

Gene map points to personal drugs

Scientists have completed a map of the most common differences in the human genome, which could lead to personalised treatments for diseases.

An international team mapped the entire genome of 269 people, and identified tiny differences in key areas of DNA.

The "HapMap" study will make it easier to look for genetic variations linked to common diseases such as diabetes.

But some experts said HapMap, detailed in Nature, told "half the story" as it could not be used for rare diseases.

Tagging

Humans are genetically 99.9% identical, but the remaining 0.1% accounts for important differences between people.

It will save a huge amount of time for researchers, but it is not a panacea

Dr Jim Wilson, Medical Research Council's Human Genetic Unit

Much of the genetic variation between individuals is caused by single letter differences in DNA called single-nucleotide polymorphisms (SNPs).

They are grouped into inherited families called "haplotypes", which are combinations of minute variations in DNA that have travelled together over evolutionary time.

There are thought to be around 10 million SNPs.

The multi-million pound HapMap study involved more than 200 scientists from the United States, Canada, the UK, China, Japan and Nigeria.

It looked at people from Africa, the Far East and western Europe.

It identified 300,000 SNPs which can provide around 90% of the information obtained by looking at all 10 million.

This report describes a remarkable step in our journey to understand human biology and disease

Professor Peter Donnelly

One of the lead research authors

This is because they act as "tags", indicating variations at a number of sites.

The researchers say this will mean a 20-fold cut in the cost of carrying out research into the genetic causes of disease.

HapMap data is already being used by scientists.

A UK team this year identified a genetic defect that substantially increases the risk of age-related macular degeneration, the leading cause of impaired vision in the elderly.

Other teams are using the data to look at conditions including diabetes, Alzheimer's disease, cancer, schizophrenia, asthma, high blood pressure and heart disease.

Human parts

In the HapMap research, the vast majority of both rare and common genetic differences were found in all the populations studied.

However, there was evidence some variations are linked to local geography and environment, including the Duffy blood group, which offers resistance to malaria and is almost exclusively seen in black Africans.

Professor Peter Donnelly, of Oxford University, one of the lead authors of the research, told the BBC News website: "HapMap heralds a new era in medical research.

"This report describes a remarkable step in our journey to understand human biology and disease.

"The human genome sequence provided us with the list of many of the parts to make a human.

"The HapMap provides us with indicators - like Post-It notes - which we can focus on in looking for genes involved in common disease."

Dr Panos Deloukas, from the Sanger Institute in Cambridge, said: "It has been both fascinating and rewarding to be part of this collaborative enterprise that has already mapped one million SNPs and will shortly add another two million to the map."

But Dr Jim Wilson, of the Medical Research Council's Human Genetic Unit in Edinburgh, said there were some drawbacks to HapMap.

"How well does this relate to rare variations - which might be very important.

"And how well do these three populations who were studied match what happens in other populations.

"If you were looking at a population of stroke patients in the UK, how well would they mirror what was found in HapMap.

"It will save a huge amount of time for researchers, but it is not a panacea."

The HapMap emerged from the Human Genome Project that produced the first human genetic blueprint in 2003.

Details of the HapMap project are being presented to a meeting of the American Society of Human Genetics this week.

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