

IN BRIEF

 SMALL RNAs

Small RNA duplexes function as mobile silencing signals between plant cells

Dunoyer, P. *et al. Science* 22 Apr 2010 (doi:10.1126/science.1185880)

Small silencing RNAs in plants are mobile and direct epigenetic modification in recipient cells

Molnar, A. *et al. Science* 22 Apr 2010 (doi:10.1126/science.1187959)

In plants, RNA interference spreads to neighbouring cells and the vasculature through mobile RNAs, but their identity was unclear. Dunoyer *et al.* found that *Arabidopsis* with no Dicer-like 4 (DCL4), which processes 21-nucleotide RNAs, lacked 21-nucleotide RNAs and thus silencing of *SULPHUR* (*SUL*) mRNA (targeted in this system). DCL4 rescue in companion cells (in the phloem) resulted in 21-nucleotide RNA production in leaves, confirming that they are mobile. Molnar *et al.* showed that 24-nucleotide RNAs are also mobile silencing elements. By grafting *Arabidopsis thaliana* roots to shoots they found that the roots accumulated 24-nucleotide RNAs from the shoots and that these mediated epigenetic reprogramming.

 PROTEIN STRUCTURE

G domain dimerization controls dynamin's assembly-stimulated GTPase activity

Chappie, J. *et al. Nature* 28 Apr 2010 (doi:10.1038/nature09032)

Structural basis of oligomerization in the stalk region of dynamin-like MxA

Gaon, S. *et al. Nature* 28 Apr 2010 (doi:10.1038/nature08972)

Two studies provide insight into the structure of the GTPases dynamin and dynamin-like myxovirus resistance protein 1 (MxA). Chappie *et al.* show that G (GTPase) domain dimerization is important for GTPase activity. They used a dynamin GTPase effector domain–G domain fusion, which dimerized in the presence of GTP or a transition mimic; this stabilized the conformation of the flexible switch regions in the catalytic core (required for GTP hydrolysis). GTP hydrolysis disengaged one of the flexible switch regions, leading to conformational changes that break up the dimer and release GDP. Gaon *et al.* find that oligomerization of MxA is important for function. MxA folds into an elongated four-helix bundle, making up the protein stalk. Wild-type MxA assembled as a stable tetramer in a criss-cross pattern in which each stalk contributes three interfaces; mutations in these inhibited oligomerization and MxA function.

 GENE EXPRESSION

Nucleosome-depleted regions in cell-cycle-regulated promoters ensure reliable gene expression in every cell cycle

Bai, L. *et al. Dev. Cell* **18**, 544–555 (2010)

Many promoters have nucleosome-depleted regions (NDRs), but their function in gene expression was unclear. The authors examined the role of NDRs in the expression of the cell cycle gene *CLN2* (activated by SCB-binding factor (SBF)) in *Saccharomyces cerevisiae*. Transcription was activated reliably in every cell cycle when the *CLN2* promoter's SBF-binding site was in an NDR. By contrast, highly variable 'on' and 'off' transcription was seen when the SBF-binding site was in a nucleosome. The authors propose that promoters are found in NDRs when unreliable gene expression may be detrimental to the cell.