

Genetic makeup of modern Europeans derived through ancient migrations from Asia

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Astounding research in four scientific papers published on January 10 in *Nature*, show that the genetic makeup of modern Europeans was largely determined through migration waves from Asia starting 45,000 years ago, and not from the adaptation to the local environment, as was previously thought.

The studies indicate that diseases such as multiple sclerosis (MS) that are prevalent in northern European populations entered via these migrations. Differences in height between taller northern Europeans and shorter southern Europeans also resulted from the migrations.

Lluís Quintana-Murci, population geneticist at the Pasteur Institute in Paris, who was not involved in the study told *Nature*, “This is a tour de force.” He explained that the research provides unprecedented detail on how ancient ancestry can influence disease risk to this day, saying, “It’s a beautiful example of how, by addressing very basic fundamental anthropological and genomic questions, you can inform medicine.”

The studies involved a large international team of 175 scientists led by evolutionary geneticist Professor Eske-Willerslev at the universities of Cambridge and Copenhagen, and Clinical Professor Thomas Werge at the University of Copenhagen, and statistical geneticist Professor Rasmus Nielsen at the University of California, Berkeley.

The researchers extracted and sequenced the DNA of 317 ancient European skeletons aged between 3,000 and 11,000 years old. These were compared to an existing database of 1,300 ancient Eurasian gene sequences. Researchers were able to develop a gene map of Eurasia, sampling the bones and teeth of 5,000 humans who lived across the land mass from 34,000 years ago. The extracted ancient DNA was compared to that of modern populations.

“Creating a gene bank of ancient DNA from Eurasia’s past human inhabitants was a colossal project, involving collaboration with museums across the region,” said Willerslev.

The research was made possible by the DNA revolution, the fact that genomes can be sequenced on a mass basis relatively cheaply and that ancient genetic material can be extracted from fossil remains.

Modern Europeans are the result of three migration waves, with the first roughly 45,000 years ago by hunter-gatherers from Asia. The second wave were farmers from the Middle East, who arrived 11,000 years ago. The last migration wave, about 5,000 years ago, consisted of pastoralists and animal herders from western Asia and

eastern Europe.

A comparison of the age, burial location and genetic characteristics of the human remains enabled the scientists to develop a genetic map and determine how the genetic makeup of the populations changed over time. Willerslev and his team found that the steppe pastoralists mostly went to northern Europe, while the Middle Eastern farmers went to the south and west.

The researchers who contributed to the paper “Population genomics of post-glacial western Eurasia” found that in some cases the new populations totally replaced the established population.

“Large-scale ancestry shifts occurred in the west as farming was introduced, including near-total replacement of hunter-gatherers in many areas, whereas no substantial ancestry shifts happened east of the zone during the same period,” the researchers state.

A similar shift occurred across Europe when the previously existing hunter-gatherer population was replaced by the Yamnaya people, who spread across western Eurasia about 5,000 years ago. The process is thought to have taken place over about 1,000 years.

The Yamnaya people are thought to have originated in what is today western Russia’s Don River basin. They became known from an excavation at a graveyard called Golubaya Krinitisa in 1903 with remains the researchers now think were from about 7,300 years ago. Previously archaeologists dated the remains at around 5,400 to 5,300 years ago.

The Yamnaya people are named after their burial practices of placing their human remains in tumuli (mounds) with simple pit chambers. The name Yamnaya means related to the pits in Russian. They are thought to have inhabited a large part of south-west Asia.

When the Yamnaya people arrived in Europe, they mated with the people known as the eastern European Globular Amphora Culture, known from their distinctive dome-shaped ceramic vessels. The resulting hybrid population known as the Corded Ware Culture became dominant in the area and then migrated to northern Europe.

The Corded Ware Culture was named after their distinctive pottery found in archaeological excavations. They are thought to have inhabited an extensive area in central Europe from the Rhine to the Volga rivers.

The Corded Ware Culture was a “hybrid population adapted rapidly to its new surroundings and formed a dominant culture,” evolutionary biologist Morten Allentoft, of Curtin University in

Perth, Australia and an author of the paper, told *Science*.

According to archaeologist Volker Heyd of the University of Helsinki, who did not participate in the new research, “These genetic discoveries align with previous archaeological evidence.”

Intriguingly, the Yamnaya migration introduced the gene associated with Multiple Sclerosis (MS) into northern European populations. Northern Europeans have double the incidence of MS than southern Europeans. Some scientists think that MS is the result of infection with the Epstein-Barr virus, but others feel there is a genetic basis for the disease.

MS is an autoimmune disease that damages the outer lining of nerve cells in the brain and spinal cord. The disease is thought to have once given a biological advantage in resisting diseases humans may have acquired from their herd animals. The neolithic period saw the development of agricultural societies, resulting in an increased prevalence of diseases due to humans living in denser populations.

The research reported in “Elevated genetic risk for multiple sclerosis emerged in steppe pastoralist populations” was led by computational biologist William Barrie from the University of Cambridge.

“Our analyses indicate that MS gene variants helped people survive in the past,” Barrie told an online news conference held by the researchers in Copenhagen in January.

Barrie and his group compared ancient Eurasian DNA to DNA collected from 410,000 white British people. The researchers looked at gene changes associated with MS.

Barrie et al. stated, “The last 10,000 years have seen some of the most extreme global changes in lifestyle, with the emergence of farming in some regions and pastoralism in others. While 5,000 years ago farmer ancestry predominated across Europe, a relatively diverged genetic ancestry arrived with the steppe migrations around this time. We have shown that this genetic ancestry contributes the most genetic risk for MS today and that these variants were the result of positive selection coinciding with the emergence of a pastoralist lifestyle on the Pontic-Caspian steppe and continued selection in the subsequent admixed populations in Europe.”

They also found evidence that genes associated with Alzheimer’s disease and Type 2 diabetes were brought to Europe by the migration of the Yamnaya people. It is not clear if those genes gave any adaptive advantage to the population.

Their genetic influence on today’s population of southern Europe is much weaker.

In another paper by Assistant Professor of Molecular Ecology and Evolution at the University of Copenhagen, Evan K. Irving-Pease and his team, “The selection landscape and genetic legacy of ancient Eurasians,” examines the transition with the Holocene period that began around 12,000 years ago and is characterized by the development of agriculture. This period saw enormous changes in human diet and general lifestyle as people started living in denser communities, which meant more likely exposure to pathogens.

The researchers found that strong selection in the HLA region of chromosome 6 that influences the immune system in this period. They found that selection occurred near the *LCT* locus,

responsible for the formation of the protein lactase, which enables lactase persistence but predates the emergence of the gene by thousands of years. This is the mechanism that enabled the digestion of milk to persist into adulthood.

In “100 ancient genomes show repeated population turnovers in Neolithic Denmark,” Morten Allentoft and his team sequenced genomes from 100 skeletons spanning 7,300 years of the Mesolithic period, Neolithic period and Early Bronze Age in Denmark. This is a critical period in human culture as it spanned the latter part of hunter-gatherer society in Europe, followed by the development of agricultural communities, up to the formation of urban societies.

The scientists found, genetic homogeneity from around 10,500 to 5,900 years before the present when neolithic farmers from Anatolia arrived. The researchers ascertained there was a very rapid population turnover thereafter, with very limited evidence of the original hunter-gatherers.

Allentoft and his team stated, “The succeeding Neolithic population, associated with the Funnel Beaker culture, persisted for only about 1,000 years before immigrants with eastern Steppe-derived ancestry arrived. This second and equally rapid population replacement gave rise to the Single Grave culture with an ancestry profile more similar to present-day Danes.”

The four papers have made an invaluable contribution, illuminating the complex history of human evolution. They show that modern Europeans are the result of mass migrations and the repeated mixing and intermingling of a variety of populations.

Importantly, this research provides critical scientific evidence against the very concept of “race,” first advanced during the period before the development of modern anthropology and genetics, and now associated with the crisis and decline of world capitalism. Science completely refutes the racist programme being promoted by the political elite of all countries against immigrants in order to divide the working class.



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