IN BRIEF

TECHNOLOGY

Conditional mutagenesis in *Drosophila*

Choi, C. M. & Vilain, S. *et al. Science* **324**, 54 (2009)

Although it is relatively straightforward to conditionally knock out genes in several species, notably in mice, analogous techniques in flies are limited by the requirement for mitotic recombination. The development of a new method, called integrase-mediated approach for gene knockout (IMAGO), now allows fly genes to be replaced by any other sequence, in the absence of cell division. The approach, which was tested successfully on the neuronal gene *atonal*, opens the door to studying gene function in postmitotic tissues, and during late differentiation or adulthood.

IMPRINTING

Germline mutation in *NLRP2* (*NALP2*) in a familial imprinting disorder (Beckwith-Wiedemann syndrome)

Meyer, E. *et al. PLoS Genet.* **5**, e10004223 (2009)

Beckwith–Wiedemann syndrome (BWS) is a human congenital overgrowth syndrome resulting from altered expression within an imprinted gene cluster on chromosome 11. These authors identified the first case of BWS caused by a genetic defect in *trans* to this cluster — a frameshift in the nucleotide-binding oligomerization domain protein *NLRP2* on chromosome 19 — that disrupts DNA methylation at the imprinted locus. Mutation of the closely related *NLRP7* has also been linked to epigenetic abnormalities, implicating this gene family in establishing or maintaining genomic imprinting.

SYSTEMS BIOLOGY

Network features of the mammalian circadian clock

Baggs, J. E. *et al. PLoS Biol.* **7**, e1000052 (2009)

An important feature of key biological networks, such as the circadian clock, is robustness to genetic perturbation. In this study, the authors systematically depleted clock components in immortalized human osteosarcoma cells in a dose-dependent manner using small interfering RNA and measured the expression levels of other clock genes. This allowed them to analyse various features of the circadian network — including proportional responses, signal propagation through interacting genetic modules and compensation by gene paralogues — all of which act as a buffering system to maintain the robustness of the circadian circuitry.

GENE REGULATION

Histone modifications at human enhancers reflect global cell-type-specific gene expression

Heintzman, N. D. *et al. Nature* 18 Mar 2009 (doi:10.1038/nature07829)

Although *cis*-regulatory sequences are important in determining specific gene expression states, little is known about the relative contributions of different types of such element. Using global ChIP–chip (chromatin immunoprecipitation and microarray) analysis, this study reveals that enhancers show much greater cell type specificity in histone modification patterns than do promoters and insulators, and that these enhancer patterns correspond to cell type-specific gene expression. The authors also predicted over 55,000 enhancers in just two cell types, suggesting that enhancers make a substantial contribution to expression differences between cell lineages.