IN BRIEF

GENE REGULATION

A stress-responsive RNA switch regulates VEGFA expression

Sarothi Ray, P. *et al. Nature* 21 Dec 2008 (doi: 10.1038/nature07598)

RNA elements, termed riboswitches, that enable gene expression changes in response to stimuli by binding to metabolites have been described in bacteria, fungi and plants. This study identifies for the first time a similar RNA switch in humans, which binds proteins rather than metabolites. This switch, in the 3′ UTR of vascular endothelial growth factor A (*VEGFA*) mRNA, undergoes a conformational change when bound by specific proteins induced by hypoxia or interferon and thereby alters the translation of *VEGFA* in response to stress stimuli.

EPIGENETICS

DNA demethylation in zebrafish involves the coupling of a deaminase, a glycosylase, and Gadd45

Rai, K. *et al. Cell* **135**, 1201–1212 (2008)

Despite growing evidence for a replication-independent (active) mode of DNA demethylation, the mechanism for this remains elusive. These authors report evidence from knockdown and overexpression experiments in zebrafish embryos that indicates that a 5-methylcytosine (5-meC) deaminase (AID) that converts 5-meC to thymine and the G•T mismatch-specific thymine glycosylase MBD4 can act together to carry out regulated DNA demethylation. The action of these two enzymes is promoted by the non-enzymatic factor GADD45. The authors propose a two-step model of demethylation involving base excision.

GENOMICS

Annotating genomes with massive-scale RNA-sequencing

Denoeud, F. et al. *Genome Biol.* **9**, R175 (2008)

This paper describes a method for genome annotation using RNA-Seq (cDNA sequencing using high-throughput, short-read sequencing) that does not rely on *a priori* information about splicing events. Existing methods for inferring exon–intron structure without such information cannot be applied for RNA-Seq. The new method builds candidate exons by mapping reads to the genome. All possible splice junctions between exons are then tested by comparing them with unmapped reads. Applying this approach to the grapevine genome, the authors successfully identified new exons for known loci and generated gene models for previously unannotated genes.

CHROMATIN

Activator control of nucleosome occupancy in activation and repression of transcription

Bryant, G. O. *et al. PLoS Biol.* **6**, e317 (2008)

Nucleosomes are thought to have important functions in transcriptional regulation, but their roles at specific stages of activation and repression are unclear. This study describes a new quantitative micrococcal nuclease protection assay that, for any genomic location, allows the fraction of sites occupied by a nucleosome to be determined at any time point. Using this method, the authors show that in *in vivo* transcriptional activation by the yeast GAL4 protein nucleosome removal is an intial step, and that repression can take place without the replacement of nucleosomes.