IN BRIEF

⮕ CHROMATIN

Role of Jhdm2a in regulating metabolic gene expression and obesity resistance

Tateishi, K. *et al. Nature* 4 Feb 2009 (doi:10.1038/nature07777)

This paper reveals a physiological role for a chromatin-modifying protein — the histone H3 lysine 9 (H3K9) demethylase JHDM2A. Disruption of *Jhdm2a* function in mice led to obesity and hyperlipidaemia. The authors showed that JHDM2A expression is induced by β-adrenergic stimulation and that this leads to direct activation of two genes that are involved in metabolic regulation — peroxisome proliferator activated receptor-α (*Ppara*) and uncoupling protein 1 (*Ucp1*) — by both decreasing levels of H3K9 dimethylation and facilitating the recruitment of transcriptional coactivators.

⮕ HUMAN GENOMICS

Population analysis of large copy number variants and hotspots of human genetic disease

Itsara, A. *et al. Am. J. Hum. Genet.* **84**, 1–14 (2009)

Using genome-wide SNP data from ~2,500 apparently normal individuals, these authors found that large (>100 kb) copy number variants are common in humans and that at least 1% of individuals carry variants longer than 1 Mb. However, individual large variants segregate at low frequencies (0.1–1%) in the general population. The authors also suggest that the anticorrelation between both the size of a variant and its gene density with allele frequency indicates that large variants are generally deleterious and so may contribute to disease phenotypes.

⮕ VIRAL GENETICS

Recombination of retrotransposon and exogenous RNA virus results in nonretroviral cDNA integration

Geuking, M. B. *et al. Science* **323**, 393–396 (2009)

This study reveals that RNA viruses, not just retroviruses, can integrate into the host genome. RNA viruses acquire this ability by recombining with an endogenous retrotransposon. The authors observed *in vitro* and *in vivo* that a mouse RNA virus (lymphocytic choriomeningitis virus) can use the reverse transcriptase and integrase functions of an endogenous retrotransposon (intracisternal A-type particle) to insert a recombinant cDNA sequence into the host genome. This finding raises the need to look closely at endogenous, largely inactive retroviral elements before attempting viral-based gene therapy.

⮕ FUNCTIONAL GENOMICS

Integrating computational biology and forward genetics in *Drosophila*

Aerts, S. *et al. PLoS Genet.* **5**, e1000351 (2009)

A new study shows that integrating genome-wide computational gene prioritization with large-scale *in vivo* genetic screening — termed systems genetics — increases the efficiency of identifying functional genes. The authors combined the ENDEAVOUR-HIGHFLY web resource for gene prioritization with genetic screening of *Drosophila* species mutant, deficiency and RNAi collections, identifying a novel gene interaction network for the *Drosophila* proneural transcription factor Atonal. They then used systems genetics to prioritize the entire *Drosophila melanogaster* genome for 10 canonical biological pathways, creating a publicly available database of prioritized pathway candidates.