Are humans evolving faster? Findings suggest we are becoming more different, not alike

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Researchers discovered genetic evidence that human evolution is speeding up – and has not halted or proceeded at a constant rate, as had been thought – indicating that humans on different continents are becoming increasingly different.

“We used a new genomic technology to show that humans are evolving rapidly, and that the pace of change has accelerated a lot in the last 40,000 years, especially since the end of the Ice Age roughly 10,000 years ago,” says research team leader Henry Harpending, a distinguished professor of anthropology at the University of Utah.

Harpending says there are provocative implications from the study, published online Monday, Dec. 10 in the journal *Proceedings of the National Academy of Sciences*:

-- “We aren’t the same as people even 1,000 or 2,000 years ago,” he says, which may explain, for example, part of the difference between Viking invaders and their peaceful Swedish descendants. “The dogma has been these are cultural fluctuations, but almost any temperament trait you look at is under strong genetic influence.”

-- “Human races are evolving away from each other,” Harpending says. “Genes are evolving fast in Europe, Asia and Africa, but almost all of these are unique to their continent of origin. We are getting less alike,

not merging into a single, mixed humanity." He says that is happening because humans dispersed from Africa to other regions 40,000 years ago, "and there has not been much flow of genes between the regions since then."

"Our study denies the widely held assumption or belief that modern humans [those who widely adopted advanced tools and art] appeared 40,000 years ago, have not changed since and that we are all pretty much the same. We show that humans are changing relatively rapidly on a scale of centuries to millennia, and that these changes are different in different continental groups."

The increase in human population from millions to billions in the last 10,000 years accelerated the rate of evolution because "we were in new environments to which we needed to adapt," Harpending adds. "And with a larger population, more mutations occurred."

Study co-author Gregory M. Cochran says: "History looks more and more like a science fiction novel in which mutants repeatedly arose and displaced normal humans – sometimes quietly, by surviving starvation and disease better, sometimes as a conquering horde. And we are those mutants."

Harpending conducted the study with Cochran, a New Mexico physicist, self-taught evolutionary biologist and adjunct professor of anthropology at the University of Utah; anthropologist John Hawks, a former Utah postdoctoral researcher now at the University of Wisconsin, Madison; geneticist Eric Wang of Affymetrix, Inc. in Santa Clara, Calif.; and biochemist Robert Moyzis of the University of California, Irvine.

No Justification for Discrimination

The new study comes from two of the same University of Utah scientists

– Harpending and Cochran – who created a stir in 2005 when they published a study arguing that above-average intelligence in Ashkenazi Jews – those of northern European heritage – resulted from natural selection in medieval Europe, where they were pressured into jobs as financiers, traders, managers and tax collectors. Those who were smarter succeeded, grew wealthy and had bigger families to pass on their genes. Yet that intelligence also is linked to genetic diseases such as Tay-Sachs and Gaucher in Jews.

That study and others dealing with genetic differences among humans – whose DNA is more than 99 percent identical – generated fears such research will undermine the principle of human equality and justify racism and discrimination. Other critics question the quality of the science and argue culture plays a bigger role than genetics.

Harpending says genetic differences among different human populations "cannot be used to justify discrimination. Rights in the Constitution aren't predicated on utter equality. People have rights and should have opportunities whatever their group."

Analyzing SNPs of Evolutionary Acceleration

The study looked for genetic evidence of natural selection – the evolution of favorable gene mutations – during the past 80,000 years by analyzing DNA from 270 individuals in the International HapMap Project, an effort to identify variations in human genes that cause disease and can serve as targets for new medicines.

The new study looked specifically at genetic variations called "single nucleotide polymorphisms," or SNPs (pronounced "snips") which are single-point mutations in chromosomes that are spreading through a significant proportion of the population.

Imagine walking along two chromosomes – the same chromosome from two different people. Chromosomes are made of DNA, a twisting, ladder-like structure in which each rung is made of a "base pair" of amino acids, either G-C or A-T. Harpending says that about every 1,000 base pairs, there will be a difference between the two chromosomes. That is known as a SNP.

Data examined in the study included 3.9 million SNPs from the 270 people in four populations: Han Chinese, Japanese, Africa's Yoruba tribe and northern Europeans, represented largely by data from Utah Mormons, says Harpending.

Over time, chromosomes randomly break and recombine to create new versions or variants of the chromosome. "If a favorable mutation appears, then the number of copies of that chromosome will increase rapidly" in the population because people with the mutation are more likely to survive and reproduce, Harpending says.

"And if it increases rapidly, it becomes common in the population in a short time," he adds.

The researchers took advantage of that to determine if genes on chromosomes had evolved recently. Humans have 23 pairs of chromosomes, with each parent providing one copy of each of the 23. If the same chromosome from numerous people has a segment with an identical pattern of SNPs, that indicates that segment of the chromosome has not broken up and recombined recently.

That means a gene on that segment of chromosome must have evolved recently and fast; if it had evolved long ago, the chromosome would have broken and recombined.

Harpending and colleagues used a computer to scan the data for

chromosome segments that had identical SNP patterns and thus had not broken and recombined, meaning they evolved recently. They also calculated how recently the genes evolved.

A key finding: 7 percent of human genes are undergoing rapid, recent evolution.

The researchers built a case that human evolution has accelerated by comparing genetic data with what the data should look like if human evolution had been constant:

-- The study found much more genetic diversity in the SNPs than would be expected if human evolution had remained constant.

-- If the rate at which new genes evolve in Africans was extrapolated back to 6 million years ago when humans and chimpanzees diverged, the genetic difference between modern chimps and humans would be 160 times greater than it really is. So the evolution rate of Africans represents a recent speedup in evolution.

-- If evolution had been fast and constant for a long time, there should be many recently evolved genes that have spread to everyone. Yet, the study revealed many genes still becoming more frequent in the population, indicating a recent evolutionary speedup.

Next, the researchers examined the history of human population size on each continent. They found that mutation patterns seen in the genome data were consistent with the hypothesis that evolution is faster in larger populations.

Evolutionary Change and Human History: Got Milk?

“Rapid population growth has been coupled with vast changes in cultures

and ecology, creating new opportunities for adaptation," the study says. "The past 10,000 years have seen rapid skeletal and dental evolution in human populations, as well as the appearance of many new genetic responses to diet and disease."

The researchers note that human migrations into new Eurasian environments created selective pressures favoring less skin pigmentation (so more sunlight could be absorbed by skin to make vitamin D), adaptation to cold weather and dietary changes.

Because human population grew from several million at the end of the Ice Age to 6 billion now, more favored new genes have emerged and evolution has speeded up, both globally and among continental groups of people, Harpending says.

"We have to understand genetic change in order to understand history," he adds.

For example, in China and most of Africa, few people can digest fresh milk into adulthood. Yet in Sweden and Denmark, the gene that makes the milk-digesting enzyme lactase remains active, so "almost everyone can drink fresh milk," explaining why dairying is more common in Europe than in the Mediterranean and Africa, Harpending says.

He now is studying if the mutation that allowed lactose tolerance spurred some of history's great population expansions, including when speakers of Indo-European languages settled all the way from northwest India and central Asia through Persia and across Europe 4,000 to 5,000 years ago. He suspects milk drinking gave lactose-tolerant Indo-European speakers more energy, allowing them to conquer a large area.

But Harpending believes the speedup in human evolution "is a temporary state of affairs because of our new environments since the dispersal of

modern humans 40,000 years ago and especially since the invention of agriculture 12,000 years ago. That changed our diet and changed our social systems. If you suddenly take hunter-gatherers and give them a diet of corn, they frequently get diabetes. We're still adapting to that. Several new genes we see spreading through the population are involved with helping us prosper with high-carbohydrate diet."

Source: University of Utah