



that are mentioned above: the lower surface of the leaf acquires upper surface-like properties, causing the leaf to roll into a cylinder and look like a trumpet. Genetic epistasis studies that involve *ago1* and genes that are required for organ polarity confirm the involvement of the RNAi pathway, as do expression studies: in *ago1* mutants, *PHB* transcripts are no longer restricted to the upper surface, which indicates that AGO1 normally downregulates *PHB* in the lower surface. The paper also provides

evidence for the specific involvement of miRNAs: in *ago1* mutants, miRNA165 is mislocalized to the upper leaf surface, and so indicates that AGO1 normally functions to regulate miRNA expression and to confine it to the lower side.

These studies back the existence of a causal link between RNAi and the establishment of polarity, and also raise the possibility that miRNAs are a movable developmental signal similar to classical developmental morphogens: for example, both papers show that miRNA forms a gradient in developing leaves, starting at the lower side but slowly accumulating in the remainder of the leaf. The signals that control the expression pattern of the miRNAs, however, remain to be seen.

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### References and links

**ORIGINAL RESEARCH PAPERS** Kidner, C. A. & Martienssen, R. A. Spatially restricted microRNA directs leaf polarity through ARGONAUTE1. *Nature* **428**, 81–84 (2004) | Juarez, M. T. *et al.* microRNA-mediated repression of *rolled leaf1* specifies maize leaf polarity. *Nature* **428**, 84–88 (2004)

**FURTHER READING** Bartel, D. P. MicroRNAs: genomics, biogenesis, mechanism, and function. *Cell* **116**, 281–297 (2004)

#### WEB SITES

**Rob Martienssen's laboratory:**  
<http://www.cshl.org/public/SCIENCE/martien.html>  
**Marja Timmerman's laboratory:**  
<http://www.cshl.edu/public/SCIENCE/timmermans.html>

complexes with the RNA-binding protein Pumilio.

Nanos–Pumilio complexes are known to bind to Nanos-response elements in target mRNAs, repressing their translation. So one future avenue of research will be to identify the mRNAs that are repressed by Nanos–Pumilio in GSCs. It will also be interesting to see how the activities of this intrinsic regulator are integrated with extrinsic signals — and whether it behaves similarly in other stem cells, and other species.

Amanda Tromans, Senior Editor,  
Nature

### References and links

**ORIGINAL RESEARCH PAPER** Wang, Z. & Lin, H. Nanos maintains germline stem cell self-renewal by preventing differentiation. *Science* **19** Feb 2004 (doi:10.1126/science.1093983)

**FURTHER READING** Lin, H. The stem-cell niche theory: lessons from flies. *Nature Rev. Genet.* **3**, 931–940 (2002)

#### WEB SITES

**Haifan Lin's laboratory:**  
<http://linweb.cellbio.duke.edu>



## IN BRIEF

### PLANT DEVELOPMENT

Mutations in the *pale aleurone color1* regulatory gene of the *Zea mays* anthocyanin pathway have distinct phenotypes relative to the functionally similar *TRANSPARENT TESTA GLABRA1* gene in *Arabidopsis thaliana*.

Carey, C. C. *et al.* *Plant Cell* **16**, 450–464 (2004)

This article reports the cloning and characterization of the *pale aleurone color 1* (*pac1*) locus, which regulates the synthesis of anthocyanin in the maize seed. An experimental comparison of *pac1* function and that of similar genes in *Arabidopsis thaliana* and *Petunia hybrida* highlights important differences in how the regulation of this pathway has evolved between monocots and dicots. For example, in monocots such as maize, the regulators of the biosynthetic genes are not under each other's control, as in dicots.

### EVOLUTION

Codon usage between genomes is constrained by genome-wide mutational processes.

Chen, S. L. *et al.* *Proc. Natl Acad. Sci. USA* **101**, 3480–3485 (2004)

In this article, Chen *et al.* use a new method to examine whether mutational forces or coding-region-specific selective forces are most important for shaping genome-wide codon bias. They found that genome-wide codon bias is well characterized by just two parameters — genome G+C content and nearest-neighbour nucleotide bias — and is determined primarily by mutational processes. The selective forces that act on translated sequences are only secondary determinants of codon bias.

### GENOMICS

Community structure and metabolism through reconstruction of microbial genomes from the environment.

Tyson, G. W. *et al.* *Nature* **428**, 37–43 (2004)

Environmental genome shotgun sequencing of the Sargasso Sea.

Venter, J. C. *et al.* *Science* **4** Mar 2004 (doi:10.1126/science.1093857)

Our inability to culture most microorganisms has prevented detailed studies of microbial communities. This problem is solved in two new studies that report shotgun sequencing of microbial communities directly from environmental samples. Tyson *et al.* reconstructed near-complete genomes from two bacterial groups and partial genomes from the three other dominant members of a well-characterized simple microbial community. By contrast, Venter *et al.* got smaller amounts of sequence from at least 1,800 genomes from the Sargasso Sea microbial community. The broader approach of Venter *et al.* identifies numerous new bacterial groups and genes, whereas the intensive genomic characterization of Tyson *et al.* provides insights into the evolution of, and metabolic interactions within, a complete community. The challenge for the future is to obtain such detailed insights into microbial communities as complex as the Sargasso Sea.