

Meeting report

The future for plants and plants for the future

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A report of the 2007 EMBO Conference Series on Plant Molecular Biology 'From basic genomics to systems biology', Ghent, Belgium, 2-4 May 2007.

The 2007 EMBO Conference on Plant Molecular Biology brought together about 150 plant scientists from 23 different countries in the beautiful town of Ghent in Belgium. This is where, some might say, plant molecular genetics received a major boost, with the work of Marc Van Montagu and Jeff Schell in the 1970s on the Ti plasmid of the plant pathogenic bacterium *Agrobacterium tumefaciens*. Plant modification with the help of the Ti plasmid of *A. tumefaciens* is now routine in many laboratories and has helped create genetically modified (GM) crops that are cultivated throughout the world.

Marc Van Montagu (Institute of Plant Biotechnology for Developing Countries, Ghent, Belgium) opened the conference by reflecting on both the past and the future of plant science. Contemplating that future, he stressed the importance of transgenic plants not only to further our basic knowledge on the function of genes, but also to cope with problems mankind will have to deal with: feeding an ever-increasing population on shrinking areas of arable land; the attrition of fossil fuels such as coal, oil and gas; and global warming. Van Montagu warned that in order to build a more sustainable economy in the future, it will be absolutely necessary for Europe to embrace the use of GM crops, as has already happened in large parts of the world. The strong reaction of consumer-rights groups and environmentalists against the use of GM crops has probably had a larger impact on plant science in Europe than generally recognized, and has been, at least in part, responsible for the drop in the numbers of students choosing plant research over the past few years.

Fortunately, the tide seems to have turned, and plant science is becoming more attractive again, on the one hand because GM plants have been used for almost 15 years without any major health hazards being reported, and on the other hand

through the growing awareness that plants might indeed hold the key to some of the most threatening problems of our time, namely energy consumption and global warming. However, here too, Europe will need to get its act together rather quickly in order not to be completely outcompeted by countries such as China or the United States, where there are already large initiatives in biofuel production.

On the positive side, much of the research presented at this meeting provided new insights that are badly needed to build a more sustainable world using plants as valuable resources. A few of the highlights are presented here.

To divide or not to divide

Although plant cell division, proliferation and cell fate are studied intensively, many questions remain. Dirk Inzé (Ghent University, Belgium) reviewed the process of endoreduplication, whereby cells undergo repeated rounds of DNA replication without mitosis and cytokinesis. Although the physiological role of endoreduplication in plants is debated, it seems to be involved in cell growth. Plants that have certain genes (for example, *CCS52A*) over-expressed and display endoreduplication often have a more rapid life cycle and improved stress tolerance than plants not displaying endoreduplication. Inzé reviewed the importance of the protein *CCS52A2* as a key regulator of endoreduplication cycles in plants. *CCS52A2* is part of the *Arabidopsis* anaphase-promoting complex (APC), and its gene is a target for the E2F/DP-like transcriptional repressor *DEL1*. Over-expression of *CCS52A2* causes excessive endoreduplication, while knock-outs have the opposite effect. Recent work by Inzé suggests that *CCS52A2*-activated APC not only promotes endoreduplication by causing the degradation of proteins essential for progression through mitosis, but that it also promotes continuing DNA replication by causing the degradation of an inhibitor of cell-cycle progression into S phase.

Eva Kondorosi (CNRS, Gif-sur-Yvette, France) studies the symbiosis between legumes, such as *Medicago*, and *Rhizobium*

bacteria that leads to the formation of nitrogen-fixing root nodules. Her talk focused on the regulation of the cell cycles of both the eukaryotic and prokaryotic partners after infection, revealing strikingly similar differentiation events in both *Medicago* and bacterial cells. In both partners, cells lose their ability to divide and become polyploid by successive rounds of endoreduplication. The development of larger bacterial and plant cells through endoreduplication might actually be a necessity for bacterial infection of the plant root. The conversion of *Sinorhizobium* cells into polyploid nitrogen-fixing bacteroids, for example, involves an unprecedented degree of prokaryotic differentiation. Kondoroski reported transcriptome and genome-analysis data suggesting that diverse peptides secreted by the host plant may act as antimicrobial peptides, inhibiting bacterial cell division.

Looking at the G₁/S transition, Crisanto Gutierrez (University of Madrid, Spain) described the recent identification of a novel protein, GEM (*GLABRA2* (*GL2*)-expression modulator protein), which interacts with CDT1, a protein that controls DNA replication at the G₁/S transition. GEM inhibits epidermal cell division and represses the expression of *GL2*, a homeobox gene that determines hair/nonhair cell fate in the root dermis of *Arabidopsis thaliana*. Gutierrez reported the participation of GEM in the maintenance of repressive histone H₃ Lys9 methylation in root-patterning genes, and was thus able to provide a clear link between cell division, cell fate and cell differentiation in *Arabidopsis* root development.

Plant development

The plant hormone auxin plays an essential role in many developmental processes. Local auxin gradients, for instance, are important in embryogenesis. Gerd Jürgens (University of Tübingen, Germany) described how they are set up by polarized auxin transport, which is dependent on auxin-efflux regulators of the PIN family. As discussed by Jiri Friml (University of Göttingen, Germany), the auxin-distribution network is modulated by both endogenous and exogenous signals to provide a common mechanism for the plasticity and adaptability of plant development. For example, gravity stimulation leads to rearrangement of subcellular polarity of auxin transport components. Consequently, auxin fluxes are redirected and the plant changes its growth to align with the new gravity vector. Equally, during embryogenesis and organogenesis, so far unknown developmental signals regulate these processes through changes of polarity of auxin transport proteins. Plant development is often synchronized to the changing seasons. In *Arabidopsis*, a circadian-clock regulated pathway that promotes flowering in response to longer day lengths is well documented. Georges Coupland (Max-Planck Institute for Plant Breeding Research, Köln, Germany) compared the regulatory network controlling flowering in *Arabidopsis* with the one found in the short-day plant *Pharbitis nil* and with the perennial plant *Arabis alpina*. Coupland showed that the *CONSTANS* (*CO*) gene,

which confers a day length response, from the short-day dicotyledonous plant *Pharbitis nil* activates the transcription of the *FLOWERING TIME* (*FT*) gene in *Arabidopsis*, which encodes a regulator of phosphorylation. Coupland is now trying to compare the protein complexes in which *CO* acts in *Arabidopsis* and *Pharbitis nil* to see how these are involved in regulating *FT* transcription as an approach to explain how diverse responses to day length in different plant species are generated.

Getting stressed

Plants cannot move to escape enemies or harsh conditions. They have therefore evolved strategies to survive grazing herbivores such as insects and snails, defenses against viral, bacterial and fungal pathogens, and protection against varying climate and other types of stress. To ward off competition from other plants, to fight infection, and to respond to the environment in general, plants make tens of thousands of different chemical compounds. Lothar Willmitzer (Max-Planck-Institut für Molekulare Pflanzenphysiologie, Golm, Germany) tries to make sense out of this enormous number of metabolites. He described a systems-biology approach for identifying putative signaling molecules involved in stress signaling by creating variability in the metabolite profiles by putting plants under many different stress conditions. Transcriptome data are then compared with metabolome data to see to what extent changes in one are coupled with changes in the other. Willmitzer also described ideas for the diagnostic use of metabolomics. One proposed application is to predict the biomass of a plant by simply measuring its metabolic composition.

Plant growth and productivity are greatly affected by abiotic stresses such as drought, salinity, and temperature. Dorothea Bartels (Max-Planck-Institut für Zuchtungsforschung, Köln, Germany) uses the 'resurrection' plant *Craterostigma plantagineum* as a model system to investigate the molecular and biochemical basis of tolerance to desiccation. *C. plantagineum* belongs to the Linderniae, a plant tribe comprising both desiccation-tolerant and desiccation-intolerant species. Although the geographical distributions of both types overlap, phylogenetic studies have shown that the desiccation-tolerant species form a monophyletic group. Comparative studies of these species have identified conserved regulatory elements and very recently evolved transposable elements in stress-relevant genes, providing clues for the evolution of drought resistance. Montserrat Pagès (Institut de Biologia Molecular de Barcelona, Spain) reported the identification and characterization of MKP5, a mitogen-activated protein kinase (MAPK) involved in seedling establishment and abscisic acid (ABA) signaling. The phytohormone ABA plays a crucial role in adaptive stress tolerance in plants. Seeds over-expressing an MKP5-GFP fusion protein show phenotypic alterations, including ABA, salt hypersensitivity, and slight drought tolerance and a severe growth arrest after germination. This

development arrest is a result of inefficient lipid reserve mobilization and is rescued by providing a source of exogenous sugar in the growth medium. Molecular analyses revealed upregulation of ABA signaling genes in those plants. These data suggest that MKP5 is a potential regulator of the ABA/stress signalling pathway and present new evidence implicating a link by MAPK activities in the control of seedling development and survival under stress conditions.

In the signal transduction network that leads from the perception of stress signals to the expression of stress-responsive genes, transcription factors play an essential role. As discussed by Chiara Tonelli (Università degli Studi di Milano, Italy) one of the MYB family of transcription factors, AtMYB60, is specifically expressed in stomatal guard cells and its expression is downregulated during drought. Tonelli reported a null mutation in AtMYB60 that results in a reduction in stomatal opening and decreased water loss, even under normal conditions, thus confirming its role. Another MYB transcription factor, AtMYB90, is upregulated in response to drought and salt stress, and she described how transgenic plants overexpressing AtMYB90 showed enhanced salt tolerance compared to wild-type plants. These findings suggest that modulation of such transcription factors might open up new possibilities for engineering plants that can better survive drought and salt stress.

Instead of abiotic stresses, Jeff Dangl (University of North Carolina, Chapel Hill, USA) focused on biotic stresses. Many plant pathogens impair plant growth and reproduction. As one of the ways of countering pathogen attack, plants have evolved a class of disease-resistance genes that encode proteins containing nucleotide-binding sites and leucine-rich repeat regions - the NB-LRR class of proteins. Dangl presented the 'guard' hypothesis, which suggests that many NB-LRR proteins might be activated indirectly by pathogen-encoded effector molecules, and not by direct recognition of the pathogens themselves, and gave examples from the response of *Arabidopsis* to the pathogenic bacterium *Pseudomonas syringae*. In particular, Dangl discussed how three different pathogen virulence factors target the *Arabidopsis* RIN4 protein, a regulator of basal host defense responses. Manipulation of RIN4 is sensed by two different plant disease resistance proteins. In contrast, Regine Kahmann (Max-Planck Institut für Terrestrische Mikrobiologie, Marburg, Germany) discussed how the fungal pathogen *Ustilago maydis* (the cause of corn smut) tries to suppress or outsmart the plant's defense responses and on the one hand this fungus actively detoxifies reactive oxygen species via a redox-controlled regulatory system, on the other hand a set of novel secreted proteins is needed to avoid plant defenses. One of these proteins is already required prior to entry, one is needed during entry and three are employed at later stages of fungal development in the host. A deeper understanding of plants' immune defenses will be crucial in the improvement of crops for food, fiber and biofuel production.

Although most of the novel insights presented during the meeting were obtained by classic molecular genetic approaches, systems-biology approaches are slowly becoming more common, although it will probably be quite some time before these have found their way to most labs. Nevertheless, a detailed systems-biological understanding of plant growth and development and a better knowledge of how plants deal with different forms of stress will offer many perspectives to improve plant yield and biomass production.