translation and correct respiratory defects? The authors used cycloheximide treatment to block cytoplasmic mRNA translation, allowing them to monitor mitochondrial protein synthesis. RIC treatment restored mitochondrial translation to almost wild-type status in MERFF and KSS cells. Furthermore, mitochondrial respiration was restored by RIC in MERFF cells (this is not possible in KSS cells as other genes that are essential for respiration are deleted in addition to *MTTK*). This rescue of respiration was dependent on the ability of RIC to import cytoplasmic $tRNA^{Lys}$.

Leishmania mitochondria import several other cytosolic tRNAs as well as $tRNA^{Lys}$, indicating that this approach could potentially be used to treat several other diseases that are caused by mitochondrial tRNA mutations. The authors point out that RIC also mediates the translocation of small RNAs, raising the exciting possibility of using this approach for a wider range of conditions by manipulating the expression of mitochondrial genes.

Louisa Flintoft

ORIGINAL RESEARCH PAPER Mahata, B. *et al.* Functional delivery of a cytosolic tRNA into mutant mitochondria of human cells. *Science* **314**, 471–474 (2006)
FURTHER READING Taylor, R. W. & Turnbull, D. M. Mitochondrial DNA mutations in human disease. *Nature Rev. Genet.* **6**, 389–482 (2005)
WEB SITE
Indian Institute of Chemical Biology: http://www.iicb.res.in

in birds and butterflies, in which males are the homogametic sex. In these species, sex-linked fitness variation can be passed from fathers to sons, allowing females to select for exaggerated male secondary sexual features more efficiently.

Several field studies indicate that intralocus sexual conflict is taxonomically widespread, but more work must be done to directly measure it outside laboratory populations of *D. melanogaster*. It can occur in any trait that is differentially selected between the sexes but is genetically constrained from diverging. Research on this topic therefore affects areas such as the evolution of imprinting, the maintenance of polymorphism, the existence of evolutionary constraints and the cost of sex.

Patrick Goymer

ORIGINAL RESEARCH PAPER Pischedda, A. & Chippindale, A. K. Intralocus sexual conflict diminishes the benefits of sexual selection. *PLoS Biol.* **4**, e356 (2006)
FURTHER READING Chenoweth, S. F. & Blows, M. W. Dissecting the complex genetic basis of mate choice. *Nature Rev. Genet.* **7**, 681–692 (2006)

IN BRIEF

GENOME EVOLUTION

Natural selection on human microRNA binding sites inferred from SNP data.

Chen, K. & Rajewski, N. *Nature Genet.* 29 October 2006 (doi:10.1038/ng1910)

Using SNP genotype data from three human populations to study *cis*-regulatory sites in the human genome, these authors show that negative selection is stronger on computationally predicted microRNA (miRNA) binding sites than on other conserved 3′ UTR sequence motifs. This finding provides evidence for the contribution of miRNAs to fitness. This approach, which can be extended to other types of *cis*-regulatory sites, indicated that 30–50% of unconserved miRNA binding sites can be functional. The probably deleterious effects of polymorphisms in predicted miRNA binding sites make them candidates for disease-causing variants.

GENOMICS

The genome of the sea urchin *Strongylocentrotus purpuratus*.

Sea Urchin Genome Sequencing Consortium. *Science* **314**, 941–952 (2006)

Sea urchin embryos have been extensively used in developmental, molecular, evolutionary and cell biology. The sequencing and analysis of the sea urchin genome has now been reported. The 814 Mb genome was sequenced at ~8× coverage using shotgun cloning and BAC sequences, and is estimated to contain ~23,300 genes. Genome analysis revealed a wealth of information about sea urchin biology (including a surprisingly sophisticated immune system), as well as vertebrate and chordate genome evolution.

CANCER GENETICS

The BRCA1/BARD1 heterodimer modulates RAN-dependent mitotic spindle assembly.

Joukov, V. *et al. Cell* **127**, 539–552 (2006)

The tumour suppressor BRCA1 functions in maintaining genomic integrity, but the details of how it does so have not been completely determined. Using *Xenopus laevis* egg extracts and human cells, this study demonstrates a previously unknown role of BRCA1 in mitotic spindle assembly. Heterodimers of BRCA1 and BARD1 work downstream of the RAN pathway to modulate the activity of spindle-pole proteins, probably through their E3 ubiquitin ligase activity. Defects in spindle-pole formation that lead to chromosome-segregation defects and aneuploidy might contribute to the genomic instability that is observed in BRCA1-deficient tumour cells.

DNA REPAIR

Age-dependent usage of double-strand-break repair pathways.

Preston, C. R. *et al. Curr. Biol.* **16**, 2009–2015 (2006)

Cells have evolved different mechanisms of DNA repair to preserve genetic information. The authors analysed the amount and quality of DNA double-strand break repair in *Drosophila* premeiotic germ cells and found that the relative use of different repair pathways changes as the organism ages. In particular, cells in old individuals use slow but accurate homologous recombination, whereas cells in younger flies opt for faster but error-prone repair mechanisms. This might contribute to the accumulation of genetic damage that takes place during ageing.