IN BRIEF

QUANTITATIVE TRAITS

Genetic variation contributing to mRNA decay

Because most expression quantitative trait locus (eQTL) studies measure the steady-state level of mRNAs, they cannot distinguish between changes in transcript production and decay rates. Pai *et al.* measured mRNA decay from 16,000 genes in 70 Yoruban HapMap lymphoblastoid cell lines. For ~10% of genes, steady-state expression levels correlated with variation in decay rate variation, and 195 loci — dubbed RNA decay quantitative trait loci (RdQTLs) — were identified as being associated with this variation.

ORIGINAL RESEARCH PAPER Pai, A. A. *et al.* The contribution of RNA decay quantitative trait loci to inter-individual variation in steady-state gene expression levels. *PLoS Genet.* **8**, e1003000 (2012)

COMPLEX DISEASE

Inflammatory bowel disease genetic association

A meta-analysis of 15 genome-wide association studies of inflammatory bowel disease (IBD) has been carried out and analysed along with data from an Immunochip study. One hundred and sixty-three loci were identified — the most for any complex disease to date. Many IBD loci were implicated in other immune-related disorders, and there was an overlap between IBD and mycobacterial infection susceptibility loci. Evidence for directional and balancing selection at IBD loci was also uncovered.

ORIGINAL RESEARCH PAPER Jostins, L. *et al.* Host–microbe interactions have shaped the genetic architecture of inflammatory bowel disease. *Nature* **491**, 119–124 (2012)

EPIGENETICS

DNA methylation discovered in nematodes

DNA methylation is an important epigenetic mark in many eukaryotes, but until now it has not been identified in nematodes. This study identified 5-methylcytosine (5mC) in the parasitic nematode *Trichinella spiralis* using MethylC-seq to generate high-resolution methylome maps. The authors found substantial changes in 5mC between life-cycle stages, both in terms of overall levels and changes at specific genes. Given that the genome of the model nematode *Caenorhabditis elegans* does not contain 5mC, these findings raise evolutionary questions about the regulation of gene expression in related species.

ORIGINAL RESEARCH PAPER Gao, F. *et al.* Differential DNA methylation in discrete developmental stages of the parasitic nematode *Trichinella spiralis*. *Genome Biol.* **13**, R100 (2012)

RNA

RNA catalytic networks

The coding and catalytic capacity of RNA has raised the possibility that early, acellular life may have been RNA-based, but whether RNAs can generate complex catalytic networks is unclear. Vaidya *et al.* engineered different versions of a catalytic RNA (known as a ribozyme) from *Azoarcus* proteobacteria that all require covalent joining of the two constituent RNA fragments for full activity. Crucially, the authors adjusted the ribozyme specificities to catalyse either their own joining or the joining of a different ribozyme variant in a cyclical network. Experimental tracking of RNA catalysis and computational modelling showed that complex RNA networks can outcompete the 'selfish' autocatalysis and can spontaneously grow in complexity.

ORIGINAL RESEARCH PAPER Vaidya, N. *et al.* Spontaneous network formation among cooperative RNA replicators. *Nature* 17 Oct 2012 (doi:10.1038/nature11549)