

RESEARCH HIGHLIGHTS

IN BRIEF

TECHNOLOGY

Potent and persistent *in vivo* anti-HBV activity of chemically modified siRNAs.

Morrissey, D. V. et al. *Nature Biotechnol.* 24 July 2005 (doi:10.1038/nbt1122)

Small interfering RNA (siRNA) molecules could be used for therapeutic approaches if an efficient and safe way to deliver them to the organism could be developed. Morrissey and colleagues have now developed such a delivery method by incorporating siRNAs into lipid-like particles. These encapsulated siRNAs are very efficient at inhibiting hepatitis B virus replication in mice, and work at low and clinically relevant doses.

PLANT EVOLUTION

Evolution through genetically controlled allometry space.

Langlade, N. B. et al. *Proc. Natl Acad. Sci. USA* **102**, 10221–10226 (2005)

Morphological differences between species involve modifications in shape and size, but the genetic basis of these changes is poorly understood. The authors have applied numerical shape and size analysis to leaves in *Antirrhinum* species and showed that most of the variation can be represented in a three-dimensional allometric space, and involves at least 15 QTLs. This representation provides a quantitative framework for relating genetic variation to evolutionary changes in shape and size.

PLANT GENETICS

The pattern of polymorphism in *Arabidopsis thaliana*.

Nordborg, M. et al. *PLoS Biol.* **3**, e196 (2005)

This study is a systematic survey of genomic DNA sequence polymorphisms in *Arabidopsis thaliana*. The authors resequenced 876 short fragments in samples from stock centres and natural populations and showed that the level of polymorphism is highly variable between genomic regions: it is negatively correlated with gene density and positively correlated with segmental duplications. They also showed that linkage disequilibrium is unusually extensive. These data will help to identify the functional polymorphisms that underlie phenotypic variation in *A. thaliana*.

GENE NETWORKS

Rewiring of the yeast transcriptional network through the evolution of motif usage.

Ihmels, J. et al. *Science* **309**, 938–940 (2005)

The authors studied the evolution of gene expression by investigating differences in transcriptional regulation in two related yeast species. Loss of a *cis*-regulatory element from many genes was found to underlie changes in the regulation of gene expression that allowed the capacity for anaerobic growth to evolve in *Saccharomyces cerevisiae*, but not in *Candida albicans*. This seems to have occurred after whole-genome duplication, indicating that such events allow rewiring of regulatory networks, as well as specialization of gene functions.