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China is the first country to begin a project to sequence the whole genomes of large numbers of private individuals.

Genomics sizes up

Next-generation human genomics has arrived. The first large-scale whole-genome sequencing project has now begun in China, and an international multi-genome sequencing programme is hot on its heels.

The Yanhuang Project, which will sequence the entire genomes of 100 Chinese individuals over 3 years was announced by the Beijing Genomics Institute (BGI) on 8 January. Ye Jia, a spokeswoman for the project, said that once it is completed, the BGI aims to sequence the genomes of thousands more people, including ethnic groups from other Asian countries.

And a large international project, which aims to sequence the genomes of close to 1,000 individuals, is expected to be formally unveiled by the US National Institutes of Health in Bethesda, Maryland, and the Wellcome Trust Sanger Institute in Cambridge, UK, later this week. As yet it doesn't have a name, but is informally called the '1,000 genomes' project and the 'Multigenome project'. It will probably include the hundreds of individuals who participated in the International HapMap Project — an ongoing study of genetic diversity — as well as hundreds of other individuals.

The BGI will also participate in the 1,000 genomes project, says director Yang Huanming. However, only participants who meet the ethics and consent rules decided on by the international collaboration will be able to join that study, he says.

The projects usher in what many scientists think will be a new era of large-scale genomics — made possible with rapid-sequencing technologies — that will lead to more powerful comparisons between and within populations. Last year, scientists Craig Venter and James Watson became the first to release their complete individual DNA sequences. And a team led by George Church at Harvard University in Cambridge, Massachusetts, has begun the 'Personal Genome Project' that will examine portions of DNA from ten individuals who have agreed to share their information with the rest of the world.

But the Yanhuang Project — named after two emperors thought to be the ancestors of China's largest ethnic group — is the first to examine the entire genomes of private individuals. The first individual sequenced in the Yanhuang Project was a researcher; the second paid 10 million yuan (about US$1.4 million) to have his genome sequenced, Yang says. It is unclear whether such people will qualify for the international project, whose rules on confidentiality of data and the informed consent of participants may differ from China's.

Whole-genome sequencing studies are expected to deepen our scientific understanding of populations such as the Chinese, whose genetics have not been studied in great detail. The findings will inform medical research specific to those populations, and improve our understanding of human history, says Rasmus Nielsen of the University of California, Berkeley. "One of the exciting things about having so many sequences from Chinese individuals is that we will be able to say how much genetic exchange there has been between continents since [early humans migrated] out of Africa. That's been very hotly debated."

> **"It's going to be very useful to sequence genomes from all populations."**

The sequencing will allow scientists to add more detail to their maps of human diversity. The last large study of diversity, the HapMap, analysed only single-nucleotide polymorphisms, or SNPs — places in which DNA differs between two individuals by just one letter of the genetic code. This approach allows scientists to hunt for relatively common genetic variants. But the evidence linking disease to rare variants is growing, says Richard Myers, director of the Stanford Human Genome Center in Palo Alto, California. Whole-genome sequencing will improve detection of these rare variants, and offer a more complete understanding of the genetics of many human traits, he predicts.

"It's going to be very useful to sequence genomes from all populations and have large enough numbers so you can do comparisons between populations," Myers says. "Even if you don't care about disease, it's going to help us look at human population history and phenotypes not relevant to disease, such as craniofacial structure, eye colour, hair colour and other fascinating things." ■

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