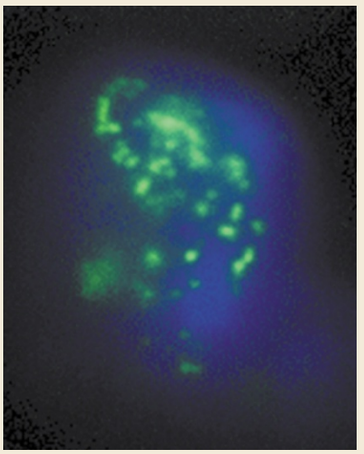
interfere with RNA processing or interact with double-stranded RNA-binding proteins. This mouse model should help to unravel the mechanisms behind this toxic effect and, more generally, the role that expanded repeats play in disease pathogenesis.

Jane Alfred



Courtesy of Charles Thornton, University of Rochester Medical Center, USA.

References and links

ORIGINAL RESEARCH PAPER Mankodi, A. *et al*. Myotonic dystrophy in transgenic mice expressing an expanded CUG repeat. *Science* **289**, 1769–1772 (2000).

FURTHER READING Tapscott, S.J. Deconstructing myotonic dystrophy. *Science* **289**, 1701–1702 (2000)

across greater phylogenetic distances? How will this knowledge affect the analysis and annotation of the *Arabidopsis* genomic sequence, which should be complete by the end of the year?

A prime selling feature of *Arabidopsis* is its small genome. But if the proposed model is correct, the genome of its ancestor would have been less of a chore to sequence, with only half as many genes as the present-day lab variety.

Tanita Casci

References and links

ORIGINAL RESEARCH PAPER Ku, H.-M. *et al*. Comparing sequenced segments of the tomato and *Arabidopsis* genomes: large-scale duplication followed by selective gene loss creates a network of synteny. *Proc. Natl Acad. Sci. USA* **97**, 9121–9126 (2000). | Grant, D. *et al*. Genome organization in dicots: genome duplication in *Arabidopsis* and synteny between soybean and *Arabidopsis*. *Proc. Natl Acad. Sci. USA* **97**, 4168–4173 (2000).

FURTHER READING Blanc, G. *et al*. Extensive duplication and reshuffling in the *Arabidopsis* genome. *Plant Cell* **12**, 1093–1102 (2000).

WEB SITES Steven Tanskley's lab | Randy Shoemaker's lab | The *Arabidopsis* Genome Initiative (AGI) | The Tomato Genomics Project (funded by the NSF) at Cornell University

IN BRIEF

ASSOCIATION STUDIES

Polymorphisms in genes involved in folate metabolism as maternal risk factors for Down syndrome.

Hobbs, C. A. et al. Am. J. Hum. Genet. ***67****, 623–630 (2000).*

This study links folate metabolism to the incidence of Down syndrome (trisomy 21), the most common genetic cause of human mental retardation. Other than advanced maternal age at conception, other risk factors are unknown. Hobbs *et al.* show that the simultaneous presence of the 677C→T polymorphism in the methylenetetrahydrofolate reductase gene and the homozygous 66A→G mutation in the methionine synthase reductase gene confer a fourfold maternal risk of having a child with Down syndrome.

MICROBIAL GENOMICS

Genome sequence of the endocellular bacterial symbiont of aphids *Buchnera* sp. APS.

Shigenobu, S. et al. Nature ***407****, 81–86 (2000).*

Because of their importance to human health and welfare, most of the bacteria whose genomes have already been sequenced are pathogens (reviewed in this issue by Brendan Wren). Shigenobu *et al.* now provide the first look at the genome of a symbiotic bacterium (*Buchnera*), which lives within the cells of an aphid. This symbiotic relationship has a 200 million year history, and the effects of this can be clearly seen in the genes that have been lost or retained in *Buchnera*'s stripped down genome.

MOUSE GENETICS

Eleven densely clustered genes, six of them novel, in 176 kb of mouse *t*-complex DNA.

Kargul, G. J. et al. Genome Res. ***10****, 916–923 (2000).*

The mouse *t*-complex encodes genes that affect embryonic development, sex ratio distortion, imprinting and male fertility, but its complicated genomic structure has hampered previous efforts to analyse it. This paper reports the first BAC to be sequenced from the region and the finding of eleven genes (some novel) in only 176 kb, making this region possibly one of the most gene-dense segments of the mouse genome.

CANCER GENETICS

PAX8-PPARγ1 fusion in oncogene human thyroid carcinoma.

Kroll, T. G. et al. Science ***289****, 1357–1360 (2000).*

A fusion protein produced by a chromosomal translocation that is associated with cancer is reported. This is news because the cancer is a carcinoma, and almost all other translocations are associated with leukaemias, lymphomas and sarcomas. This translocation produces a fusion between *PAX8* and a peroxisome proliferator-activated receptor gene. The fusion protein is associated specifically with one form of thyroid carcinoma, and so provides new avenues for diagnosis and, possibly, treatment.