On the Inside

Further Insights into a Gene for Big Tomatoes (Lycopersicon esculentum)

The quantitative trait locus fw2.2 is responsible for approximately 30% of the difference in fruit size between large-fruited, domestic varieties of tomato and their small-fruited wild relatives. It had been demonstrated previously that fw2.2 encodes for a RAS-like G protein and is associated with altered cell division in ovaries. Although increased fruit size is the most obvious phenotypic manifestation of this quantitative trait locus, in this issue, Nesbitt and Tanksley (pp. 575–583) examine the possibility that the gene may be pleiotropic, possibly effecting other changes in plant morphology or overall fruit yield. Field observations on near-isogenic lines (NILs) differing at the fw2.2 locus revealed that although a small-fruited NIL produced smaller ovaries and fruits as expected, this was compensated for by a larger number of inflorescences and fruits. Overall, however, there was no net change in total fruit mass yield. In a flower removal experiment that controlled for differences in inflorescence size and number, the fruit size remained significantly different between the NILs. These experiments reinforce the conclusion that the primary effect of fw2.2 is in controlling ovary and fruit size, and that other associated phenotypic effects, such as differences in photosynthate partitioning between fruits, are secondary.

Progress in the War on Limp Lettuce (Lactuca sativa)

The wilting and yellowing that accompanies leaf senescence is a major postharvest problem for leafy vegetables such as lettuce.

Water Movement in Early and Late Wood

Although computed tomography (CT) has been used previously to monitor the water distribution in a single tree over periods of days, months, or years, the spatial resolution of these measurements was low. In this issue, Fromm et al. (pp. 416–425) report on the use of a new, high-resolution CT technique to measure the water contents in spruce (Picea abies) and oak (Quercus robur) stems and branches. The spatial resolution (0.1225 mm$^3$) of this new technique is so acute that the water content differences within single annual rings can be studied. The authors report that tree rings of the sapwood show steep water gradients from latewood to earlywood, whereas those of the heartwood reflect water deficiency in both species. Although it had previously been suggested that only the youngest two annual rings of ring porous species are actually involved in water transport, the
high-resolution CT technique reveals similar amounts of water in all the rings of oak sapwood. This indicates at the very least that water storage is important in the entire sapwood (Fig. 2).

**Phosphate Acquisition and Acid Phosphatase**

P is among the most limiting factors for plant growth due to its immobilization by inorganic and organic components in the soil. Anywhere from 30% to 80% of soil P occurs in organic complexes. Under P-deficient conditions, plant roots typically increase the synthesis of acid phosphatases and their secretion into the soil. White lupine (Lupinus albus) is an N₂-fixing legume that is highly efficient at acquiring soil P even though it lacks mycorrhizal associations. One of the major adaptations that facilitate its acquisition of P is the formation of proteoid roots (cluster roots) under low P conditions. Proteoid roots are specialized sites for the production and secretion of both organic acids such as malate and citrate, and acid phosphatase. In this issue, Miller et al. (pp. 594–606) characterize the secreted acid phosphatase and its gene from white lupine. The secreted acid phosphatase is a glycoprotein with broad substrate specificity. It appears to be encoded for by a single gene containing seven exons. The putative 5’-upstream promoter contains a 50-bp region having 72% identity to an Arabidopsis promoter that is responsive to low P conditions. The authors propose that the phosphatase promoter and targeting sequence may be useful tools for genetically engineering important proteins from plant roots.

**Did Higher Plants Inherit Their Cellulose Synthase from Cyanobacteria?**

Cyanobacterial extracellular polysaccharides are involved in a wide range of functions including desiccation tolerance, protection from UV light, adhesion to substrates, as well as motility. Although cellulose biosynthesis among the bacteria has been suggested previously, Nobles et al. (pp. 529–542) provide conclusive evidence of the widespread occurrence of cellulose in the extracellular polysaccharides of these organisms. Based on the results of x-ray diffraction, electron microscopy, and cellubiohydrolase-gold labeling experiments, evidence for cellulose synthesis is reported in nine cyanobacterial species representing three of the five major groups of cyanobacteria. The amino acid sequences of the cellulose synthase A (CesA) enzymes from higher plants revealed greatest homology to putative cellulose synthases from *Anabaena* sp. and *Nostoc punctiforme*. Phylogenetic analyses indicate that the cyanobacterial cellulose synthases share a common branch with the CesA proteins of higher plants in a manner similar to the relationship observed between cyanobacterial and chloroplast 16S rRNAs, indicating that plants may have originally obtained CesA by lateral transfer from cyanobacteria. Because no sequences with similarity to cellulose synthase have been reported in the genomes of chloroplasts or cyanelles to date, translocation of the gene to the nucleus must have occurred relatively early in the evolution of the green algae.

**Genomics of Arabidopsis Ribosomal Protein Genes**

The eukaryotic ribosome is typically a complex structure composed of four rRNAs and about 80 ribosomal proteins (r proteins). In contrast to the information available on r proteins and their corresponding genes in prokaryotes and a few eukaryotic models (rats and yeast), much less is known about the molecular biology of r proteins in plants. In this issue, Barakat et al. (pp. 398–415) identify 249 genes (including some pseudogenes) corresponding to 80 (32 small subunit; 48 large subunit) cytoplasmic r-protein types in Arabidopsis. None of the r-protein genes are single copy and most are encoded by three or four expressed genes, indicating substantial internal duplication of the Arabidopsis genome. An examination of the frequency of expressed sequence tags for the different r-protein gene family members and reverse transcriptase-PCR analysis of several r-protein gene families demonstrated differential patterns of gene expression with no clear relationship between expression levels and gene number. The identification of the r-protein genes and the determination of their primary structure and organization constitutes an important first step in determining their biological roles, the mechanisms controlling their expression, and the molecular structure of ribosomes in plants.

Peter V. Minorsky
Department of Biology
Vassar College
Poughkeepsie, NY 12604