RESEARCH HIGHLIGHTS

IN BRIEF

SMALL RNAS

An epigenetic role for maternally inherited piRNAs in transposon silencing

Brennecke, J. et al. Science 322, 1387-1392 (2008)

In Drosophila melanogaster the offspring of wild-caught males and laboratory-strain females are sterile, but genetically identical offspring from the reciprocal cross are fertile. This phenomenon, called hybrid dysgenesis, is thought to be due to the mobilization of transposable elements in the progeny. This paper shows that maternally inherited small RNAs — piRNAs — can protect offspring by silencing transposons. Both genetic and environmental factors shape the RNA population passed on by the mother and can influence the fate of the offspring.

EVOLUTION

A novel gene family controls species-specific morphological traits in *Hydra*

Khalturin, K. et al. PLoS Biol. 6, e278 (2008)

A family of genes that is unique to the *Hydra* genus has been found to control the morphology of the tentacles of this basal metazoan lineage. Differences in the temporal and spatial expression patterns of these *Hym301* genes between closely related, yet morphologically distinct *Hydra* species are shown to control species-specific tentacle growth. This illustrates how genes without any known homologues in other lineages can generate diversity within a genus, and that such 'orphan' gene families can be responsible for novel morphological features.

AGEING

Telomerase reverse transcriptase delays aging in cancer-resistant mice

Tomas-Loba, A. et al. Cell 135, 609-622 (2008)

Dissecting the role of telomerase in ageing has been problematic, owing to the cancer-promoting activity of this enzyme. A new study circumvents this problem by constitutively expressing the telomerase reverse transcriptase (TERT) component in mice that have been engineered to be cancer-resistant through overexpression of the tumour suppressor proteins p53, p16 and p19ARF. The TERT-overexpressing mice had increased longevity and the authors suggest that the anti-ageing effects of TERT might be mediated by slowing telomere attrition and maintaining the proliferative potential of stem cells.

GENE REGULATION

Single-RNA counting reveals alternative modes of gene expression in yeast

Zenklusen, D. et al. Nature Struct. Mol. Biol. 16 Nov 2008 (doi:10.1038/ nsmb.1514)

According to this study, genes are subject to different modes of regulation that determine the tempo and variability of mRNA output. The authors developed a fluorescence *in situ* hybridization (FISH)-based method to count single mRNA molecules from single yeast cells. Using mathematical modelling to evaluate the kinetics of gene expression, they found that although bursts of transcription occur from some genes — as has been proposed to happen in mammalian cells — other genes are characterized by single, clearly spaced initiation events, leading to lower expression variability.