

FLOWER DEVELOPMENT

Compounding a raceme

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Although our understanding of the gene networks that control inflorescence development in *Arabidopsis* has been significantly advanced, little is known about the development of more complex inflorescence architecture. Using the pea plant (*Pisum sativum*) as a model, Frances C. Sussmilch, at the University of Tasmania, and colleagues now find that a homologue of the bZIP transcription factor FD, VEGETATIVE2 (VEG2), plays a vital role in compound inflorescence development.

Unlike the inflorescence of *Arabidopsis*, a simple ‘raceme’, peas have secondary inflorescences bearing flowers on lateral branches, known as compound racemes. The researchers focused on two pea mutants, *veg2-1* and *veg2-2*, that exhibit nonflowering and delayed-flowering phenotypes, respectively. The late-flowering *veg2-2* mutant showed abnormal inflorescence and floral morphology. Through genetic mapping and

sequence analysis, they confirmed the *VEG2* gene to be a homologue of *FD*. Examination of the mutant phenotypes and gene expression showed that *VEG2* is expressed in the apex and functions throughout the developmental stages of the compound raceme — that is from flower initiation to secondary inflorescence development.

VEG2 regulates flowering and meristem identity genes as these genes were misexpressed in the *veg2* mutants. The researchers showed that the regulatory effect of *VEG2* on the downstream genes might be mediated through its interaction with the five FT proteins in pea. This significant mechanistic understanding of compound inflorescence development may facilitate the future breeding of legume crop species with modified inflorescence architecture. JL

ROOT DEVELOPMENT

Subterranean specialization

Proc. Natl Acad. Sci. USA <http://doi.org/4qc> (2015)

Existing as they do beneath the surface of the soil, the diverse forms and behaviours of roots are often overlooked. Caroline Gutjahr *et al.* have employed proteomic techniques to illuminate the molecular variations underlying the morphological variety of rice roots and the different ways particular root types respond to arbuscular mycorrhizae.

The authors collected three main root types from rice: crown roots — which connect directly to the stem of the rice plant — as well as large- and fine lateral roots. The roots showed distinct patterns of transcription with over 5,000 genes expressed

at significantly different levels between crown roots and fine laterals. Crown roots produced more transcripts involved in responses to hormones and secondary cell wall metabolism. Lateral roots had higher levels of inorganic-ion transporters showing their greater involvement in nutrient uptake. All root types showed large changes in response to inoculation with the mycorrhizal fungus *Rhizophagus irregularis*. Although less heavily colonized than lateral roots, the crown roots changed the most. The profile of a colonized crown root was more similar to that of a large lateral root than to its former, uncolonized state.

Gutjahr *et al.* provide a detailed picture of the differing character of root types illustrating both the diversity of a plant’s belowground organs and their plasticity in response to the subterranean environment. CS

ECOLOGY

Grassland growth

Ecology <http://dx.doi.org/10.1890/14-1902.1> (in the press)

Human activities have significantly increased the amount of reactive nitrogen in the environment, with consequences for carbon cycling, climate and biodiversity. An analysis of grassland productivity spanning four continents suggests that nitrogen deposition is a key determinant of grassland growth worldwide.

Carly Stevens, of Lancaster University, UK, and colleagues assessed the effect of anthropogenic nitrogen deposition on aboveground grassland productivity, using biomass data collected from 42 sites around the globe and a chemistry transport model. Grassland production increased with nitrogen deposition across sites, rising by 3% for every additional kilogram of nitrogen deposited per hectare per year. Overall, nitrogen deposition explained 16% of the variation in aboveground net primary production. In contrast, mean annual temperature, potential evapotranspiration and elevation each explained just 7% of the variation.

Nitrogen deposition is predicted to rise in many parts of the world over the coming decades. The researchers note that in the absence of other limiting factors, this additional nitrogen could boost the productivity of grasslands, with potential consequences for terrestrial carbon storage. AA

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IMMUNITY

Antagonistic acetylases

Plant Cell <http://doi.org/4sq> (2015)

Cytosolic immune receptors detect the presence of specific effectors secreted by microbes, and induce a potent response to limit the growth and spread of the invading pathogen. However, if too abundant, autoimmune phenotypes such as necrosis and dwarfism may occur. Xin Li and colleagues discover a new mechanism to regulate the stability of one immune receptor called SNC1, through the opposite effects of two N-terminal acetyltransferases in *Arabidopsis*.

A screen designed to isolate enhancers of SNC1-induced autoimmunity leads to a subunit of the N-terminus acetyl transferase complex NatA. The partial loss-of-function allelic mutant exhibits autoimmunity and higher SNC1 accumulation, while a null mutant is lethal. Proteomic, genetic and molecular analyses show that NatA acetylates the first methionine of SNC1, leading to degradation of the protein. When the adjacent second methionine residue is acetylated by the distinct complex NatB, however, the opposite effect is observed: it stabilizes SNC1. Control of the receptor stability by these two antagonistic pathways also modulates immunity.

This balancing act could dynamically adjust other important low-abundance and fast-turnover proteins. The study by Xin Li and co-workers highlights the double role of N-terminal acetylation in protein stability in general, but also specifically in immunity. GT