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How Likely Are You To Get Sick?

A new DNA database could gauge your risk for disease

Gattaca, a science fiction movie released in 1997, portrays a dystopian future in which a person's place in society is determined by an analysis of his or her DNA, and the likelihood of disease is ascertained at birth. The movie would seem to have little connection with reality -- except that an international consortium has just completed the groundwork for a version of this future. Ultimately an individual's DNA could be decoded at an early age to spot a predisposition to illness. But here's where life improves on art: The goal will be to counter the risk of disease, not pigeonhole the person.

On Oct. 27 the three-year old International HapMap Consortium published a comprehensive catalog of more than 1 million human genetic variations, grouped in blocks called haplotypes. The DNA sequences of any two individuals are 99.9% the same, but the range of variations in the remaining 0.1% is enormous. That 0.1% is responsible for a predisposition to asthma, diabetes, cancer, heart disease, schizophrenia, and many other ailments.

The HapMap database, which is freely available to all, allows researchers to connect genetic variations to a disease. Once such a link is made, drugmakers hope to come up with a treatment that can zero in on the cause and possibly even prevent the illness. "This type of information is completely changing the way we do drug discovery," says Paul Herrling, head of corporate research for Novartis AG. "It is certainly an important step in the direction of personalized medicine."

Given the exceedingly slow pace of drug discovery, it will probably take a decade or two for new treatments to spin out from the HapMap data. But within five years doctors may be able to test a patient's DNA for variations that cause adverse reactions to any of a broad range of drugs, predicts Dr. Francis S. Collins, director of the National Human Genome Research Institute. "Ultimately each of us will have our complete DNA in a medical record," says Collins.

Such predictions were rife after the Human Genome map was completed in 2001, but they proved premature. The genome map identified only the 22,000 or so genes common to all humans, not the tiny genetic variations that make each individual unique. Mapping all the differences in the population would be a Herculean task, but geneticists discovered in 2001 that the variations regularly bunch together in haplotype blocks.

These blocks turn up over and over in the same places on the genome, across a wide range of populations. That makes them likely markers for gene-based diseases. By comparing people who have the same disease, such as diabetes, scientists hope to find which haplotypes they have in common. Lifestyle and environment would still determine whether a person with a specific variation would develop the disease. But genetic testing could at least identify susceptible individuals, who could then avoid triggers.

The HapMap consortium was formed by 15 public and private groups from the U.S., Japan, China, Nigeria, Canada, and Britain. The consortium based its research on 269 DNA samples taken from four categories of volunteers: the Yoruba tribe of Nigeria, Han Chinese in Beijing, Japanese from the Tokyo area, and people of Northern European ancestry in Utah.

Ethicists have raised concerns that such an ethnically based approach might contribute to race-based medical practices. But Dr. Aravinda Chakravati, director of genetic medicine at Johns Hopkins University, says the HapMap should diminish considerations of race in medical treatment. The consortium found that the vast majority of both rare and common genetic variations were found in all the populations studied.

Meanwhile, the group is close to finishing a second version of the HapMap with three times as much detail. The effort is already producing results: In March, using preliminary HapMap data, researchers reported the discovery of a genetic

variation that significantly increases the risk of age-related macular degeneration, the leading cause of blindness in the elderly.

As the project moves ahead, scientists admit to worrying about a Gattaca-like future. "The only adequate protection is federal legislation that would ban genetic discrimination," says Collins. One such bill has been passed by the Senate but has yet to see any action in the House. Perhaps Congress should watch the movie.

By Catherine Arnst in New York

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