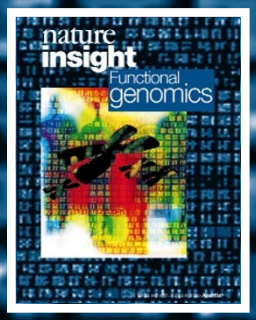
nature insight

Functional genomics



Cover illustration courtesy of Jacey.

Functional genomics has leapt from being a surrealistic, or at least futuristic, concept in the 1980s to an accepted (if not yet everyday) part of science in the year 2000. How has this transformation come about? Since worldwide efforts to sequence genomes began formally in 1990, astounding technological advances have been introduced. Among the eukaryotes, yeast, worm and fly sequences have been completed, alongside more than 20 prokaryotic genomes. The expected date for completion of the entire human genome is 2003, with a first draft due this autumn.

But what is the value of all this sequence data? An inventory of genes will impact molecular medicine the greatest, leading to improved diagnosis of disease. Sequencing of prokaryotic genomes will aid vaccine design and allow exploration of new microbial energy sources, while knowledge of other animal and plant genomes should enhance agriculture. Gaining the DNA sequences heralds the end of the beginning. The next step in this biological revolution is 'functional genomics', not simply the assignation of function to the identified genes but the organization and control of genetic pathways that come together to make up the physiology of an organism. This month's *Nature* Insight focuses on the challenges to biology brought about by the avalanche of DNA sequence information.

Vukmirovic and Tilghman provide an overview to the genomic revolution on page 820 and discuss what it will mean to scientists interested in the fundamentals of life. The progression of biology into a data-rich science has been orchestrated by computational biologists. On page 823, David Eisenberg and colleagues look at the role computers will play in predicting the function of a gene and even modelling signalling pathways in which it may act. At the molecular level, functional information can be acquired through the analysis of DNA and RNA expression arrays and on page 827 Lockhart and Winzeler examine the current status of this technology. On page 837, Pandey and Mann discuss the sophisticated machinery being used in proteomics — the large-scale analysis of proteins and their interactions. The past couple of decades have witnessed an explosion in the identification of genes for several inherited human disorders. But successes have been limited mainly to diseases caused by mutations in a single gene. Neil Risch discusses on page 847 how having the human genome at our fingertips will present new opportunities for geneticists studying complex human disorders. Finally, on page 857 Allen Roses introduces pharmacogenetics — the study of how genetic differences influence the variability in patient response to drugs and allow custom-drug design.

We are pleased to acknowledge the financial support of Aventis in producing this Insight. Of course, *Nature* carries the sole responsibility for all editorial content and rigorous peer-review. In 1953, *Nature* published the structure of the DNA helix. Today, as the first human chromosome sequences appear in our pages, we stand at the brink of the next biological revolution. We hope that our readers will find the following reviews enlightening as well as thought provoking. The sequence for the human chromosomes and published genomes can be accessed online through *Nature*'s Genome Gateway at http://www.nature.com/genomics.

Ritu Dhand Insight Editor

Publisher and liaison for corporate support Liz Allen (e.allen@nature.com)