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IN BRIEF

RNA WORLD

Sorting of *Drosophila* small silencing RNAs.

Tomari, Y. *et al. Cell* **130**, 299–308 (2007)

Drosophila microRNAs are sorted into functionally distinct Argonaute complexes after production by Dicer-1.

Förstemann, K. *et al. Cell* **130**, 287–297 (2007)

Given their similar features, what is the basis for the different modes of gene regulation by small interfering RNAs (siRNAs) and microRNAs (miRNAs)? Tomari and colleagues showed that *Drosophila melanogaster* siRNAs and miRNAs are actively sorted into distinct complexes that contain different Argonaute (AGO) proteins. This sorting occurs independently of the different biogenesis pathways that are used to produce these two classes of small RNA, and instead depends on the structure of the double-stranded miRNA and siRNA duplexes that are produced as intermediates. Förstemann and colleagues also demonstrated active sorting of siRNAs and miRNAs. They also showed that it is the nature of the AGO complex into which the small RNA is sorted that determines the mode of repression. These results indicate that, in the fly at least, it is the intrinsic structures of siRNAs and miRNAs that determine the mechanism by which their targets are repressed.

MICROBIAL GENETICS

A comprehensive genetic characterization of bacterial motility.

Girgis, H. S. *et al. PLoS Genet.* e154.eor (doi:10.1371/journal.pgen.0030154.eor)

The authors describe a powerful genome-wide approach to identify the genetic bases of complex bacterial phenotypes. They used libraries of transposon-mutagenized cells, enriched them for cells with abnormal phenotypes by competitive selection, and analysed the genetic determinants of the phenotypes by microarray-based genetic footprinting. Analysis of *Escherichia coli* motility through this method revealed more than 95% of the previously known flagellar and chemotaxis genes and more than 30 new genes, some of which had not been characterized before. The authors also show the feasibility of this approach for studying gene-by-gene and gene-by-environment interactions.

GENE REGULATION

MTERF3 is a negative regulator of mammalian mtDNA transcription.

Park, C. B. *et al. Cell* **130**, 273–285 (2007)

Although components of the basal mitochondrial transcription machinery have been defined at the molecular level, the members that fine-tune levels of mitochondrial transcription to modulate oxidative phosphorylation capacity are poorly understood. The authors show that mitochondrial transcription termination factor 3 (MTERF3) functions as a transcriptional repressor — the first example of a mitochondrial protein that acts as a specific repressor of mammalian mitochondrial DNA transcription initiation *in vivo*. The gene is essential — knocking it out in mice is embryonic lethal. Moreover, heart-specific MTERF3 inactivation results in increased transcription initiation and, ultimately, severe respiratory-chain deficiency.