molecular biology courses to plant cell biology. This integration attempts to break down the

barrier so plant cell biology is seen as an entrance into higher science. Distinguishing this book from papers that are often used for teaching the subject which use a single plant to demonstrate the techniques of molecular biology, this book covers all aspects of plant cell biology without emphasizing any one plant, organelle, molecule, or technique. Although most examples are biased towards plants, basic similarities between all living eukaryotic cells (animal and plant) are recognized and used to best illustrate for students cell processes.

Audience: Plant Biology and Plant Cell Biology courses; researchers and scientists with a background in plant anatomy, plant physiology, plant growth and development, plant taxonomy, plant biochemistry, and plant molecular biology needing a reference in plant biology.

ENVIRONMENTAL BIOTECHNOLOGY: A BIOSYSTEMS APPROACH

Daniel Vallero

Academic Press 2010

ISBN: 978-0-12-375089-1

Key Features: Provides a systems approach to biotechnologies which includes the physical, biological, and chemical processes in context. Case studies include cutting-edge technologies such as nanobiotechnologies and green engineering. Addresses both the applications and implications of biotechnologies by following the life-cycle of a variety of established and developing biotechnologies

For more than a century, biotechnology has acted as a vital buffer between people, pollution and the environment. The field is designed to moderate, if not eliminate, the stresses we inflict upon the world's ecosystems. In order to do this effectively, a systems approach must be employed to maximize the sustainability of our efforts and improve the long term health our environment.

This book will address the questions of how and why knowledge and understanding of the physical, chemical, and biological principles of the environment must be achieved for the effective development of biotechnology applications. Using a systems biology approach, Environmental Biotechnology will provide a context for researchers and practitioners in environmental science. It will serve as a complement to the useful guidebooks which provide the necessary specifications and criteria for a wide range of environmental designs and applications by providing the underlying principles for the specifications, an area which is most

important to scientific researchers in this arena to develop further technologies.

Readership: researchers in environmental biology, nanotechnology, systems biology and microbiology; environmental engineers; scientists at engineering and remediation companies and public organizations; practitioners in applied biology fields; graduate and post-doctoral students in these areas of science.