IN BRIEF

AGEING

Analysis of long-lived *C. elegans daf-2* mutants using serial analysis of gene expression.

Halaschek-Wiener, J. *et al. Genome Res.* 18 April 2005 (doi:10.1101/gr.3274805)

This is the first study to use serial analysis of gene expression (SAGE) to understand gene-expression patterns involved in the ageing process. By comparing control and long-lived (*daf-2* mutant) worms the authors identified whole gene families that were differentially regulated between the two groups. As long-lived worms showed a 'hypo-metabolic' state in early life, the authors speculate that the apparent metabolic repression contributes substantially to the observed longevity.

HUMAN DISEASE

A common sex-dependent mutation in a *RET* enhancer underlies Hirschsprung disease risk.

Sproat Emison, E. *et al. Nature* **434**, 857–863 (2005)

Hirschsprung disease (HSCR) is a complex, non-Mendelian disorder that has been linked to mutations in the coding sequence of the *RET* receptor tyrosine kinase. The authors used family-based association studies combined with comparative genomics analysis of *RET* sequences from several organisms to further the molecular understanding of this multifactorial disorder. Using this new approach, they show that the most common HSCR-associated mutation in *RET* is non-coding, has low penetrance and has sex-dependent effects.

GENE EXPRESSION

Special feature: Gene regulatory networks

Proc. Natl Acad. Sci. USA **102**, 5 April 2005

How do gene-regulatory networks control animal development? And what are the current approaches used to dissect those networks? A recent issue of *PNAS* addressed these questions in a special feature that contains commentaries and research articles. Understanding why, when and where genes are specifically expressed are the key issues that scientists are trying to tackle using different models — from nematodes and flies to sea urchins, frogs and mammals. Advanced technologies are also discussed, including a combination of DNA microarrays and bioinformatics that promises to accelerate regulatory-network studies.

HUMAN EVOLUTION

A scan for positively selected genes in the genomes of humans and chimpanzees.

Nielson, R. *et al. PLoS Biol.* **3**, e170 (2005)

Humans and chimpanzees have undergone pronounced changes in anatomy and cognitive ability in the 5 million years since their divergence. Nielson *et al.* compared the sequences of 13,731 annotated human genes to their orthologues in chimpanzees. They found that those genes with the strongest signatures of positive selection encode proteins that are involved in immunity, sensory perception, spermatogenesis and, surprisingly, tumour suppression and apoptosis. Unexpectedly, they found no evidence of positive selection on those genes that are maximally expressed in the brain.