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Genetic GPS: Your mutations reveal where your ancestors lived

An Israeli-American research team teases out origin based on DNA, with remarkable accuracy.

By Asaf Shtull-Trauring | Jun.06, 2012 | 12:38 PM | 1

2

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Must be his side of the family: A cranium of Australopithecus sediba. Photo by Reuters

Who are you? Where were your grandparents from, and their grandparents, and theirs? Anecdotes aside, can anybody really peer into the darkness of history and know where his family originated?

That's a yes, thanks to a remarkably accurate method created by an Israeli-American research team, based on genetics, to pinpoint geographic origins. The method represents a leap forward in geneticists' ability to trace the origins of people with mosaic ancestry.

Beyond the fascinating glimpse into history that comparative genetic mapping can provide, a more immediately useful function could be to predict a propensity for certain diseases based on genetic lineage.

The researchers, Eran Halperin from Tel Aviv University and Eleazar Eskin from the University of California, Los Angeles, studied DNA samples from 1,157 people from across Europe. They analyzed about half a million genomic sites prone to mutation, forming a genetic fingerprint of mutation that differed from person to person.

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A new exhibit at Tel Aviv's Museum of the Jewish People pays tribute to volunteer soldiers now in their 80s and 90s.

By Andrew Esensten | Anglo File | 3

How therapy became a multimillion dollar industry

By Eva Illouz | Magazine | 2

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By Naomi Darom | Magazine

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By Maya Sela | Week's End

The mutations they were looking for were variations in a single nucleotide— the building blocks of DNA.

DNA is a giant polymer molecule comprised of four basic types of nucleotide: adenine (A), cytosine (C), guanine (G) and thymine (T). A mutation is when a given nucleotide, say C, gets replaced by another one, say G.

These differences between people – where a T shows up instead of a C, for instance – are known as single-nucleotide polymorphisms. While they are not necessarily expressed physiologically (though they can be), they are powerful tools for mapping genetic relations between individuals and populations.

The closer the blood relation between two people, the less likely they are to have such genetic differences.

"In our research, we think of the frequency of a given nucleotide's appearance in a certain genomic site as a function of a person's geographic origin," said Halperin.

For instance, the nucleotide C might appear at a given genomic site in 80 percent of Parisians and 40 percent of Barcelonans, he says. By combining the probabilities of certain mutations appearing across hundreds of thousands of genomic sites, Halperin and his colleagues were able to guess the geographic origins of the study's participants to within a few hundred kilometers, on average.

They found the method worked outside of Europe as well.

"We were able to map individuals from all over the world on a three-dimensional globe," says Halperin. "So it's fair to say that the approach is applicable to many populations."

One of the method's biggest advantages is that it can distinguish between the different geographic origins of a person's parents. If a person has a Barcelonan mother and a Parisian father, older methods will simply, and wrongly, assume that he is from somewhere in between – say Lyon, France, says Halperin. The new method, on the other hand, can reach the correct conclusion.

"The combined genetic fingerprint of the mother and father is manifested in the child," said Halperin. "We are able to 'reverse engineer' this information to detect the parents' origins without ever observing their genetic fingerprints directly. In principle our approach could be extended to grandparents, great grandparents, etc."

However, the further the new method reaches back, the more its geographic resolution decreases. Moreover, it can be blurred by ongoing population migrations.

"Analyses of populations such as North Americans or Jews are more complicated, because they have been mixing with other populations or mixing among themselves regardless of their geographic origins," Halperin said.

Karl Skorecki, director of medical and research development at Rambam Medical Center, was involved in similar genome-wide association studies and considers the new research "outstanding." "It adds an important further dimension to understanding the genetic architecture and demographic history of global populations and communities," Skorecki says. Not only is the new method likely to supplant existing approaches, he points out: it could even contribute to human health research one day.



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By Neri Livneh | Neri Livneh

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By Chemi Shalev | West of Eden

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By Hagai Amit | Week's End

IDF chief of staff-turned-vice premier: 'We are not bluffing'

By Ari Shavit | Magazine | 4

FEATURES

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By Avi Issacharoff | 04:23 PM |

2



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By Amir Teig, Ami Ginsburg, Inbal Orpaz | 03:56 PM



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By Anshel Pfeffer | 06:02 PM

