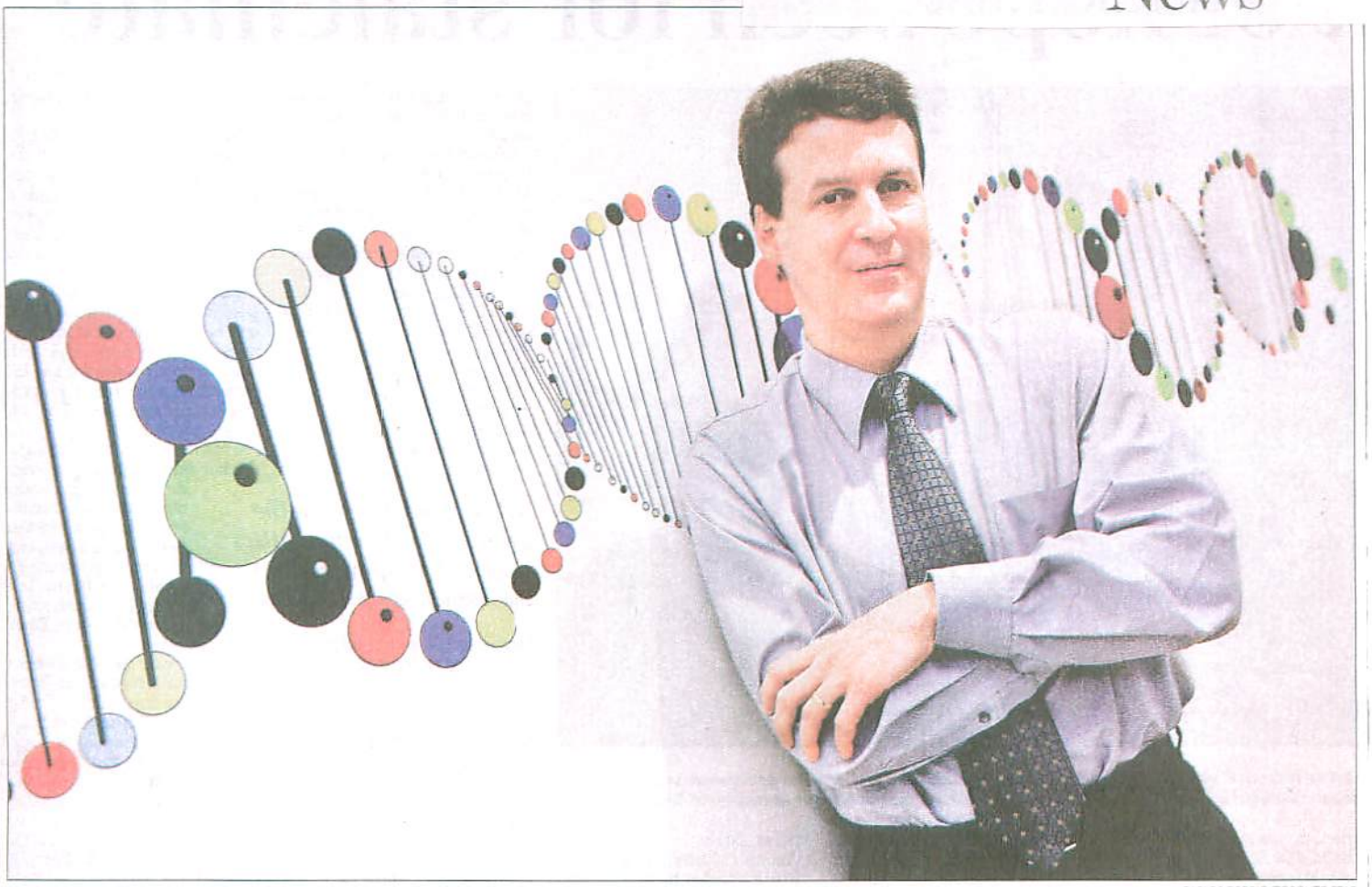
GROUNDBREAKING STUDY



CARLOS OSORIO/TORONTO STAR

Dr. Stephen Scherer, senior scientist at Sick Kids and professor of medicine at U of T, was on the research team that discovered major variations in DNA among individuals.

A genome gem uncovered

Redrawn map will boost research into the genetic variation between human beings and the origin of diseases

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HEALTH REPORTER

A Toronto-led team of international researchers has revealed a new map of the human genome that will break new ground in finding out the genetic origins of disease, including heart disease, diabetes, Alzheimer's and various cancers.

Stephen Scherer, senior scientist at the Hospital for Sick Children, has found new kinds of genetic variations hidden within the genome, which scientists say could change their entire understanding of inheritance of disease and evolution.

The study, published yesterday in the journal *Nature*, also reveals that genetic variation between humans is much greater than previously thought.

"We have a common heritage through our common humanity, but we also have a lot of differences that make us unique," says Scherer, who is also a professor of medicine at the University of Toronto. "Now we have more biology to explain the differences between brothers or cousins or spouses."

The map will soon be used in 20,000 labs around the world, says Tom Hudson, president and scientific director of the new Ontario Institute for Cancer Research.

In the six years since scientists mapped the human genome, researchers continue to find new information hidden deep within our genes. Scherer and his team discovered many hundreds of genetic variations called copy number variants (CNVs), large segments of DNA that either have an extra or missing part, as opposed to a single pair.

Scherer and his colleagues at several different research centres in the United States, Japan and Europe, used state-of-the-art technology to locate CNVs within the human genome, creating a new map that shows 1,477 new locations for this form of genetic variation.

This is a big leap forward from the Human Genome Project that helped identify millions of base-pair changes in the DNA code. These single nucleotide polymorphisms (SNPs) have been mapped in more detail and scientists have long thought that they were the primary source of genetic variation within humans.

But as Scherer continued to build on his research, the team found that CNVs had a much wider reach.

Techniques and tools gleaned from the study are immediately available to researchers in 20,000 labs around the world

They compared chunks of DNA from 270 people with African, Asian or European ancestry and found nearly 1,500 CNV regions, which covers 12 per cent of the human genome.

"We were shocked at the number of these things that we found," says Scherer, who adds that the team spent six months checking and double-checking their data to make sure it was valid. "We knew they existed, but we never predicted this many of them."

Roderick McInnes, scientific director of the Institute of Genetics at the Canadian Institutes for Health Research, says that Scherer and colleagues were right in concluding that scientists will have to incorporate CNV analysis in every new study on genomes. Last month, Scherer released the CNV map to the scientific community via his website, and scientists from all over the world, working in clinical science, evolutionary biology and basic science, began using the new database.

Hudson, a founding member of the Human Genome Project, says the CNV study is a significant step forward because the techniques and tools are immediately available to the research community. Hudson is now leading a new project called Assessment of Risk for Colorectal Tumours in Canada to find ways of predicting a person's genetic susceptibility to colon cancer. He is eager to see if CNVs can push his research forward.

Scherer says that CNVs could influence how genetic tests and personalized genome sequencing methods are developed, and may be used in the field of pharmacogenetics to explain the body's response to different drugs. CNVs could also provide clues to evolutionary biologists about how chromosomes evolved between species, he says. Scientists have found CNVs in the genome of other animal species, including mice and chimpanzees.

For Scherer, the next step is to look for CNVs at an even higher resolution to create a second-generation map and a more complete database. There are likely many, many more.

"We would like to sample 1,000 people from around the world to get a better survey of the characteristics and content of CNVs," he says.

"We want to know where all of them are in a human population and fully understand their implications in development and disease."