

## IN BRIEF

## RNA SILENCING

A link between mRNA turnover and RNA interference in *Arabidopsis*.

Gazzani, S. *et al. Science* **306**, 1046–1048 (2004)

MicroRNA binding sites in *Arabidopsis* class III HD-ZIP mRNAs are required for methylation of the template chromosome.

Bao, N. *et al. Dev. Cell* **7**, 653–662 (2004)

These papers provide new insights into RNA-mediated silencing. RNA-dependent RNA polymerase (RdRP) promotes RNA interference in several species, but its substrate is unknown. Gazzani *et al.* showed that mutation of the *Arabidopsis thaliana* *XRN4* exonuclease gene promotes RdRP-dependent silencing of a transgene. Plants that lack both RdRP and *XRN4* accumulate decapped transgene mRNA, implicating uncapped transcripts as RdRP substrates. Bao *et al.* investigated the regulation of the *A. thaliana* *PHB* and *PHV* leaf-patterning genes. Both genes are heavily methylated in wild-type plants, but this is reduced by mutation of microRNA binding sites that are present in *PHB* and *PHV* mRNAs, but not in the corresponding genomic sequences. MicroRNAs therefore seem to regulate expression of these genes by interacting with their transcripts to produce epigenetic changes at the genomic level.

## EPIGENETICS

DNA methylation profiling of the human major histocompatibility complex: a pilot study for the human epigenome project.

Rakyan, V. K. *et al. PLoS Biol.* **2**, e405 (2004)

DNA methylation has a crucial function in vertebrate development, gene regulation and disease. The Human Epigenome Project (<http://www.epigenome.org>) aims to identify and catalogue the pattern of cytosine methylation across the human genome. As a prelude to this large-scale project, Rakyan and colleagues have analysed the DNA-methylation profile of the human major histocompatibility complex. The project, which involved the development of high-throughput analysis methods, revealed that most regions of the 90 genes studied were either hypo- or hypermethylated.

## TECHNOLOGY

A reverse genetic, nontransgenic approach to wheat crop improvement by TILLING.

Slade, A. J. *et al. Nature Biotechnol.* 5 December 2004 (doi:10.1038/nbt1043)

Modifying the wheat genome is an attractive goal for agriculture and industry, but the size of this large, polyploid genome makes the application of transgenic methods particularly challenging. Ann Slade and colleagues have now applied a reverse genetic, non-transgenic method called TILLING to isolate 246 alleles of a gene (*GBSSI*) that is involved in starch biosynthesis, showing that this method can be used effectively for crop improvement. Plants with null alleles of *GBSSI* produce highly branched starches that have unique and commercially valuable properties.

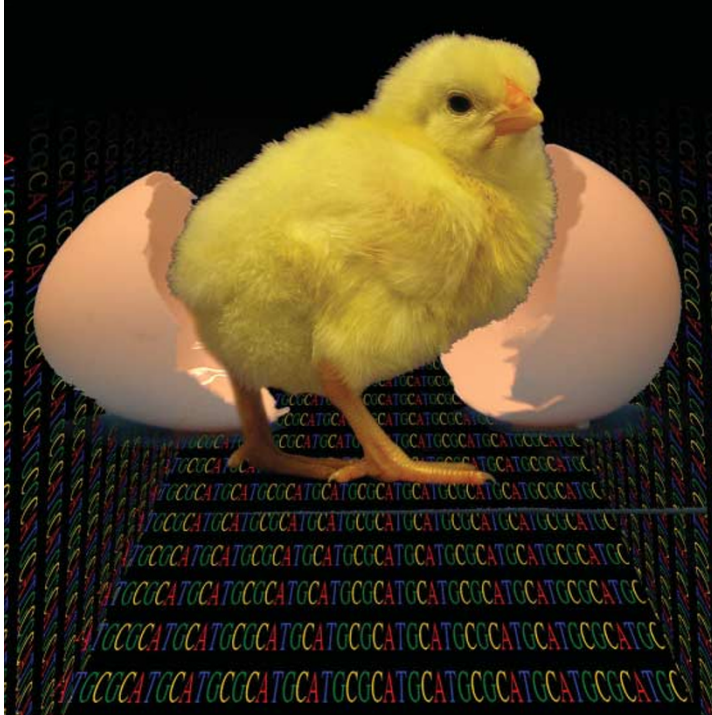


Image courtesy of Mary E. Delany, University of California, Davis. Graphic design courtesy of Washington University Medical Public Affairs.

## References and links

**ORIGINAL RESEARCH PAPERS** International Genome Sequencing Consortium. Sequence and comparative analysis of the chicken genome provide unique perspectives on vertebrate evolution. *Nature* **432**, 695–716 (2004) | International Chicken Polymorphism Map Consortium. A genetic variation map for chicken with 2.8 million single nucleotide polymorphisms. *Nature* **432**, 717–722 (2004) | Wallis J. W. *et al.* A physical map of the chicken genome. *Nature* **432**, 761–764 (2004)

**FURTHER READING** Schmutz, J. & Grimwood, J. Fowl sequence. *Nature* **432**, 679–680 (2004)

## WEB SITES

AvianNET: <http://www.chicken-genome.org>  
Chicken variation database:  
<http://chicken.genomics.org.cn/index.jsp>

at least one fact for you to share in the pub: the discovery of hundreds of olfactory-receptor genes contributes to a long-standing debate by indicating that chickens have at least the genetic capability for a well-developed sense of smell. Who says genomics can't be controversial?

Chris Gunter, Senior Editor, Nature

within seven generations. So, although other fitness effects might also contribute to the even shorter time to extinction seen in the experiments, decreased fertility seems to have an important role.

This fits in with evolutionary models which suggest that increased longevity is selected against owing to adverse effects on reproductive fitness earlier in life. Given the conserved nature of the IGF-I pathway, it seems likely that this will apply to other species as well, reinforcing the need to learn more about the factors that determine lifespan before we can even consider manipulating our own.

Louisa Flintoft

## References and links

## ORIGINAL RESEARCH PAPERS

Jenkins, N. L., McColl, G. & Lithgow, G. J. Fitness cost of extended lifespan in *Caenorhabditis elegans*. *Proc. R. Soc. Lond. B* 24 November 2004 (doi:10.1098/rspb.2004.2897)

## WEB SITE

Gordon Lithgow's Laboratory:  
<http://www.buckinstitute.org/lithgow/>

