

## Ancient DNA Tells a New Human Story

Armed with old bones and new DNA sequencing technology, scientists are getting a much better understanding of the prehistory of the human species.

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By

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Imagine what it must have been like to look through the first telescopes or the first microscopes, or to see the bottom of the sea as clearly as if the water were gin. This is how students of human prehistory are starting to feel, thanks to a new ability to study ancient DNA extracted from bodies and bones in archaeological sites.

Low-cost, high-throughput DNA sequencing—a technique in which millions of DNA base-pairs are automatically read in parallel—appeared on the scene less than a decade ago. It has already transformed our ability to see just how the genes of human beings, their domestic animals and their diseases have changed over thousands or tens of thousands of years.

The result is a crop of new insights into precisely what happened to our ancestors: when and where they migrated, how much they intermarried with those they met along the way and how their natures changed as a result of evolutionary pressures. DNA from living people has already shed some light on these questions. Ancient DNA has now dramatically deepened—and sometimes contradicted—those answers, providing a much more dynamic view of the past.

It turns out that, in the prehistory of our species, almost all of us were invaders and usurpers and miscegenators. This scientific revelation is interesting in its own right, but it may have the added benefit of encouraging people today to worry a bit less about cultural change, racial mixing and immigration.

Consider two startling examples of how ancient DNA has solved long-standing scientific enigmas. Tuberculosis in the Americas today is derived from a genetic strain of the disease brought by European settlers. That is no great surprise. But there's a twist: 1,000-year-old mummies found in Peru show symptoms of TB as well. How can this be—500 years before any Europeans set foot in the Americas?

In [a study published late last year](#) in the journal *Nature*, Johannes Krause of the Max Planck Institute for the Science of Human History in Jena, Germany, and his colleagues

found that all human strains of tuberculosis share a common ancestor in Africa about 6,000 years ago. The implication is that this is when and where human beings first picked up TB. It is much later than other scientists had thought, but Dr. Krause's finding only deepened the mystery of the Peruvian mummies, since by then, their ancestors had long since left Africa.

Modern DNA cannot help with this problem, but reading the DNA of the tuberculosis bacteria in the mummies allowed Dr. Krause to suggest an extraordinary explanation. The TB DNA in the mummies most resembles the DNA of TB in seals, which resembles that of TB in goats in Africa, which resembles that of the earliest strains in African people. So perhaps Africans gave tuberculosis to their goats, which gave it to seals, which crossed the Atlantic and gave it to native Americans.

Another genetic puzzle has been the fact that most modern Europeans have certain DNA sequences that are similar to those of some American Indians but different from those of most Asians, including natives of Siberia. How can this be, since American Indians are supposedly descended from Asians who migrated across the Bering land bridge from Siberia to Alaska about 14,000 years ago? Were there ancient seafarers in the Atlantic? Or is it simply from mating between European settlers and American Indians after Columbus? Neither, as it happens.

Modern DNA could not resolve these issues, but ancient DNA provides answers. Eske Willerslev's research group at the University of Copenhagen, working with Russian scientists, read the genomes of two bits of human remains found near Lake Baikal in Siberia; one of these individuals lived 24,000 years ago, the other 17,000.

Both had genes similar to modern Europeans and modern American Indians but distinct from modern Siberians or other East Asians. As the researchers say [in a paper published early last year in Nature](#), this implies that a population of hunter-gatherers lived in northern Eurasia in the last ice age and partly gave rise to the first Americans in the East and to Europeans in the West, before they themselves died out in Siberia and were replaced by immigrants from elsewhere in Asia.

This may help to explain the enigma known as Kennewick Man, a 9,000-year-old skeleton from Washington state, which seems to have features more like those of a modern European than of a modern American Indian. The earliest inhabitants of the Americas seem to have been distant cousins of Europeans, connected through Siberia, with their genes later diluted by other Asians migrating through Alaska.

As this example shows, one of the common themes of research on ancient DNA is that the mixing of native and immigrant populations happened much more often than previously suspected. The new research allows us to identify the many different elements of that complex history. It is like watching a cake being reverse-engineered into flour, sugar, eggs, milk and its other ingredients. The familiar textbook notion that, for most of human existence, people native to one region developed in isolation from those native to a different region no longer makes sense.

A long-running debate in archaeology revolves around how to explain such key events as the advent of agriculture or the replacement of a certain type of tool by another. The key divide is over what caused the change: Did hunter-gatherers take up farming, or did farmers move in and replace hunter-gatherers? This is sometimes called the “pots versus people” debate.

Geneticists studying the genes of people alive today have leaned toward theories based on “serial founder effects” rather than on mass migrations. The idea is that while most people stayed put, small groups of farmers would have moved short distances and started new colonies, which would then have expanded. This would account for the fact that the further from Africa a population lies, the lower is its genetic diversity: The populations had been through a series of genetic bottlenecks caused by small numbers of founders.

The study of ancient DNA has challenged this view. We now know that mass migrations occurred repeatedly, overwhelming natives while absorbing some of their genes. In a study published in 2009 in the journal *Science*, analysis of ancient DNA by Joachim Burger and Barbara Bramanti of Johannes Gutenberg University in Mainz, Germany, and Mark Thomas at University College London, showed that the first farmers of central Europe could not have been descended solely from their hunter-gatherer forerunners.

In response to such research and to their own findings, Joseph Pickrell of Columbia University and David Reich of Harvard University argue that “major upheavals” of human population have been “overwriting” the genetic history of the past 50,000 years. The result, they say, is that “present-day inhabitants of many places in the world are rarely related in a simple manner to the more ancient peoples of the same region.” In short, we are none of us natives or purebred.

Perhaps the most striking example of this is a discovery announced by Dr. Reich’s team [in a paper recently published in Nature](#): Just 4,500 years ago, long after the arrival of farming in Europe from the near East—a transition that had largely displaced the genes of the indigenous hunter-gatherers—another “massive migration into the heartland of Europe from its eastern periphery” occurred. People from the steppes northeast of the Black Sea swamped the European genome with their DNA, and that relatively new pool of DNA is still ubiquitous among Europeans today.

This tips the balance in another long-running argument among anthropologists about the origin of the “Indo-European” languages. From Irish to Sanskrit, there are close similarities of vocabulary among most of the languages of Europe and those spoken in parts of Central Asia, Iran and India—connections not shared by languages like Basque, Turkish, Arabic, Hungarian and Finnish.

Two main rival theories have been offered to explain this pattern. The first holds that proto-Indo-European was spoken by the first farmers who left the fertile crescent of Syria, Turkey and Iraq for adjacent regions. The second view is that the foundational language was spoken not by these early farmers but, as certain shared words seem to

suggest, by horse-riding sheep and cattle herders who spilled out of the Ukrainian steppe a few thousand years later.

The recent research of Dr. Reich and his colleagues supports this latter hypothesis: Indo-European languages probably originated in the steppes just two millennia before the Christian era.

The discovery of the massive migration from the steppes 4,500 years ago was made possible by the analysis of DNA from 69 different individual bodies from between 8,000 and 3,000 years ago and the comparison of nearly 400,000 different sections on their genomes. This sort of massive analysis would have been impossible just a decade ago, but since the advent of low-cost, high-throughput DNA sequencing, as well as advances in statistical analysis, it is now almost routine.

Before these technical innovations, reading DNA required the laborious amplification of short segments, one at a time. By 2008, companies such as 454 Life Sciences in Branford, Conn., and the San Diego-based Illumina began marketing machines that could read millions of DNA samples in parallel. In the past, researchers wanting to study ancient or modern DNA had to sip from raindrops; now they can drink from fire hoses.

For now, such work can only be done in a few laboratories—not just because the sequencing requires big machines but also because the procedures needed to avoid contamination of ancient samples by modern DNA are elaborate and expensive, to say nothing of the skills required to analyze the massive amounts of data produced. As a result, says Greger Larson, head of a new ancient-DNA research group at Oxford University, scientists are conducting this work not at many different laboratories but in huge teams gathered around the leading experts in the field, such as David Reich at Harvard Medical School, Eske Willerslev of the University of Copenhagen or [Svante Pääbo of the Max Planck Institute for Evolutionary Anthropology in Leipzig](#).

Dr. Pääbo is best known for his achievement in sequencing the Neanderthal genome in 2009 and for his discovery that a small amount (up to 4%) of Neanderthal DNA is found in modern Europeans and other non-Africans. This suggests that when African emigrants overwhelmed the Neanderthal populations of Europe and western Asia some 40,000 to 30,000 years ago, they interbred with them to some small extent—thus anticipating the scenarios of admixture described by studies of later waves of migration.

In 2010, Dr. Pääbo and his colleagues startled the world again by discovering (from the DNA in a 50,000-year-old finger bone found in a cave at Denisova in the mountains of western Siberia) that a hitherto unsuspected third type of early human lived in Asia at this time. These “Denisovans” are as distantly related to the Neanderthals as they are to us “Africans.” A small amount (up to 6%) of their DNA survives in the genomes of Melanesians and Australian aborigines, which suggests that somewhere on their way east from Africa, probably in southeast Asia, modern humans mated occasionally with Denisovans.

Now comes evidence that Tibetans also have a Denisovan connection. In the thin air of the Tibetan plateau, the local people can survive only because of specially evolved versions of a gene called EPAS1. [In a study published last summer in Nature](#), Emilia Huerta-Sánchez and Rasmus Nielsen of the University of California, Berkeley, and their colleagues found this version of the DNA sequence around EPAS1 in the ancient genetic material of the Denisovans. Mating with Denisovans seems to have enabled people to survive at high elevations in Tibet.

Ancient DNA is telling us, in short, not only who mated with whom and when but which genes were then promoted by natural selection in the resulting offspring to improve their chances of survival. As Dr. Thomas of University College London points out, changes in the frequency of particular DNA sequences are the stuff of evolution itself. Directly measuring how DNA changed over time, by comparing samples from different periods of human history, allows us to see evolution not in the survival rates of organisms (that is, through a middleman of sorts) but in genetic material itself.

Consider, for example, the invention of farming in Europe about 8,500 years ago, a shift that caused rapid evolutionary change in the genes of Europeans as they adapted to new diets, new pathogens and new social structures. Some of this can be inferred from the study of modern DNA, but ancient DNA can catch it in the act.

[A forthcoming paper](#) by Dr. Reich's group looks at 83 individuals from the period before, during and after the arrival of agriculture. The study analyzes 300,000 different sections of their genomes and pinpoints just five genes that changed rapidly.

The strongest signal came from the mutation for lactase persistence—that is, the ability to continue digesting the milk sugar lactose after infancy. Normally, mammals don't need to digest lactose as adults, and the necessary lactase gene switches off when a baby is weaned from its mother.

This changed for human beings, however, when dairy farming introduced milk into the adult diet. A mutation that prevented the weaning switch-off spread in Europeans fairly late, around 4,300 years ago, probably long after dairy farming was invented, but it gave its possessors a significant advantage: They derived more nutrition from drinking milk (and suffered less indigestion) than their rivals.

Two genes that affect skin color were also subject to rapid evolutionary selection as early farmers tried to subsist on grain-rich, vitamin-D-poor diets in northern areas with low levels of sunlight. (Sunlight helps the body to convert a form of cholesterol into a form of vitamin D.) The shift to pale skin—which produces vitamin D more efficiently than darker skin—among northern Europeans after the advent of farming [appears to have proceeded rapidly](#), pointing to some of the strongest selection pressures ever recorded in human genetics.

Since the discovery of DNA's structure more than a half-century ago, genetic science has promised—and begun to deliver—a medical revolution, but it keeps producing other

kinds of revolutions too. In the 1990s, it transformed the field of forensics, for example, and now it is having a similar effect on history and archaeology. Today, the prehistory of humanity is an open book as never before.

The lessons of this DNA revolution are not just scientific, however; they are social and political as well. The discoveries made possible by our new access to ancient DNA show that very few people today live anywhere near where their distant ancestors lived. Virtually no one on the planet is a true native—an instructive fact to consider at a time when ethnic and national differences still abound and the world continues to throw human beings together in new and unexpected ways.

*Mr. Ridley is the author of “The Rational Optimist: How Prosperity Evolves” and “The Evolution of Everything: How Ideas Emerge,” to be published in November.*

<http://www.wsj.com/articles/ancient-dna-tells-a-new-human-story-1430492134>