Flowering: A Role for DNA Topoisomerase

Transitions to flowering occur in response to multiple internal and external cues, including photoperiod, vernalization, GA, temperature, and an autonomous pathway. In Arabidopsis (Arabidopsis thaliana), these various cues by way of their respective signal transduction pathways eventually regulate the expression of two major floral pathway integrators, SUPPRESSOR OF OVEREXPRESSION OF CONSTANS1 and FLOWERING LOCUS T, which in turn activate floral meristem identity genes, such as APETALA1 and LEAFY, to transform a vegetative shoot meristem into an inflorescence meristem. Gong et al. (pp. 642–654) now report on a novel role for DNA topoisomerase Iα (TOP1α) in controlling floral initiation in Arabidopsis. DNA topoisomerases are essential enzymes that mediate proper DNA topology by resolving unfavorable DNA supercoils, knots, and other over-wound intermediates accumulated during replication and transcription. In Arabidopsis, the only two type I topoisomerase genes, TOP1α and TOP1β, are tandemly linked loci on chromosome 5, and their encoded proteins share more than 60% similarity. Down-regulation of TOP1β does not display observable phenotypes, whereas loss of function of TOP1α affects primordium initiation in shoot apical meristems and floral meristems, resulting in abnormal phylotaxis and plant architecture. The authors report that the loss of function of TOP1α results in early flowering under both long and short days. This is attributed mainly to a decrease in the expression of a central flowering repressor, FLOWERING LOCUS C (FLC), and its close homologs during the floral transition. TOP1α physically binds to the genomic regions of FLC and its homologs and promotes the association of RNA polymerase II complexes to their transcriptional start sites. These effects may facilitate the expression of key flowering repressors to prevent precocious flowering in Arabidopsis.

A Novel GA Receptor Agonist

GAs are tetracyclic diterpenoid carboxylic acids that are important growth regulators in higher plants. The active forms of gibberellin (GA3, GA4, GA5, and GAs) control various developmental processes in plants, including seed germination, stem elongation, and flowering. In agriculture, GAs are used as plant growth promoters, whereas GA biosynthesis inhibitors (e.g. paclobutrazol) are used to retard or prevent plant growth. However, several factors limit the agronomical application of GA to crops. For example, GA causes some unfavorable changes in plant growth, resulting in taller plants that are prone to lodging. GAs are also expensive to produce. Jiang et al. (pp. 825–835) now report that AC94377, a substituted phthalodimide, mimics the growth-regulating activity of GAs in various plants. AC94377 has an equal or even stronger effect on seed germination and growth than GAs, despite the lack of structural similarity between AC94377 and GAs. The authors confirm that AC94377 exhibits GA-like activities in Arabidopsis, including the promotion of seed germination, hypcotyl elongation, and bolting. They also demonstrate that AC94377 binds to the Arabidopsis GID1 receptor (AtGID1), forms the AtGID1-AC94377-DELLA complex, and induces the degradation of DELLA protein. AC94377 is apparently selective for a specific subtype among Arabidopsis’s three subtypes of AtGID1s, and the selectivity of AC94377 is attributable to a single residue at the entrance to the hydrophobic pocket of GID1. As a bona fide agonist of GID1, AC94377 might potentially be used to develop even more effective agonists or antagonists with selectivity for specific GID1 in structure-activity relationship studies, using an assay system similar to that used in this study.

cis-Cinnamic Acid and Auxin Efflux

Cinnamic acid (CA) is found in plants, both as trans (t)- and cis (c)-isomers, though not in equal concentrations. t-CA is synthesized through the deamination of Phe by PHENYLAMONIA-LYASE, after which it is hydroxylated to p-coumaric acid by CINNAMIC ACID-4-HYDROXYLASE, a key enzyme of the phenylpropanoid pathway. Besides being a crucial intermediate of this pathway, t-CA itself has also been described as a bioactive compound. Depending on the experiment, t-CA

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The Function of Plant Extracellular Vesicles

The extracellular vesicles (EVs) or exosomes of animal cells were originally thought to function as waste disposal systems, but more recent findings indicate that they mediate intercellular communication and are capable of modulating immune responses. Exosomes secreted by immune cells present antigens on their surface and contribute to adaptive immunity by activating T cells. Exosomes also can down-regulate immune cells, facilitate normal growth and development, or promote the spread of tumors and viruses. Exosomes also mediate intercellular communication by shuttling mRNAs and various species of small noncoding RNAs between cells. These molecules remain functional after delivery and can elicit effects in the recipient cell. Plants are also known to produce EVs, particularly in response to pathogen infection. The contents of plant EVs have not been analyzed, however, and their function is unknown. 

Rutter and Innes (pp. 728–741) describe a method for purifying EVs from the apoplastic fluids of Arabidopsis leaves. Proteomic analyses of these EVs revealed that they are highly enriched in proteins involved in biotic and abiotic stress responses. Consistent with this finding, EV secretion was enhanced in plants infected with Pseudomonas syringae and in response to treatment with salicylic acid. These findings suggest that EVs may represent an important component of plant innate immune responses and may mediate intercellular communication in plants.

Molecular Biology of the Weedy Habit

The progress of agricultural biotechnology has been hampered by political, economic, intellectual property, and ecological concerns that have restricted widespread acceptance of genetically modified organism technology. Genetic selection markers are critical components of molecular breeding programs for crop improvement. Selectable markers using chemicals as selection agents that confer resistance to phytotoxic substances such as antibiotics and herbicides have been a particular point of contention with genetically modified organism critics who fear the escape of these transgenes to other organisms. Selectable markers derived from plant genes circumvent the potential risk of antibiotic- or herbicide-resistance gene transfer into neighboring plant species, endophytic bacteria, or mycorrhizal fungi. Toward this goal, Hu and Lagarias (pp. 366–375) have engineered and validated a novel dominant plant gene-based selectable marker cassette consisting of a heat shock-inducible promoter for tight regulation of a phyB allele with a single missense mutation (YHB). Genes encoding both components of this system are already present ubiquitously in plant genomes, including those of crop species. The introduced single missense mutant variants of phyB are thus unlikely to trigger immune responses or other unexpected consequences if/when consumed by humans or livestock. YHB-expressing transformants could be identified by their constitutive photomorphogenic phenotype with short hypocotyls and fully expanded cotyledons that were easily distinguished from a taller lawn of nontransformants. Thus, eYHB-based alleles are robust substitutes for antibiotic/herbicide-dependent marker genes. Moreover, YHB’s intense red fluorescence provides the added benefit of the ability to noninvasively monitor its expression in vivo.

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