PLANT DEVELOPMENT

A TOPLESS
two-step to
polarity

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The familiar architecture of green plants — shoots at the top and roots at the bottom — relies on the correct formation of the apical–basal axis during embryogenesis. Most studies of how this polarity is set up have focused on the initiating role of the hormone auxin, but recent work reveals a second layer of regulation that relies on chromatin modification and transcriptional repression.

Jeff Long and colleagues had previously identified a temperature-sensitive mutation in *Arabidopsis thaliana*, *topless 1* (*tpl1*), that produces a unique phenotype — the shoot pole of the embryo is transformed into a second root. The authors have now looked at the expression of an apical marker, which revealed that although the apical–basal axis is initially set up

in *tpl1* mutants, apical identity is subsequently lost. Mapping of *tpl1* localized the mutation to a gene that shares a similar domain organization with known transcriptional co-repressors. A screen for second-site mutations in *TPL* revealed that changes that are predicted to down-regulate the activity of the protein suppress the *tpl1* phenotype, which the authors conclude must result from a gain of function.

Long and colleagues also carried out a screen for suppressors of *tpl1* at the restrictive temperature. This screen identified mutations in *HAG1*, which encodes the *A. thaliana* homologue of the histone acetyltransferase GCN5 — a protein that is well known in other eukaryotes for its role in transcriptional activation. Interestingly, the co-repressors to which TPL shows similarity collaborate with RPD3-family histone deacetylases (HDACs) to inhibit transcription, suggesting that the regulation of gene expression through modulating histone acetylation might be a key pathway in apical–basal

axis formation. Consistent with this, mutations in *HDA19* — which encodes an RPD3-family HDAC — have phenotypes similar to *tpl1*, and analysis of combinations of *hag1*, *tpl* and *hda19* mutations suggested that TPL and HDA19 regulate an overlapping set of genes.

Altogether, these findings support a two-step model of axis specification in the developing plant embryo: after polarity is initiated by a gradient of auxin, the axis is fixed in place by chromatin-modifying enzymes. The authors propose that transcriptional inactivation by promoter histone deacetylation is required in apical cells to turn off genes that otherwise lead to root development. Identifying the genes that are regulated in this way will provide further insights into how the top and bottom ends of developing plants are allocated their very different fates.

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ORIGINAL RESEARCH PAPER Long, J. A., Ohno, C., Smith, Z. R. & Meyerowitz, E. M. TOPLESS regulates apical embryonic fate in *Arabidopsis*. *Science* **312**, 1520–1523 (2006)