IN BRIEF

➔ ADAPTATION

Selective sweeps and parallel mutation in the adaptive recovery from deleterious mutation in *Caenorhabditis elegans*

Denver, D. R. *et al. Genome Res.* 29 Oct 2010 (doi:10.1101/gr.108191.110)

A new study represents the first molecular characterization of adaptive recovery from deleterious mutations in a multicellular eukaryote. The authors used high-throughput sequencing to study the recovery of mutation-accumulation *Caenorhabditis elegans* lines with reduced fitness. After 60 generations, all lines regained wild-type fitness and 28 fixed mutations were detected, indicating that the mutations responsible for recovery were subject to positive selection. The authors suggest that compensatory epistatic interactions between mutations in the recovery lines and the mutation-accumulation lines can restore fitness.

➔ HUMAN GENOMICS

Fine-scale recombination rate differences between sexes, populations and individuals

Kong, A. *et al. Nature* **467**, 1099–1103 (2010)

This paper reports the first human recombination map to be constructed from directly observed recombination events. The authors used SNP data from more than 15,000 parent–offspring pairs to map recombination events down to a resolution of 10 kb. This mapping provides interesting insights into differences in recombination patterns between individuals, between the sexes and between populations. For example, in both males and females, ~15% of recombination hot spots were found to be specific to one sex, and recombination tends to act on different features of genic regions in the two sexes.

➔ GENE EXPRESSION

The honey bee epigenomes: differential methylation of brain DNA in queens and workers

Lyko, F. *et al. PLoS Biol.* **8**, e1000506 (2010)

The authors have examined the distribution of methyl cytosine in the brains of queen and worker honeybees (*Apis mellifera*) to establish whether a unique brain DNA methylome might underlie the diet-controlled difference in behaviour between the two castes. The analysis identified over 550 genes at which methylation patterns differed between the castes; moreover, the methylated sites correlated strongly with splicing sites, suggesting that methylation differences could mediate behavioural differences by modulating alternative splicing.

➔ EVOLUTION

Rapid construction of empirical RNA fitness landscapes

Pitt, J. N & Ferré-D'Amaré, A, R. *Science* **330**, 376–379 (2010)

By using a combination of next-generation sequencing, computational analysis and *in vitro* selection, the authors have generated the first experimental fitness landscape of a catalytic RNA (a ribozyme). They showed that peak fitness is correlated to genotype abundance, and this information was used to quickly generate a detailed fitness map of ~10^7 unique RNA sequences. This detailed fitness map could be used to study host–pathogen interactions or to inform vaccine and drug development.