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Introducing the Mouse— in As, Cs, Ts, and Gs

Despite the fanfare surrounding its publication in June 2001, the sequence data from the human genome has been of limited use. This could change, however, following the publication of the genetic sequence of the mouse in the 5 December 2002 issue of *Nature*. This major milestone in biomedical research may yet provide the key to unlocking the secrets of the human genome.

Using the whole genome shotgun method, which is quicker than the clone-by-clone method used to produce the public version of the human genome, the international Mouse Genome Sequencing Consortium determined the sequence of the 2.5 billion nucleotides that comprise the genome of the C57BL/6J mouse—the strain most commonly used in biomedical research.

The *Mus musculus* genome contains roughly 30,000 genes, about 99% of which have a human counterpart. Despite having diverged from a common ancestor around 75 million years ago, the mouse and human genetic sequences are sufficiently similar that the consortium could identify long stretches where the linear order of genes has been conserved. In fact, the team was able to assemble the sequence using a physical map of the mouse genome that was based in part on the human genome sequence.

Celera Genomics (Rockville, MD) has previously published a draft sequence of the mouse genome, but the data are only available to customers willing to shell out \$15,000 per year for access. The consortium's results, however, have been deposited in public databases, making this valuable information accessible to the general scientific community.

Direct comparison of the human and mouse genetic sequence data has already proven informative, but thorough functional analysis of the newly sequenced genes will require the creation of new genetically engineered mice. Indeed, there is talk of developing knockout strains for all 30,000 mouse genes. The combined data from the mouse and human genomes will accelerate the identification of genes of particular scientific and medical interest and will increase the ease with which novel mouse models can be derived.

But with these advances will come challenges to the laboratory animal care community. These new mutant mice will require housing, characterization, and veterinary care. Many institutions are already scrambling to build new animal facilities as their existing ones fill up. Thus, the pace of new construction may, at least in part, determine the pace at which new mouse models can be created. Murine pathologists, who analyze mutant mice and diagnose often subtle or unexpected problems, are already in short supply. Without thorough phenotypic analysis, studies of mutant mice may prove fruitless, as potentially important traits can be missed. Additionally, the shortage of laboratory animal veterinarians begs the question of whether there will be an adequate veterinary presence to provide top-notch care for these mice.

The US National Human Genome Research Institute (Bethesda, MD)—one of the main funding agencies for sequencing projects—recently listed the chimpanzee and dog among the top priorities for genomic sequencing. Coupled with the fact that the Rat Genome Project is nearing completion, this means that the field of comparative genomics will continue to grow rapidly, and current issues, such as the need to expand the pipeline of veterinarians into biomedical research, will become even more important.

Tanja Schub

Tanja Schub, Editor