

ECOPHYSIOLOGY

Root-cluster control

New *Phytol.* <http://doi.org/zjh> (2014)

BYRON LAMONT, CURTIN UNIVERSITY



Densely packed clusters of short, hairy roots enhance nutrient uptake in many plants. A series of controlled-environment experiments suggest that soil bacteria that stimulate plant growth promote production of these root clusters.

Although particularly important in nutrient-scarce environments, the factors that regulate root-cluster formation have remained unclear. Byron B. Lamont, of Curtin University, Australia, and colleagues tested the effects of two species of plant-growth-promoting soil bacteria on cluster formation in representatives of the major root-cluster-bearing families — Fabaceae and Proteaceae — under four nutrient regimes. The bacteria stimulated cluster formation in six of the sixteen treatments. The stimulation, which was underpinned by increases in root length and the number of clusters per unit root length, was more pronounced in the presence of nitrogen.

The researchers attribute the stimulation of cluster formation to bacterial secretion of the plant hormone auxin, known to promote the growth of these root systems. They suggest that the variable response observed stems from bacterial-dependent differences in auxin secretion, and plant-dependent differences in auxin sensitivity. AA

GUARD CELLS

Finding a MATE

Nature Commun. **6**, 6057 (2015)

Stomatal pores allow gas exchange between plant leaves and their environment. They open to allow entry of carbon dioxide for photosynthesis, and close to prevent excessive water loss. Wang Tian and Congcong Hou, of the Capital Normal University, Beijing, and colleagues, describe

how elevated CO₂ concentration is perceived in the guard cells that surround the pore and how this triggers stomatal closure.

Using a genetic screen in *Arabidopsis*, the authors identified the gene *RESISTANT TO HIGH CO₂ 1 (RHC1)*, required for stomatal closure in response to high CO₂ concentration. *RHC1* encodes a multi-antimicrobial extrusion (MATE) protein that interacts with carbonic anhydrase in guard cells. Carbonic anhydrase converts CO₂ to bicarbonate thus linking CO₂ levels to the guard-cell signalling pathway. *RHC1* also represses the activity of HT1, a kinase that negatively regulates the CO₂ response. This relieves HT1-mediated inactivation of OST1, a positive regulator of SLAC1 ion channels, whose activity mediates changes in guard-cell turgor. By heterologous expression of these components in frog oocytes, the authors are able to reconstitute the core molecular pathway that links perception of CO₂ to ion-channel activity.

These findings trace a pathway by which increasing CO₂ in the atmosphere can influence stomatal aperture and gas exchange in plants, thereby connecting photosynthesis to the control of water availability. RP

RICE YIELD

Swelling the grain

Proc. Natl Acad. Sci. USA **112**, 76–81 (2015)

Grain weight is an important component of crop yield. Although a few genes responsible for the grain weight of rice have been found, the precise regulatory mechanisms

underlying this trait remain largely unknown. Now Xianjun Song, of Nagoya University, and colleagues have identified a histone acetyltransferase (OsglHAT1, a chromatin modifier) that controls the grain weight of rice.

The gene encoding OsglHAT1 was pinpointed to a 4-kb region of chromosome 6 by genetic mapping. Transgenic assays confirmed the positive regulatory effects of this gene on grain weight in both rice and *Arabidopsis*. A beneficial allele from the *indica* rice variety Kasalath, increased grain weight and biomass as a result of higher promoter activity and expression levels — compared with the more common allele from the *japonica* variety Nipponbare. OsglHAT1 increases cell numbers and consequent grain length, which facilitates grain filling.

That the underlying molecular mechanism stems from the transcription regulatory effect of OsglHAT1 was suggested by its histone acetyltransferase activity and nuclear localization. Indeed, OsglHAT1 transgenes modulate the expression of a large number of genes, consistently upregulating those involved in the cell cycle.

The beneficial Kasalath allele, present in only a few cultivated varieties, has not been actively explored by human selection. Therefore, its function as a chromatin modifier could be a promising new target for yield improvement in both rice and other crops. JL

Written by Anna Armstrong, Jun Lyu, Richard Pattison and Guillaume Tena.

CELL WALL FORMATION

Xylem differentiation

Nature <http://doi.org/zjj> (2014)

The secondary cell walls of xylem are composed of polysaccharide fibres embedded in a lignin matrix, providing mechanical support for the plant. The chemical composition of this hard shell depends on biosynthetic enzymes regulated by transcription factors. Siobhan Brady, of UC Davis, Samuel Hazen, of UMass Amherst, and colleagues have taken a systems biology approach to decipher the gene network controlling the biosynthesis of this major component of wood. Their analysis links its complex topology to plant responses to external perturbations.

The authors built a map of all protein–DNA interactions between the promoter sequences of the fifty most important xylem-specific genes and hundreds of transcription factors, based on individual assays in yeast. The network is dominated by highly redundant connections, ‘power edges’, between groups of transcription factors and promoters. Multiple feed-forward loops, both directly and indirectly affecting target genes, make for a robust transcriptional network structure. However, abiotic stresses modify specific sub-networks, allowing the plant to precisely adapt the properties of their cell walls to the environment.

This work again shows how a systems biology approach to signalling pathways can bypass the limitations of genetic screens, and so get closer to the true complexity of biological responses. It may also translate into more efficient biofuel crops through cell-wall engineering. GT