A Possible Strategy for Increasing Met Titer in Seeds

Met is a nutritionally essential sulfur-containing amino acid found at low levels in plants and in their seeds. It often limits the nutritional value of crop plants as a source of dietary protein for humans and animals. In plants, Met plays key roles in protein synthesis and mRNA translation, and regulates indirectly a variety of cellular processes through its main catabolic product S-adenosyl-Met (SAM). SAM serves as the precursor for the synthesis of the plant hormone ethylene, polyamines, and biotin, and donates a primary methyl group that is essential for methylation reactions involved in a variety of developmental processes in plant cells. Genetic and biochemical studies suggest that in seeds, Met can be synthesized de novo as in vegetative tissues via the classical Asp family pathway by the activity of its main regulatory enzyme, CYSTATHIONINE-γ-SYNTHASE (CGS). However, isotope-labeling experiments suggest that Met can be synthesized in seeds through an alternative pathway by which Met produced in vegetative tissues is converted to S-methyl-Met (SMM) that is then transported via the phloem into the reproductive tissues, where it is converted to Met. Cohen et al. (pp. 1322–1333) have previously produced transgenic Arabidopsis (Arabidopsis thaliana) RNAi seeds with lower transcript expression of AtCGS and found unexpectedly that the seeds accumulated significantly higher levels of Met compared with controls. Using radiolabels, the authors now show that SMM synthesized in the rosette leaves of the RNAi plants significantly contributed to the accumulation of Met in their seeds at late stages of development. Seed-specific repression of AtCGS in RNAi seeds triggered the induction of genes operating in the SMM cycle of rosette leaves, leading to elevated transport of SMM toward the seeds, where higher reconversion rates of SMM to Met were detected. The results of this study suggest new strategies for improving Met contents in seeds.

ABA Is Required for Cuticle Formation Independent of Water Stress

The waxy cuticle, a key barrier to desiccation and pathogen entry, is a dynamic structure, the composition, area, permeability, and thickness of which can change in response to environmental conditions. For example, water deficit in Arabidopsis triggers an increase in the accumulation of both cutin monomers and waxes, resulting in a thicker, less permeable cuticle. While the abiotic stress-related hormone abscisic acid (ABA) is known to up-regulate wax accumulation in response to drought, the hormonal regulation of cuticle biosynthesis during organ ontogeny is poorly understood. To address the hypothesis that ABA also mediates cuticle formation during normal shoot ontogeny, Martin et al. (pp. 1384–1398) assessed the effect of ABA deficiency on cuticle formation in three ABA biosynthesis-impaired tomato (Solanum lycopersicum) mutants: notabilis, flaca, and sitiens. The severity of the phenotypes of these mutants correlates with the ABA concentrations in their shoots: notabilis had the mildest phenotype and the highest level of ABA, while sitiens had the most severe phenotype and the lowest ABA levels. The mutant leaf cuticles were thinner, had structural abnormalities, and had a substantial reduction in levels of cutin. The exogenous application of ABA partially rescued these phenotypes, confirming that they were a consequence of reduced ABA levels. The ABA mutants also showed reduced expression of genes involved in cutin or wax formation. This difference was again countered by exogenous ABA, further indicating regulation of cuticle biosynthesis by ABA. Fruit cuticles were less affected by the ABA-associated mutations, suggesting that ABA action influences cuticle formation in an organ-dependent manner. These results suggest dual roles for ABA in regulating leaf cuticle formation: one that is fundamentally associated with leaf expansion, independent of abiotic stress, and another that is drought induced.

Is All Root Hair Development the Same?

Root hairs are long tubular extensions of root epidermal cells that greatly increase the root surface area and thereby assist in water and nutrient absorption. Root hairs are found in nearly all vascular plants, including angiosperms, gymnosperms, and lycophytes, and they exhibit similar cellular features, suggesting a common evolutionary origin. However, different plant species are known to vary in their root hair distribution patterns and their root hair morphology, implying that genetic differences exist in root hair development programs. Root hairs have been studied intensively in Arabidopsis. In particular, molecular genetic analyses have led to the identification of numerous root hair genes, which provide insight into the mechanisms of Arabidopsis root hair development. Root hair-bearing cells in Arabidopsis are specified by a set of early acting patterning genes that generate a cell position-dependent distribution of root hair cells and nonhair cells via a complex transcriptional regulatory network. To understand the extent to which this program might operate in other plants, Huang et al. (pp. 1697–1712) conducted a large-scale comparative analysis of root hair development genes from diverse vascular plants, including eudicots, monocots, and a lycophyte. Combining phylogenetics and transcriptomics, the authors have discovered conservation of a core set of root hair genes across all vascular plants, which may derive from an ancient program for unidirectional cell growth co-opted for root hair development during vascular plant evolution. Interestingly, they also discovered diversification in the structure and expression of root hair development genes, relative to other root hair- and root-expressed genes, among these species. The greatest divergence appears to have occurred in the composition and expression of genes used for root hair patterning, suggesting that the Arabidopsis transcriptional regulatory mechanism is not shared by other species. Altogether, this broad analysis of gene expression in a single cell type across multiple species provides new insight into the conservation and diversification of plant cell differentiation programs in vascular plants.

Auxin Regulates Growth of a Characean Alga

Auxin regulates many aspects of growth and development in land plants,
but the origin and evolution of auxin signaling and response mechanisms remain largely unknown. Genome analyses of the moss Physcomitrella patens revealed the presence of the principal gene families involved in auxin homeostasis and signaling in tracheophytes, suggesting that the last common ancestor of land plants had already acquired the core auxin machinery of land plants. However, as we peer further back into phyllogenetic time, things get murkier. To address this knowledge deficit, Ohtaka et al. (pp. 1621–1632) analyzed auxin responses in the charophyte alga Klebsormidium nitens, whose ancestor diverged from a green algal ancestor during the evolution of land plants. The authors have previously identified gene homologs for several auxin-biosynthesis and auxin-signaling-related factors (IAA, YUCCA, PIN, AUX/LAX, and ABP1) in K. nitens; furthermore, the auxin indole-3-acetic acid (IAA) has been detected in K. nitens. On the other hand, a draft genome sequence of the moss K. nitens analyzed auxin responses in the charophyte alga Klebsormidium nitens, whose ancestor diverged from a green algal ancestor during the evolution of land plants. The authors now report that exogenous TIR1-Aux/IAA-ARF-mediated auxin-biosynthesis and inhibitors of polar auxin transport. Moreover, exogenous IAA rapidly induced expression of the LATERAL ORGAN BOUNDARIES-DOMAIN transcription factor. These results suggest that K. nitens has acquired the part of the auxin system that regulates transcription and cell growth without the requirement for the central players that govern auxin signaling in land plants.

**Phenotyping Water Deficit Acclimation Responses**

Water deficit (WD) is one of the main environmental stress factors affecting crops and global food security. Acclimation to WD, however, enables plants to maintain growth under unfavorable environmental conditions. To shed light on the molecular mechanisms underlying WD acclimation, Rymaszewski et al. (pp. 1913–1930) investigated the natural variation of long-term acclimation to moderate and severe soil WD in 18 Arabidopsis accessions using PHENOPSIS, an automated phenotyping platform. Studies of plant acclimation to WD are labor intensive because they require frequent monitoring and correction of soil water content. Thus, it is essentially impossible to manually perform acclimation experiments on multiple plants at the same time. For plants grown in pots, this problem is solved by plant phenotyping platforms such as PHENOPSIS, which enable automatic maintenance of soil water content and automated measurements of multiple plant traits. Using this technology, the authors investigated the long-term acclimation to constant WD at the morphophysiological and molecular levels in 18 Arabidopsis accessions isolated from different natural habitats. These accessions were chosen for study because they displayed differences in the transcript level of the drought response-related marker ANNEXIN1 in the absence of stress treatments. Plants were subjected to two severities of constant WD, in addition to well-watered controls. The authors measured a large subset of plant traits related to plant growth and water use to analyze for WD effects. In parallel, they performed expression analyses of a set of 16 genes related to physiological responses to WD. Contrary to most published studies, the transcript levels were analyzed after a long acclimation period using plant material collected before dawn to minimize the effect of circadian oscillations on transcript levels. As expected, severe WD conditions had a greater effect on most of the measured morphophysiological traits than did moderate WD conditions. The results, however, also revealed that different accessions displayed different types of acclimation responses to long-term WD and that morphophysiological traits, such as rosette area, transpiration rate, and rosette water content, were closely linked to expression levels of certain stress-response genes. The results point to the potential of using gene expression levels as a predictor of morphophysiological WD responses, which would be particularly useful for breeders because it would not be necessary to apply WD during the process of cultivar selection.

**The Role of an Animal-Like Cryptochrome in a Green Alga**

Light is an essential environmental factor for photosynthetic organisms, serving as a source of energy and signal information. To precisely perceive and respond to different wavelengths of light, microorganisms and higher plants have developed different classes of light-sensitive receptors, including phototropins (PHOT), phytochromes, and blue-light-absorbing cryptochromes (CRYs). Four CRYs are encoded in the green alga Chlamydomonas reinhardtii, including an animal-like CRY (aCRY) that also absorbs red light. Light conditions influence the sexual life cycle of Chlamydomonas. Illumination, for example, provokes the transition from pregametes to gametes, which achieve full mating ability. The conversion from pregametes to gametes is mainly influenced by blue light, but to some extent also by red light, indicating the participation of blue and/or red light photoreceptors. These considerations led Zou et al. (pp. 1334–1347) to investigate whether aCRY is involved in the regulation of the sexual life cycle of C. reinhardtii. They show that aCRY plays an important role in the sexual life cycle of C. reinhardtii. The authors demonstrate that aCRY acts in combination with the C. reinhardtii plant cryptochrome (pCRY) as a negative regulator for mating ability, opposite to the function of phototropin. In contrast, aCRY controls the vegetative germination of the alga in a positive manner, similar to the regulation of this process by PHOT and pCRY.

**Peter V. Minorsky**

Division of Health Professions and Natural Sciences

Mercy College

Dobbs Ferry, New York 10522