IN BRIEF

GENOMICS

Initial sequence and comparative analysis of the cat genome.

Pontius, J. U. *et al. Genome Res.* **17**, 1675–1689 (2007)

The assembly and annotation of the domestic cat (*Felis catus*) genome has been reported. The genome of Cinnamon, an Abyssinian cat, was sequenced at twofold coverage and annotated by comparison with the genomes of other sequenced mammals. The analysis identified chromosomal rearrangements, thousands of genomic variants, microRNAs and many transposable elements. The sequence will be relevant not only for improving cat health but also for mapping disease-susceptibility genes, including those for the >250 hereditary disorders shared with humans.

CANCER

An elaborate pathway required for Ras-mediated epigenetic silencing.

Gazin, C., Wajapeyee, N. *et al. Nature* **449**, 1073–1077 (2007)

A genome-wide RNAi screen in human cancer cells in culture identifies a network of genes that converts a normal cell to a cancerous one. *KRAS*-transformed cells were screened for epigenetic regulators in the Ras pathway that silence the pro-apoptotic gene *FAS*. The 28 epigenetic modifiers — most of which were not previously connected to Ras — belong to a common pathway of 'Ras epigenetic silencing factors' that also silence other, unrelated genes that are required for cell transformation.

GENOME EVOLUTION

A sex-ratio meiotic drive system in *Drosophila simulans*. I: An autosomal suppressor.

Tao, Y. *et al. PLoS Biol.* **5**, e292 (2007)

A sex-ratio meiotic drive system in *Drosophila simulans*. II: An X-linked distorter.

Tao, Y. *et al. PLoS Biol.* **5**, e293 (2007)

Sex-ratio distortion occurs in many species and leads to the overrepresentation of one sex among offspring. Two papers identify for the first time, in *Drosophila simulans*, an X-linked distorter gene (*DOX*) and the autosomal gene (*not much yang*, *NMY*) that has evolved to suppress the action of the distorter. The sequence similarity of the two genes suggests that the suppression occurs by RNAi. The authors also report that the physiological cause of the distortion is a failure to produce mature sperm.

GENE NETWORKS

A gene regulatory network subcircuit drives a dynamic pattern of gene expression.

Smith, J. *et al. Science* **318**, 794–797 (2007)

The authors have defined a *cis*-regulatory subcircuit that defines the dynamic expression pattern of genes in the early sea urchin embryo. *Blimp1* is expressed at the centre of an expanding ring at early cleavage stages and, while the expression domain moves radially outwards, it is progressively extinguished in the more central domains. In the experimentally resolved circuit, which involves at least three key genes, extinction of *Blimp1* expression is caused by autorepression, whereas its radial expansion follows Wnt8 signalling.

GENE EXPRESSION

Proteins in profile

A new profiling method that overcomes the limitations of large-scale proteomic studies has been applied to map the QTLs that control protein levels and to compare them with those that affect transcript abundance.

The number of transcriptomics studies has rocketed in recent years, but the weak correlation between transcript and protein abundance means that transcript profiles are of limited use for understanding variation in protein levels. Existing proteomics methods are not powerful enough to monitor proteome changes across many samples: the concentration of a protein can be compared across experiments but, in practice, corresponding proteins in different experiments are difficult to match. The new, more direct approach also relies on the established technique of mass spectrometry (which separates peptides according to mass and charge), but introduces a key innovation: an algorithm that aligns peptides across samples — this made it possible to compare the levels of 569 proteins in more than 400 samples.

The samples in question derive from the parents and offspring of a cross between two strains of *Saccharomyces cerevisiae*. Protein levels in the segregants varied continuously, that is, they behaved like quantitative traits. To determine the QTLs that control protein abundance, 221 of the most reliable peptides were chosen for linkage studies. Perhaps surprisingly, most control loci seem to function in *trans*, as they map to chromosomes other than those that contain the genes encoding the corresponding proteins. Furthermore, the regulatory QTLs are clustered in four 'hotspots', one

HORIZONTAL GENE TRANSFER

Unclonable, that's what you are!

Computation analysis allied with experimental proof has been used to show that genes that are toxic to a new host fail to transfer by horizontal gene transfer (HGT).

Rotem Sorek and colleagues reasoned that cloning genes into a foreign host (*Escherichia coli*) using plasmid vectors is akin to HGT by conjugation. Microbial genome sequences are typically assembled from sequenced fragments that have been cloned in *E. coli*. Sequence stretches that cannot be cloned are closed by clone-independent PCR-based 'finishing'. With this in mind, the authors examined the original genome sequence data sets for evidence of genes that could (cloned genes) or could not (uncloned genes) be transferred by HGT.

Using the original data from 79 complete microbial genome sequences, they mapped the positions of all the clones used to generate the completed genomes against annotated genes, excluding genes larger than 1.5 kb. Some 'uncloned' loci were not represented in plasmid multicopy libraries, and a quarter of these (124 genes) were absent from fosmid low-copy libraries, indicating that the unclonability of many genes is copy-number independent.