these genes and in many interactions between RNA and protein molecules in the cell.

In a third paper, Dermitzakis *et al.* directly compared the sequences on most of human chromosome 21 to their counterparts in mice. Even the gene-poor region of the chromosome shows extensive similarity between the two organisms, and conserved sequences seem to be under selective constraint in the mouse, despite the fact that they seem not to be encoding transcripts. Further exploration is needed into the non-coding regions of both genomes to explain the differences between us.

As the sequence has all been deposited in public databases, the mouse genome should provide a huge boost to genetic researchers. For example, crosses between the C57BL/6J strain and others are often used to map mutations that mimic human disease. In another paper in the issue, Wade *et al.* compare the C57BL/6J genome with 17 Mb of finished sequence from strain 129/Sv as well as a genome-wide sample of reads from multiple strains, finding regions of high and low polymorphism in single nucleotides between the strains. Extensive mapping of high-polymorphism areas will be extremely useful for mapping quantitative trait loci, and therefore possibly the genes that contribute to the inheritance of complex traits. Given the bonanza of information they've just received, scientists might now consider the laboratory mouse to be "man's best friend".

Chris Gunter,
Associate Editor, Nature

References and links

ORIGINAL RESEARCH PAPERS Mouse Genome Sequencing Consortium. Initial sequencing and comparative analysis of the mouse genome. *Nature* **420**, 520–562 (2002) | The FANTOM Consortium and the RIKEN Genome Exploration Group Phase I & II Team. Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs. *Nature* **420**, 563–573 (2002) | Dermitzakis, E. T. *et al*. Numerous potentially functional non-genic conserved sequences on human chromosome 21. *Nature* **420**, 578–582 (2002) | Wade, C. M. *et al*. The mosaic structure of variation in the laboratory mouse genome. *Nature* **420**, 574–590 (2002)

WEB SITES

Ensembl mouse genome browser: http://www.ensembl.org/Mus_musculus

***Nature* mouse web focus:** http://www.nature.com/nature/mousegenome

UCSC Genome Bioinformatics site: http://www.genome.ucsc.edu

NIH Mouse Genome Resources: http://www.ncbi.nlm.nih.gov/genome/guide/mouse

chromosome regions, as recently reported in worms and flies, which hints at how chromatin structure might govern gene expression.

Mapping the gene expression of an entire chromosome at high resolution provides the next level of genome annotation and brings researchers closer to identifying the function of every human gene — the most important issue in genomic biology.

Natalie DeWitt,
Senior Editor, Nature

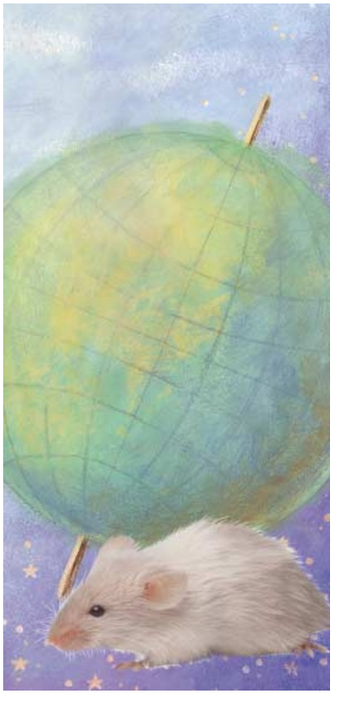
References and links

ORIGINAL RESEARCH PAPERS Reymond, A. *et al*. Human chromosome 21 gene expression atlas in the mouse. *Nature* **420**, 582–586 (2002) | The HSA21 Expression Map Initiative. A gene expression map of human chromosome 21 orthologues in mouse. *Nature* **420**, 586–590 (2002)

WEB SITES

Supplementary information for Reymond, A. *et al.*: http://www.tigem.it/ch21exp

Supplementary information for The HSA21 Expression Map Initiative: http://chr21.molgen.mpg.de/data



IN BRIEF

DEVELOPMENTAL BIOLOGY

BMP4 initiates human embryonic stem cell differentiation to trophoblast.

Xu, R.-H. *et al. Nature Biotechnol.* **20**, 1261–1264 (2002)

Although embryonic stem (ES) cells are well known for their controversial application in transplantation therapy, they are also important for understanding the development and function of different cell types. This paper shows that human ES cells can be induced to differentiate into trophoblast — which develops before the three embryonic germ layers — by bone morphogenetic protein 4. This result reinforces the value of human ES-cell research as mouse and human trophoblast are significantly different and mouse ES cells differentiate poorly into trophoblast.

DISEASE GENETICS

A defect in a novel Nek-family kinase causes cystic kidney disease in the mouse and in zebrafish.

Liu, S. *et al. Development* **129**, 5839–5846 (2002)

Mice with the juvenile cystic kidney (*jck*) mutation are good models for the human disorder polycystic kidney disease (PKD). The authors have positionally cloned the *jck* mutation, which corresponds to a point mutation in the kinase-encoding gene *Nek8*. The role of Nek8 in PKD was confirmed by *in vitro* overexpression studies and the polycystic phenotype of zebrafish in which the Nek8 orthologue was inactivated using antisense oligonucleotides. Gene function can therefore be successfully investigated using comparative analyses.

FUNCTIONAL GENOMICS

Integrating interactome, phenome, and transcriptome mapping data for the *C. elegans* germline.

Walhout, A. J. M. *et al. Curr. Biol.* **12**, 1952–1958 (2002)

Gene clustering based on RNAi phenotypes of ovary-enriched genes in *C. elegans*.

Piano, F. *et al. Curr. Biol.* **12**, 1959–1964 (2002)

Integration of functional genomics approaches and protein–protein interaction data on a global scale provides an opportunity for the thorough testing of biological hypothesis. Such an integrative analysis has already been carried out in yeast, and now Walhout *et al.* have done a similar analysis for the *Caenorhabditis elegans* germline. They have combined a protein–protein interaction map (obtained from yeast two-hybrid data for 600 germline-expressed transcripts) with large-scale phenotypic analysis of germline-specific genes (based on RNA interference (RNAi) data from Piano *et al.*) and transcriptome profiling (obtained by clustering transcripts from several expression profiling experiments). They find that, in a quarter of germline interactions, both partners have RNAi phenotypes that are either embryonic lethal or masculinizing, indicating that these interactions might be most relevant for germline biology.