

IN BRIEF

FUNCTIONAL GENOMICS

Identification of genes needed for regeneration, stem cell function, and tissue homeostasis by systematic gene perturbation in *Planaria*.

Reddien, P. W. *et al. Dev. Cell* **8**, 635–649 (2005)

The authors developed an RNAi-based screening strategy to carry out the first large-scale survey of gene function in planarian biology. Among the 1,065 genes that were inactivated, 240 generated phenotypes associated with stem-cell function, regeneration and tissue homeostasis. This study demonstrates the great potential of RNAi for the identification of gene function in under-studied organisms and establishes planarians as a powerful model for studying regeneration.

SYSTEMS BIOLOGY

Cell fates as high-dimensional attractor states of a complex gene regulatory network.

Huang, S. *et al. Phys. Rev. Lett.* **94**, 128701 (2005)

The robustness of development to external perturbations has led to the suggestion that differentiated cell fates represent stable attractor states, which can be reached through more than one pathway. The authors provide the first experimental evidence for this, taking advantage of the fact that the differentiation of human neutrophils can be induced by two different chemicals. Using microarray analysis, they showed that the gene-expression pathways induced by the two chemicals were almost entirely different, but resulted in the same biological endpoint.

METAGENOMICS

Genomic sequencing of Pleistocene cave bears.

Noonan, J. P. *et al. Science* 2 June 2005 (doi:10.1126/science.1113485)

Genome sequencing of extinct species is hampered by the degradation of ancient DNA, but a metagenomics approach could help to address this problem. Noonan *et al.* tested this idea by making libraries from a mixture of DNA fragments obtained from two 40,000-year-old extinct cave bears. They compared these libraries with the annotated dog genome (bears and dogs are closely related) and identified 26,861 bp of cave-bear genome sequence. The phylogeny generated from this and sequences from modern bears is topologically equivalent to bear phylogenies previously obtained using mitochondrial DNA.

GENE THERAPY

Non-viral gene delivery regulated by stiffness of cell adhesion substrates.

Joon Kong, H. *et al. Nature Mater.* **4**, 460–464 (2005)

Considerable efforts are being made to improve the levels of gene transfection and expression achieved using non-viral gene-therapy vectors. Rather than trying to improve the efficiency of this process by manipulating the vector, Joon Kong *et al.* focused on the cellular environment. They show that gene-transfer efficiency and levels of gene expression increase as the rigidity of the cell-adhesion substrate increases. This effect is related to the influence of the substrate on cell proliferation.