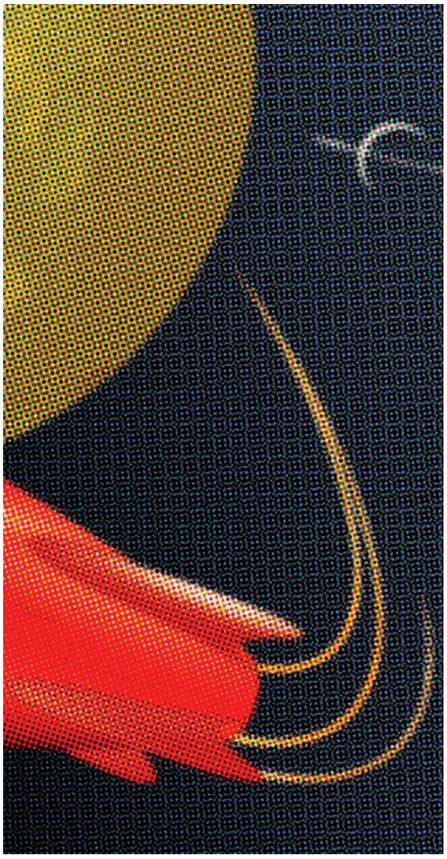

travels to and from the mammalian X chromosome. However, is the cement still wet on this busy genomic highway or is it a well-worn track? Emerson and colleagues answer this question with a comparative analysis of the mouse and human genomes, which showed that most retrogenes that have escaped the X (12/15) or have moved to it (10/13) did so before the mouse–human divergence. Clearly, the turnover of genes on the X chromosome is an ancient but ongoing process.

The fascinating picture of dynamic X-chromsome evolution that Emerson and colleagues have revealed invites a bit of genomic crystal-ball gazing. Is it just a matter of time before the X chromosome becomes the exclusive preserve of genes that are advantageous to males when hemizygous and that are silenced in female tissues, whereas all genes that are favourable to males when homozygous will be shifted to the autosomes?

Nick Campbell

References and links

ORIGINAL RESEARCH PAPER Emerson, J. J. *et al.* Extensive gene traffic on the mammalian X chromosome. *Science* **303**, 537–540 (2004)

FURTHER READING Long, M. *et al*. The origin of new genes: glimpses from the young and old. *Nature Rev. Genet*. **4**, 865–875 (2003) | Betran, E. *et al.* Retroposed new genes out of the X in *Drosophila*. *Genome Res.* **12**, 1854–1859 (2002)

WEB SITES

Esther Betran's laboratory: http://www3.uta.edu/faculty/betran

Henrik Kaessmann's laboratory: http://www.unil.ch/cig/page6396_en.html

Manyuan Long's laboratory: http://pondside.uchicago.edu/~longlab/longlab.html

However, before robot scientists appear in laboratories everywhere, there is still a lot of work to be done. The authors are now testing whether their system can uncover the role of genes for which no functional information is available. This will require the translation of many bioinformatic databases into logical formulae and the extension of their hypothesis-generation method. But it does seem that the potential of this system to be applied to many scientific problems will ensure that, one day, the use of robot scientists will be commonplace.

Natalie Wilson

References and links

ORIGINAL RESEARCH PAPER King, R. D. *et al*. Functional genomic hypothesis generation and experimentation by a robot scientist. *Nature* **427**, 247–252 (2004)

WEB SITES

ASE-Progol: ftp://www.comp.rgu.ac.uk/pub/staff/chb/systems/ase_progol/version_1.0

KEGG: http://www.genome.ad.jp/kegg

IN BRIEF

DEVELOPMENTAL BIOLOGY

fgf8 mRNA decay establishes a gradient that couples axial elongation to patterning in the vertebrate embryo.

Dubrulle, J. & Pourquié, O. *Nature* **427**, 419–422 (2004)

Axial development in vertebrate embryos proceeds in a stereotypical manner whereby cells differentiate according to their position in a protein gradient. This paper shows how the Fgf8 gradient that controls this process might form in the chick. *fgf8* is transcribed only in tail-bud cells but this process stops as these cells move anteriorly during development. The protein gradient is consequently formed as the cells' supply of mRNA dwindles, therefore providing the answer to a long-standing question.

POPULATION GENETICS

Evidence for extensive transmission distortion in the human genome.

Zöllner, S. *et al. Am. J. Hum. Genet.* **74**, 62–72 (2004)

Mendel's laws predict that a diploid organism should transmit each chromosome at a similar frequency. Deviations from this 1:1 ratio — known as segregation distortion — occur in many species and for various reasons. By examining genome data from 148 families, the authors conclude that segregation distortion is extensive in humans and that many loci underlie this effect.

GENE REGULATION

A noncoding RNA is required for the repression of RNApol II-dependent transcription in primordial germ cells.

Martinho, R. G. *et al*. *Curr. Biol*. **14**, 159–165 (2004)

Unlike somatic cells, primordial germ cells (PGCs) — those that will develop into eggs and sperm — need to remain undifferentiated: they are thought to do so by inhibiting RNApolII transcription. Ruth Lehmann's group has now found that a non-coding RNA that is encoded by the *polar granule component* (*pgc*) gene blocks RNApolII activity in PGCs, possibly by preventing transcription-activating enzymes from reaching the nucleus.

MEDICAL GENETICS

Molecular and comparative genetics of mental retardation.

Inlow, J. K. & Restifo, L. L. *Genetics* (in the press)

Mental retardation (MR) is a common and genetically heterogeneous form of cognitive impairment. Jennifer Inlow and Linda Restifo estimate there to be hundreds of MR genes, 282 of which they have identified by data mining the Online Mendelian Inheritence in Man (OMIM) database and the literature. A total of 76% of these genes have functional orthologues in *Drosophila*, which indicates that this fly could be the ideal model to use to dissect the genetic basis of MR.