

# Human genome sequences — a potential treasure trove, but how useful?

Imagine trying to understand a country and its culture without knowing its language. Only a comprehensive knowledge of the language would give a newcomer the tools *to begin* to explore and understand the country. Publication of the human genome sequence in February this year (see box) was a little like equipping scientists with the language of the human body.

The scientific community's reaction has been positive, but tempered by uncertainty over the time it will take for practical results to emerge. "Now," says Dr Virander Chauhan, director of the International Centre for Genetic Engineering and Biotechnology in New Delhi, India, "we can truly start to turn the genetic sequences into information important for medicine." But, cautions Dr Barry Bloom, dean of the Harvard School of Public Health in the USA, "there will be a long haul before the human genome is fully exploited — even in the West." And Dr Allan Bradley, head of the Sanger Centre in Cambridge, UK, which is

sequencing one third of the human genome, says: "When it comes to disentangling and understanding the human genetic message, we are only at the end of the beginning."

Nevertheless, no one involved in biological research doubts that publication of the human genome is a milestone. Just how the exploration will proceed, though, is anyone's guess and will depend on the complexity of the disease being studied and on the relative needs and resources of each country. "Every country has its own dynamics," says Chauhan. "In India, 50% of the population are TB carriers and we are the world's largest repository for leishmaniasis, so I am advising our department of biotechnology that TB and leishmaniasis as well as malaria and HIV should be our priorities."

Whatever the national priorities, genetic medicine has the potential to produce diagnostics, vaccines, and therapies. Already, there are sequence-based genetic tests of rare monogenetic diseases (i.e. caused by single

genes). Huntington's chorea and cystic fibrosis are two better-known examples.

These genes, says Professor Newton Morton, professor of human genetics at Southampton University, in the UK, and a member of the WHO committee on human genetics before it was disbanded, are genes which when faulty can alone have a large visible effect.

The Huntington's and cystic fibrosis genes have led to prenatal diagnostic tests and to tests that reveal whether the parents are carriers, but not yet to therapies developed directly from knowledge of the sequence. The catastrophic impact that these monogenetic diseases have and their rarity means that researchers were able to locate the individual genes by family studies, then isolate and sequence the genes. These projects were not part of the wholesale genome sequencing effort, but they showed the potential and limitations of sequence data.

Clearly diagnostic tests are important, but their value is limited, argues Bloom, "if patients do not have access to genetic

**Sequencing, genetics and medicine** A genome comprises essentially four main types of molecules, or bases — adenine, thiamine, guanine and cytosine — arranged in pairs in a double helical structure. There are 3 billion base pairs and their order carries the instructions to make a human being. Of the entire human genome sequence, only 1.1–1.4% contains genes.

Two sequences of the human genome were published simultaneously in February (see main text). They are roughly 92–94% complete. The published sequences suggest that there are 31 000 genes in the human body, far fewer than originally estimated — vs about 26 000 genes for plants, 18 000 for worms, 13 000 for flies and 6000 for yeast. One sequence was the work of the publicly funded International Human Genome Sequencing Consortium and was published in *Nature* (15 February 2001). The consortium has made its data freely available to the public via the Internet on a daily basis. Its work was undertaken by about a thousand scientists in six countries, including one developing country, China.

The other sequence and its analysis were published by the US commercial company Celera Genomics in *Science* (16 February 2001). Access to Celera's sequence data is more restricted and there has been much controversy and rivalry between the public and private ventures. The question is complex but what is clear is that Celera's entry into the mass sequencing game spurred the public effort to complete its task earlier than it would have done otherwise.

"Making the data publicly available," says Dr Virander Chauhan, director of the International Centre for Genetic Engineering and Biotechnology in New Delhi, India, "has levelled the playing field, so that for the first time a university in New Delhi can compete directly with a university such as Harvard in the States."

Though the Human Genome Project was conceived in 1985 and began in earnest in 1990, since the beginning of the century scientists have attempted to identify traits passed down through the generations. Then, with the advent of molecular biology tools, individual genes were isolated and sequenced. In the mid-1980s, biologists, mainly in the USA, began to consider sequencing the whole genome. Sequencing began in the late 1980s. About a decade later, the project got under way in earnest, moving away from earlier concerns about the function of genes and concentrating on the sequencing itself.

To transform sequence data into diagnostic tests, vaccines, and therapies, scientists have important questions to answer. Although the location of most of the genes is now known, scientists need to know which gene makes which protein, in which cell and at what stage of life. Then they need to know a protein's specific tasks and how different proteins interact with one another. Equally importantly, researchers want to know how environmental factors influence gene expression.

Now that the human genome sequence is known, the focus is firmly back on gene function, only this time researchers will be learning and exploring with an entire genetic language, not only the few words interpreted from isolated observations.

counselling about the possible consequences of their carrier status or to abortion clinics if needed”.

Science targeted the monogenetic diseases first because they could be tackled through current knowledge. The holy grail, however, is to understand the complex noncommunicable diseases — cardiovascular disease, hypertension, diabetes, cancer, mental illness — that affect all of humanity.

Morton, an expert in the genetics of complex diseases, says hundreds of genes are associated with each of these classes of disease, each gene having, perhaps, a small effect. Moreover, extragenetic factors, from diet to pollution to lack of exercise, affect regulation of the genes.

Laboratories around the world are focusing on the complex diseases. Take type 2 diabetes in the general population (as distinct from specific families), which affects adults in both developed and developing countries. To date scientists are not absolutely sure of even a single causative gene (although one gene, called Colpain 10, is a possible contributing cause of type 2 diabetes

among Mexican Americans). About a dozen locations on the human genome, however, have been identified where the DNA sequences of people with diabetes are different from those of someone without diabetes. Work to match those sequences with the human genome and to investigate whether the sites are in a region that includes genes or gene sequences regulating gene expression is now under way. The human sequence data are speeding up the process, says Dr Don Bowden, professor of biochemistry and medicine in the human genetic unit at Wake Forest University, North Carolina, USA, but it is hard to say when this work will result in either a therapy or a diagnostic kit.

For the infectious diseases there is an added hurdle: it is not just the human genome that must be understood, but also the genome of the infectious agent and, for malaria and other vector-borne diseases, of the vector. “When we have the complete sequence of the malaria parasite,” says Chauhan, “we might compare it with the human genome to find genes that are not

present in humans, and then develop a drug that kills the parasite but does not affect the human host.”

And then, of course, there are the many ethical considerations that this new technology raises. Among them are questions like: Who is to decide if and when genome data should be used to “enhance” genomes that are basically healthy (a critical question, since such re-engineered genomes could affect future generations)?

The debate on such issues has started. Whatever its outcome, though, “in 20 years time,” says Morton, “the sequence data will be central to every branch of medical science.” And as US scientist and Nobel laureate Dr David Baltimore of the California Institute of Technology wrote in *Nature’s* special genome issue (15 February 2001), “Although I’ve seen a lot of exciting biology emerge over the past 40 years ... chills still ran down my spine when I first read the paper that describes the outline of our genome.” ■

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## Measles eradication still a long way off

Until recently, many people assumed that once polio had been eradicated, measles would be next in line. Now there are doubts about whether measles could — or even should — be a target for global eradication.

Five years ago, an international meeting of experts sponsored by the US Centers for Disease Control and Prevention, the Pan American Health Organization, and WHO, recommended that the World Health Assembly should consider setting a target for the global eradication of measles some time between 2005 and 2010.

That target date has never been set. Why not?

Not because the disease no longer constitutes a major public health burden. With an annual toll of some 30 million cases and 900 000 deaths, mostly in children, it still does. Measles in fact kills more than half of the 1.6 million children who die annually from vaccine-preventable diseases. And among those who survive measles, up to 10% may suffer disabilities, such as blindness, deafness, and irreversible brain damage.

Nor is it because measles fails to meet the technical criteria for eradication. It does. Humans constitute the only natural reservoir for the causative virus and there are no healthy carriers of the virus (as there are for viral hepatitis, for example). Also, an effective vaccine has been available for over three

decades and today costs only US\$ 0.26 for a single dose, including safe injection equipment. And finally, natural immunity to the virus is of lifelong duration.

There is also evidence that interrupting transmission of the virus is possible in large areas of the world — a necessary preliminary to eradication. Several regions — foremost among them the Americas — have shown that it is operationally feasible to interrupt transmission of the disease. Transmission of measles virus has almost ceased in the Americas, where it is now believed to be confined to the Dominican Republic and Haiti. Two other WHO regions — the European and Eastern Mediterranean regions — have set targets to eliminate the disease by 2007 and 2010, respectively.

Even in sub-Saharan Africa, where transmission of the virus is intensive and where over half the world’s measles cases occur, a handful of countries have made remarkable progress in reducing the number of measles cases and deaths. In six southern African countries, mass vaccination campaigns during 1996–98 reduced reported measles deaths from over 300 in 1996 to only two between January 1999 and September 2000. In Malawi — one of the world’s poorest countries — the number of measles cases plummeted from 7000 in 1997 to

only two in 1999. And for the first time ever there were no measles deaths.

So why is there reluctance today to make plans to eradicate the disease?

One reason is the ongoing effort to eradicate polio, scheduled for 2005 (five years later than the original deadline) and now in its, hopefully, final but most difficult stage (see WHO News story p. 582). “We have to finish polio eradication before considering measles eradication,” says Dr Ana-Maria Henao-Restrepo, medical officer and measles focal point within WHO’s vaccine programme. “But in the meantime, we are working with countries throughout the world to reduce measles deaths through immunization plus, where needed, vitamin A administration. There is a lot we can do even before polio is eradicated.”

In late March this year, WHO and UNICEF issued a “global measles strategic plan” to halve measles deaths by 2005. Because measles is a highly contagious disease, the new plan calls for immunization of at least 90% of children worldwide, vs the current 74% global vaccine coverage rate. And because the initial dose of vaccine is only about 85% effective in developing countries, the plan recommends a second dose of vaccine for all children, through either routine vaccination or mass immunization campaigns. Improved surveillance and la-