

literature focus

A shield against the sun

Niyogi, K.K., Grossman, A.R. and Björkman, O. (1998) *Arabidopsis* mutants define a central role for the xanthophyll cycle in the regulation of photosynthetic energy conversion, *Plant Cell* 10, 1121–1134

Too much light can damage plants, as absorption of excessive light energy causes an oxidative stress for the photosynthetic apparatus and reduces photosynthetic efficiency. Almost all photosynthetic eukaryotes are able to protect themselves against excess light by using the light harvesting complexes (LHC) associated with PSII to dissipate energy in the form of heat. This process is called non-photochemical quenching (NPQ) of chlorophyll fluorescence and is triggered by an increase in the *trans*-thylakoidal (Δ pH) proton gradient.

In this paper, the authors investigated the role played by the xanthophyll cycle during NPQ. Using a chlorophyll fluorescence video

imaging system, they were able to isolate several *Arabidopsis* mutants with altered NPQ activity. Two of these mutants, *npq1* and *npq2* were then characterized: *npq1* lacks violaxanthin de-epoxidase activity, whereas *npq2* lacks zeaxanthin epoxidase activity.

Induction of NPQ in excessive light is severely impaired in *npq1*, indicating that de-epoxidation of violaxanthin to antheraxanthin and zeaxanthin is necessary for most of the NPQ in *Arabidopsis*. This perturbation in NPQ activity in *npq1* is associated with greater sensitivity to photoinhibition. In the *npq2* mutant, NPQ induction is faster than in wild type and decreases more slowly. Previous studies

indicated that the *aba1* mutant, which is allelic to *npq2*, does not show any increased sensitivity to photoinhibition with respect to wild type.

This raises the question, if zeaxanthin is necessary for the induction of the NPQ (as shown by the *npq1* mutant) and constitutively high levels of zeaxanthin (as in *npq2*) do not appear to modify the sensitivity to photoinhibition with respect to wild type, then what is the advantage of a xanthophyll cycle? The authors show that more energy is dissipated by the *npq2* mutant at moderate, sub-saturating light intensities; thus an enhanced NPQ could decrease the efficiency of photosynthesis in limiting light conditions.

One MADS-box gene does not a flower make

Tandre, K., Svenson, M., Svensson, M.E. and Engström, P. (1998) Conservation of gene structure and activity in the regulation of reproductive organ development of conifers and angiosperms, *Plant J.* 15, 615–623

Rutledge, R., Regan, S., Nicolas, O., Fobert, P., Côté, C., Bosnich, W., Kauffeldt, C., Sunohara, G., Séguin, A. and Stewart, D. (1998) Characterization of an *AGAMOUS* homologue from the conifer black spruce (*Picea mariana*) that produces floral homeotic conversions when expressed in *Arabidopsis*, *Plant J.* 15, 625–634

The flowers of angiosperms and cones of conifers look very different, but they perform the same reproductive role, and homologous genes are expressed in both flowers and cones. This is illustrated in these recent papers, in which two different spruce homologues of the MADS-box gene *AGAMOUS* have been functionally analyzed in transgenic *Arabidopsis* plants. MADS-box proteins are transcription factors involved in developmental regulation. According to the ABC model of flower development, MADS-box proteins of three classes, A, B and C, act together to regulate organ formation in the angiosperm flower.

Tandre *et al.* and Rutledge *et al.* found that constitutive expression of the *AGAMOUS* homologues from conifers (*DAL2* from Norway spruce and *SAG1* from black spruce, respectively) in *Arabidopsis*, induced the same aberrations in flower development (including homeotic transformation of floral organs) as seen for the ectopic expression of *AGAMOUS* and other angiosperm C class genes. The two spruce genes are highly homologous to *AGAMOUS*, and *DAL2* groups with C class genes in phylogenetic analyses. In addition,

the expression patterns of the two genes are consistent with a role in determining organ identity in the cone.

Thus, these spruce genes are both structurally and functionally related to the angiosperm class C MADS-box genes. Their effects in transgenic *Arabidopsis* plants indicate that the encoded proteins can interact with other regulatory proteins in the angiosperm, suggesting that these mechanisms are highly conserved – even between such distantly related plant groups. As Rutledge *et al.* point out, this should make it possible to study the function of other putative regulatory proteins from conifers in *Arabidopsis*. This would be a great advantage in furthering studies on

conifer development and could be conducted while waiting for a transgenic spruce to 'flower'.



This month's **literature focus** articles were contributed by Irene Murgia and Christina Johansson. We are keen to expand coverage of interesting research papers by selecting from as wide a range of primary journals as possible. So, whether your interest is in ecology, genetics, or palaeobotany, if you have read a recent research paper that you think deserves more attention, then please contact the editor (plants@elsevier.co.uk).