

IN BRIEF

EVOLUTION

Widespread parallel evolution in sticklebacks by repeated fixation of *Ectodysplasin* alleles.

Colosimo, P. F. *et al. Science* **307**, 1928–1933 (2005)

Stickleback body armour is reduced in freshwater populations, which arose after many separate marine-to-freshwater migrations. The authors showed that polymorphism in a single gene underlies the loss in most cases. Rather than arising several times, the causal variants exist at low levels in marine populations, and are selected for repeatedly in freshwater environments. This supports a key role of standing genetic variation in parallel evolution.

HUMAN DISEASE

Deletion of active ADAMTS5 prevents cartilage degradation in a murine model of osteoarthritis.

Glasson, S. S. *et al. Nature* **434**, 644–648 (2005)

ADAMTS5 is the major aggrecanase in mouse cartilage *in vivo* and *in vitro*.

Stanton, H. *et al. Nature* **434**, 648–652 (2005)

The proteoglycan aggrecan allows cartilage to resist compression, and its degradation causes osteoarthritis. Some ADAMTS (a disintegrin and metalloproteinase with thrombospondin motifs) family members can cleave aggrecan, and two research groups have now identified ADAMTS5 as an important culprit in osteoarthritis. They found that mice lacking functional ADAMTS5 are resistant to cartilage destruction following joint injury or inflammation. Furthermore, the knockout mice apparently suffered no other problems, making ADAMTS5 a promising drug target.

FUNCTIONAL GENOMICS

Functional genomic analysis of RNA interference in *Caenorhabditis elegans*.

Kim, J. K. *et al. Science* 24 March 2005 (doi:10.1126/science.1109267)

The authors performed a genome-wide screen in an engineered RNAi sensor strain of worms to identify components of the RNAi pathway. Among the 90 genes identified are those that are required for germline- and somatic-transgene silencing. Physical interactions between some of these gene products indicate links to other RNA-dependent gene-regulatory pathways.

COMPARATIVE GENOMICS

Systematic discovery of regulatory motifs in human promoters and 3' UTRs by comparison of several mammals.

Xie, X. *et al. Nature* **434**, 338–345 (2005)

By comparing 3' UTR and promoter regions from human, mouse, rat and dog genomes the authors created a catalogue of regulatory motifs contained in these regions. They describe 105 new promoter motifs and 106 motifs in 3' UTR regions that are likely to be involved in post-transcriptional regulation. Importantly, their analysis indicates that at least 20% of human genes might be regulated by miRNAs.