ANTHROPOLOGY CURRENT AFFAIRS MAGAZINE
MAY 2020

VISHNUIAS.COM

WE PROVIDE A PATH FOR YOUR SUCCESS

CURRENT AFFAIRS ANTHROPOLOGY

A MAGAZINE FOR CIVIL SERVICES PREPARATION

(Welcome To Vishnu IAS online)

(Research and Training Institute for the best civil services preparation in India)

Telegram link – https://t.me/vishnuiasmentor http://vishnuias.com/

(+91-7702170025)

CONTENTS

10. Supercomputer model simulations reveal cause of Neanderthal extinction

11. Tracing the evolution of self-control

12. Neandertals were choosy about making bone tools

13. Research shows even animals benefit from social distance to prevent disease

14. Earliest evidence of Italians' extraordinary genetic diversity dates back to 19,000 years ago

15. Maharashtra Governor modifies law on forest rights

16. Dozens of mammoth skeletons found under future Mexico City airport

1. Ancient DNA unveils important missing piece of human history

Newly released genomes from Neolithic East Asia have unveiled a missing piece of human prehistory, according to a study conducted by Prof. Fu Qiaomei's team from the Institute of Vertebrate Paleontology and Paleoanthropology (IVPP) of the Chinese Academy of Sciences.

The study, published in *Science* on May 14, reveals that population movement played a profound role in the early genetic history of East Asians.

The researchers used advanced ancient DNA capture techniques to retrieve ancient DNA from 25 individuals dating back 9,500-4,200 years and one individual dating back 300 years from northern and southern East Asia. The newly sequenced DNA casts a spotlight on an important period in East Asia's early history: the transition from hunter-gathering to agricultural economies.

One hypothesis for population movement in East Asia is that during the Neolithic, a "second layer" of agriculturalists replaced a "first layer" of hunter-gatherers in East and Southeast Asia. While the genetics of ancient humans in Southeast Asia, Siberia, and the Japanese archipelago have been well-studied, little has been known until now about the genetics of ancient humans in northern and southern China.

Prof. Fu and her team found that these Neolithic humans share the closest genetic relationship to present-day East Asians who belong to this "second layer." This suggests that by 9,500 years ago, the primary ancestries composing the genetic makeup of East Asians today could already be found in mainland East Asia.

Skull of Qihe 2, a 8400 old individual from qihe cave Fujian

While more divergent ancestries can be found in Southeast Asia and the Japanese archipelago, in the Chinese mainland, Neolithic populations already displayed genetic features belonging to present-day East Asians.

Notably, this includes the Early Neolithic southern East Asians dating to ~8,000 years from this study that should have been "first layer" early Asians, according to the earlier hypothesis. In fact, Prof. Fu and her team showed that they shared a closer relationship to present-day "second layer" East Asians. Thus, the results of the current study fail to support a "two layer" dispersal model in Neolithic East Asia in this area.

The scientists also found that Early Neolithic East Asians were more genetically differentiated from each other than present-day East Asians are. In early Neolithic East Asia since 9,500 BP, a northern ancestry existed along the Yellow River and up into the eastern steppes of Siberia, distinct from a southern ancestry that existed along the coast of the southern Chinese mainland and islands in the Taiwan Strait since 8,400 BP.

Population movement may have already started impacting East Asians by the Late Neolithic. For example, the Late Neolithic southern East Asians may have shared a connection to coastal northern East Asians and the former's ancestry may have extended north as well.

Today, most East Asian populations are not clearly separated into two distinct groups. Present-day mainland East Asians from both the north and south share a closer genetic relationship to northern Neolithic East Asians along the Yellow River than to southern Neolithic East Asians on the southern coast of China.

Further analyses show that they are almost all a mixture of northern and southern ancestry from Neolithic East Asia, with northern ancestry playing a larger role. Population movement, particularly from the north along the Yellow River southward was a prominent part of East Asian prehistory after the Neolithic. Interestingly, present-day Han Chinese in all provinces, north and south, show a similar amount of northern and southern influences.

Southern ancestry, while less represented in mainland East Asia today, had extensive influence on other regions. Present-day Austronesian speakers, who share a close genetic relationship to present-day mainland East Asians but live across a wide swath of islands in Southeast Asia and the Southwest Pacific, show a remarkably close genetic relationship to Neolithic populations from the southern coast of China.

Archaeological materials dating back to the Middle Neolithic have long hinted at the connection between Austronesian islanders and populations in mainland East Asia. Now, the genetic relationships uncovered by Prof. Fu and her team show unambiguous evidence that Austronesian speakers today originated from a proto-Austronesian population that derived from southern China at least 8,400 year ago. The history revealed by these 26 ancient humans highlights the profound impact that population movement and mixture had on human history, but they also reveal continuity that extends back

9,500 years. Unlike in Europe, influences from Central Asia had no role in the formation of East Asian ancestry, with mixing largely occurring regionally between northern and southern populations in East Asia.

The whole slate of ancestries present across East Asia during the Neolithic is still unknown, as genome-wide data have not been retrieved from many inland regions of mainland East Asia.

But coastal connections between ancient populations in Siberia, Japan, China, and Southeast Asia suggest that as more ancient DNA is retrieved and studied, a complex history of population contact and admixture in East Asian human prehistory will be revealed.

2. Chimpanzees help trace the evolution of human speech back to ancient ancestors

Summary:

> One of the most promising theories for the evolution of human speech has finally received support from chimpanzee communication.

The evolution of speech is one of the longest-standing puzzles of evolution. However, inklings of a possible solution started emerging some years ago when monkey signals involving a quick succession of mouth open-close cycles were shown to exhibit the same pace of human spoken language.

In the paper 'Chimpanzee lip-smacks confirm primate continuity for speech-rhythm evolution', published today, the 27th May, in the journal *Biology Letters*, a consortium of researchers, including St Andrews University and the University of York, led by the University of Warwick, have found that the rhythm of chimpanzee lip-smacks also exhibit a speech-like signature -- a critical step towards a possible solution to the puzzle of speech evolution.

Just like each and every language in the world, monkey lip-smacks have previously shown a rhythm of about 5 cycles/second (i.e. 5Hz). This exact rhythm had been identified in other primate species, including gibbon song and orangutan consonant-like and vowel-like calls.

However there was no evidence from African apes, such as gorillas, bonobos and chimpanzees -- who are closer related to humans, meaning the plausibility of this theory remained on hold.

Now, the team of researchers using data from 4 chimpanzee populations have confirmed that they too produce mouth signals at a speech-like rhythm. The findings show there has been most likely a continuous path in the evolution of primate mouth signals with a 5Hz rhythm. Proving that evolution recycled primate mouth signals into the vocal system that one day was to become speech.

African great apes, the closest species to humans, had never been studied for the rhythm of their communication signals. Researchers investigated the rhythm of chimpanzee lip-smacks, produce by individuals while they groom another and found that chimpanzees produce lip-smacks at an average speech-like rhythm of 4.15 Hz.

Researchers used data across two captive and two wild populations, using video recordings collected at Edinburgh Zoo and Leipzig Zoo, and recordings of wild communities including the Kanyawara and the Waibira community, both in Uganda.

Dr Adriano Lameira, from the Department of Psychology at the University of Warwick comments:

"Our results prove that spoken language was pulled together within our ancestral lineage using "ingredients" that were already available and in use by other primates and hominids. This dispels much of the scientific enigma that language evolution has represented so far. We can also be reassured that our ignorance has been partly a consequence of our huge underestimation of the vocal and cognitive capacities of our great ape cousins.

"We found pronounced differences in rhythm between chimpanzee populations, suggesting that these are not the automatic and stereotypical signals so often attributed to our ape cousins. Instead, just like in humans, we should start seriously considering that individual differences, social conventions and environmental factors may play a role in how chimpanzees engage "in conversation" with one another.

"If we continue searching, new clues will certainly unveil themselves. Now it's a matter of mastering the political and societal power to preserve these precious populations in the wild and continue enabling scientists to look further."

3. Dual hand use in early human relative

Summary:

Research by anthropologists has identified hand use behavior in fossil human relatives that is consistent with modern humans. The human lineage can be defined by a transition in hand use. Early human ancestors used their hands to move around in the trees, like living primates do today, whereas modern human hands have evolved to primarily perform precision grips.

Research by anthropologists at the University of Kent has identified hand use behaviour in fossil human relatives that is consistent with modern humans.

The human lineage can be defined by a transition in hand use. Early human ancestors used their hands to move around in the trees, like living primates do today, whereas modern human hands have evolved to primarily perform precision grips.

However, new research led by Dr Christopher Dunmore, Dr Matthew Skinner and Professor Tracy Kivell from Kent's School of Anthropology and Conservation has revealed that the hand of an ancient human relative was used for both human-like manipulation as well as climbing.

Their discovery came from analysing and comparing the internal bony structures of fossil knuckle and thumb joints from the hands of several fossil species from South Africa, eastern Africa and Europe. These included: *Australopithecus sediba*, *Australopithecus africanus*, *Australopithecus afarensis*, *Homo neanderthalensis* and *Homo sapiens* dated between 12 thousand and three million years old.

The knuckles at the base of *Australopithecus sediba*'s fingers were found to have an internal trabecular structure consistent with branch grasping, but that of their thumb joints is consistent with human-like manipulation. This unique combination is different to that found in the other *Australopithecus* species studied and provides direct evidence that ape-like features of this species were actually used, probably during in climbing. Furthermore, it supports the idea that the transition to walking on two legs was gradual in this late surviving member of the *Australopithecus* genus.

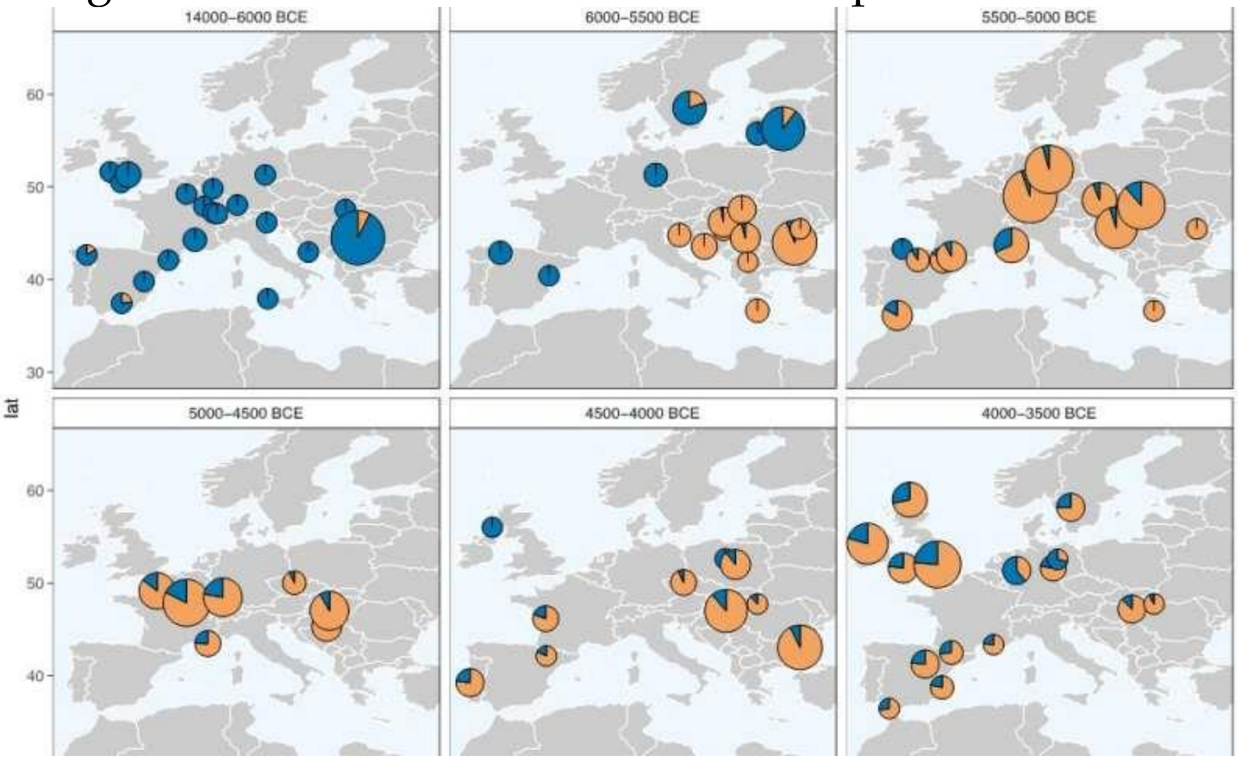
Dr Dunmore said: 'Internal bone structures are shaped by frequent behaviours during life. Therefore, our findings can support further research into the internal structure of hands in relation to stone tool use and production. This approach may also be used to investigate how other fossil hominin species moved around and to what degree climbing might have remained an important part of their lifestyle.'

Professor Kivell said: 'The internal bone structure can reveal hidden evidence that gives us insight into how our fossil human relatives behaved. We were really excited to see this particular hand-use pattern in *Australopithecus sediba* as it was so different from other australopiths. The fossil record is revealing more and more diversity in the ways our ancestors moved around, and interacted with, their environments - the human evolutionary story is even more complex and interesting than we previously thought.'

4. Heightened interaction between neolithic migrants and hunter-gatherers in Western Europe

Summary:

This study reports new genome-wide data for 101 prehistoric individuals from 12 archaeological sites in today's France and Germany, dating from 7000-3000 BCE, and documents levels of admixture between expanding early Neolithic farmers and local hunter-gatherers seen nowhere else in Europe.



Maps showing inherited genetic component from hunter-gatherer (blue) and Anatolian Neolithic (orange) populations along time slices. The expansion of the Anatolian component carried by Neolithic migrants and the differences in proportions observed regionally and chronologically illustrate the diversity of processes at work during the Neolithic expansion in Europe.

The Neolithic lifestyle, including farming, animal domestication and the development of new technologies, emerged in the Near East around 12,000 years ago and contributed profoundly to the modern way of life. The Neolithic spread rapidly across Europe, mainly along the Danube valley and the Mediterranean coastline, reaching the Atlantic coast around 5000-4500 BCE. The existing archaeogenetic data from prehistoric European farmers indicates that the spread of farming is due to expanding populations of early farmers who mixed little, if at all, with indigenous hunter-gatherer groups. However, until now, no archaeo genetic data were available for France.

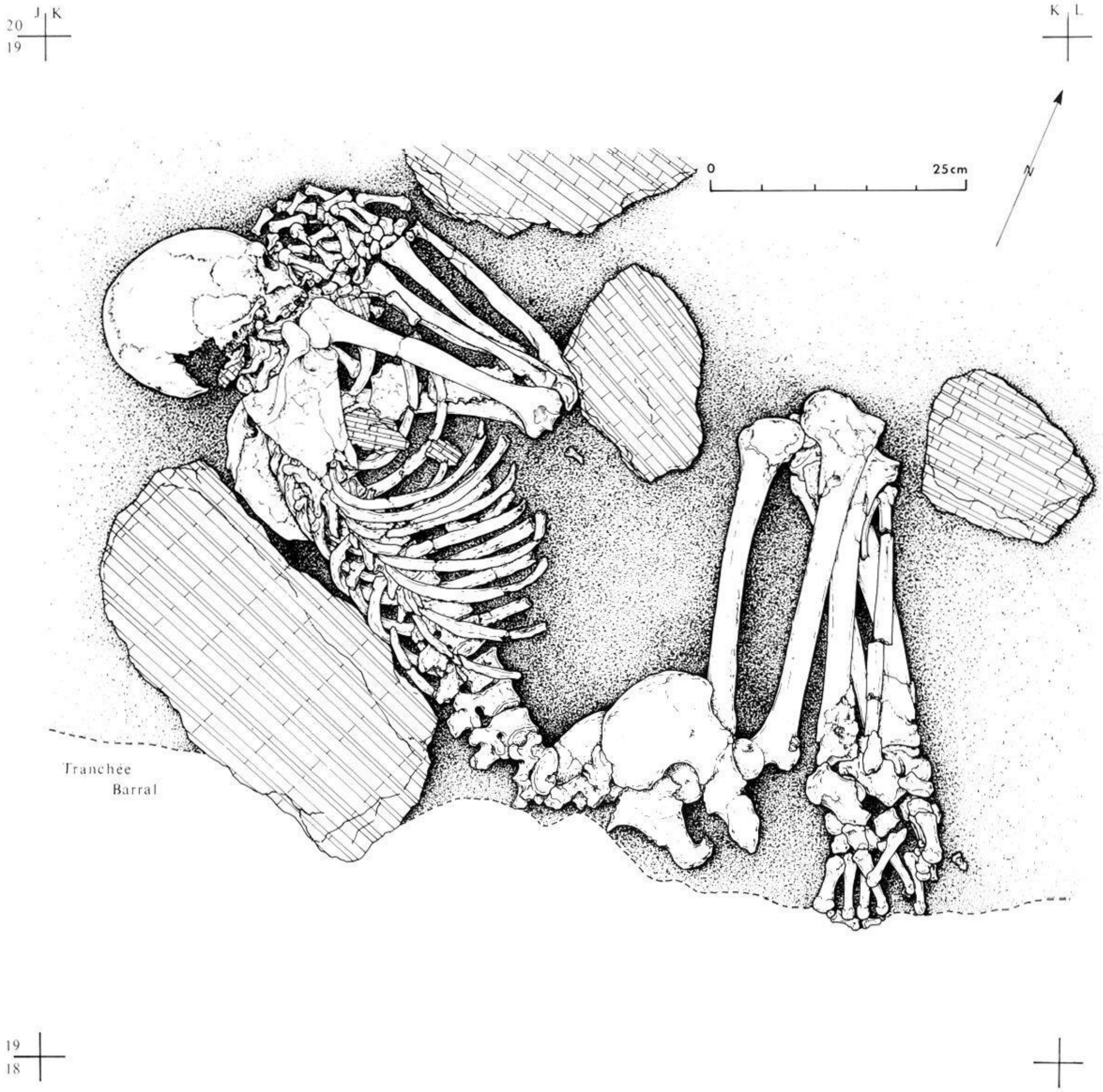
"France is where the two streams of the Neolithic expansion overlapped, so understanding how these groups interacted would fill in a big piece of the puzzle," says Wolfgang Haak, senior author of the study. "The data we're collecting suggests a more complex scenario than elsewhere in Europe, with more interaction between early farmers and hunter-gatherers."

These interactions seem to vary greatly from one region to another, attesting to a diverse cultural mosaic in early Neolithic Western Europe. In order to document the biological interactions during this transition period, researchers from the Max Planck Institute for the Science of Human History teamed up with colleagues from the

PACEA laboratory (1*) in Bordeaux, the CEPAM laboratory (2*), the RGMZ (3*), and other international partners. The study, published in *Science Advances*, reports new genome-wide data for 101 prehistoric individuals from 12 archaeological sites in today's France and Germany, dating from 7000-3000 BCE

High levels of hunter-gatherer ancestry in early farmers from France

The new results showed evidence for a higher level of admixture, or the combination of genetic information from genetically distant populations, between early migrant farmers and local hunter-gatherers in France. The genetic mixture in this region is unprecedented in the rest of Europe for the early stages of the Neolithic expansion. The genetic contribution of hunter-gatherers is particularly high in the south of France, roughly 31% on average, compared with 3% in Central Europe or 13% in the Iberian Peninsula.



The burial of Pendimoun F2 (5480-5360 BC), woman carrying about 55% of hunter-gatherer component.

Intriguingly, in an individual from the Pendimoun site in Provence (5480-5360 BCE), the genetic contribution of local hunter-gatherers was as high as 55%. The team could show that the admixture in this individual occurred recently, about four generations before, shortly after the first Neolithic farmers settled on that part of the French coast. "These findings suggest continuous contacts between both groups for at least a century."

Genetic evidence for the two routes of the Neolithic expansion

Leveraging the genetic substructure observed in European hunter-gatherers, the team was able to retrace the dynamics of admixture in various European regions. Neolithic farmers in central Europe carry a very small hunter-gatherer component, which had already been mixed in and brought in from southeastern Europe. This accounts for the rapid spread of Neolithic groups with a negligible amount of interaction with local hunter-gatherers. On the other hand, Neolithic farmers from west of the Rhine river (in France, Spain, Great Britain) carry a genetic component inherited from local Mesolithic groups, implying a process of late and local admixture.

The new data highlight the complexity and regional variability of biological and cultural interactions between farmer and hunter-gatherer communities during the Neolithic expansion. "This study shows that we can add a lot more detail with focused sampling and unravel the regional dynamics of the farmer-forager interactions." "With the increasing amount of genetic data, we gain the much-needed resolution to investigate biological processes in the past and to understand their relations with observed cultural phenomena."

5. Homo naledi juvenile remains offers clues to how our ancestors grew up

This rare case of an immature fossil hominin sheds light on the evolution of human development

Summary:

A partial skeleton of Homo naledi represents a rare case of an immature individual, shedding light on the evolution of growth and development in human ancestry, according to a study.

Much research has gone into the evolution of ancient hominins -- human relatives and ancestors -- but little is known about their growth and development. Most hominin fossils represent adult individuals, and remains of developmentally young hominins are rare. This has left a gap in our understanding of how our ancient relatives grew from young into adults, and how modern human growth patterns evolved.

In this study, Bolter and colleagues examined fossils from the Dinaledi Chamber of the Rising Star Cave System in South Africa. This site is famous for providing abundant remains of the hominin *Homo naledi*, including individuals ranging from infants to adult. These fossils date to the late

Middle Pleistocene, between 335,000 and 226,000 years ago, possibly overlapping in time with the earliest members of our own species. The team identified a collection of arm and leg bones and a partial jaw as the remains of a single young individual designated DH7.

The bones and teeth of DH7 were not fully developed and display a mixture of maturity patterns seen in modern humans and earlier hominins. DH7 is estimated to be similar in its developmental stage to immature specimens of other fossil hominins between 8-11 years old at death. The authors note, however, that if *Homo naledi* had a slower growth rate like modern humans, DH7 might have been as old as 15. Further study is needed to assess how *Homo naledi* grew and where it fits into the evolution of human growth and development.

Bolter adds: The rare juvenile *Homo naledi* partial skeleton will shed light on whether this extinct species is more human-like in its development, or more primitive. The findings help reconstruct the selective pressures that shaped extended maturity in our own species.

6. Increased fertility for women with Neanderthal gene, study suggests

Summary:

One in three women in Europe inherited the receptor for progesterone from Neanderthals -- a gene variant associated with increased fertility, fewer bleedings during early pregnancy and fewer miscarriages, according to new research.

One in three women in Europe inherited the receptor for progesterone from Neandertals -- a gene variant associated with increased fertility, fewer bleedings during early pregnancy and fewer miscarriages. This is according to a study published in *Molecular Biology and Evolution* by researchers at the Max Planck Institute for Evolutionary Anthropology in Germany and Karolinska Institutet in Sweden.

"The progesterone receptor is an example of how favourable genetic variants that were introduced into modern humans by mixing with Neandertals can have effects in people living today," says Hugo Zeberg, researcher at the Department of Neuroscience at Karolinska Institutet and the Max Planck Institute for Evolutionary Anthropology, who performed the study with colleagues Janet Kelso and Svante Pääbo.

Progesterone is a hormone, which plays an important role in the menstrual cycle and in pregnancy. Analyses of biobank data from more than 450,000 participants -- among them 244,000 women -- show that almost one in three women in Europe have inherited the progesterone receptor from Neandertals. Twenty-nine percent carry one copy of the Neandertal receptor and three percent have two copies.

Favourable effect on fertility

"The proportion of women who inherited this gene is about ten times greater than for most Neandertal gene variants," says Hugo Zeberg. "These findings suggest that the Neandertal variant of the receptor has a favourable effect on fertility."

The study shows that women who carry the Neandertal variant of the receptor tend to have fewer bleedings during early pregnancy, fewer miscarriages, and give birth to more children. Molecular analyses revealed that these women produce more progesterone receptors in their cells, which may lead to increased sensitivity to progesterone and protection against early miscarriages and bleeding.

The research was supported by the NOMIS Foundation and the Max Planck Society.

7. Information technology played key role in growth of ancient civilizations

Summary:

> A new article shows the ability to store and process information was as critical to the growth of early human societies as it is today.

When it comes to the great civilizations of human history, the pen really might have been mightier than the sword.

That's according to a new paper in Nature Communications that shows the ability to store and process information was as critical to the growth of early human societies as it is today.

"There's a fundamental relationship between the way in which societies process information and how large they are able to become," said Tim Kohler, an archaeologist at Washington State University and a corresponding author of the paper. "Early innovations in information processing such as writing and coinage appear to be as important to the sociopolitical development of our ancestors as something like the internet is to us today."

For their study, Kohler and colleagues at the Santa Fe Institute set out to discover more about the role information technology played in the growth of human societies from the Neolithic to the last millennium.

They dug into what's called the Seshat Global History Databank, a massive assembly of historical and archaeological information spanning more than 400 societies, six continents and 10,000 years of human history.

The databank enabled the researchers to quantitatively analyze things like how large were civilizations when they developed writing, systems of coinage and other innovations in information processing and what were the effects of these advances on the growth of the overall state.

Their findings show that sociopolitical development historically underwent three phases. Initially, population growth was the dominant force in a society's complexity.

Then, once a civilization reached a certain size, it needed to develop more sophisticated ways of dealing with information and economic transactions, through inventions like writing and currency. Once these innovations were discovered, the society could once again continue growing in size and scale.

"Our findings show that ancient civilizations ran into an information bottleneck when they reached a certain size, a point we call the scale threshold. "Without innovations like writing or a system of currency, further expansion became very rare. However, once these advances in information processing and storage were achieved, you start to see the big empires of history emerge."

One of the more intriguing findings of Kohler and colleagues' study is a possible explanation for the technology gap that existed between old and new world societies.

Their work shows very few civilizations in the ancient Americas ever crossed the scale threshold. Consequently, there was less pressure to develop writing and other forms of information processing in the Americas that spurred further technological development in Europe and Asia.

"One of the main reasons we think the vast majority of Native American civilizations never reached the scale threshold was the absence of horses, oxen and other large animals capable of carrying people or sizeable loads,". "Such animals helped create agricultural surplus, facilitated trade and generally facilitated the expansion of empire in Europe and Asia."

Moving forward, the researchers hope to use the Seshat database to investigate other intriguing, long-standing questions from history such as why did some civilizations collapse when there weren't any apparent external causes such as natural disaster, famine or war.

"We think as the Seshat database gets larger and larger there will be more data points and we will be able investigate these kinds of questions,".

The researchers' work could also have interesting implications for the study of contemporary society.

"We have enormous new capabilities for storing and processing data that are just well beyond the scope of anything in the past,". "Does this imply that we're going to have another growth in scale for human civilizations? And if so, what would that look like?"

8. Migration patterns reveal an Eden for ancient humans and animals

Summary:

Researchers have discovered a new migration pattern (or lack of) at Pinnacle Point, a now-submerged region in South Africa. While it was first believed large omnivores would travel to follow the growth of vegetation to survive, our researcher came to a completely new conclusion through studying

> antelope teeth! They discovered that this region was an Eden to all living species that called it home, including the earliest humans.

Pinnacle Point, a series of archaeological sites that overlook a now submerged section of South Africa's coastline and one of the world's most important localities for the study of modern human origins, was as much of an Eden for animals as it was for early humans. Jamie Hodgkins, PhD, assistant professor of anthropology at University of Colorado Denver, and her team drilled ancient herbivore teeth to find that many local animals stayed put in the ecologically rich ecosystem, which may explain why humans flourished there, too.

Home to the Earliest Modern Humans

Home to some of the richest evidence for the behavior and culture of the earliest clearly modern humans, the submerged shelf called the Palaeo-Agulhas Plain (PAP) once formed its own ecosystem. Co-author Curtis Marean, PhD, Arizona State University, has worked with teams of scientists for decades to reconstruct the locale back into the Pleistocene, the time period that spanned from 2.6 million to 11,700 years ago.

In this study, the researchers looked specifically at antelope migratory patterns at Pinnacle Point. This series of cave sites that sit on the modern South African coast offers archaeological materials from humans who were living and hunting there back to 170,000 years ago.

"During glacial cycles, the coastal shelf was exposed," said Hodgkins. "There would have been a huge amount of land in front of the cave sites. We thought it was likely that humans and carnivores were hunting animals as they migrated east and west over the exposed shelve."

A Lack of Migratory Pattern

Hodgkins and her team wanted to understand those migratory patterns. They studied the carbon and oxygen isotopes within the tooth enamel of many large herbivores, including *Redunca*, or reedbuck, a nonmigratory antelope. Tooth enamel can reveal a pattern of migration by tracking changing levels of carbon from the plants an animal eats as its teeth grow.

In general, wetter, cooler environments are home to C3 plants; hotter, drier environments are home to C4 plants. Animals like lush vegetation, which means they tend to follow the rain patterns: in this case east for summer rain (C4 grasses), and west for winter rain (C3 grasses). If animals were migrating between summer and winter rainfall zones, their tooth enamel would register that annual C3 and C4 plant rotation as a sinusoidal curve as their teeth grew.

A) Map of South Africa (SA) showing the distribution of C4 grasses associated with the percentage of summer rain from east to west along the coast, and with the winter rainfall zone in the west (modified from Vogel, 1978); B) A map of SA showing the area of the Greater Cape Floristic Region with the expanded PAP and hypothesized animals migration (i.e. It is hypothesized that animals would have been undertaking long-distance migrations between the east coast in summer rainfall zone and west coast in the winter rainfall zone)

But when Hodgkins and her team used the nonmigratory reedbuck as their control animal, they found that the enamel from its typically migratory pals -- like the wildebeest, hartebeest, and springbok -- showed no discernible migratory pattern. Most animals seemed happy right where they were.

"They weren't struggling at Pinnacle Point," says Hodgkins. "We now know that powerful river systems supplied the expanded coast, thus animals didn't have to be migratory. It was a great location, resource-wise. During interglacials when the coast moved closer to the caves humans had shellfish and other marine resources, and when the coast expanded in glacial times hunters had access to a rich, terrestrial environment. Hunters wouldn't need to be as mobile with all of these herbivores wandering around."

Thriving in an Ecogeological Haven

Hodgkins' team's findings of this prehistoric Eden echoed another recent discovery. Seventy-four-thousand years ago, one of Earth's largest known eruptions at Mount Toba in Sumatra, Indonesia, created a global winter, causing population crashes. In 2018, researchers from Marean's group found that humans at Pinnacle Point not only survived, but thrived in the haven.

Hodgkins says this is just a first attempt at using isotopic data to test the hypothesis of east and west migration patterns at these sites and further research will be done.

"It is quite possible that animal migration patterns changed as the coastline moved in and out during glacial and interglacial cycles," said Hodgkins.

Funders for this project include the National Science Foundation, the Hyde Family Foundations, and the John

Templeton Foundation at the Institute of Human Origins (IHO) at Arizona State University.

9. Reexamining the origins of human fatherhood

Dads emerged to reap the benefits of partnerships with females and other males, researchers say

Summary:

The origins of paternal care, a key differentiator between humans and other primates, have long been tied to ancestral females trading their own sexual fidelity for food provided by their mates. A new theory developed by economists and anthropologists states that ecological changes, beginning roughly 5-8 million years ago, placed a premium on partnerships -- both between and within sexes -- and fueled the emergence of males who provided food for their offspring.

Humans differ from other primates in the types and amounts of care that males provide for their offspring. The precise timing of the emergence of human "fatherhood" is unknown, but a new theory proposes that it emerged from a need for partnership in response to changing ecological conditions, U.S. and French researchers report in the *Proceedings of the National Academy of Sciences*.

The new theory was developed using tools of economists and knowledge of the economic and reproductive behavior of human foragers. The theory focuses on the benefits of a "fit" between exclusive partners that enabled the strengths of males and females to provide for one another and their offspring, according to researchers from Boston College, Chapman University, University of New Mexico, and the University of Toulouse in France.

Scientists have long tried to explain how human fatherhood emerged. Paternal care -- those investments in offspring made by a biological father -- is rare among mammals but widespread across modern human subsistence societies. Much of men's parental investment consists of provisioning relatively helpless children with food for prolonged periods of time -- for as long as two decades among modern hunter-gatherers. This is a sharp break with other great apes, whose observed mating systems do not encourage paternal provisioning.

That paternal provisioning arose in humans seems remarkable and puzzling and has revolved around a discussion about two groups of males dubbed "Dads" and "Cads."

With promiscuous mating, a would-be Dad who provides food for a mate and their joint offspring without seeking additional mates risks being outcompeted in terms of biological fitness by a Cad, who focuses only on promiscuous mating instead of investing in offspring. Such a competitive disadvantage creates a formidable barrier for Dads to emerge when Cads abound.

An oft-invoked explanation for the evolution of paternal provisioning in humans is that ancestral females started mating preferentially with males who provided them with food, in exchange for female sexual fidelity. This explanation is insufficient for several reasons, the researchers write.

Instead, the team of anthropologists and economists argues that ecological change would have sufficed to trigger the spread of Dads, even in the face of female sexual infidelity, according to the report, "Paternal provisioning results from ecological change."

The key force in the theory of paternal provisioning is complementarities -- in essence the cooperation between females and males, as well as between males. Complementarities are synergistic effects that increase per-capita benefits, which may arise from dividing labor and/or pooling resources. The path to complementarities began roughly five to eight million years ago, with a gradual drying in Africa, and a progressively greater need to rely on nutritious, diverse, spatially dispersed and relatively hard-to-obtain foods, including animal products.

In response to ecological change, ancestral hominins adapted in various ways, including efficient bipedal locomotion, dietary flexibility, and an ability to thrive in diverse environments, facilitated by tool use. Complementarities between males and females would have resulted from the nutrients that each sex specialized in acquiring: protein and fat acquired by males paired well with carbohydrates acquired by females.

Complementarities between males would have resulted from higher returns from hunting in groups instead of in isolation, and from food sharing to lower starvation risk.

Dietary reliance on animal products is thus a key feature underlying these complementarities between and within sexes.

These complementarities would have led to a substantial increase in the impact of food provided by a Dad on the survival of his mate's offspring.

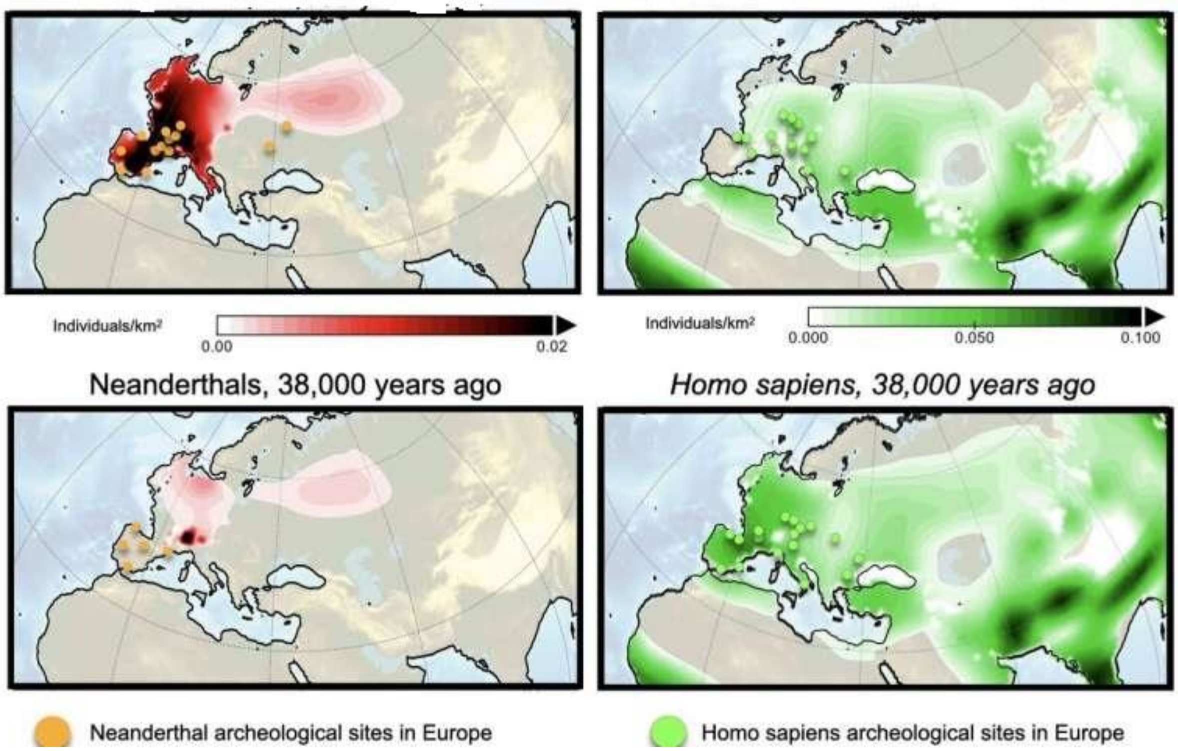
Using evolutionary game theory, the authors show that this impact can lead Dads to gain a fitness advantage over Cads, although Cads may still co-exist with Dads under certain conditions. If sons inherit their biological father's traits, then over time Dads will increase in number in a population. Theoretically connecting the evolution of paternal provisioning to ecological change allows the authors to make novel predictions about the paleontological and archeological record.

10. Supercomputer model simulations reveal cause of Neanderthal extinction

Summary:

> Climate scientists discover that according to new supercomputer model simulations, only competition between Neanderthals and Homo sapiens can explain the rapid demise of Neanderthals around 43 to 38 thousand years ago.

Neanderthals, 43,000 years ago Homo sapiens 43,000 years ago



Climate scientists from the IBS Center for Climate Physics discover that, contrary to previously held beliefs, Neanderthal extinction was neither caused by abrupt glacial climate shifts, nor by interbreeding with *Homo sapiens*. According to new supercomputer model simulations, only competition between Neanderthals and *Homo sapiens* can explain the rapid demise of Neanderthals around 43 to 38 thousand years ago

Neanderthals lived in Eurasia for at least 300,000 years. Then, around 43 to 38 thousand years ago they quickly disappeared off the face of the earth, leaving only weak genetic traces in present-day *Homo sapiens* populations. It is well established that their extinction coincided with a period of rapidly fluctuating climatic conditions, as well as with the arrival of *Homo sapiens* in Europe. However, determining which of these factors was the dominant cause, has remained one of the biggest challenges of evolutionary anthropology.

To quantify which processes played a major role in the collapse of Neanderthal populations one needs to use mathematical models that can realistically simulate the migration of Neanderthals and *Homo sapiens*, their interactions, competition and interbreeding in a changing climatic environment. Such models did not exist previously.

In a new paper published in the journal *Quaternary Science Review*, Axel Timmermann, Director of the IBS Center for Climate Physics at Pusan National University, presents the first realistic computer model simulation of the extinction of Neanderthals across Eurasia. The model which is comprised of several thousands of lines of computer code and is run on the IBS supercomputer Aleph, solves a series of mathematical equations that describe how Neanderthals and *Homo sapiens* moved in a time-varying glacial landscape and under shifting temperature, rainfall and vegetation patterns. In the model both hominin groups compete for the same food resources and a small fraction is allowed to interbreed. The key parameters of the model are obtained from realistic climate computer model simulations, genetic and demographic data.

"This is the first time we can quantify the drivers of Neanderthal extinction," said Timmermann. "In the computer model I can turn on and off different processes, such as abrupt climate change, interbreeding or competition" he said. By comparing the results with existing paleo-anthropological, genetic and archeological data, Timmermann demonstrated that a realistic extinction in the computer model is only possible, if *Homo sapiens* had significant advantages over Neanderthals in terms of exploiting existing food resources. Even though the model does not specify the details, possible reasons for the superiority of *Homo sapiens* could have been associated with better hunting techniques, stronger resistance to pathogens or higher level of fecundity.

What exactly caused the rapid Neanderthal demise has remained elusive for a long time. This new computer modeling approach identifies competitive exclusion as the likely reason for the disappearance of our cousins. "Neanderthals lived in Eurasia for the last 300,000 years and experienced and adapted to abrupt climate shifts, that were even more dramatic than those that occurred during the time of Neanderthal disappearance. It is not a coincidence that Neanderthals vanished just at the time, when *Homo sapiens* started to spread into Europe" says Timmermann. He adds "The new computer model simulations show clearly that this event was the first major extinction caused by our own species."

A research team at the IBS Center for Climate Physics is now improving the computer model to also include megafauna and implement more realistic climate forcings. "This is a new field of research in which climate scientists can interact with mathematicians, geneticists, archeologists and anthropologists," said Axel Timmermann.

11. Tracing the evolution of self-control

Summary:

Advances in the craftsmanship of stone hand axes around 500,000 years ago suggest individuals at this time possessed characteristics which demonstrate significant self-control, such as concentration and frustration tolerance.

Human self-control evolved in our early ancestors, becoming particularly evident around 500,000 years ago when they developed the skills to make sophisticated tools, a new study suggests.

While early hominins such as Homo erectus could craft basic hand axes as early as 1.8 million years ago, our hominin ancestors began to create more elaborate and carefully designed versions of these tools sometime before 500,000 years ago.

The authors of the study, from the University of York, say these advances in craftsmanship suggest individuals at this time possessed characteristics which demonstrate significant self-control, such as concentration and frustration tolerance.

The study highlights a collection of 500,000 year-old flint axes unearthed from a gravel quarry in the village of Boxgrove in West Sussex. The axes are highly symmetrical suggesting careful workmanship and the forgoing of immediate needs for longer term aims.

Senior author of the study, Dr Penny Spikins, from the Department of Archaeology said: "More sophisticated tools like the Boxgrove hand axes start to appear around the same time as our hominin ancestors were developing much bigger brains.

"The axes demonstrate characteristics that can be related to self-control such as the investment of time and energy in something that does not produce an immediate reward, forward planning and a level of frustration tolerance for completing a painstaking task.

"In the present day our capacity for self-control has become particularly important. Without the advanced levels of self-control we possess as a species, lockdown would be impossible. It takes self-control to put the needs of the community first rather than focus on our own immediate ends. Our study offers some clues as to where in human history this ability originated."

The researchers also point to evidence that the production of highly symmetrical and elaborate axes would have required knowledge and skill accumulated over a life time.

In one study, it took people trying to replicate the axes discovered at Boxgrove 16 hours of practice to even produce a recognisable handaxe.

Lead author of the study, James Green, a PhD student in the Department of archaeology at the University of York, added: "By deciphering the mental and physical processes involved in the production of prehistoric artefacts, we can gain valuable insights into the abilities of the individuals who made them.

"These axes demonstrate social learning and effortful activity directed at honing skills. They also provide some of the earliest evidence of something being deliberately made in a sequence from a picture in someone's mind.

"Self-control is not unique to humans, but may have played an important role in our evolution. It's key to many of the traits which define modern humans such as pro-sociality, cooperation and caring for the vulnerable."

12. Neandertals were choosy about making bone tools

Evidence continues to mount that the Neandertals, who lived in Europe and Asia until about 40,000 years ago, were more sophisticated people than once thought. A new study from UC Davis shows that Neandertals chose to use bones from specific animals to make a tool for specific purpose: working hides into leather.

Naomi Martisius, research associate in the Department of Anthropology, studied Neandertal tools from sites in southern France for her doctoral research. The Neandertals left behind a tool called a lissoir, a piece of animal rib with a smoothed tip used to rub animal hides to make them into leather. These lissoirs are often worn so smooth that it's impossible to tell which animal they came from just by looking at them.

Martisius and colleagues used highly sensitive mass spectrometry to look at residues of collagen protein from the bones. The method is called ZooMS, or zooarchaeology by mass spectrometry. The technique breaks up samples into fragments that can be identified by their mass to charge ratio and used to reconstruct the original molecule.

Normally, this method would involve drilling a sample from the bone. To avoid damaging the precious specimens, Martisius and colleagues were able to lift samples from the plastic containers in which the bones had been stored and recover enough material to perform an analysis.

Favoring bovine ribs over deer

The results show that the bones used to make lissoirs mostly came from animals in the cattle family, such as bison or aurochs (a wild relative of modern cattle that is now extinct). But other animal bones from the same deposit show that reindeer were much more common and frequently hunted for food. So the Neandertals were choosing to use only ribs from certain types of animals to make these tools.

"I think this shows that Neandertals really knew what they were doing," Martisius said. "They were deliberately picking up these larger ribs when they happened to come across these animals while hunting and they may have even kept these rib tools for a long time, like we would with a favorite wrench or screwdriver."

Bovine ribs are bigger and more rigid than deer ribs, making them better suited for the hard work of rubbing skins without wearing out or breaking.

"Neandertals knew that for a specific task, they needed a very particular tool. They found what worked best and sought it out when it was available," Martisius said.

13. Research shows even animals benefit from social distance to prevent disease

Microorganisms living inside and on our body play a crucial role in both the maintenance of our health and the development of disease. Now researchers at UTSA have uncovered evidence about the importance of maintaining physical distance to minimize the spread of microbes among individuals.

The scientists observed monkeys in the wild to understand what role genetics, diet, social groupings and distance in a social network play when it comes to the microbes found inside an animal's gut.

"Social microbial transmission among monkeys can help inform us about how diseases spread. This has parallels to our current situation in which we are trying to understand how social distancing during the COVID 19 pandemic and future disease outbreaks may influence disease transmission," said Eva Wikberg, an assistant professor in UTSA's Department of Anthropology who studies the interaction between ecology, behavior and genetics in primates.

The gut microbiome refers to all the microorganisms inhabiting the digestive tract, starting with the stomach and ending with the colon. Over the past decade the microbiome has come under more scientific focus because it's believed that an unhealthy gut microbiome can lead to obesity, impaired immune function, weakened parasite resistance and even behavioral changes.

However, researching microbiomes is difficult because of the variation in microbial composition between individuals. One long-standing question is whether this variation is driven by genetic makeup, diets or social environments.

This research inquiry has been especially hard in wild populations because of the lack of detailed data necessary to tease apart the myriad factors that shape the microbiome.

To find an answer, Wikberg and fellow researchers studied the fecal matter of 45 female colobus monkeys that congregated in eight different social groups in a small forest by the villages of Boabeng and Fiema in Ghana. The scientists saw major differences among social groups' gut microbiomes.

However, individuals from different groups that were more closely connected in the population's social network had more similar gut microbiomes. This discovery indicates that microbes may be transmitted during occasional encounters with members of other social groups.

A similar setting may be when people come into one-meter proximity of each other at a store. Being in close proximity or accidentally brushing up against someone else may be all it takes to transmit certain microbes.

This study suggests that microbes transmitted this way help the colobus monkeys digest the leaves in their diet. However, further research is needed to investigate whether this type of transmission yields health benefits, which could explain why different social groups occasionally have friendly between-group encounters.

"Studies of wild animals can teach us a lot about the importance of using interventions, such as social distancing, to ensure a safer community during this pandemic," said Wikberg.

14. Earliest evidence of Italians' extraordinary genetic diversity dates back to 19,000 years ago

In Europe, Italians have the highest genetic diversity. The gradient of their genetic variability, scattered all over the peninsula, encloses on a small scale the whole genetic variance between southern and continental Europeans. This amazing diversity started to accumulate soon after the Late Glacial Maximum, which ended approximately 19,000 years ago.

This is what researchers of the University of Bologna have reported in a paper published in *BMC Biology* . It is the first time that researchers have traced Italians' genetic history. Results also show that there are genetic peculiarities characterizing people living in the north and south of Italy that evolved in response to different environments. These peculiarities contribute to reducing the risk of kidney inflammation and skin cancers, and the risk of diabetes and obesity, favoring a longer lifespan.

"Gaining an understanding of the evolutionary history of the ancestors of Italians allows us to better grasp the demographic processes and those of environmental interactions that shaped the complex mosaic of ancestry components of today's European populations," explains Marco Sazzini, one of the principal investigators of this study and professor of molecular anthropology at the University of Bologna. "This investigation provides valuable information in order to fully appreciate the biological characteristics of the current Italian population. Moreover, it let us understand the deep causes that can impact on this population's health or on its predisposition to a number of diseases."

An unexpected outcome

To carry out this study, researchers sequenced the entire genome of 40 participants who were selected as representatives of the biological variability of the Italian population with a good approximation. The analysis brought to the fore more than 17 million genetic variants. Scientists then made a twofold comparison. First, they compared these data against the genetic variants observed in other 35 populations from Europe and from the Mediterranean. Second, they compared the same data against the genetic variants found in studies on almost 600 human remains dating from the Upper Palaeolithic (approx. 40,000 years ago) to the Bronze Age (approx. 4,000 years ago).

These comparisons reached such high levels of precision that it was possible to extend the investigation to very remote time periods with respect to those achieved by previous studies. Eventually, the researchers identified traces left in the gene pool by events that followed the last glaciation, which ended more or less 19,000 years ago.

The bulk of the scholarship in this field has so far suggested that the oldest events leaving a trace in Italian

DNA were the migrations during the Neolithic and the Bronze Ages, between 7,000 and 4,000 years ago. The results of this study show, on the contrary, that the earliest biological adaptations to the environment and migrations underlying Italians' extraordinary genetic diversity are much older than previously thought.

Climate changes and post-glacial migrations

Researchers traced the evolutionary history of the two groups at the opposite ends of Italians' gradient of genetic variability. This means that they evaluated and measured differences between the gene pools of participants from southern and northern Italy and observed when these differences became evident.

"We observe some partially overlapping demographic trends among the ancestors of these two groups from 30,000 years ago and for the remaining years of the Upper Palaeolithic," says Stefania Sarno, researcher at the University of Bologna and one of the co-first authors of the paper. "However, we observed a significant variation between their gene pools from the Late Glacial period, thus some thousands of years before those great migrations that happened in Italy from the Neolithic onward."

Here, the main hypothesis is that with temperatures rising and glaciers shrinking, some groups of people who made it through the glaciation period thanks to "glacial refugia" in central Italy, moved north and drifted away, thus progressively isolating themselves from the inhabitants of southern Italy.

The DNA of people living in northern Italy shows traces of these post-glacial migrations. If compared to individuals from southern Italy, Italians from the north present a close genetic relation to human remains attributed to ancient European cultures such as the Magdalenian and the Epigravettian cultures and dated respectively between 19,000 and 14,000 years ago and between 14,000 and 9,000 years ago. Moreover, in northern Italians' gene pool, the researchers observed ancestry components that were even more ancient, such as those proper of eastern European hunter-gatherers, which are thought to characterize all European populations between 36,000 and 26,000 years ago, and that later on spread to western Europe with migratory movements from "glacial refugia" during the Late Glacial period.

Conversely, in southern Italians, these post-glacial migrations traces seem to vanish, as more recent events significantly reshaped their gene pool. This is confirmed by their closer genetic relation with Neolithic human remains from Anatolia and the Middle East, and with Bronze-Age remains from south Caucasus. Differently from the north of Italy, the south was a main hub for migratory movements, which first spread agriculture to the Mediterranean area during the Neolithic transition, and then, during Bronze Age, fostered a new ancestry component. The latter differs from the ancestry component associated with populations of the Eurasian steppe that spread during the same time across continental Europe and northern Italy.

Genetic adaptations: differences and peculiarities across Italy

Nineteen thousand years ago, after the end of the Last Glacial Maximum, ancestors of northern and southern Italians started living in increasingly different environmental and ecological contexts, which gradually led to the emergence of differences and peculiarities in their gene pools.

For millennia, the populations resettling in northern Italy endured abrupt climate changes and environmental pressures similar to those of the Last Glacial Maximum. These circumstances brought to the evolution of specific biological adaptations. For instance, populations in northern Italy developed a metabolism optimized for a diet rich in calories and animal fat, which are essential to survive in cold climates. "In the subjects from northern Italy, we observed changes in the gene networks regulating insulin and body-heat production as well as in those responsible for fat tissue metabolism," says Paolo Garagnani, professor of experimental medicine and pathophysiology at the University of Bologna. "These changes could have resulted in key factors reducing the susceptibility to diseases like diabetes and obesity."

While this was happening in northern Italy, in the south, a warmer climate exposed its populations to different kinds of environmental pressures. The genomes of people from southern Italy show changes in the genes encoding for mucins, which are proteins found in the mucous membranes of the respiratory and gastrointestinal systems and that prevent pathogens from attacking the tissues. "These genetic adaptations may have evolved in response to ancient micro-organisms," says Paolo Abondio, Ph.D. student at the University of Bologna and another co-first author of this study. "Some scholars have linked some of these genetic variants with a reduced susceptibility to Berger's disease, which is a common inflammation affecting the kidneys and is indeed less frequent in the south than in the north of Italy."

Researchers also identified other peculiarities in the genome of southern Italians. For example, there are some modifications in the genes regulating the production of melanin, the pigment that provides colour to the skin. Most probably, these alterations developed in response to more intense sunlight and to a higher number of sunny days that characterise the Mediterranean regions. In turn, these alterations may also have contributed to a lower incidence of skin cancers among southern Italians.

"We observed that some of these genetic variants have been also linked to a longer lifespan. This is also true for other genetic modifications which are characteristic of southern Italians. These are found on genes involved in the arachidonic acid metabolism and on those encoding for FoxO transcription factors," according to Claudio Franceschi, emeritus professor of the University of Bologna.

The study, titled "Genomic history of the Italian population recapitulates key evolutionary dynamics of both Continental and Southern Europeans," was published in *BMC Biology*.

15. Maharashtra Governor modifies law on forest rights

Context: Maharashtra Governor Bhagat Singh Koshyari has modified the Scheduled Tribes and Other Traditional Forest Dwellers (Recognition of Forest Rights) Act, 2006, allowing rightful claimants of forest rights to appeal against decisions of the district level committee (DLC).

The Governor has modified Section 6 of the Act, in its application to Scheduled Area of the State of Maharashtra, in exercise of the powers conferred on him by Schedule V of the Constitution.

Significance:

- The notification is important to provide justice to tribals whose 'individual or community forest right' has been rejected by the DLC, constituted under the Forest Rights Act (FRA).

- The notification applies to areas covered in the Panchayats (Extension to Scheduled Areas) Act in the State and allows appeal provision against the DLC's decision.
- The notification states that divisional level committees under the chairmanship of divisional commissioners have been constituted to hear the appeals against the DLC's decisions. In the case of an order passed by the DLC before commencement of the notification, the appeal needs to be made within six months. However, if an order has been passed after commencement of the notification, the application has to be made within 90 days.

Criticisms:

Activists, however, are concerned that this will lead to further delays in implementation of forest laws. They say the notification is a double-edged sword. A tribal farmer will find it difficult to go to the district headquarters. They fear this committee will further delay implementation of FRA. Delay means denial of justice and increased scope for fake claims.

What is 5th schedule?

The Fifth Schedule of the Constitution deals with the administration and control of Scheduled Areas as well as of Scheduled Tribes residing in any State other than the States of Assam, Meghalaya, Tripura and Mizoram.

Special Provisions for Fifth Schedule Areas:

1. The **Governor of each State having Scheduled Areas (SA)** shall annually, or whenever so required by the President, make **a report to the President regarding the administration of Scheduled Areas in that State.**
2. The **Union Government shall have executive powers to give directions to the States as to the administration of the Scheduled Areas.**
3. Para 4 of the Fifth Schedule provides for establishment of **a Tribes Advisory Council (TAC)** in any State having Scheduled Areas.
4. **Composition**: Consisting of not more than twenty members of whom, three-fourths shall be the representatives of the Scheduled Tribes in the Legislative Assembly of the State. If the number of representatives of the STs in the Legislative Assembly of the State is less than the number of seats in the TAC to be filled by such representatives, the remaining seats shall be filled by other members of those Tribes.
5. **Functions**: The TAC shall advise on such matters pertaining to the welfare and the advancement of the STs in the State as may be referred to them by the Governor.

The Governor may make rules prescribing or regulating:

1. The number of members of the Council, the mode of their appointment and the appointment of the Chairman of the Council and of the officers and servants thereof, the conduct of its meetings and its procedure in general.
2. The Governor may, by public notification, direct that **any particular Act of Parliament or of the Legislature of the State shall or shall not apply to a SA or any part thereof in the State, subject to such exceptions and modifications, as specified.**
3. The Governor may make regulations for the peace and good government of any area in the State which is for the time being a SA. Such regulations may prohibit or restrict the transfer of land by or among members of the Scheduled tribes in such area; regulate the allotment of land to members of the STs in such area.
4. In making such regulations, **the Governor may repeal or amend any Act of Parliament or of Legislature of the State or any existing law after obtaining assent of the President.**

16. Dozens of mammoth skeletons found under future Mexico City airport

A team of archaeologists have found the remains of more than 60 mammoths at the site of a new airport being built to serve Mexico City. Excavators have also

found animal and human bones in the area.

© picture-alliance/AP/M. Tapia

A team of archaeologists working near Mexico City has discovered the remains of more than 60 mammoths at the city's future airport.

Mexico's National Institute of Anthropology and History (INAH) said the bones, found at the construction site of the planned Felipe Angeles International Airport, date back some 15,000 years.

The remains were uncovered close to the spot where the airport's future control tower is to be built. INAH excavators have been working at the site – some 50 kilometers (about 30 miles) north of the capital – since April last year, seeking animal remains from the Pleistocene era.

The team reported in December that that it had found the bones of a far smaller number of animals at the old Santa Lucia Air Base, a military airport being converted for civilian use.

The area was formerly submerged under the Xaltocan Lake, part of the Mexican Basin and a focal point of the country's pre-Colombian civilization. Traps for the hunting of mammoths, thought to have been dug soon after the lake dried up, were found at the site last year.

Almost all of the giant skeletons are thought to belong to the Colombian mammoth species.

Other types of fauna, including bison, camels and horses were also found, as well as bones of humans buried in the pre-Hispanic era and various artefacts.

"The main challenge is that the richness of fauna and relics is greater than we had considered," Pedro Francisco Sánchez Nava, INAH's national anthropology coordinator told.