**EVOLUTION**

Cryptic genetic variation promotes rapid evolutionary adaptation in an RNA enzyme

Hayden, E. J., Ferrada, E. & Wagner, A. Nature **474**, 92–95 (2011)

This study gives experimental support to the hypothesis that cryptic variation facilitates adaptation to new environments. Ribozymes that were evolved in vitro under purifying selection to retain native levels of enzymatic activity adapted to a different environment (a new substrate) at a rate proportional to their cryptic variation levels. A sequence comparison of the ribozyme lineages showed that the adaptation was mediated by more than one mutation, either via epistasis or gene-by-environment interactions.

**COMPUTATIONAL BIOLOGY**

Assembly of full-length transcripts from RNA-seq data without a reference genome

Grabherr, M. G. et al. Nature Biotech. 15 May 2011 (doi:10.1038/nbt.1883)

The authors present Trinity, a sensitive program for reconstructing full-length transcriptomes in the absence of a sequenced reference genome. The approach — a three-step process that is based on analysing de Bruijn graphs — was tested on fission yeast, mice and whiteflies and efficiently mapped most of the transcriptome, including alternatively spliced isoforms and transcripts from recently duplicated genes. Unlike previous de novo assembly programs, Trinity was devised specifically for the transcriptome, instead of being adapted from a genome-assembly program.

**MICRORNA**

Identification of a microRNA that activates gene expression by repressing nonsense-mediated RNA decay

Bruno, I. G. et al. Mol. Cell **42**, 500–510 (2011)

This study shows that microRNAs can control the expression of large sets of transcripts by regulating nonsense-mediated decay (NMD). Levels of miR-128, which is specifically expressed in the mammalian brain, increase during development to repress two key NMD components. As a result, a large battery of transcripts involved in neural development is upregulated, as repression of these transcripts by NMD is relieved. This function of miR-128 in regulating NMD is conserved in frogs and chickens.

**EPIGENETICS**

Temporal uncoupling of the DNA methylome and transcriptional repression during embryogenesis

Bogdanovic, O. et al. Genome Res. 2 Jun 2011 (doi:10.1101/gr.114843.110)

Little is known about the role of DNA methylation in non-mammalian vertebrates. These authors profiled this epigenetic mark in Xenopus tropicalis embryos, compared its location with those of key histone modifications and used promoter–reporter constructs to address the relationship between DNA methylation and transcription. Strikingly, DNA methylation and transcriptional repression are correlated in X. tropicalis oocytes and late embryos but not at the blastula or gastrula stage. This suggests that the effect of this mark on gene expression changes during development.