Overexpression of Talin Alters Auxin-Mediated Responses
The polar transport of auxin has been identified as a key process in axis formation and the developmental patterning of plants. The polarity of transport depends on transcellular gradients of auxin-efflux carriers that continuously cycle between plasma membrane and intracellular compartments. Although it has been proposed that this cycling depends on actin filaments, the role of actin in the polarity of auxin transport is far from clear. By means of overexpressing the actin-binding protein talin, Nick et al. (pp. 155–167) have generated transgenic rice (Oryza sativa) lines in which actin filaments are bundled to variable extents. They show that the bundling of actin filaments is directly correlated with impaired gravitropism and a reduction in the polar transport of auxin. In support of the idea that interactions of auxin and actin are bidirectional, the authors were able to restore a normal actin configuration by the addition of exogenous auxins. When the actin configurations were restored, so too were gravitropism and polar auxin transport. This rescue is mediated by indole-3-acetic acid and 1-naphthyl acetic acid, but not by 2,4-dichlorophenoxyacetic acid, an auxin that does not exhibit polar transport. The authors interpret these findings in the context of a self-referring regulatory circuit between polar auxin transport and actin organization. This circuit might contribute to the self-amplification of auxin transport that is a central element in current models of auxin-dependent patterning.

Carotenoid Biosynthesis in Transplastomic Tomatoes
Carotenoids are isoprenoid molecules that aid in the harvesting of light during photosynthesis and in protecting plants against light stress. Carotenoids are also essential components of the human diet, providing the body with β-carotene, the precursor of vitamin A. In tomato (Solanum lycopersicum) fruits, carotenoids accumulate in specialized plastids, the chloroplasts. Although the enzymology of the carotenoid biosynthetic pathways in plants is now reasonably well understood, questions still remain about the regulation of carotenoid biosynthesis and what limits total carotenoid accumulation in fruit chromoplasts. Apel and Bock (pp. 59–66) have introduced the lycopene β-cyclase genes from the eubacterium Erwinia herbicola and the higher plant daffodil (Narcissus pseudonarcissus) into the tomato plastid genome. Whereas the bacterial gene elicited no significant change in carotenoid accumulation, expression of the lycopene β-cyclase from the higher plant daffodil not only triggered efficient lycopene-to-violaxanthin A conversion, but also led to a massive increase in total fruit carotenoid content. A plausible explanation of these findings could be that the daffodil enzyme is less susceptible to negative feedback regulation by β-carotene than the bacterial enzyme. The expression of the daffodil lycopene β-cyclase also resulted in altered carotenoid composition in leaves. The levels of zeaxanthin and violaxanthin were increased at the expense of lutein. Thus, there appears to be substrate competition between lycopene β-cyclase and lycopene ε-cyclase. The presence of elevated amounts of lycopene β-cyclase, therefore, directed more lycopene to be channeled into the zeaxanthin/violaxanthin pathway of carotenoid biosynthesis. This alteration in flux through the pathway, however, did not result in any phytotypic effect, which is not unexpected: Lutein has previously been shown to be dispensable for photosynthesis in higher plants. These results provide new insights into the regulation of carotenoid biosynthesis and demonstrate the potential of plastid genome engineering for the nutritional enhancement of food crops.

Mechanosensing by Poplar
The modification of growth by external mechanical loading is known as thigmomorphogenesis. External mechanical loadings cause a decrease in elongation and a stimulation of diameter growth. Trees, however, can become acclimated to mechanical stress when they are repetitively loaded, and it appears that it is mechanical strain (i.e. the relative length changes of each element) that the plants are sensing rather than mechanical stress per se. Thus, the study of the effect of a single mechanical loading appears to be a
prerequisite for studying the effect of different loading frequencies. A biophysical model—the “sum-of-strains” model—has been put forth to explain mechanosensing. This hypothesis proposes that mechanosensitive tissue produces a secondary signal proportional to the strain experienced by the individual elements. The thigmomorphogenic signal thus produced is proportional to the sum of the applied strains, and this sum provides a quantitative model of the integrated mechanical stimulus on the plant. Coutand et al. (pp. 223–232) employed a bending device to study stem responses over a range of strains in poplar (Populus tremula × alba). In particular, they have assessed the sum-of-strains model by quantifying short-term local responses of poplar at two spatial scales: the whole organ modification of stem diameter growth and the cellular expression of the mechanosensitive gene PtaZFP2. They report that a single bending episode altered plant diameter growth and increased the relative abundance of PtaZFP2 transcripts. Moreover, the maximal diameter growth rate reached after bending and the relative abundance of PtaZFP2 mRNAs were linearly correlated with the integrals of longitudinal strains. Thus, the sum-of-strains model of mechanosensing is applicable for local responses at two scales: diameter growth and gene expression.

A Nitrate Transceptor?

In addition to serving as a major plant nutrient, nitrate also acts as a signal. When plants are exposed to nitrate, genes in the nitrate assimilation pathway are rapidly induced as are other genes required for reprogramming carbon metabolism and providing chemical energy for reduction and assimilation. Transcriptome analyses have shown that more than 1,500 genes are induced or repressed by nitrate within 20 to 180 min of treatment. The nitrate transporter gene NRT1.1 has also been implicated in nitrogen regulation. A transcriptome analysis using serial analysis of gene expression showed that about 300 genes were misregulated in nrt1.1 mutant roots. However, because NRT1.1 functions as a nitrate transporter, it is difficult to distinguish between its proposed regulatory and transport functions. To shed light on this question, Wang et al. (pp. 472–478) used a genetic screen that employed a nitrate-inducible promoter fused to the yellow fluorescent protein marker gene YFP to identify nitrate regulatory mutants of Arabidopsis. Two mutations mapped to a region containing the NRT1.1 (CHL1) nitrate transporter gene. These mutations were shown to disrupt nitrate regulation of three well-known nitrate-responsive genes. However, since NRT1.1 encodes a nitrate transporter, it is possible that the loss of nitrate induction in the nrt1.1 mutants is due to reduced nitrate uptake. To test this idea, nitrate induction of a nitrate-inducible gene in the wild type and the two nrt1.1 mutants were assayed at various concentrations of nitrate in the presence of ammonium. The induction of nitrate-regulated genes was virtually abolished in both mutants at all nitrate concentrations tested. True, nitrate accumulation was lower in the mutants, but the amount of accumulation was still substantial enough (36%–77% of wild type) to support nitrate induction. Thus, the loss of nitrate induction in the two nrt1.1 mutants was not explicable in terms of reduced nitrate uptake. These results strongly support the model that NRT1.1 acts as a nitrate regulator or sensor in Arabidopsis. The most consistent model to explain all the published results and the present findings is that NRT1.1 senses nitrate directly and thus acts as a nitrate transceptor. Transceptors, which are transporters that also act as sensors, have been described in yeast. If NRT1.1 is in fact a transceptor, it should be possible to isolate mutants that separate the transport from sensing functions.

Polyphenoloxidase and Latex Coagulation

Latex, a milky sap that coagulates upon exposure to air, is produced by more than 12,500 plant species spanning 20 families. Latex is a complex mixture of proteins, carbohydrates, oils, secondary metabolites, and rubber that deter herbivores and protect wound sites against infection. The latex produced by Taraxacum kok-saghyz (Russian dandelion) is a good source of rubber and was investigated as an alternative to Hevea brasiliensis for natural rubber production during World War II until it was deemed that its rapid coagulation during extraction hampered its efficient utilization. The latex secreted by Taraxacum officinale (common dandelion) and T. kok-saghyz are also rich in polyphenols. The rapid wound-induced browning of dandelion latex suggests that it may contain phenoloxidizing enzymes. Wähter et al. (pp. 334–346) present a comprehensive analysis of the major latex proteins from T. officinale and T. kok-saghyz, as well as enzymatic studies showing that polyphenoloxidase (PPO) is responsible for latex browning. PPOs are plastid-localized copper metalloenzymes that catalyze the oxidation of o-diphenols to o-diquinones. By means of electrophoresis and N-terminal sequencing, the authors show that the most abundant proteins in the aqueous latex fraction are three PPO-related proteins generated by the proteolytic cleavage of a single precursor (pre-PPO). Silencing the PPO gene by constitutive RNA interference in transgenic plants reduced PPO activity compared to wild-type controls, allowing T. kok-saghyz RNA interference lines to expel 4 to 5 times more latex than controls. The fluidity of latex in silenced plants showed a strong correlation between residual PPO activity and the coagulation rate, indicating that laticifer-specific PPO plays a major role in latex coagulation and wound sealing in dandelions. In contrast, very little PPO activity is found in the latex of H. brasiliensis, suggesting that latex proteins have functionally diverged during plant evolution.

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