

IN BRIEF

▶ COMPUTATIONAL GENOMICS

Computational prediction of methylation status in human genomic sequences.

Das, R. *et al. Proc. Natl Acad. Sci. USA* **103**, 10713–10716 (2006)

Computational approaches to epigenomics have lagged behind molecular ones. This report describes a pattern-recognition method that, based on DNA sequence alone, evaluates methylation propensity for an 800-bp region around a CpG. The program, HDFINDER, can predict methylation with an accuracy of 86%. The authors used human brain DNA to produce a map of DNA methylation across the human genome. They invite researchers to compare these results with those for other tissues in future studies.

▶ SMALL RNAs

A distinct small RNA pathway silences selfish genetic elements in the germline.

Vagin, V. V. & Sigova, A. *et al. Science* 29 June 2006 (doi:10.1126/science.1129333)

Repeat-associated small interfering RNAs (rasiRNAs) protect the fly against genomic instability by silencing endogenous selfish elements in the germ line. These authors show that rasiRNAs are a product of a third, distinct silencing pathway — they arise mainly from the antisense strand and their production does not require Dicer 1 or 2 (which are involved in miRNA and siRNA production, respectively). Moreover, unlike siRNA and miRNA-mediated silencing, which require Ago proteins, rasiRNA function is mediated by Piwi.

▶ HUMAN GENETICS

Linkage disequilibrium and heritability of copy-number polymorphisms within duplicated regions of the human genome.

Locke, D. P. *et al. Am. J. Hum. Genet.* **79**, 275–290 (2006)

Duplication-rich regions of the genome are expected to be recombination hotspots. The authors looked at 130 such regions from the International HapMap Project data set. Forty-six showed no variation in copy number, implying that rearrangements in them might be pathogenic. Copy-number variation showed Mendelian inheritance but lower than expected linkage disequilibrium with nearby SNPs, implying that the same variants could have arisen on multiple haplotypes. There was also a bias against copy-number losses, suggesting purifying selection.

▶ PLANT EVOLUTION

A genome-wide survey of *R* gene polymorphisms in *Arabidopsis*.

Bakker, E. G. *et al. Plant Cell* 23 June 2006 (doi:10.1105/tpc.106.042614)

Specific alleles of plant resistance (*R*) genes interact with pathogen virulence proteins to produce a hypersensitive response. The authors assessed SNP variation within 27 such genes. There were high levels of non-synonymous polymorphism in *R* genes but little evidence for selective sweeps and only weak evidence for balancing selection, arguing against evolutionary arms races. Instead, the results were consistent with selection for many novel alleles that are rarely maintained in populations over the long term.

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URLs