

DEVELOPMENTAL GENETICS

Micromasters

New work from Javier Palatnik and colleagues provides the first direct evidence that microRNAs (miRNAs) control aspects of plant development by guiding the cleavage of mRNAs.

Like small interfering RNAs (siRNAs), which are the effectors of RNA interference, miRNAs can bind to complementary mRNAs and silence the genes that encode them. Despite evidence that they can silence plant genes, previously there was no support for any specific biological function for miRNA silencing.

In an *Arabidopsis* developmental mutant (*jaw-D*) that has uneven leaf shape and curvature in adult plants, Palatnik and colleagues identified five *TCP* genes that were downregulated, which were closely related to a snapdragon gene (*CIN*) that is involved in leaf morphogenesis. In all five *TCP* genes, the authors found a motif that was partially complementary to a previously identified plant miRNA and a sequence at the *JAW* locus.

By hybridizing a probe that was based on the *JAW* sequence to a low molecular-mass RNA blot, the authors showed that it encoded a 20-nucleotide miRNA (miR-JAW). To try to understand the interaction between miR-JAW and the *TCP* genes, the authors engineered miRNA-resistant forms of *TCP4*. Constructs with mutant *TCP4* produced stable transcripts that were unaffected by the

co-injection of a *JAW* construct into a heterologous host, unlike wild-type *TCP4* constructs, which led to an accumulation of cleavage products.

The same mutations introduced into *TCP4 in situ* resulted in a range of developmental defects, most of which led to growth arrest at the seedling stage. This clearly showed that miRNA-guided cleavage of *TCP4* is essential for normal plant development.

Neatly completing the circle, the authors then showed that miRNA-resistant *TCP2* could rescue the *jaw-D* phenotype. So, the production of *TCP2* transcripts that are resistant to miRNA-mediated degradation might correct aberrant phenotypes that are associated with lower expression levels of the gene.

As miRNA target sequences were found in *TCP* genes from plants with a range of leaf forms, including lotus and maize, it seems that these micromasters might have a ubiquitous role in controlling leaf development. Perhaps the time is now ripe for a wider search for such motifs to help identify other developmental pathways that could be influenced by miRNAs.

Nick Campbell

References and links

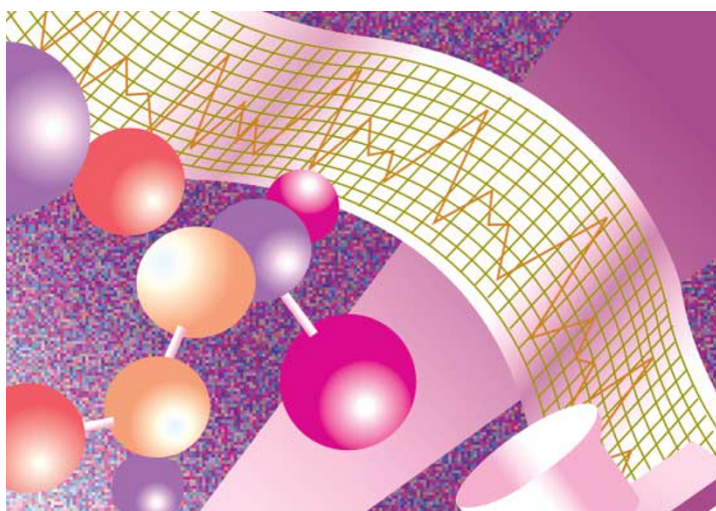
ORIGINAL RESEARCH PAPER Palatnik, J. *et al.* Control of leaf morphogenesis by microRNAs. *Nature* 20 August 2003 (10.1038/nature.01958)

FURTHER READING McManus, M. T. & Sharp, P. A. Gene silencing in mammals by small interfering RNAs. *Nature Rev. Genet.* 3, 737–747 (2002)

WEB SITES

Detlef Weigel's laboratory:
<http://weigelworld.org>

Arabidopsis small RNA project in James Carrington's laboratory:
<http://cgrb.orst.edu/smallRNA/index.html>



IN BRIEF

DEVELOPMENTAL BIOLOGY

Conserved role of *nanos* proteins in germ cell development.

Tsuda, M. *et al. Science* 301, 1239–1241 (2003)

In *Drosophila*, *nanos* encodes an RNA-binding protein that is required maternally for the migration of the primordial germ cells into the gonad. Now, two mouse *nanos* homologues, *nanos2* and *nanos3*, have been cloned. The knockout phenotypes of these two genes — lack of male germ cells in *nanos2*^{-/-} mice and lack of germ cells in both sexes in *nanos3*^{-/-} animals — indicate that despite apparent differences, the mechanism of germ-cell specification is conserved between vertebrates and invertebrates.

DEVELOPMENTAL BIOLOGY

GATA-3: an unexpected regulator of cell lineage determination in skin.

Kaufman, C. K. *et al. Genes Dev.* 17, 2108–2122 (2003)

The GATA-3 transcription factor is known to be required in lymphocyte differentiation. A microarray screen showed that *GATA-3* is also expressed in the inner root sheath (IRS) cells — those that guide the developing hair shaft to the skin surface — early during hair morphogenesis. This evidence, together with the absence of the IRS in *GATA-3*-null mice and the aberrant structure of the mutant hair, points to a new function for *GATA-3* in the differentiation of epidermal stem cells.

EVOLUTION

Parasite selection for immunogenetic optimality.

Wegner, K. M. *et al. Science* 301, 1343 (2003)

Theoretical models predict that the highly polymorphic genes of the vertebrate major histocompatibility (MHC) complex, which help to fight parasite infection, should exist at an intermediate level of diversity: too little diversity would impair pathogen recognition whereas too much would increase the likelihood of reacting against self-peptides. Wegner and colleagues have now tested the theory by infecting stickleback fish of varying levels of MHC diversity with several parasites. As predicted, fish with intermediate MHC diversity levels had the lowest infection rate.

FUNCTIONAL GENOMICS

The human transcriptome map reveals extremes in gene density, intron length, GC content, and repeat pattern for domains of highly and weakly expressed genes.

Versteeg, R. *et al. Genome Res.* 13, 1998–2004 (2003)

The authors construct a new human transcriptome map to physically characterize clusters of highly expressed genes. They find that they are GC rich and contain many SINE but few LINE repeats. Genes that lie within these so-called ridges have shorter introns than genes that lie elsewhere. They also find evidence of clusters of weakly expressed genes, which they call antiridges.