from *D. simulans*. Among the rapidly diverging candidates (a hallmark of a Dobzhansky–Muller gene) they found *CG18468*; it contained a BESS domain, which mediates protein–protein interactions and is often associated with MADF domains. It turns out that the *Lhr*[1] strain that rescues hybrid incompatibility carries a ~4 kb insertion in the predicted 5′ UTR of *CG18468*, and that transcription of *CG18468* is reduced in this strain.

Barbash and colleagues introduced *D. simulans CG18468* into *D. melanogaster* on an inducible vector. In a series of crosses, they proved that *CG18468* is *Lhr* — a major-effect hybrid-lethality gene. Using an *Hmr* hypomorphic mutation, the authors showed that the hypomorph-mediated rescue of hybrid lethality is suppressed by *Lhr*[1]. Moreover, male hybrids that carry a null *Hmr* mutation are fully viable even when they carry the induced *Lhr* transgene — in other words, the lethal effects of *D. simulans Lhr*[1] require functional *Hmr*.

Conversely, the *D. melanogaster Hmr* requires functional *D. simulans Lhr* to exert its lethal effects.

Having shown that their pair fulfils all three Dobzhansky–Muller criteria, the authors wondered about the evolutionary forces that drive the divergence of *Lhr*. Because the *Lhr* protein localizes to heterochromatin, they propose that it "…may be coevolving with rapidly evolving heterochromatic repetitive DNAs", consistent with a previously proposed hypothesis on how repetitive DNAs might contribute to hybrid incompatibilities and speciation.

*Magdalena Skipper*

**ORIGINAL RESEARCH PAPER** Brideau, N. J., Flores, H. A. & Wang, J. *et al.* Two Dobzhansky–Muller genes interact to cause hybrid lethality in *Drosophila*. *Science* **314**, 1292–1295 (2006)
**FURTHER READING** Noor, M. A. F. & Feder, J. F. Speciation genetics: evolving approaches. *Nature Rev. Genet.* **7**, 851–861 (2006) | Wu, C.-I. & Ting, C.-T. Genes and speciation. *Nature Rev. Genet.* **5**, 114–122 (2004)

rates in the mouse — such as chromosome, position within a chromosome and sex.

Sequence is also important. The motif CCTCCCT — the sequence that is most strongly associated with recombination hotspots in the human genome — also predicts the approximate positions of jungles in the mouse. Furthermore, the positions of human hotspots and mouse jungles are correlated. In fact, the CCTCCCT motif occurs at similar densities in similar places in the human, mouse, rat, dog and chimpanzee genomes.

The authors conclude that many factors influence the density of recombination events, and that not only are recombination patterns well conserved on a large scale, they are influenced by similar chromosomal and sequence characteristics across mammals. The new maps are already proving their worth as a genetic tool — the map of the outbred lines has been used in QTL analysis — and are now freely available to the mouse community.

*Jenny Bangham*

**ORIGINAL RESEARCH PAPER** Shifman, S. *et al.* A high-resolution single nucleotide polymorphism genetic map of the mouse genome. *PLoS Biol.* **4**, e395 (2006)
**FURTHER READING** Peters, L. L. *et al.* The mouse as a model for human biology: a resource guide for complex trait analysis. *Nature Rev. Genet.* **8**, 58–69 (2006)
**WEB SITES**
**Genetic Architecture of Complex Traits in Heterogeneous Stock Mice:**
http://gscan.well.ox.ac.uk/#genetic_map
**Mouse SNP Selector:**
http://well.ox.ac.uk/mouse/snp.selector

# IN BRIEF

## FUNCTIONAL GENOMICS

### Genome-wide prediction of conserved and nonconserved enhancers by histone acetylation patterns.

Roh, T.-Y. *et al. Genome Res.* 29 November 2006 (doi:10.1101/gr.5767907)

This study combines epigenomics and comparative genomics to improve the identification of functional non-coding sequences. The authors identified thousands of sequences that are conserved between humans and pufferfish, or between humans and mice, and that also correspond to islands of histone H3 diacetylation in human T cells. Many of the conserved sequences were found to have enhancer activity in T cells, and patterns of epigenetic modification were conserved in the mouse. This combined approach therefore aids the search for functional elements from among large numbers of conserved sequences.

## MOLECULAR EVOLUTION

### Robustness–epistasis link shapes the fitness landscape of a randomly drifting protein.

Bershtein, S. *et al. Nature* 19 November 2006 (doi:10.1038/nature05385)

Bershtein and colleagues subjected a bacterial enzyme to random mutational drift and purifying selection. The resulting effects on fitness indicated negative epistasis, in which the combined effect of mutations is greater than expected from their individual impacts on fitness. This negative epistasis was correlated with mutational robustness. The authors propose a model of robustness in which mutational effects are buffered up to a certain threshold, above which stability breaks down and the deleterious effects are unleashed to their full extent.

## RNA WORLD

### A late-acting quality control process for mature eukaryotic rRNAs.

LaRiviere, F. J. *et al. Mol. Cell* **24**, 619–626 (2006)

The existence of quality-control pathways for mRNAs is well established; this study now shows that ribosomal RNAs (rRNAs) are also subject to such monitoring mechanisms. The authors showed that rRNAs that contain point mutations in sites that are essential for ribosome function are significantly downregulated in *Saccharomyces cerevisiae*. The mechanism that is involved results in decreased stability of rRNAs that have already been assembled into ribosomes or ribosomal subunits. This provides a means by which eukaryotic cells might ensure the structural and functional integrity of the protein-translating machinery.

## SEX CHROMOSOMES

### Clustered DNA motifs mark X chromosomes for repression by a dosage compensation complex

McDonel, P. *et al. Nature* **444**, 614–618 (2006)

In *Caenorhabditis elegans* hermaphrodites, expression from each X chromosome is repressed by half so that total expression is the same as that in males, which possess only one X chromosome. These authors have identified the sequence elements that mark the X chromosomes for such repression by the dosage compensation complex. These *rex* (recruitment element on X) sites contain at least two motifs, which are not enriched on the X chromosome, but the distribution of which within *rex* sites marks the correct chromosomes for repression.