Paleogenetics, Part 11, 2022

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September 2022
Science Update

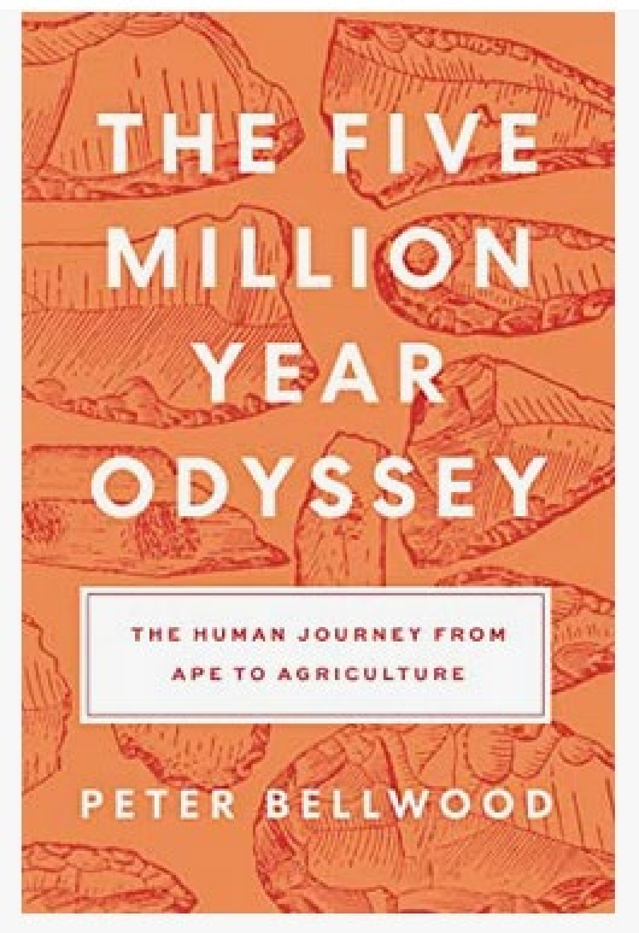
If MH and N are 99.7% genetically identical, how can MHs have 2% Neandertal

- The 99.7% refers to all 3 Billion base pairs of your genome, thereby leading to a 0.3% difference between MHs and Ns.

- You have ~2% N DNA.

- The 2% refers to 2% of that 0.3% difference -- roughly 0.0006% of 3 billion, or 180,000 N base pairs.

The Five Million Year Odyssey – Peter Bellwood



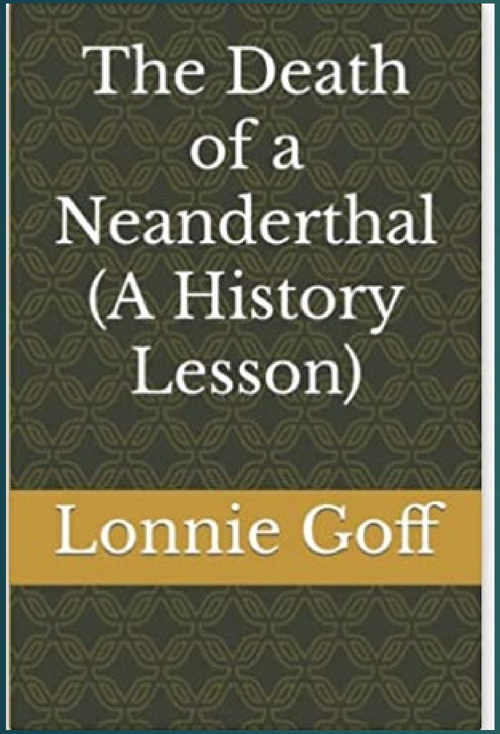
Archeologist Peter Bellwood, one of the foremost expert on the spread of farming and human migrations

Reviews Human evolution, emphasizing movement and migrations

Believes farmers, and not the Yamnaya, introduced Indo-European languages to Europe

Author of 2004 book *First Farmers*

The Death of a Neanderthal by Lonnie Goff, 2022


The Death
of a
Neanderthal
(A History
Lesson)
Lonnie Goff

A 40-year old Neanderthal died in Northern Iraq 50,000 years ago.
His death was not an accident. It was the culmination of something that had happened in Southern Africa a very long time ago. It was a snapshot of a new world order.

An 100-page review of the bow and arrow in human history

Neptune has rings? Five. New image from James Webb Space Telescope

4D scans of fetuses

- 4D ultrasound scans of 100 pregnant women to see how their unborn babies responded after being exposed to flavors from foods eaten by their mothers.
- Scanned the mothers, aged 18 to 40, at both 32 weeks and 36 weeks of pregnancy to see fetal facial reactions to the kale and carrot flavors.
- Researchers looked at how the fetuses reacted to either carrot or kale flavors just a short time after the flavors had been ingested by the mothers.
- Exposure to just a small amount of carrot or kale flavor was enough to stimulate a reaction.
- Fetuses exposed to carrot showed more "laughter-face" responses while those exposed to kale showed more "cry-face" responses.

A 4D scan image of a fetus showing a neutral face.

A 4D scan image of the same fetus showing a laughter-face reaction after being exposed to the carrot flavor.

Same fetus showing a cry-face reaction after being exposed to the kale flavor

True cause of ageing: study of 200 species

- The age of almost any mammal can now be accurately estimated from a tissue sample by analyzing methylation chemical tags added to DNA.
- Mammals seem to have the same "ageing clocks" shows that ageing is the result of developmental programs that have been retained during the evolution of mammals, rather than being solely due to accumulating damage.
- The new finding is a result of looking at DNA which have chemical tags called methyl groups added to them. These methyl groups get added to or removed to alter the activity of genes, in what are known as epigenetic changes

Aging cause: epigenetic clock

- 2011, Horvath: certain bits of DNA accumulate methyl groups in a consistent way over time, and so can be used to roughly estimate a person’s age.
- In 2013, his team identified another “epigenetic clock’” that signals the age of any human tissue suggesting there is an ageing process common to all human cells.
- The latest clocks are based on studies of nearly 12,000 samples from 59 different tissue types across 185 species of mammal.

Failure to switch off developmental processes

- There are these certain locations – genomic regions – that gain methylation in an extremely consistent way in all of these very different mammalian species. Methyl tags control gene activation & deactivation.
- The current dominant idea of cause of aging is that it is due to accumulation of damage (i.e. oxidative stress). But epigenetic clocks add to growing evidence for an alternative idea that is called the programmatic theory.
- The basic idea of this is that the body’s failure to completely switch off the developmental processes that build our bodies is the key to ageing. For instance, pruning connections between neurons in the brain is a key part of development when we are young, but might contribute to cognitive decline in later life.

Ageing: conserved developmental processes in all mammals

- Many of the sites that gain methylation with age are next to genes related to development.
- These results support the idea that ageing is linked to developmental processes common to all mammals.
- “That to me is a smoking gun, that there are these processes that are conserved,” he says. “There must be some sort of a program.”

Where you get your PhD: *n* = 295,089 faculty in 10,612 depts

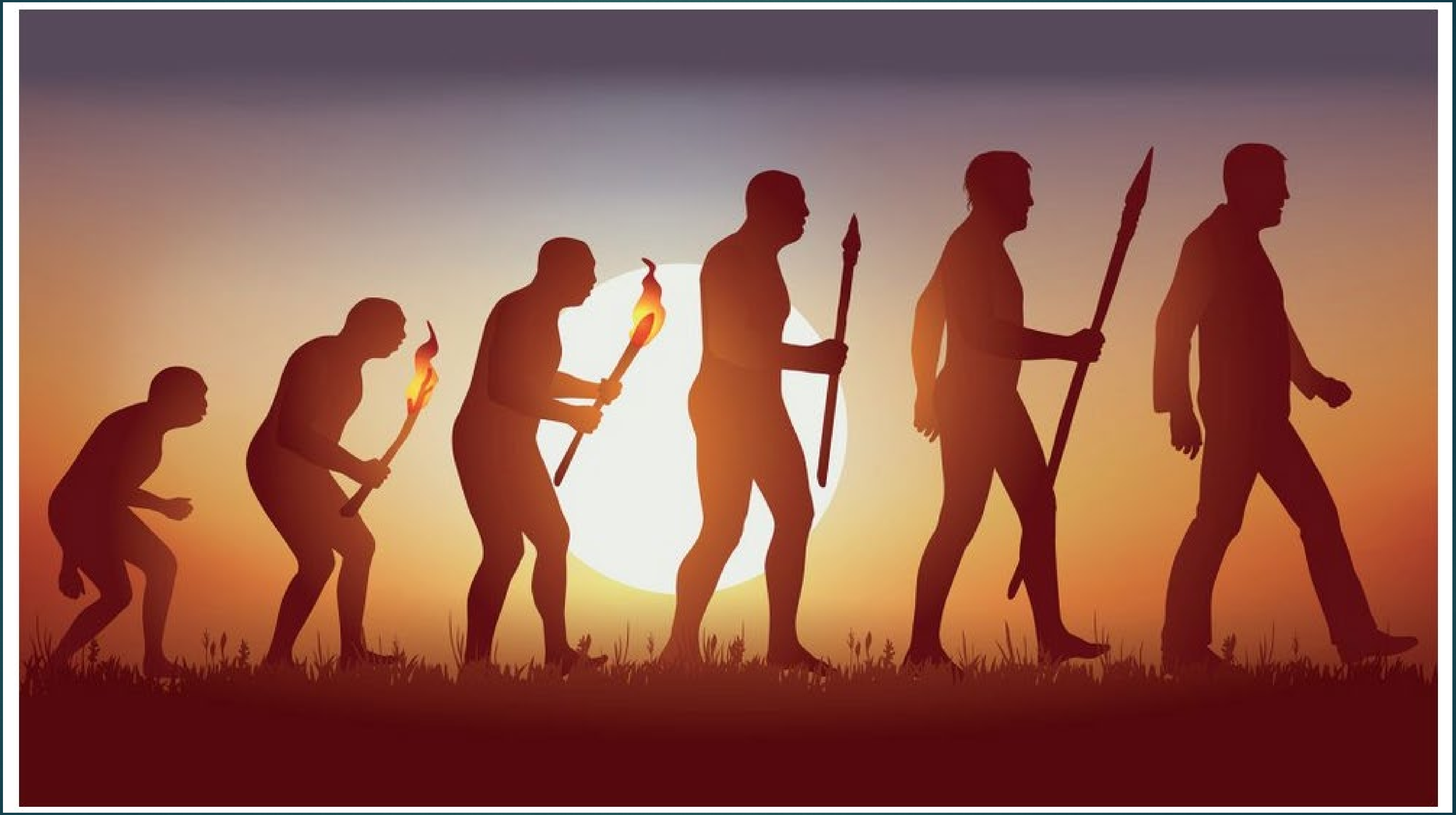
- Analysis the academic employment and doctoral education of tenure-track faculty at all PhD-granting US universities over the decade 2011–2020, quantifying stark inequalities in faculty production, prestige, retention and gender.
- Our analyses show universal inequalities in which a small minority of universities supply a large majority of faculty across fields, exacerbated by patterns of attrition and reflecting steep hierarchies of prestige.
- We identify markedly higher attrition rates among faculty trained outside the United States or employed by their doctoral university.

PhDs

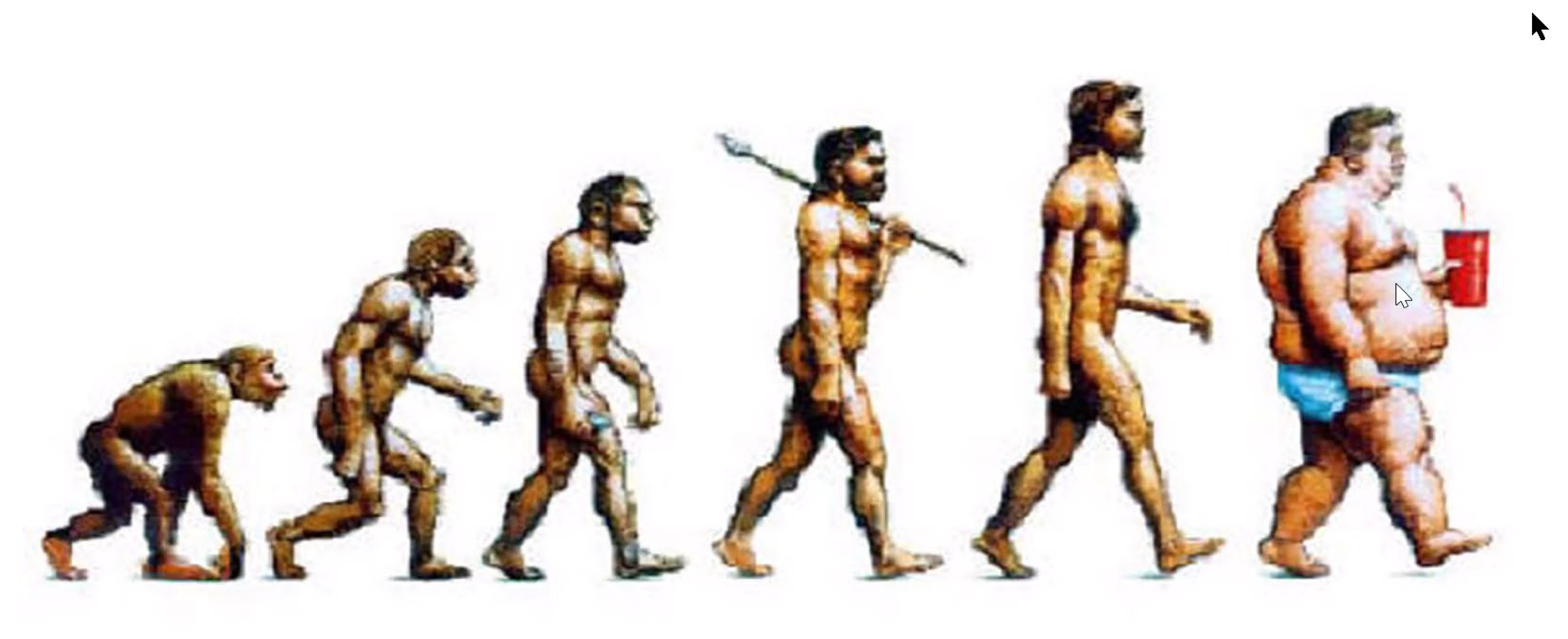
- US tenure-track faculty hiring is dominated by a small minority of US universities that train a large majority of all faculty and sit atop steep hierarchies of prestige.
- Moreover, the five most common doctoral training universities—UC Berkeley, Harvard, University of Michigan, University of Wisconsin-Madison and Stanford—account for just over one in eight domestically trained faculty
-
- 80% of all domestically trained faculty were trained at just 20% of universities.

How many ants are there on planet Earth? 20 quadrillion = 20,000,000,000,000,000

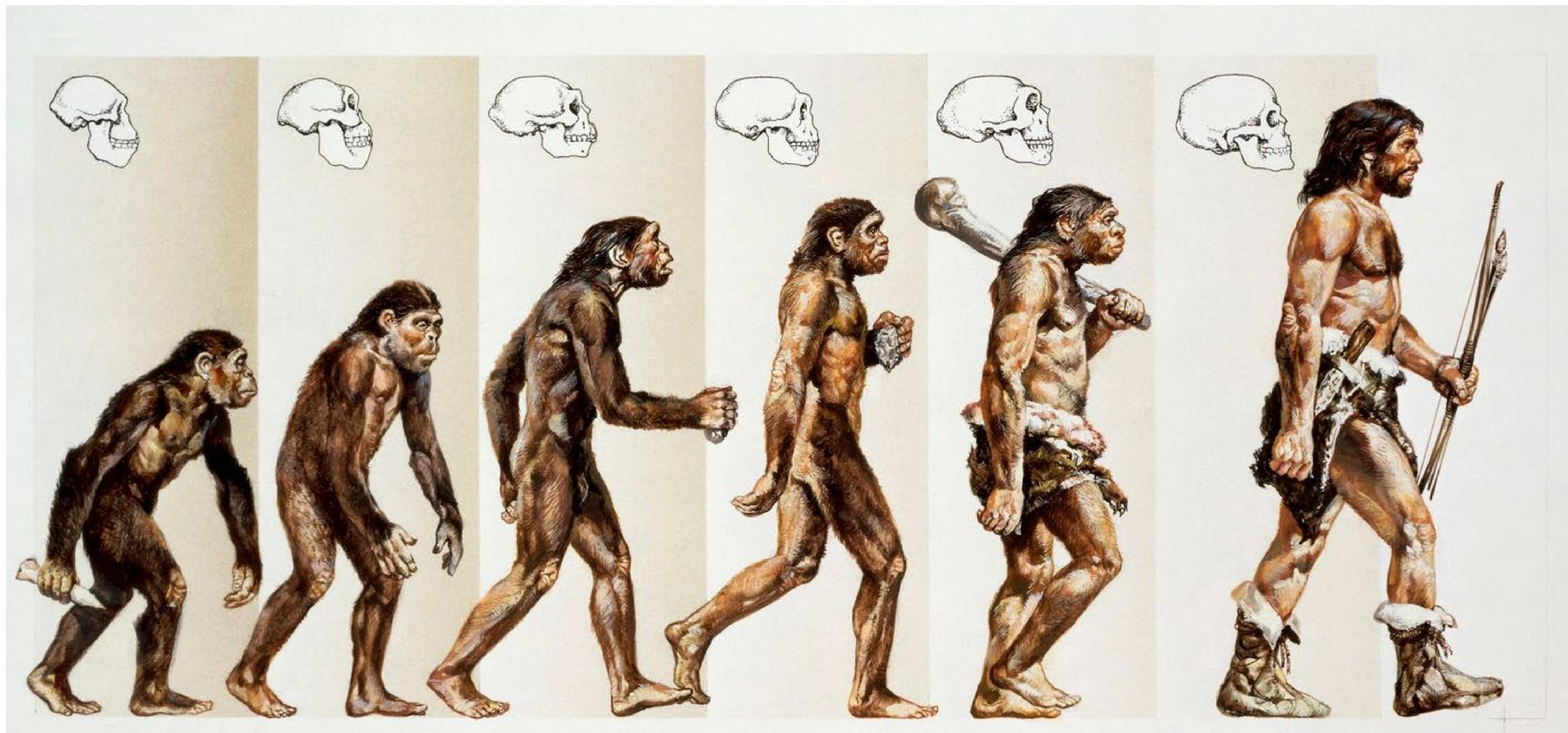
- According to current estimates, the global ant population is 20 x 10 to the power of 15—that is, 20 quadrillion animals. That is a 20 with 15 zeros, which is hard to grasp and appreciate.
- The biomass of the ants = 12 megatons of carbon. That exceeds the combined biomass of wild birds and mammals, = about 20 percent of humanity's biomass.
- Evaluated about 500 papers, and combined them in a database.
- Tropics have the highest ant density.
- Per hectare, ants move up to 13 tons of soil mass per year



New March of Progress



March of Progress concept = Wrong!!



Berger on the March of Progress

- “We are a cur, a mutt, a series of chance interactions and genetic introgressions with everything that was out there. We are just this amalgamation of encounters that occurred as populations of different species expanded and contracted, met each other, shared DNA, and that’s what we are today. We’re no purebred destiny that came marching out of Africa.“
- There is no evolutionary progress line to humans or to increasing complexity.
- We have to remove this innate separation that humans have in their perception of nature.

Steps per day: UK Biobank study of 78 K people

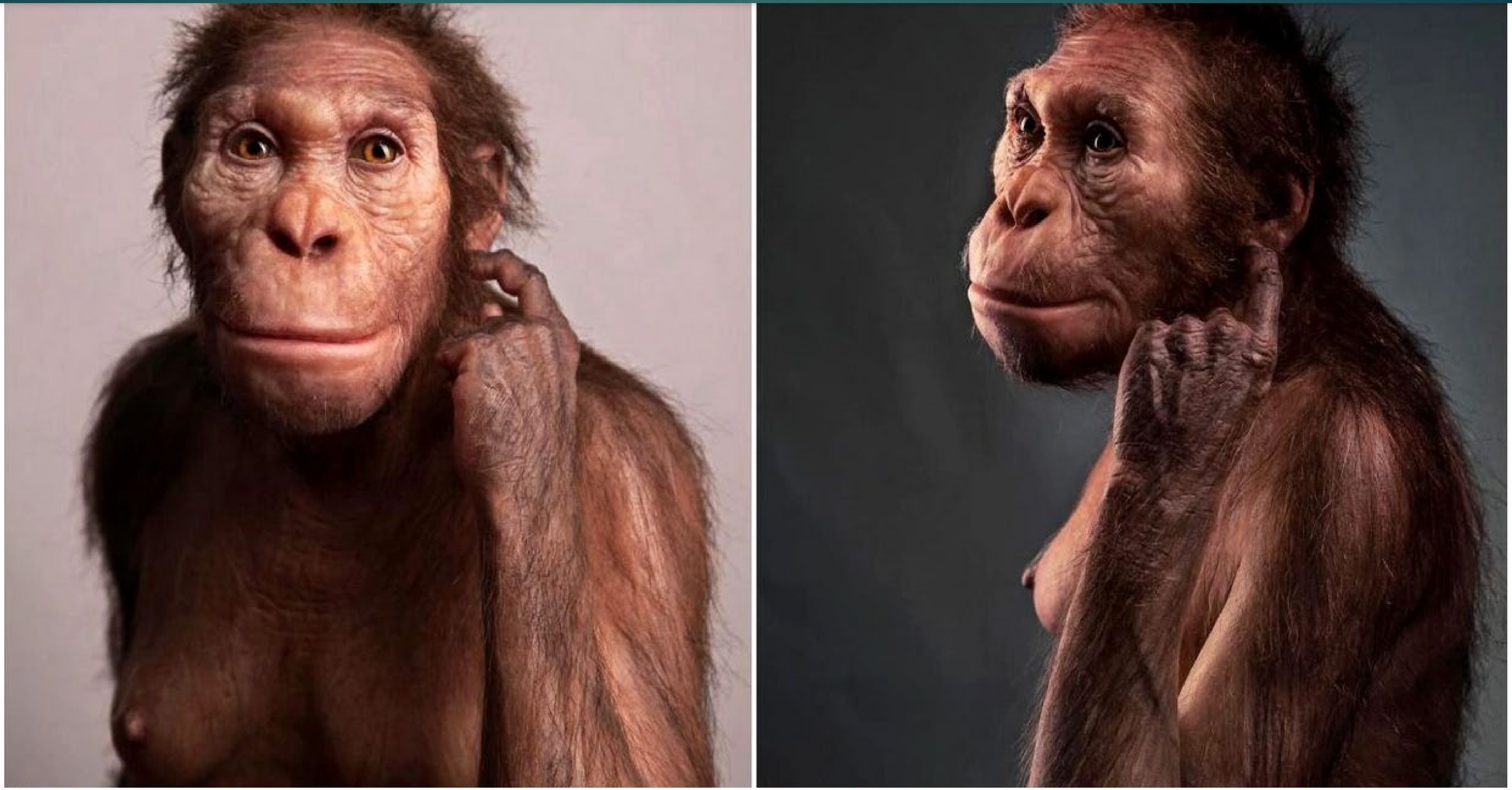
- Every 2,000 steps lowered risk of premature death incrementally by 8 to 11 percent, up to approximately 10,000 steps a day.
- Similar associations were seen for cardiovascular disease and cancer incidence.
- A higher number of steps per day was associated with a lower risk of all-cause dementia
- 9,800 steps was the optimal dose linked to lower risk of dementia by 50 percent, however risk was reduced by 25 percent at as low as 3,800 steps a day
- Stepping intensity or a faster pace showed beneficial associations for all outcomes (dementia, heart disease, cancer and death) over and above total daily steps.

440-lb, lion sized otters prowled Ethiopia 3 million years ago

The species, named *Anhydride omoensis*, lived about 3.5 to 2.5 Ma and co-existed with the australopithecines. Its teeth suggest it was not aquatic. Had a diet of terrestrial animals.

The axolotl: endangered amphibian who can regrow its brain post injury

New reconstruction of *H. sediba*



Life reconstruction of Australopithecus sediba, commissioned by the University of Michigan Museum of Natural History. (Sculpture: Elisabeth Daynes / Photo: S Entressangle)

Expect a major new discovery from Rising Star Cave

- Lee Berger is hinting there will be a major new announcement soon.
- Together with two articles presently under peer review
- At the Rising Star Cave, collectively, between 30 and 60 H. naledi individuals have been identified, who are certainly of the same species, and this is a “powerful tool for scientists to unlock human processes like growth, difference in sexes, disease and ageing. We have never had an assemblage like this for any other hominin species,” says Berger.

Homo naledi, 335-236 Ka

Hibernation in hominins from Atapuerca, Spain half a million years ago (2020 paper submission to PeerJ for review)

- Both animal hibernation and human renal osteodystrophy are characterized by high levels of serum parathyroid hormone.
- To test the hypothesis of hibernation in an extinct human species, we examined the hominin skeletal collection from Sima de los Huesos, Cave Mayor, Atapuerca, Spain, for evidence of hyperparathyroidism -- 28 individuals, 430 Ka
- We studied the morphology of the fossilized bones by using macrophotography, microscopy, histology and CT scanning.
- Bone damage evidence: found trabecular tunneling and osteitis fibrosa, subperiosteal resorption, ‘rotten fence post’ signs, brown tumors, subperiosteal new bone, chondrocalcinosis, rachitic osteoplaques and empty gaps between them, craniotabes, and beading of ribs mostly in the adolescent population of these hominins

Hominin hibernation?

- Since many of the above lesions are pathognomonic, these extinct hominins suffered annually from renal rickets, secondary hyperparathyroidism, and renal osteodystrophy associated with Chronic Kidney Disease - Mineral and Bone Disorder (CKD-MBD).
- We suggest these diseases were caused by poorly tolerated hibernation in dark cavernous hibernacula.
- This is particularly evidenced by the rachitic osteoplaques and the gaps between them in some of the adolescent individuals along with the evidence of healing mainly in the adults. The sublayers in the rachitic osteoplaques indicate bouts of arousal from hibernation.

Hibernation: period of extreme glaciation

- The strong projection of the external lip of the femoral trochlea, the rachitic osteoplaques with the empty gaps between them, the “rotten fence post" sign, and the evidence of annual healing also point to the presence of annually intermittent puberty in this extinct human species.
- The hypothesis of hibernation is consistent with the genetic evidence and the fact that the SH hominins lived during an extreme glaciation.
- The above bone evidence shows that the SH hominins used hibernation as a survival strategy to face winter famine and cold.
- *Homo antecessor*, from the nearby caves (Sima del Elefante cave site) does not bear any evidence of the pathologies

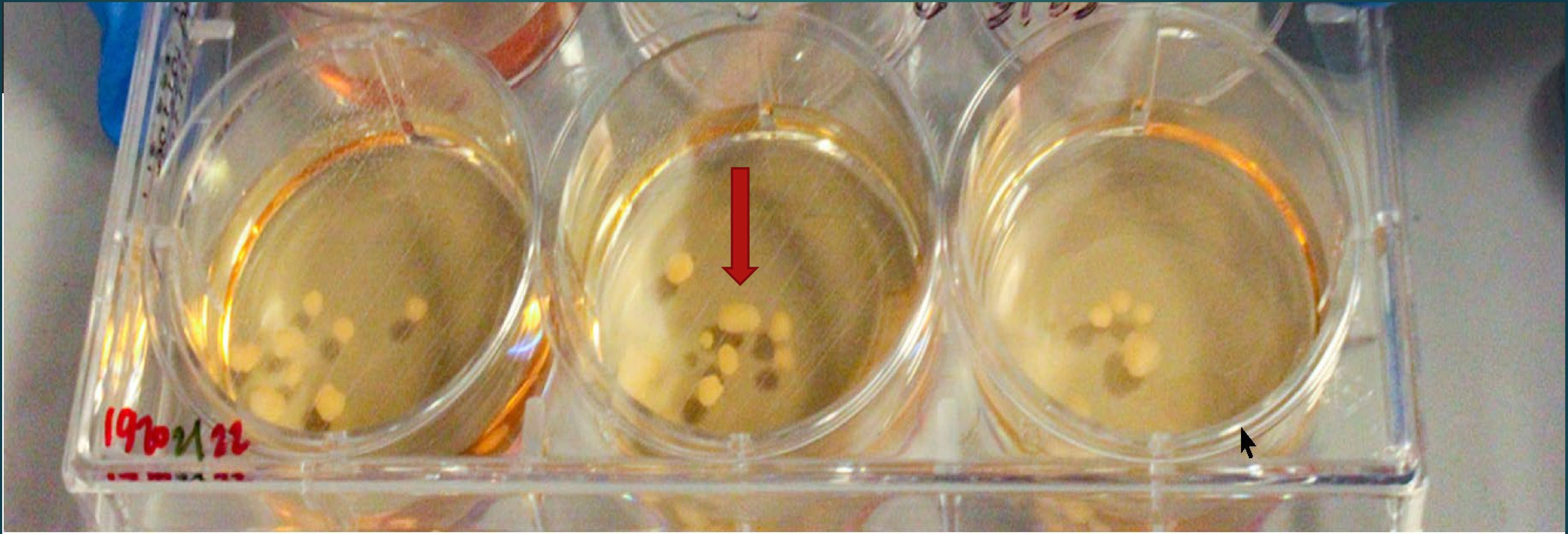
Antonis Bartsiokas, Juan-Luis Arsuaga 2020

MH and N brains were roughly the same size

What Makes Your Brain Different From a Neanderthal's?

- Neanderthal brains were elongated, whereas humans have a more spherical shape. Scientists can't say what accounts for those differences.
- One possibility is that various regions of our ancestors' brains changed size.
- 96 human-specific mutations that changed the structure of a protein.
- 1 of these altered a gene called TKTL1. TKTL1 becomes active in the developing human cortex, especially in the frontal lobe.

Brain organoids: from human stem cells edited with N gene



Alysson Muotri's lab grew these brain organoids from human stem cells that had a developmental gene edited into the version once possessed by Neanderthals. J.

Increased Neurogenesis

- Caused both mice and ferrets to make more neurons.
- Neanderthal brain organoids: made fewer neurons than did organoids with the human version of TKTL1.
- When the TKTL1 gene mutated, our ancestors could produce extra neurons in the frontal lobe. May have reorganized neuronal wiring.
- Human TKTL1 implies greater neurogenesis in frontal neocortex of modern humans than Neanderthals
- Other recent discoveries: two other mutations change the pace at which developing brain cells divide. Last year: another mutation appears to increase the synaptic connections human neurons make with each other.

Eurasia's oldest human remains outside Dmanisi

- Dmanisi: five *H. erectus* skulls and a multitude of postcranial remains and lithic industry of Oldowan type dated to 1.8 Ma. Oldest human presence outside of Africa
- Shangchen, in northern China, 2.1 Ma; *Homo*
- Qvemo Orozmani, Georgia, 20 km from Dmanisi: Oldowan (Mode 1) stone tools and faunal bones, 1.8 Ma)
- Orce: deciduous tooth from Barranco León at 1.4 Ma; earliest evidence in Western Europe
- Sima del Elefante, Atapuerca: a maxilla, 1.4 Ma; found in 2022
- Kocabaş in Turkey: a partial skull, 1.2 Ma

Eurasia's oldest human remains outside Dmanisi

- Descendants of *H. ergaster* gave rise 1 MYA to *H. antecessor* in Africa, before .9 Ma
- Cueva Victoria in Southern Spain, with some human fossils dated to 0.8-0.99 Ma and the near Cueva Negra with Acheulean tools dated to also c. 0.9 Ma
-
- La Boella in Northern Spain, with a set of 50 flint tools dated to between 0.8-1 Ma, along with skeletal remains and coprolites of big mammals.

First known surgical amputation: 31 Ka

The left tibia (left two images) and left fibula of an individual who lived some 31,000 years ago show healed amputation sites. (T. R. Maloney *et al.*/*Nature*)

Healed left tibia and left fibula

Tim Ryan Maloney, et al., 2022

Surgical amputation of a limb 31,000 years ago in Borneo

- Prior record at 7 Ka: the oldest known indication of an ‘operation’ in skeletal remains of a European Neolithic farmer (found in France) whose left forearm had been surgically removed and then partially healed
- Current discovery of skeletal remains of a young individual from Borneo who had the distal third of their left lower leg surgically amputated, probably as a child, at least 31,000 years ago.
- The individual survived the procedure and lived for another 6–9 years, before their remains were intentionally buried in Liang Tebo cave, in East Borneo, in a limestone karst area that contains some of the world’s earliest dated rock art.
- Leg bone shows a clean sloping cut rather than the more irregular physical hallmarks expected for an accidental injury that caused the loss of part of the limb. Bone was well healed.
- Early accident?: Also had a very well healed neck fracture and trauma to their collar bone that may have occurred during the same event,

Surgically amputated site of the left tibia and fibula. Left and right legs with pelvic girdle, demonstrating the complete absence of the distal third of the left lower leg.

Earliest amputation

- Person died between 31,201 and 30,714 years ago. Their age at death was estimated to be about 19 or 20 years old.
- The amputation occurred during childhood and at least six to nine years before death.
- A lump of red ochre pigment accompanied the person's remains, which were found in a cave decorated with hand stencils.
- This individual evidently did not suffer from an infection severe enough to leave permanent skeletal markers and/or cause death.

Artistic reconstruction

La Torre-La Janera (Huelva), Spain, future avacado farm site: 526 megaliths, 3-6 Ka

Another submerged site: Discovered in 1926 by a German archaeologist, then was voluntarily covered by water in 1963 as part of a rural development project wanted by Franco, the site of Guadalperal is therefore once again visible. It would have been erected ~7 Ka

Near Prague: remains of a Stone Age structure that's older than Stonehenge and even the Egyptian pyramids: an enigmatic complex known as a roundel.

7 Ka structure near Prague: Woodhenge

- Roundels consist of one or more wide, circular ditches with several gaps that functioned as entrances. The inner part of each roundel was likely lined with wooden poles, perhaps with mud plastering the gaps,
- 7,000 years ago during the late Neolithic; Some roundels are astronimically aligned.
- The excavated roundel is large — about 180 feet (55 meters) in diameter, or about as long as the Leaning Tower of Pisa is tall. They were part of the Stroked Pottery culture, which flourished between 4900 B.C. and 4400 B.C. After three centuries of popularity, roundels suddenly disappeared from the archaeological record around 4600 B.C.

Map of the Laurentide Ice Sheet at the Last Glacial Maximum.

Laurentide Ice Sheet

- Laurentide Ice Sheet, covering much of Canada and the northern United States with a mass of ice that was nearly 4 km thick in some places.

- After 20,000 years ago, Earth started to warm, and the Laurentide Ice Sheet began to disappear.

- Around 8,200 yr ago, there was an abrupt cooling of 1–3 °C (34-37 °F) across large parts of the Northern Hemisphere which lasted around 160 years. Resulted from the rapid draining of glacial Lake Agassiz into the North Atlantic via the Great Lakes and St. Lawrence drainage

Glacial Lake Agassiz: drained ~8,200 ya

Louisiana State University Mounds, 20 feet high: geological or anthropological?

The LSU Mounds can be found at the north end of Louisiana State University's campus. (Image credit: LSU)

Louisiana State University Mounds: oldest known human-made structures in the Americas

- Two of more than 800 similar human-made mounds in Louisiana, built by Indigenous Americans.
- Oldest mound is 11,000 years old, making it the oldest human-made structure discovered in either North or South America.
- Found layers of clay and ash from burned reed and cane plants, as well as microscopic animal bone fragments.
- Because the flames from reed and cane are too hot to cook food with, the researchers think that the mounds were built up and used for religious or ceremonial purposes.
- Mound B is 11,000 years old, while Mound A is around 7,500 years old. The finding reveals that both mounds are older than the ancient Egyptian pyramids (4700 ya)

Louisiana State University Mounds: aligned with star Arcturus

- Around 8,200 years ago, Mound B was abandoned — and researchers aren't sure why. But a rapidly changing climate could have had an impact. Starting around 8,200 years ago, temperatures in the Northern Hemisphere suddenly dropped around 35 degrees Fahrenheit, and stayed that way for about 160 years.
- No evidence of human activity at Mound B for the next 1,000 years. Then, around 7,500 years ago, ancient people started constructing Mound A about 30 feet (9 m) away, using mud from a floodplain where today's LSU Tiger Stadium now sits.
- The researchers also discovered a stellar characteristic of the mounds — they line up just 8.5 degrees east of north, which is where the giant red star Arcturus would have risen several thousand years ago. Around 6,000 years ago, both mounds were completed to align toward Arcturus,

Most embryos die

- Most human embryos die before anyone, including doctors, even know they exist. This embryo loss typically occurs in the first two months after fertilization, before the clump of cells has developed into a fetus.

- Total abortion bans that would define personhood at conception mean that full legal rights exist for a 5-day-old blastocyst, a hollow ball of cells roughly 0.008 inches (0.2 millimeters) across with a high likelihood of disintegrating within a few days.

Most embryos die

- Most human embryos die due to random genetic errors.
- Around 60% of embryos disintegrate before people may even be aware that they are pregnant.
- Another 10% of pregnancies end in miscarriage, after the person knows they're pregnant.
- These losses make clear that the vast majority of human embryos don't survive to birth.

Most embryos die

- In people, the most common outcome of reproduction by far is embryo loss due to random genetic errors.
- An estimated 70% to 75% of human conceptions fail to survive to birth.
- Between 1973 and 2005, over 400 women were arrested for miscarriage in the U.S.
- With the current shift toward restrictive abortion policies, the continued criminalization of pregnancies that don't result in birth, despite how common they are, is a growing concern.

Who is Ancestor X? The biggest mystery in human evolution

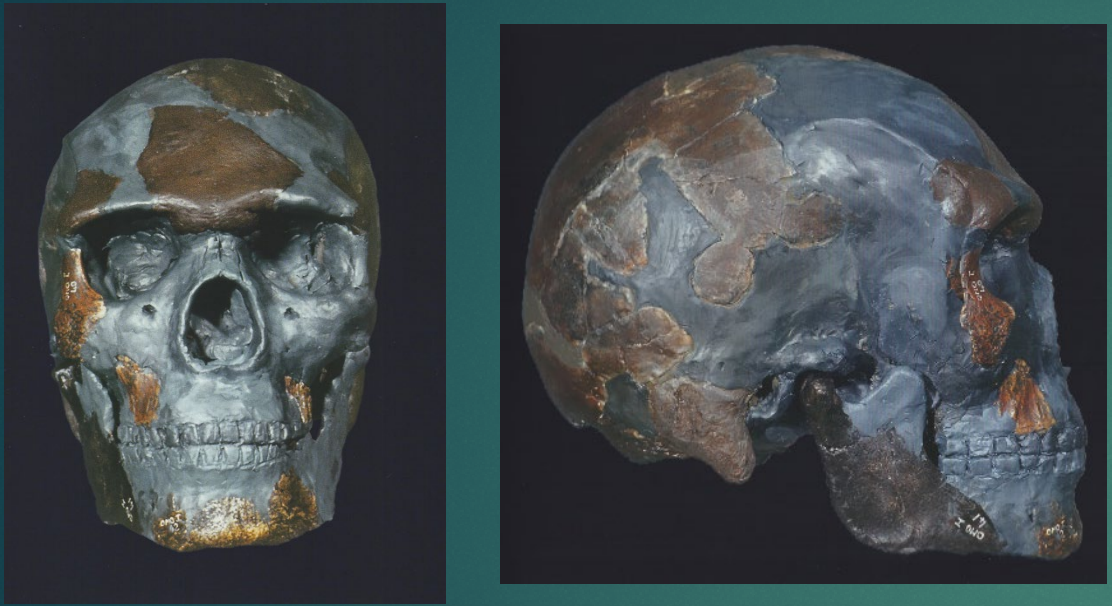
- Enigmatic Ancestor X – the species that gave rise to humanity. The search for the direct ancestor of humans, Neanderthals and Denisovans has been protracted and puzzling.

- Big picture of human evolution:
  - 1- all living people today are so genetically similar to one another that *H. sapiens* must have emerged no more than a few hundred thousand years ago.
  - 2 - this happened in a corner of Africa – since most of the genetic diversity that exists in our species today is largely concentrated in Africa.

Colin Barras 2022

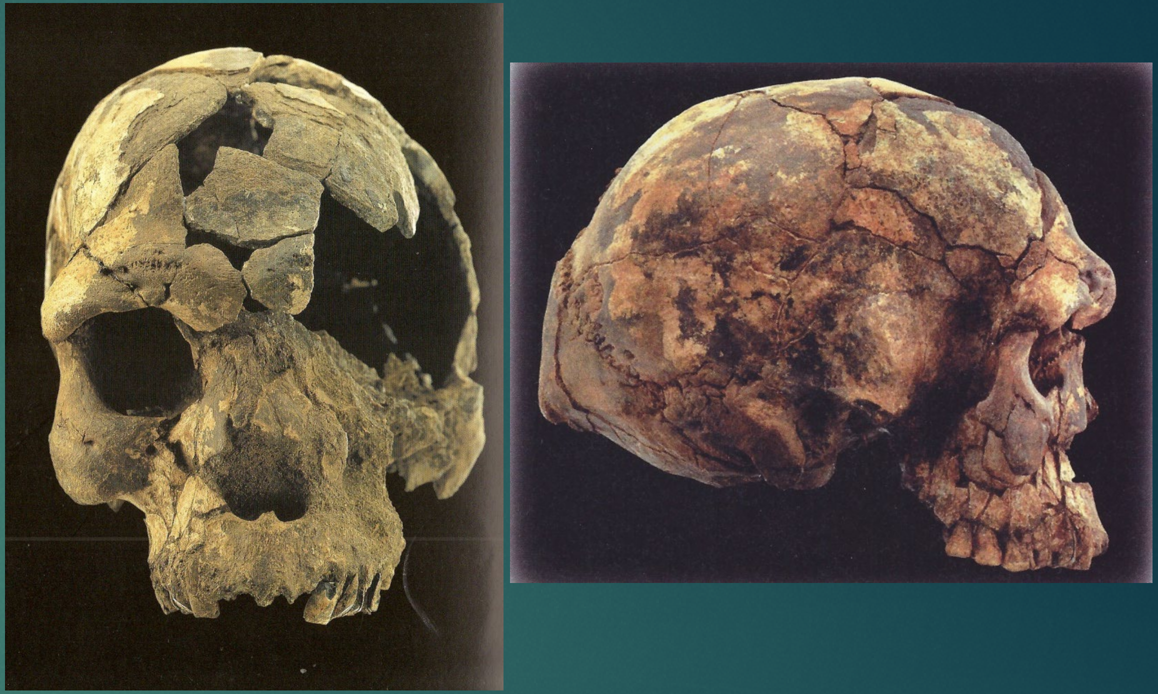
1967: 2 oldest *Homo Sapiens,* Omo 196 Ka & Herto, 160 Ka:

Curved parietal, high forehead, chin



Homo sapiens (Omo I)

At 196 Ka, the oldest known fully anatomically modern human fossil



Homo sapiens idaltu, 160K
Herto, Ethiopia; Bou-VP-16-1

2017: Oldest *Homo sapiens*, Jebel Irhoud, Morocco, 300 Ka

A composite computer reconstruction of fossils from Jebel Irhoud shows a modern, flattened face paired with an archaic, elongated braincase; 100 K older than Omo II skull. Evolutionary processes behind the emergence of H. sapiens involved the whole African continent. The fossils suggest that faces evolved modern features before the skull and brain took on the globular shape seen in the Herto fossils and in living people.

Anne Gibbons, Science, 2017

Ancestor X

  - 3 - Our parent species also gave rise to a second species, *Homo neanderthalensis*, the Neanderthals.
  - In other words, the two species share a common ancestor, dubbed Ancestor X.
- Several hundred thousand years ago, our parent species was present in parts of Africa and Europe.
- Then, a small population of this Ancestor X became isolated in Africa for long enough to evolve new genetic and physical traits and give rise to *H. sapiens*.
- At roughly the same time, another small population of Ancestor X became isolated in Europe and evolved into the Neanderthals.
- Eventually, the isolation ended. *H. sapiens* and Neanderthals both began to spread, consigning all remaining populations of Ancestor X to extinction.

The search for Ancestor X: *H. heidelbergensis*

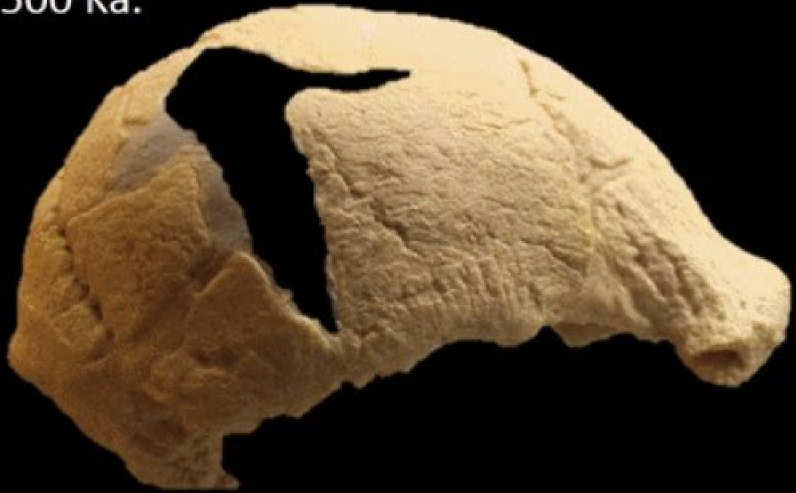
- By the early 1980s, Chris Stringer: spent years scrutinizing the shape of Neanderthal and *H. sapiens* skulls to work out what they had in common: features they had probably inherited from Ancestor X.
- Both had large brains, similarly shaped temporal bones and other features.
- These were also seen in a third hominin, *Homo heidelbergensis*.
- *H. heidelbergensis* had been present in parts of Africa and Europe between about 300,000 and 500,000 years ago. “I thought: well there you are,” says Stringer. “It’s in the right place at the right time to be the common ancestor.”

African Middle Pleistocene specimens

Bodo (Ethiopía)
600 Ka.

Kabwe (Zambia)
300 Ka.
Broken Hill

Saldanha (Sudáfrica)
500 Ka.



Ndutu (Tanzania)
350 Ka.

The search for Ancestor X

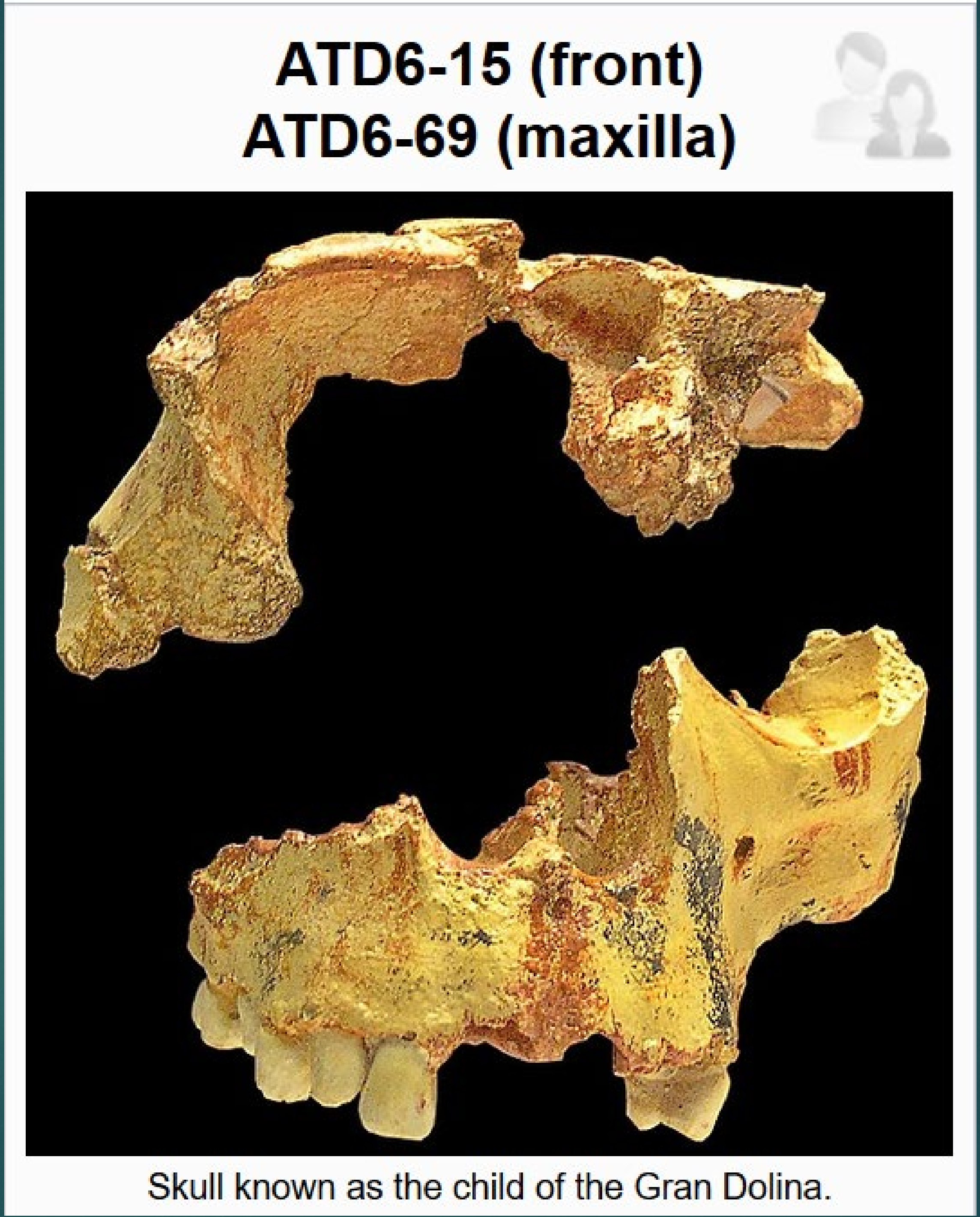
- But in the 2010s, he and many other researchers had second thoughts.
- Some of the best evidence about *H. heidelbergensis* had come from fossils found at Sima de los Huesos in Spain, and by the mid 2010s, it was clear that they actually looked more like proto-Neanderthals.
- Analysis of their nuclear DNA in 2016: Sima fossils were early Neanderthals.
- Their age of 430 Ka required the estimate for when Ancestor X existed to be upgraded to between 550,000 and 765,000 years ago.
- An underestimate. A 2019 analysis of Neanderthal and *H. sapiens* teeth suggested that Ancestor X was on Earth 800,000 years ago or more.
- The message was clear: *H. heidelbergensis* was too young to be Ancestor X.

Neanderthals and modern humans diverged at least 800,000 years ago, substantially earlier than indicated by most DNA-based estimates

- Ancient DNA analyses have generally indicated that both lineages diverged around 300,000 to 500,000 years ago. This divergence time, however, is not compatible with the anatomical and genetic Neanderthal similarities observed in the hominins from Sima de los Huesos.
- 2019 Analysis of dental evolutionary rates across different hominin species, focusing on early Neanderthals. It shows that the teeth of 430 Ka hominins from Sima de los Huesos, Spain diverged from the modern human lineage earlier than 800 Ka.
- Simplest explanation is that the divergence between Neanderthals and modern humans was older than 800,000 years (.9 -1.2 Ma).

Aida Gómez-Robles, et al., 2019

Gran Dolina, TD6, 860 Ka *H. antecessor*



ATD6-15 (front)
ATD6-69 (maxilla)

Skull known as the child of the Gran Dolina.

Ancestor X

- A new Ancestor X candidate was already waiting in the wings. Curiously, this suspect – *Homo antecessor* – had been discovered at a site just a few hundred meters to the north of Sima de los Huesos. At 800 Ka - 1 Ma, it a far more likely Ancestor X, at least on the grounds of age.
- *H. antecessor* exhibits the oldest known modern face so far found. Its delicate cheekbones and flattened features are similar to those seen in living humans and are unlike the heavily built faces of Neanderthals.
- Because of this, there is now a surprising hypothesis about Ancestor X: perhaps it looked a little like us. “Our so-called modern face is an ancient face,” says Stringer. The Neanderthal face might actually be far more evolved.

Ancestor X

- Stringer doesn’t think *H. antecessor* is Ancestor X itself.

- In a 2016 analysis: Stringer concluded that Ancestor X had a face like H. antecessor combined with teeth that were more Neanderthal-like, while the part of the skull encasing the brain looked like that of a primitive *H. heidelbergensis* cranium discovered in Ceprano, Italy.

- Recent phylogenetic study has concluded that H. antecessor is a sister group to Ancestor X.

Ancestor X

- There are still a few researchers betting on *H. heidelbergensis*, including Axel Timmermann at Pusan National University in South Korea.
- They ran a climate model on a supercomputer for six months to reconstruct how temperature and rainfall might have shaped what resources were available to hominins over the past 2 million years. They then combined their results with thousands of fossils and other archaeological evidence to work out where and when six species of humans – including the early *H. sapiens* – could have lived.
- Among other things, their results suggested that our species evolved from *H. heidelbergensis* in southern Africa as conditions became hotter and more arid.

Ancestor X

- It is a minority view, though.
- Most researchers now see hints in the fossils that *H. heidelbergensis* was more closely related to the proto-Neanderthals than to our species.
- They could be wrong. The problem is that we appear to have fundamentally misunderstood the way human evolution works.
- “The idea humans originated from a small region [of Africa] doesn’t make much sense,”

Ancestor X: African multiregionalism or pan-African evolution.

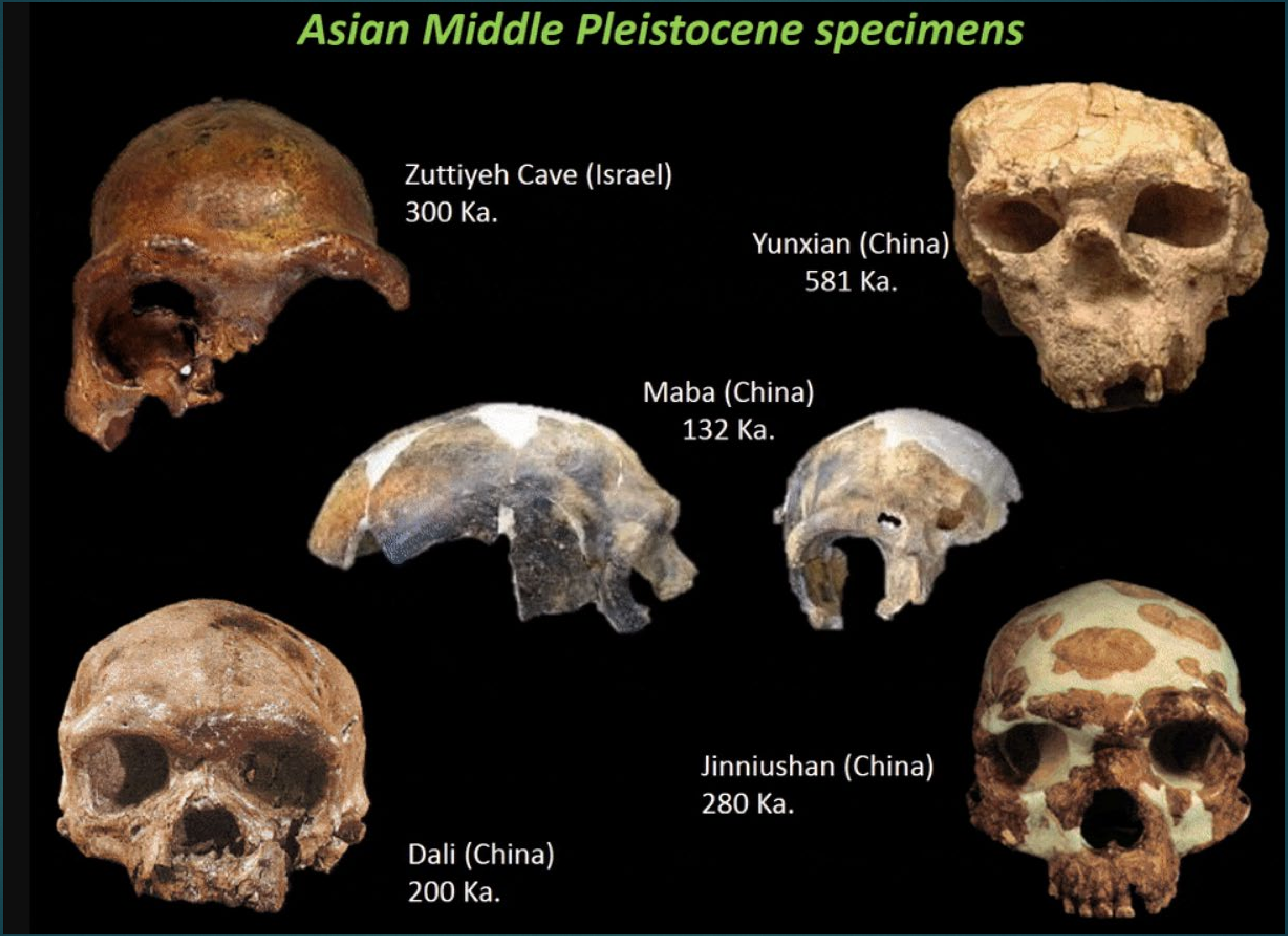
- The genetic signals in living humans imply that *H. sapiens* emerged as a "metapopulation" spread over a wide geographical area where several "subpopulations" were interconnected by genetic exchange. Each of these subpopulations was characterized by distinct genetic signatures – and a distinct look.
- Across Africa, there are fossils between about 200,000 and 300,000 years old that look superficially like *H. sapiens*, but that each carry a unique mix of physical features.
- They appear to be representatives of some of the subpopulations that mixed and interbred to establish our species as a metapopulation. This idea, published in 2018, has come to be known as African multiregionalism or pan-African evolution.

‘Kabwe’ or ‘Broken Hill 1’ Homo heidelbergensis skull. Discovered: 1921 in Kabwe (formerly Broken Hill), Zambia. It combines primitive features such as a wide face, thick arching browridges. and a sloping forehead, but with a large brain capacity of 1280 cc.

Ancestor X

- This phenomenon may have implications for *H. heidelbergensis*.
- The "Kabwe skull" or "Broken Hill skull" from Zambia, originally labelled as *H. heidelbergensis*, originally dated at 40 Ka, has recently been redated to 300 Ka.
- This means *H. heidelbergensis* was still in Africa at the time H. sapiens was emerging across the continent. And although *H. sapiens* probably traces most of its ancestry to Ancestor X, Stringer says it is possible that one or more *H. heidelbergensis* groups were among the subpopulations that contributed some DNA to our species.
- Arguably, an even bigger implication of the pan-African evolution model is that it probably applies to the origin of other hominins – including Ancestor X.
- If so, our immediate ancestor also evolved through the mixing of numerous subpopulations of its own parent species spread over a wide geographical area. But where in the world did that happen?

Asia



Asian Middle Pleistocene specimens

Zuttiyeh Cave (Israel)
300 Ka.

Yunxian (China)
581 Ka.

Maba (China)
132 Ka.

Jinniushan (China)
280 Ka.

Dali (China)
200 Ka.

Ancestor X

- Asia is another hotbed of human evolution

- Chinese Harbin skull. Like *H. antecessor*, it had a face strikingly similar to our own. Dated to 146 Ka.

- Phylogenetic study suggested the Harbin skull – and a few other fossils, many of them unearthed in China – belong to a previously unrecognized ancient human population that is evolutionarily even closer to *H. sapiens* than the Neanderthals.

- Ni and some of his colleagues identified it as a new species: *Homo longi*. Nickname: Dragon Man.

Ancestor X

- Stringer speculates that Dragon Man might have emerged from Ancestor X at around the same time *H. sapiens* and Neanderthals did, implying that our species is one of triplets, not one of twins. Perhaps, he adds, this third human group will turn out to contain the mysterious Denisovans.
- Harbin-like fossils imply that the search might be harder than we thought, because Ancestor X could have lived almost anywhere within a truly vast geographical region.
- “It could have been in Africa,” says Stringer. “But it could have been in Europe – that’s where *H. antecessor* is – or it could have been in west Asia. It could even have been in east Asia. We just don’t know yet.”

East-West Relations

- Sheela Athreya at Texas A&M University suspects that cultural influences may help explain our belief of an African origin.
- Concept of “A single ‘pure’ form evolving and spreading to replace all others? That’s colonialism in Europe and that’s manifest destiny in the United States,” she says.
- To be clear, she doesn’t mean that all researchers of European ancestry are racist, but that racist cultural ideas may influence their work, if unconsciously. What’s more, a few of these same researchers have been quick to criticize their colleagues in Asia and elsewhere of being under the influence of perceived cultural biases, she says. This has discouraged collaboration and made it difficult to work out how the extraordinary fossil finds made in Asia fit into the bigger picture of human evolution.

East-West

- The view is that Asian scientists are biased and ethnocentric, that they like the idea of long-standing regional continuity because the alternative is a replacement model that suggests they haven’t been in the area for as long.
- This view is incorrect, offensive and – above all – counterproductive because it has encouraged some Western researchers to dismiss almost all scientific findings made by human evolution scientists in Asia.
- Fortunately, attitudes are changing.

Ancestor?

- **Ancestor X =** .9-1.2 Ma
- **Homo antecessor** - 900,000 years old. Now a sister group to our ancestor
- **Sima hominin** - 430,000 years old. Neanderthal, not a direct ancestor as thought
- **Jebel Irhoud human - 315,000** years old. Oldest known remains of a *Homo sapiens*
- **Florisbad human** - 260,000 years old. Surprisingly modern-looking for its age
- **Omo I human** - 230,000 years old. Shows a mix of archaic and modern features
- **Herto human - 160,000** years old. Archaic/modern mix, but distinct from Omo I
- **Laetoli human** - 120,000 years old. More modern but more archaic-looking

Human brain size reduction? Did the transition to complex societies in the Holocene drive a reduction in brain size?

- DeSilva et al. (2021) hypothesize that modern human brain size has decreased, starting at roughly 3,000 years ago. Claim changes in modern human brain size around 3 ka driven by transitions to agriculture and social complexity in the Holocene. They offer a model in which directional selection for decreased brain size, and/or stabilizing selection for maintaining large brains, was relaxed due to the ability to store information externally in social groups. Under this model, which they analogize from ants, following the development of complex societies, the cumulative intelligence and knowledge of the social group acted to relax the strong forces of selection that had been present in earlier human populations. They propose that “group-level cognition may select for reduced brain size and/or adaptive brain size variation.

Brian Villmoare and Mark Grabowski, 2022

Human brain size reduction? NO - based on study of 987 fossils.

- Populations from around the globe are lumped together, with only 23 crania sampled over what we would argue to be a critical window with regards to their hypothesis, 5–1 ka; and finally, 165 crania (28% of the total sample) are from Australian pre-Neolithic hunter-gatherer populations and dated in DeSilva et al. (2021) to 100 years ago.

- The sample of DeSilva et al. (2021) generates a modern human mean of 1,297 cc in the final 100-year category, which is well below other published estimates of contemporary world-wide modern mean human cranial capacity that range from 1,340 cc up to 1,460 cc; more than half of the specimens of a 9.8-million-year analysis are placed in the final 100 years
- Current study: They reduced sample to last 30 Ka.

- With regards to testing the hypothesis in question, our analyses showed no changes in brain size associated with the transition to agriculture during the Holocene. Overall, our conclusion is that, given a dataset more appropriate to the research question, human brain size has been remarkably stable over the last 300 ka. Thus, hypotheses of recent change are not supported by the evidence

2nd killer asteroid?

2^{nd} meteor may have struck at end of dinosaur era

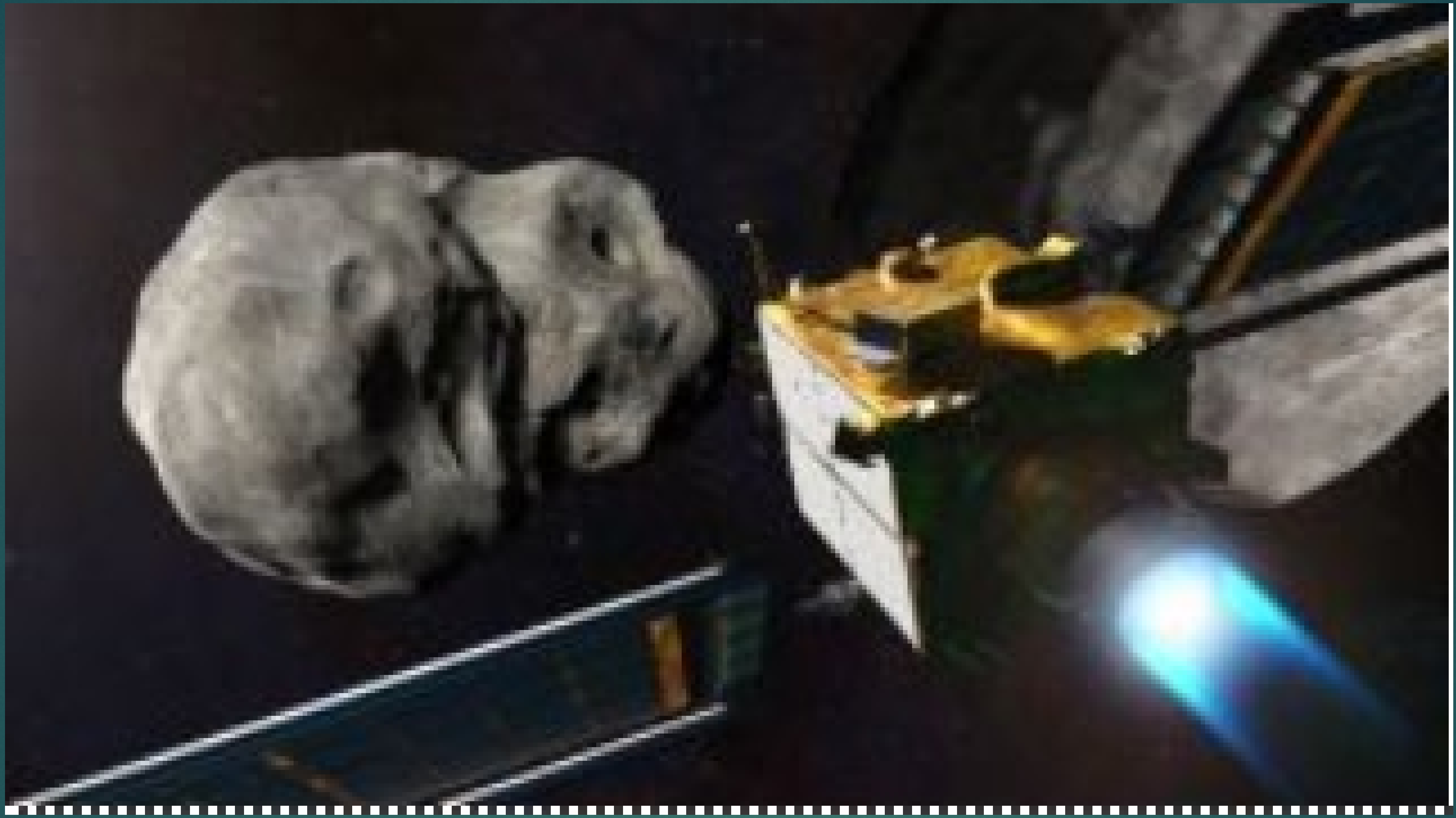
- 9 km crater discovered buried beneath the sea floor near the coast of West Africa. It was made around the time of the larger Chicxulub impact that wiped out most dinosaurs, leading to speculation that it was caused by a chunk that broke off the Chicxulub asteroid.

- Spotted the feature in seismic reflection data supplied by the oil and gas industry. The likely crater, named the Nadir crater after a nearby seamount, is on the continental shelf a few hundred kilometers off the coast of Guinea, buried beneath around 300 meters of sediment in an area where the water is 900 meters deep.

Second Asteroid

- The structure has all the features characteristic of an impact crater of this size, including a raised rim and signs of ejected material outside the crater itself.
- Asteroid size = 400 meters round
- Nadir crater appears to have formed around 66 million years ago, the same time as the 180-kilometer-wide Chicxulub crater in what is now Mexico. This asteroid was 13 km wide

NASA's DART mission slammed into an asteroid's moon today



Dimorphos measures 525 feet across; accelerate to 13,421 miles per hour (21,600 kilometers per hour) and crash into the moon nearly head-on. The spacecraft is about 100 times smaller than Dimorphos,

Sex toy hypothesis: Monkeys use stones for pleasure.

- Many monkeys are skilled stone handlers, using rocks to dig up roots, cut plants and crack open an array of delicacies, including fruits and nuts.
- A population of free-ranging, long-tailed macaques that live in or near the Sacred Monkey Forest Sanctuary in Ubud, a Balinese town in Indonesia. Regularly fed by humans
- Some macaques frequently rub or tap stones around their genitals. The monkeys appear to engage in “a form of self-directed, tool-assisted masturbation.
- To systematically investigate the hypothesis, Ms. Cenni and her colleagues analyzed the stone-handling actions of 173 monkeys. They found that young males engaged in the genital tapping and rubbing more than adult males did, and were especially likely to engage it in during sexually charged situations, such as when they or another macaque nearby was soliciting a mate or showing signs of sexual arousal. Moreover, the behavior tended to precede physical signs of male sexual arousal, and it lasted longer when arousal occurred — patterns that did not hold true for other kinds of stone handling.

Midfacial Morphology and Neandertal–Modern Human Interbreeding

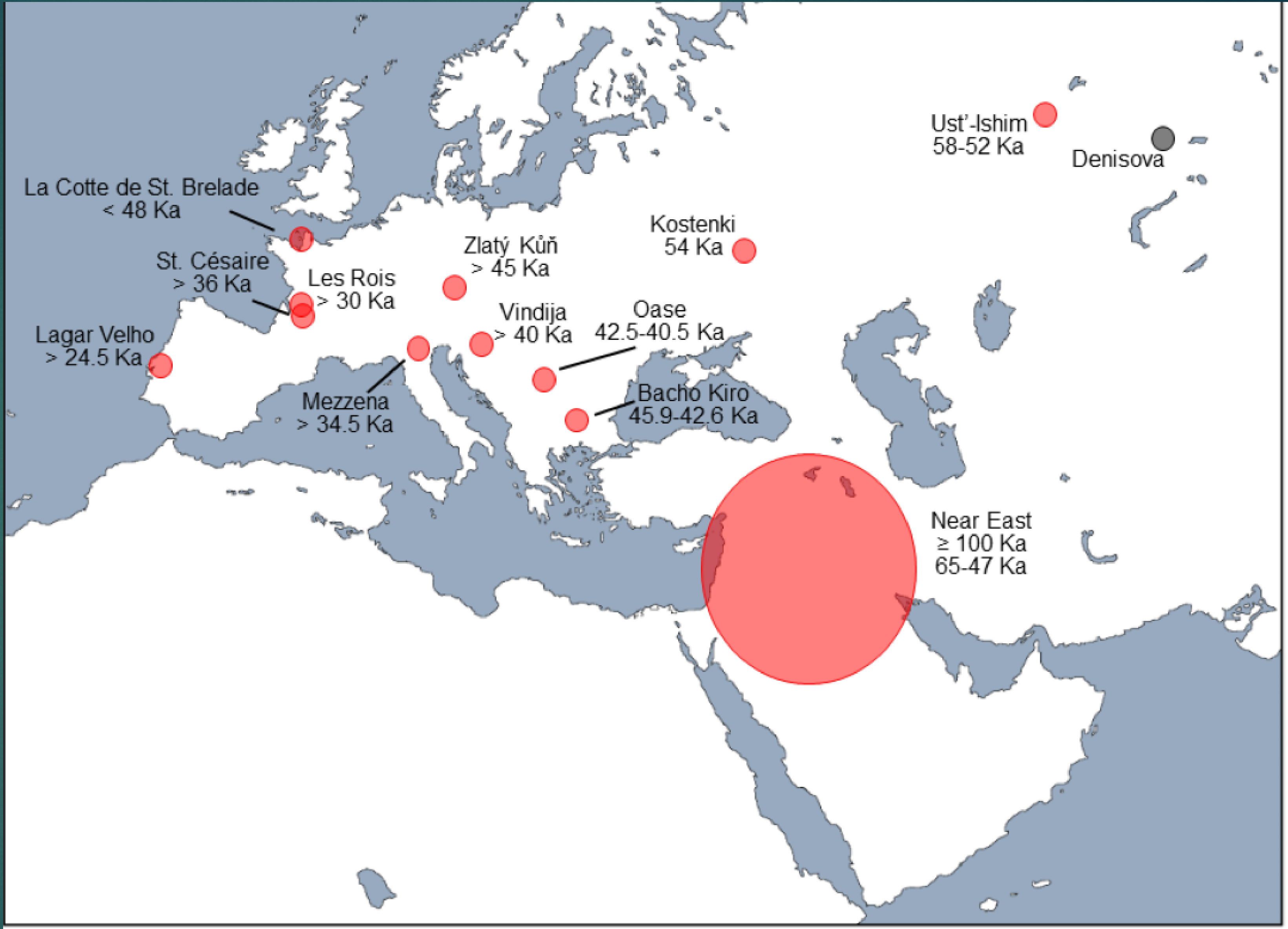
- Used published data on six measurable features of craniofacial morphology for 13 Neandertals, 233 ancient *Homo Sapiens*, and 83 modern humans to see where Neanderthal features like prominent brow ridges showed up most strongly.
- Found certain facial features “retained evidence of inbreeding with Neanderthals” generations later.
- During both the middle and late Palaeolithic era, the Near East and northeast Africa were populated by people whose features place them between Neanderthals and modern humans, suggesting considerable dual inheritance. Any subsequent hybridization in Europe appears to have left much less of a mark.

S. Churchill, et al., 2022

N Facial characteristics

- Neandertals possessed distinctive facial morphology, characterized by:
  - large, superoinferiorly tall yet
  - mediolaterally narrow faces with
  - pronounced midfacial prognathism,
  - absolutely and relatively tall orbits,
  - flat or convex infraorbital plates (and thus, no canine fossae),
  - wide nasal apertures and
  - strongly projecting external noses, and
  - prominent, double-arched supraorbital tori

More hybridization of MHs & Ns produced more N facial features In current MHs



igure 1. Map of western Eurasia showing areas and estimated dates of possible Neandertal–modern uman hybridization (in red) based on fossil samples from indicated sites. Ancient DNA from a

Medieval cemetery

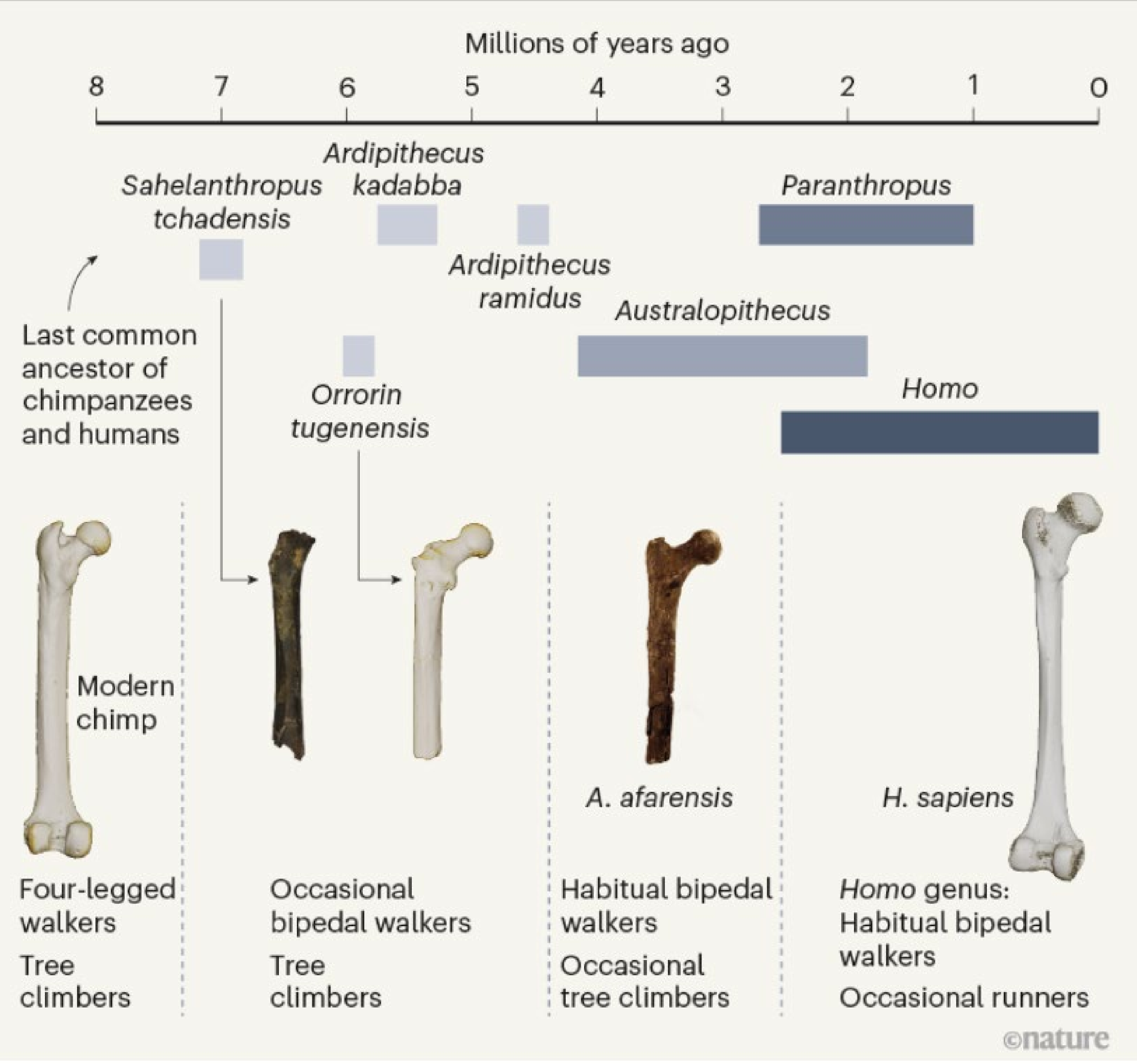
Intestinal parasites in medieval monks

- Augustinian friars in medieval England were nearly twice as likely to suffer from intestinal parasites as other people, despite most monasteries being equipped with washing facilities -- a rarity for ordinary citizens.
- Researchers from the University of Cambridge's Department of Archaeology excavated the remains of 19 friars from the grounds of a former Augustinian friary in Cambridge, England.
- By comparing soil samples taken from around the pelvises of the friars and 25 townspeople of low socioeconomic status from the same 12th-14th-century era, the researchers were able to compare the prevalence of parasites in people with vastly different lifestyles.
- The analysis revealed that 11 of the friars (58%) were infected with worms, compared with just eight of the locals (32%).

Monks

- Of the parasite eggs, the most common species found was roundworm, followed by whipworm, both of which are spread by "poor sanitation."
- Difference in the infection rate must be due to differences in dealing with human waste.
- One possibility is that the friars manured their vegetable gardens with human feces; may have led to repeated infection with the worms.

History of bipedalism



Which hominin? Or hominoid?

2001: *Sahelanthropus tchadensis*, Chad, 7-6 M

Remarkably complete but distorted cranium & 2 mandibles; no postcranials?

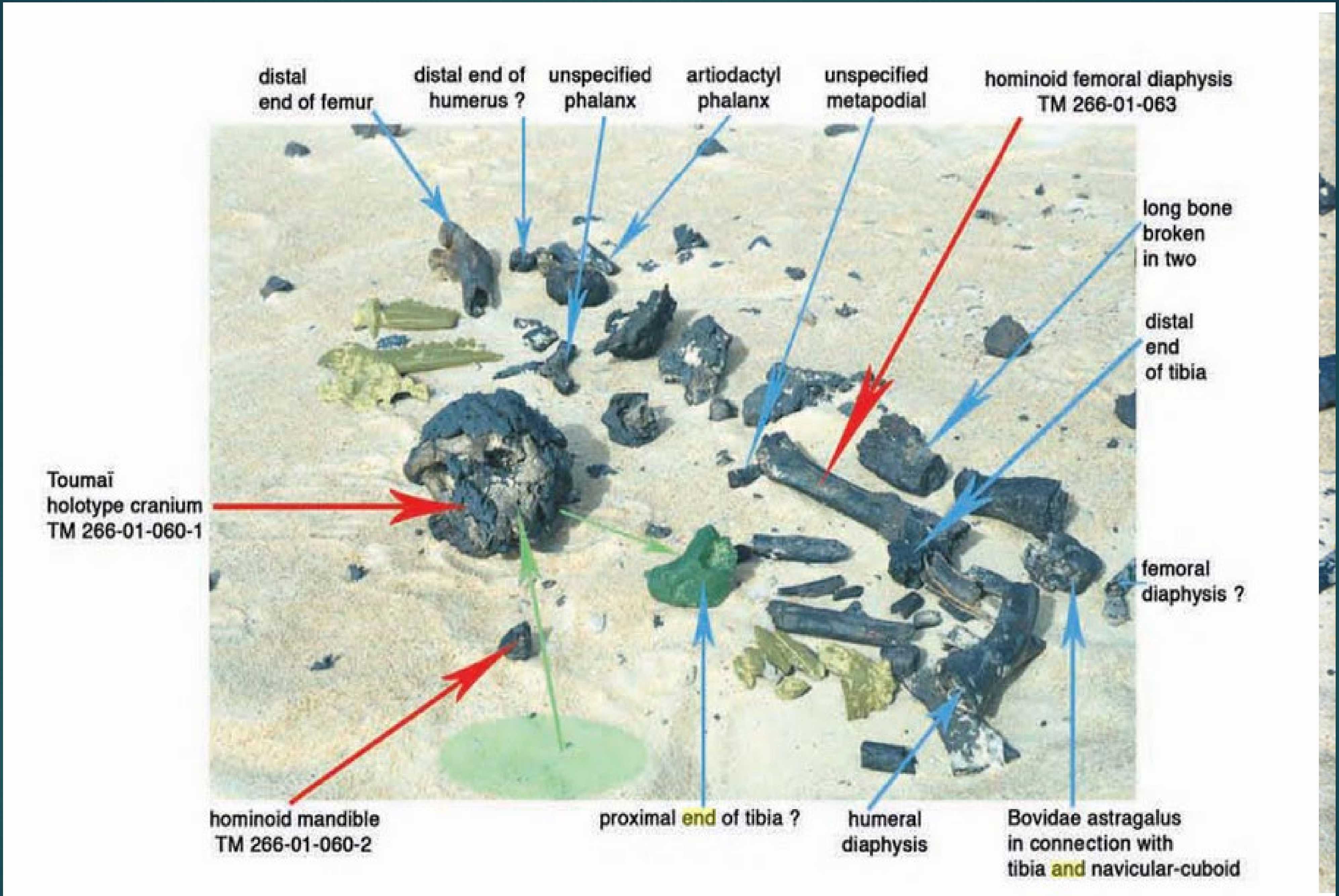
Has been virtually remodeled

Largest hominoid browridge ever discovered

Smaller size than Ardi

Foramen magnum shape and forward positioning indicate bipedalism (like Ardi; both upright posture)

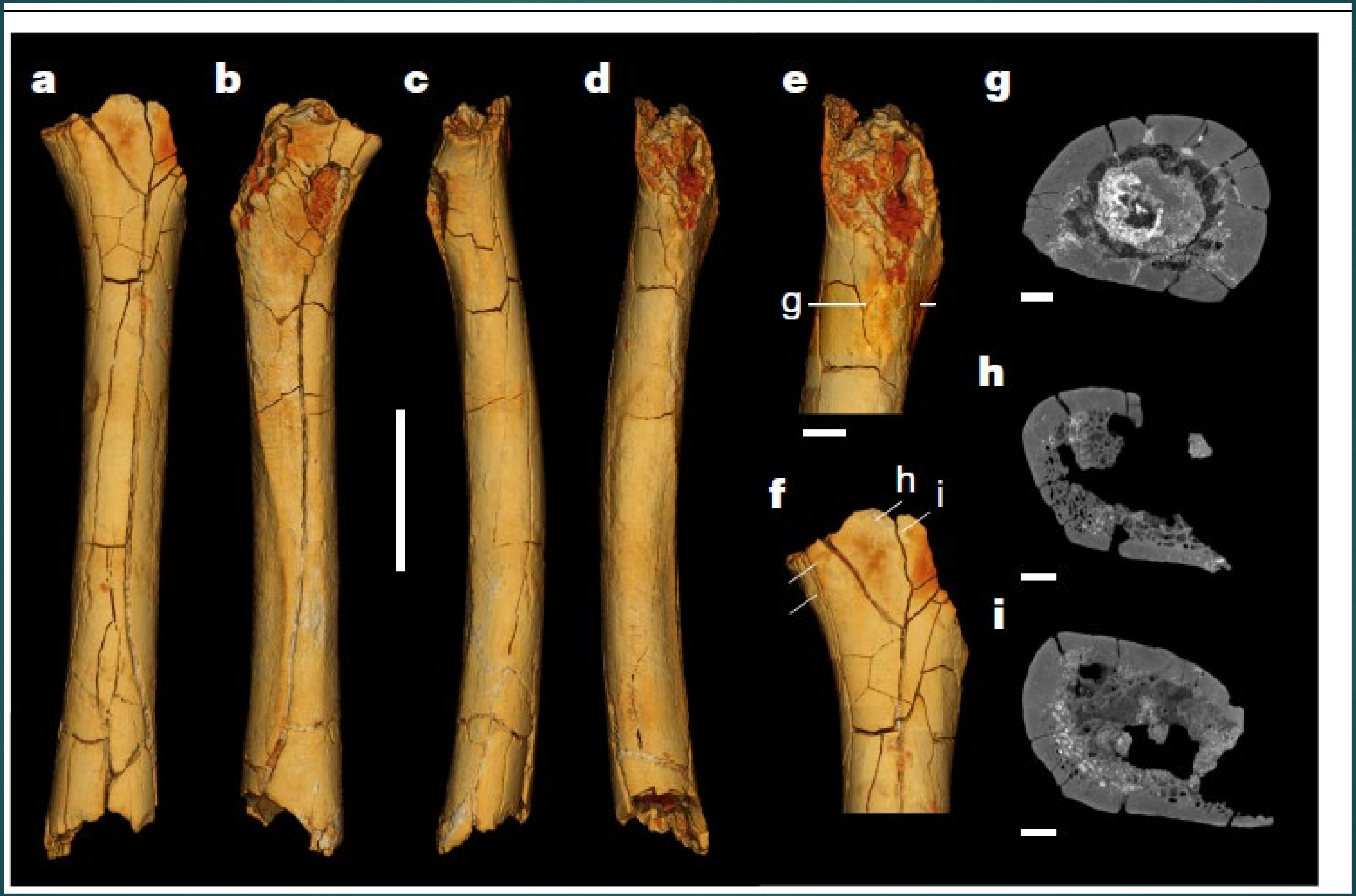
Canines smaller and shorter than those of the male chimp; thick enamel



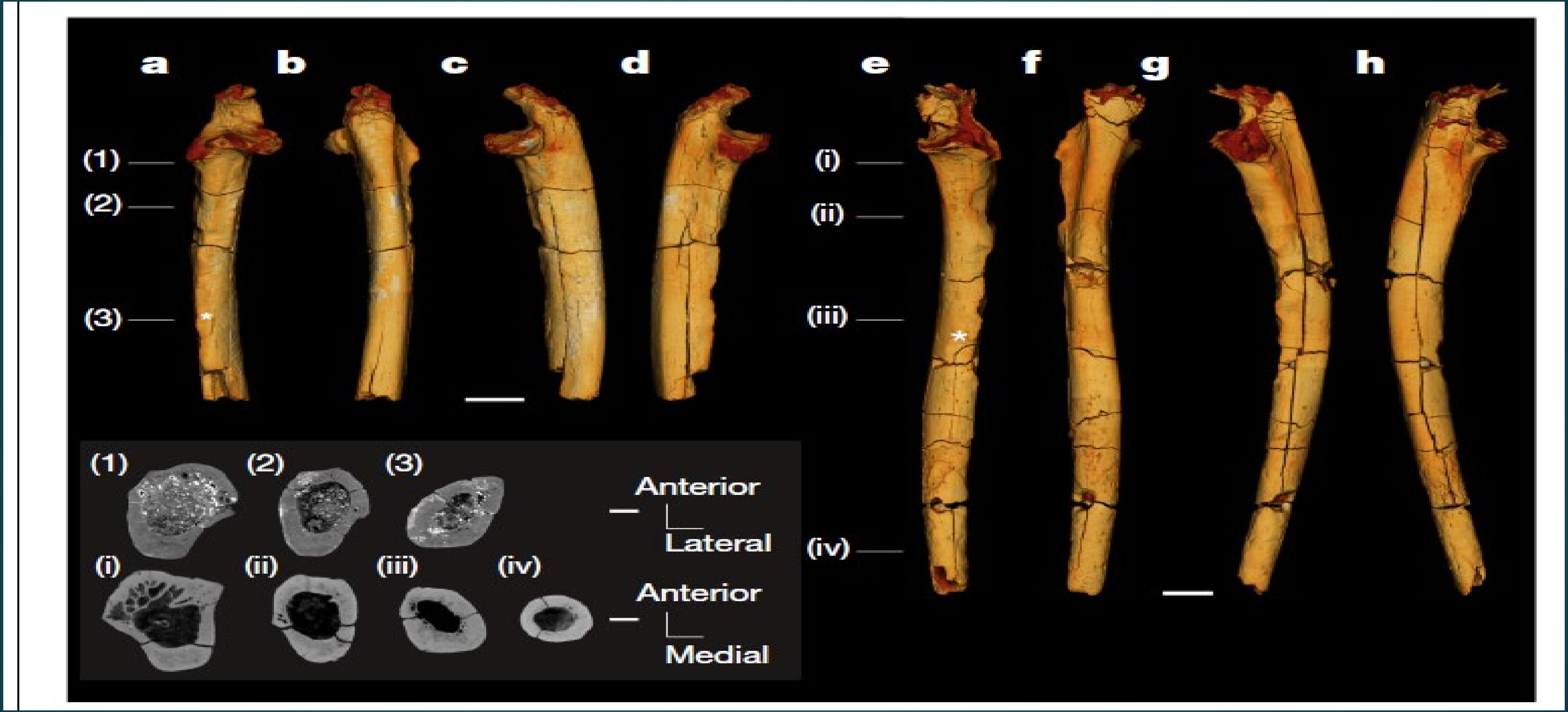
Did camel herders rebury Toumai facing Mecca?

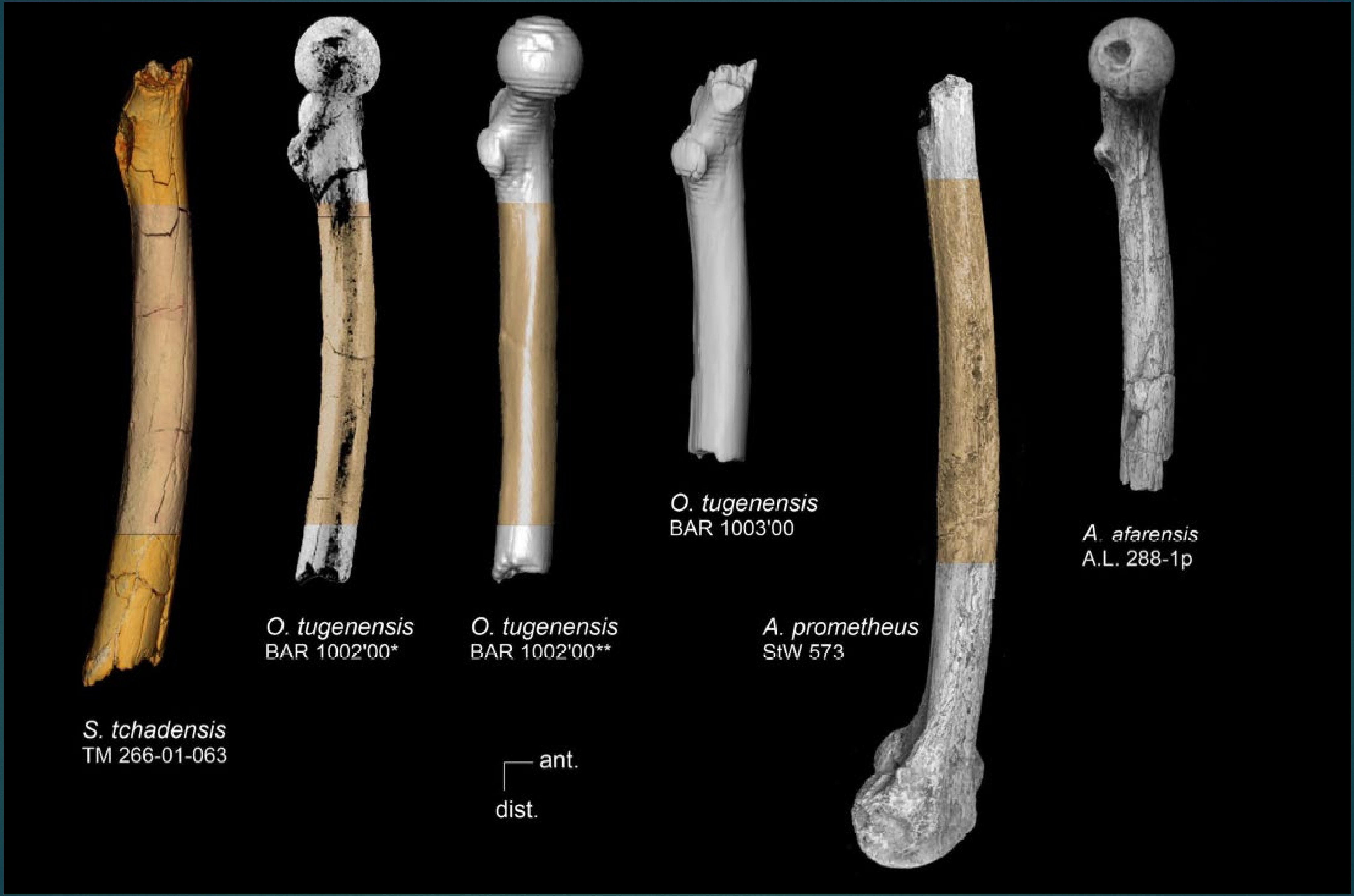
New Study: 1 femur & 2 ulnas of *S. tchadensis*

The femur of *Sahelanthropus tchadensis*



Ulnar remains of *Sahelanthropus tchadensis*




S. tchadensis
TM 266-01-063
O. tugenensis
BAR 1002'00*
O. tugenensis
BAR 1002'00**
O. tugenensis
BAR 1003'00
A. prometheus
StW 573
A. afarensis
A.L. 288-1p
ant.
dist.

The evolution of bipedalism.

- Hominins (species more closely related to humans than to chimpanzees) evolved from an ancestor shared with African great apes (such as chimpanzees and gorillas), which move by walking on four legs and climbing trees.
- *Sahelanthropus tchadensis* is the oldest known hominin species. It has features that suggest it was an occasional bipedal walker, including leg-bone characteristics that Daver *et al*. report.
- The authors indicate that arm bones of this species were adapted for tree climbing.
- A similar mix of adaptations for occasional bipedal walking and tree climbing characterizes early hominins of the genus *Orrorin* and *Ardipithecus*

Bipedalism

- Species of the genus *Australopithecus* were comparatively more effective habitual bipedal walkers, but retained adaptations for climbing trees.
- Species in the genus *Homo* have numerous adaptations for effective bipedal walking and for running, but have lost most adaptations for tree-climbing.
- *Sahelanthropus* femur is missing joints at the end of the femur bone, which would have provided insights into how this species moved.

Foramen magnum

- Perhaps the most exciting feature that Toumaï shares with other hominins is the anatomy of the skull opening (foramen magnum) at the base of the skull where the spine connects and the spinal cord emerges.

- The foramen magnum of four-legged animals is typically located towards the back of the skull and is oriented backwards, whereas in *Sahelanthropus* it is positioned near the middle of the skull and is oriented downwards.

- Combined with the horizontal angle of the back of the skull where the neck muscles attach, a downwards-oriented foramen magnum provides strong evidence that, like bipeds, *Sahelanthropus* balanced its head on a vertical neck.

Sahelanthropus

- An account of the femur's discovery was published in 2009. A subsequent analysis argued that the femur's shape was more similar to that of apes than to that of known bipedal hominins, although this assessment was based on just a few measurements of the femur and on 2D photographs
- The ulna found in 2001 and another discovered in 2003 were subsequently recognized as being those of hominins.
- Despite the new study, don't expect a full resolution just yet, because the femur consists mostly of a shaft that doesn't have the joints at either end that would provide most of the information needed to infer *Sahelanthropus*'s posture and how it walked.
- Whatever you might think about the femur, the arm ulnae are unquestionably chimpanzee-like and are clearly well adapted to climbing trees.

Foramen magnum positions

Figure 2: A comparison of the position of the foramen magnum (marked by white arrows) in chimpanzee, modern human and *Sahelanthropus*.

Daniel Lieberman

- The *Sahelanthropus* femur doesn’t have ‘smoking-gun’ traces of bipedalism, but it looks more like that of a bipedal hominin than that of a quadrupedal ape. When considered in conjunction with the orientation of the foramen magnum, which is compatible only with bipedalism, it seems reasonable to infer that *Sahelanthropus* was some type of biped and that, like later hominins such as *A. ramidus*, it was also well adapted to climbing trees.
- A mixed repertoire of walking and climbing makes sense given that *Sahelanthropus* lived near a lake with woodland adjacent to it.
- It bears repeating that, apart from bipedalism and slightly more hominin-like teeth and face, many *Sahelanthropus* features are similar to those of a chimpanzee. This resemblance makes sense if the last common ancestor of humans and chimpanzees was chimpanzee-like and *Sahelanthropus* evolved very soon after humans and chimpanzees diverged.

Guy Diver, et al., 2022: Postcranial evidence of late Miocene hominin bipedalism in Chad

- Bipedality of *Sahelanthropus tchadensis* was hitherto inferred about 7 Ma in central Africa (Chad) based on cranial evidence.
- The original material was discovered at locality TM 266 of the Toros-Ménalla fossiliferous area and consists of one left femur and two, right and left, ulnae. The morphology of the femur is most parsimonious with habitual bipedality, and the ulnae preserve evidence of substantial arboreal behavior.
- Taken together, these findings suggest that hominins were already bipeds at around 7 Ma but also suggest that arboreal clambering was probably a significant part of their locomotor repertoire.

G. Daver, et al., 2022

Sahelanthropus tchadensis

- A battered fossil leg bone discovered more than 20 years ago in Chad is finally making its scientific debut. Researchers say that the remains, described today in *Nature*, show that a species called *Sahelanthropus tchadensis* was an ancient human relative that walked on two feet.
- At seven million years old, *S. tchadensis* is a candidate for the earliest known member of the hominin lineage — the evolutionary branch that leads from the common ancestor of humans and chimpanzees to modern humans.
- A French and Chadian team discovered *S. tchadensis* in July 2001, during an expedition in the Lake Chad basin. The key find was a nearly complete, but heavily damaged, skull that was described in *Nature* the following year.

Sahelanthropus tchadensis

- The skull was nicknamed Toumaï, which means ‘hope of life’ in the Chadian Daza language. Researchers led by paleoanthropologist Michel Brunet at the University of Poitiers, France, argued that, despite the small, chimp-like size of its brain, Toumaï possessed other features of later hominins, such as in its teeth and face. The probable angle at which the base of Toumaï’s skull would have met its spine also hinted at upright walking on two feet.
- The researchers collected hundreds of other bone fragments during the expedition, but didn’t initially spot the shaft of an upper leg bone.
- The blackened femur fragment was first noticed in 2004 by graduate student Aude Bergeret-Medina at the University of Poitiers; Roberto Macchiarelli, a paleoanthropologist there. He supervised Bergeret-Medina and agreed with her assessment that the bone belonged to a primate, probably *S. tchadensis*.

Confirms that *Sahelanthropus* was a hominin.

- Over the years, the undescribed fossil — sometimes dubbed Toumaï's femur, even though it's not clear whether the skull and leg bone belonged to the same individual — became one of palaeoanthropology's worst kept secrets.
- Macchiarelli et al, 2020 : In 2020, a team including Macchiarelli and Bergeret-Medina published a brief description of the femur, based on several days of study done in 2004. Their preliminary analysis concluded that the remains probably did not belong to a species that routinely walked upright.
- In the 2022 paper now describing the femur, alongside the two arm bones, Guy's team comes to the opposite conclusion. The team contends that more than a dozen features of the femur suggest that Toumaï's kind walked on two feet, and the ape-like arm bones suggest its species would also have been comfortable clambering in trees.

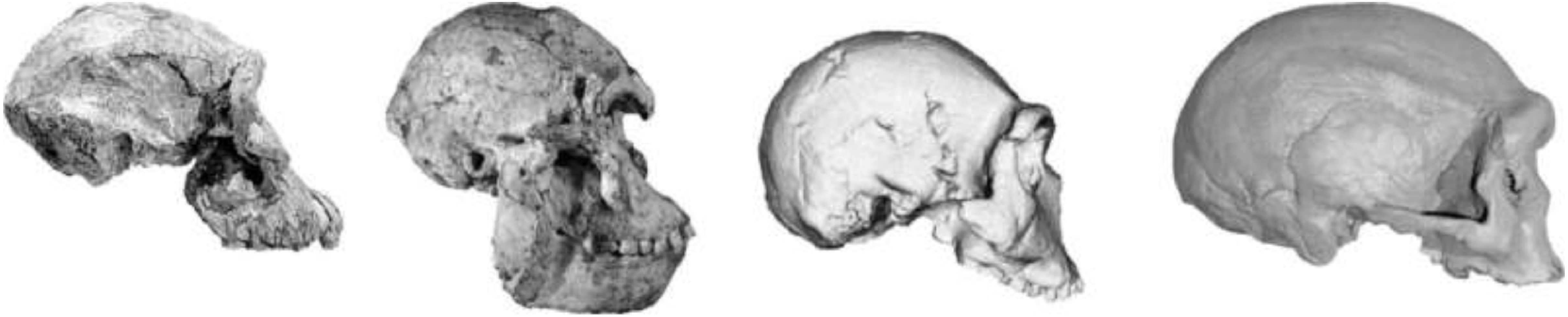
Critique

- Other scientists are less swayed by the analysis. One of the features Guy's team cited as evidence for bipedalism is the presence of a bony ridge that supports the femur during upright walking. But significance is debated.
- "They cherry-pick what they think is information which is consistent with the femur shaft being a biped, and they studiously ignore information to the contrary," adds Bernard Wood, a palaeoanthropologist at George Washington University in Washington DC who co-authored the 2020 analysis with Macchiarelli and Bergeret-Medina.
- Guy and his co-authors said in an e-mail that *Sahelanthropus* is marked as an upright walker not by any single trait, but rather by the combination of numerous features that are more common in bipedal hominins than knuckle-walking apes.

Sahelanthropus

- Still, Macchiarelli thinks *Sahelanthropus* is more likely to be an ape than a hominin, and one that lived not long after the two lineages diverged, in the past ten million years.
- Researchers know little about how the common ancestor of humans and chimps looked or moved, and Macchiarelli thinks that the *Sahelanthropus* remains, including its infamous femur, might offer some clues. "These are extraordinarily important specimens."

Paleontologists reveal new data on the evolution of the hominin cranium



Australopithecus anamensis (MRD-VP-1)

Australopithecus prometheus (StW573)

Homo naledi (LES-1)

Homo longi (HBSM2018-000018(A))

Human evolution uniquely combines an increase in brain size with the acquisition of an increasingly juvenile cranial shape.

Juan Antonio Pérez-Claros, Paul Palmqvist, 2022

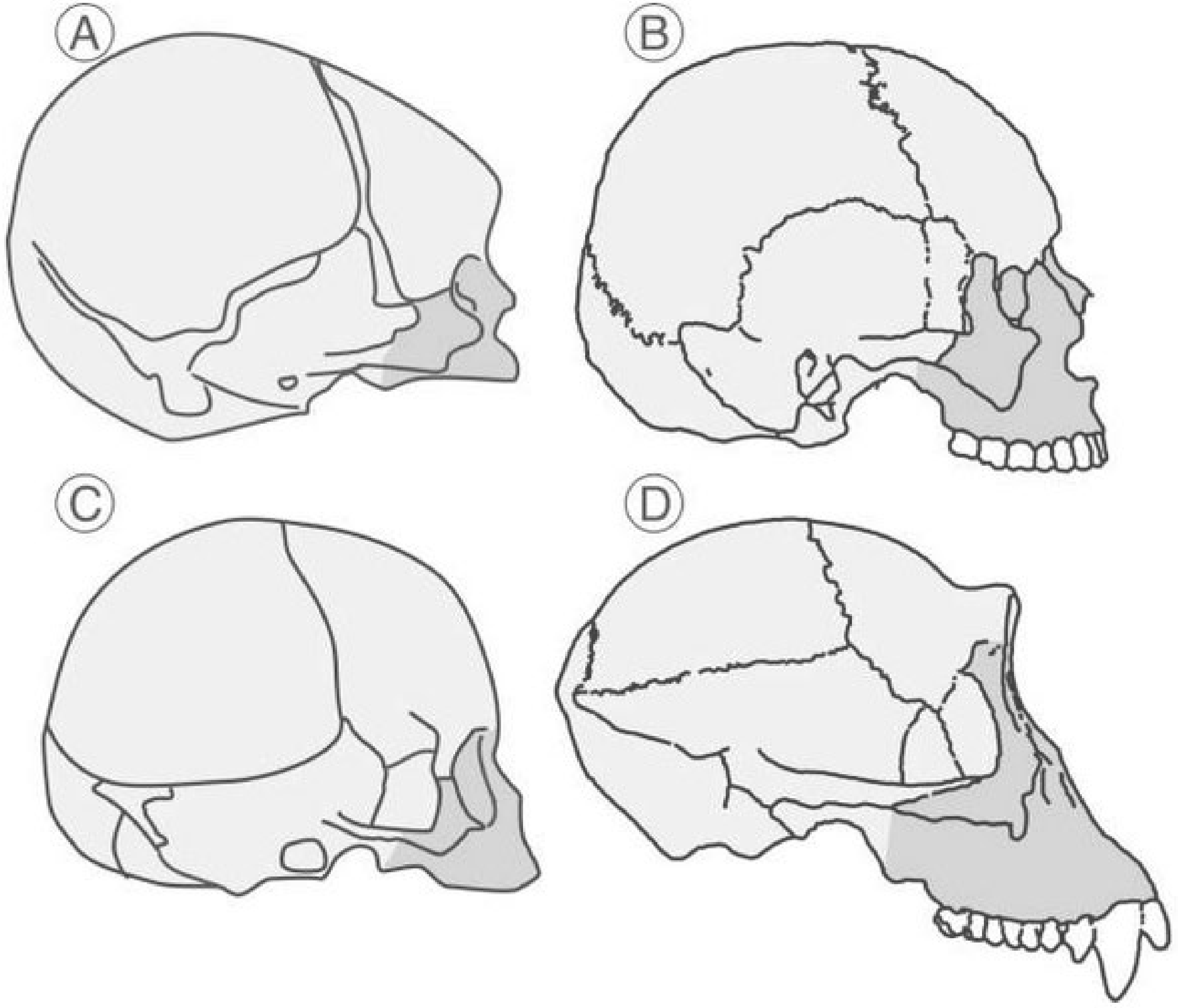
Human cranium

- Sample: 4 new skull specimens: Australopithecus anamensis, Australopithecus prometheus, Homo naledi and Homo longi. As well as juvenile samples of modern species of great apes.
- The great apes and modern humans share a pervasive negative ontogenetic allometry in the neurocranium (reduced cranial size) and a positive one in the splanchnocranium (larger face).
- The representatives of the genus Homo, as well as the australopithecines share with orangutans, gorillas and chimpanzees a negative growth of the neurocranium—the cranial vault, which measures brain development, grows at a slower pace than the rest of the cranium—and a positive one in the splanchnocranium—the dimensions of the face, which correlate with the size of dentition, grow faster throughout development.
- This means that bigger crania present higher relative sizes in the face and more reduced sizes in the cranial vault

Juvenilization: higher relative sizes in the face and more reduced sizes in the cranial vault

- A "juvenilization" of cranial proportions: adults retained the characteristics of the infant crania of the ancestral species

- Demonstrated that the cranium of *Homo naledi*, despite being a relatively recent species, show proportions that are similar to those of the the Homo habilis, which are more than 2 million years old.



Comparison of the development of human and chimpanzee brains. Credit: ...

Eran Elhaik, PhD, Univ. of Lund

- Israeli-American geneticist and bioinformatician, and an associate professor of bioinformatics at Lund University in Sweden.
- Highly published in peer reviewed journals
- In 2013, published a paper claiming that Ashkenazi Jews originated in Turkey; it was highly criticized
- 2022 study: Principal Component Analyses (PCA)-based findings in population genetic studies are highly biased and must be reevaluated, by Eran Elhaik, 2022. The study is published in *Scientific Reports*.

Study reveals flaws in popular genetic method

- The most common analytical method within population genetics is deeply flawed.
- This may have led to incorrect results and misconceptions about ethnicity and genetic relationships.
- Massive and highly complex datasets, dubbed the "Big Data revolution." To make these data more manageable, researchers use statistical methods that aim to compact and simplify the data while still retaining most of the key information.
- Perhaps the most widely used method is called PCA (principal component analysis).

PCA: unreliable

- Principal Component Analysis (PCA) is a multivariate analysis that reduces the complexity of datasets while preserving data covariance. The outcome can be visualized on colorful scatterplots,
- PCA is extensively used as the foremost analyses in population genetics
- .
- We analyzed twelve common test cases using an intuitive color-based model alongside human population data. We demonstrate that PCA results can be artifacts of the data and can be easily manipulated to generate desired outcomes.
- PCA results may not be reliable, robust, or replicable as the field assumes.

PCA history

- In population genetics, PCA is primarily used to reduce the dimensionality of multivariate datasets by linearly transforming the genotypes into a set of mutually uncorrelated principal components (PCs) ranked according to their variances.
- As most of the original variability is contained in the primary two PCs, they are typically visualized on a colorful scatter plot.
- The early work of Cavalli-Sforza suggested that PCA can detect ancient migrations and population spreads in the genomic data.

Principal Components Analysis

- According to Elhaik, the method helped create old perceptions about race and ethnicity.
- It plays a role in manufacturing historical tales of who and where people come from, not only by the scientific community but also by commercial ancestry companies.
- PCA is used to create a genetic map that positions the unknown sample alongside known reference samples. Thus far, the unknown samples have been assumed to be related to whichever reference population they overlap or lie closest to on the map.

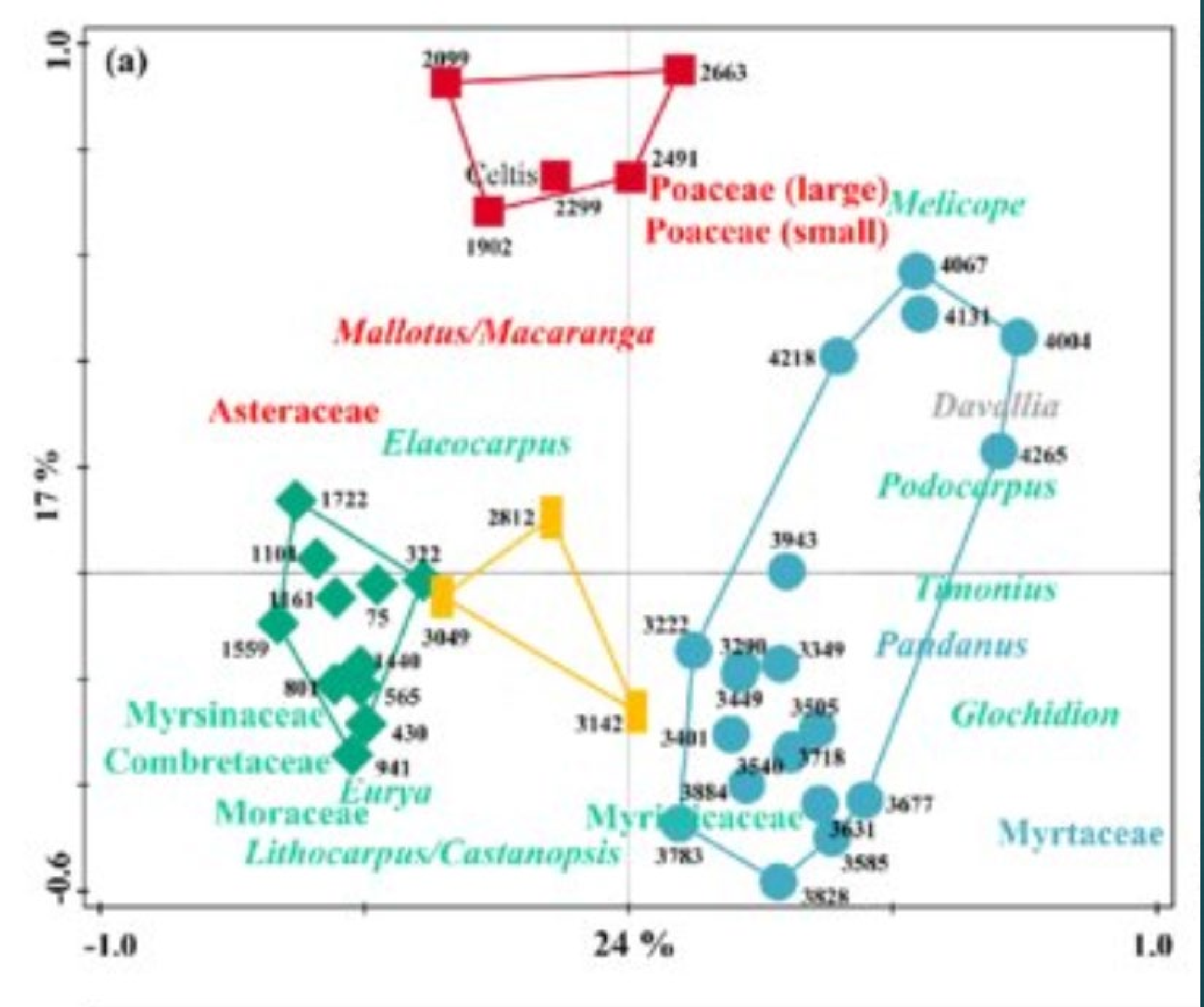
PCA: every paper in population genetics

- PCA became the foremost utility in population genetic investigations, reaching "fixation" by 2013, the point where it is used almost in every paper in the field

- First, PCA typically explains a tiny part of the variation that may have a genealogical interpretation, but not only does it grow smaller as more samples are added, it also grows in inaccuracy.

- This leads to a paradox, whereas increasing the sample size, which intuitively should be expected to increase the accuracy of analyses, decreases the proportion of explained variance and accuracy.

Example: A PCA study graph: buffalos in Sumatra



PCA: too flexible

- Our findings raise concerns about the validity of results reported in the population genetics literature and related fields that place a disproportionate reliance upon PCA outcomes
- .
- We conclude that PCA may have a biasing role in genetic investigations and that 32,000-216,000 genetic studies should be reevaluated.

- In the study, Elhaik has examined the twelve most common population genetic applications of PCA. He has used both simulated and real genetic data to show just how flexible PCA results can be. According to Elhaik, this flexibility means that conclusions based on PCA cannot be trusted since any change to the reference or test samples will produce different results.

PCA

- The question of who the ancestors of admixed populations are and the extent of their contribution to other groups is at the heart of population genetics.
- PCA is the primary tool in paleogenomics, where ancient samples are initially identified based on their clustering with modern or other ancient samples.
- Elhaik states that a sample could be made to lie close to virtually any reference population just by changing the numbers and types of the reference samples, generating practically endless historical versions, all mathematically "correct," but only one may be biologically correct.

PCA

- Specifically, in analyzing real populations, showed that PCA could be used
  - to generate contradictory results and lead to absurd conclusions (*reductio ad absurdum*),
  - “correct” conclusions cannot be derived without *a prior*i knowledge
  - *cherry-picking* or *circular reasoning* are always needed to interpret PCA results.
  - This means that the difference between the a posteriori knowledge obtained from PCA and a priori knowledge rests solely on belief.
- The conflicting PCA outcomes shown here via over 200 figures demonstrate the high experimenter’s control over PCA’s outcome. By manipulating the choice of populations, sample sizes, and markers, experimenters can create multiple conflicting scenarios with real or imaginary historical interpretations, *cherry-pick* the one they like, and adopt *circular reasoning* to argue that PCA results support their explanation.

PCA studies often leave out variances

- Concludes that authors misinterpret PCA findings and do not disclose the amount of variation explained by PCA.
- Fascinatingly, in 2008 Reich and colleagues found it necessary to assess "whether the proportion of the variance explained by the first PC is sufficiently large," most likely before they realized just how small this variation really is. To the best of our knowledge, they omitted this information in their numerous publications that employed PCA.
- Although authors were aware that PCA results depended on the sample cohort, they continued using it, presenting only the results that fit their a priori hypotheses.
- Our findings, albeit in population genetics, demonstrate that with the exceptions discussed above, all PCA results are wrong and are independent of the level of "cautiousness" exhibited by the experimenter even for "exploration" purposes.

PCA = no null hypothesis

- Overall, the positioning of a method that lacks any measurable power, a test of significance, or a null model, which any diligent scientist should seek at the forefront of population genetic analyses, is problematic at the very least.
- It would not be an exaggeration to consider PCA the Rorschach of population genetics, a procedure that is almost entirely open to manipulations and consequent interpretations, where researchers may see “geographical maps” or “Neolithic clines” as they will.
- In PCA-driven science, almost all the answers are equally acceptable, and the truth is in the eyes of the beholder.

PCA: often low variance in human populations

- PCA is a mathematical transformation that reduces the dimensionality of the data to a smaller set of uncorrelated dimensions called principal components (PCs).
- In population genetics alone, PCA usage is universal. PCA is typically the first and primary analysis, and its outcomes determine the study design.
- That PCA is completely non-parametric is the source of its strength. Any genotype dataset can be rapidly processed with no concerns about parameters or data validity.

PCA

- It is also a weakness because the answer is unique and depends on the particular dataset, which is when reliability, robustness, and reproducibility become a concern.
- The implicit expectation employed by PCA users is that the variance explained along the first two PCs provides a reasonable representation of the complete dataset. When this variance is minuscule (as often with human populations), it poorly represents the data.
- Authors often choose not to report the variation explained by PCA. Regardless, it is not a proxy for the reliability of the results.

PCA: conclusions

- As PCA lacks any measurable significance or accuracy, we argue that its dominance in population genetics could not have been achieved without the adoption of two fallacies:
  - *cherry-picking* or *circular reasoning* (i.e., "exploration"), the screening and selecting PCA scatterplots that fit preconceived hypotheses while ignoring the other plots, and
  - the a priori where PCA results are interpreted based on pre-existing knowledge because PCA scatterplots are uninformative a posteriori.
  - We consider PCA scatterplots analogous to Rorschach plots. We find PCA unsuitable for population genetic investigations and recommend reevaluating all PCA-based studies.

PCA

- CJV: Have not yet found a significant critique of the use of PCA in population genetics study

- "The idea that archaeological units of classification represent human groups of a shared social, or ethnic identity has been proven wrong many times during the history of research," says Martin Furholt.
- Ethnicity is founded on shared ancestry, whereas identity is more about culture.
- "Geneticists are basically looking at ethnicity. But archaeologists are foremost looking at identity," says archeologist VolkerHeyd.

Drink coffee!!

- The impact of coffee subtypes on incident cardiovascular disease, arrhythmias, and mortality: long-term outcomes from the UK Biobank:
- 450 K participants (median 58 years, 55.3% females) were followed over 12.5 years.
- Decaffeinated, ground, and instant coffee, particularly at 2–3 cups/day, were associated with significant reductions in incident CVD and all cause mortality.
- Ground and instant but not decaffeinated coffee was associated with reduced arrhythmia.

Science, 2022: 3 major genetics papers by Leipzig group

- The genetic history of the Southern Arc: A bridge between West Asia and Europe by Iosif Lazaridis…David Reich – 206 authors
- A genetic probe into the ancient and medieval history of Southern Europe and West Asia
- Ancient DNA from Mesopotamia suggests distinct Pre-Pottery and Pottery Neolithic migrations into Anatolia

- Review: Ancient genomes and West Eurasian history

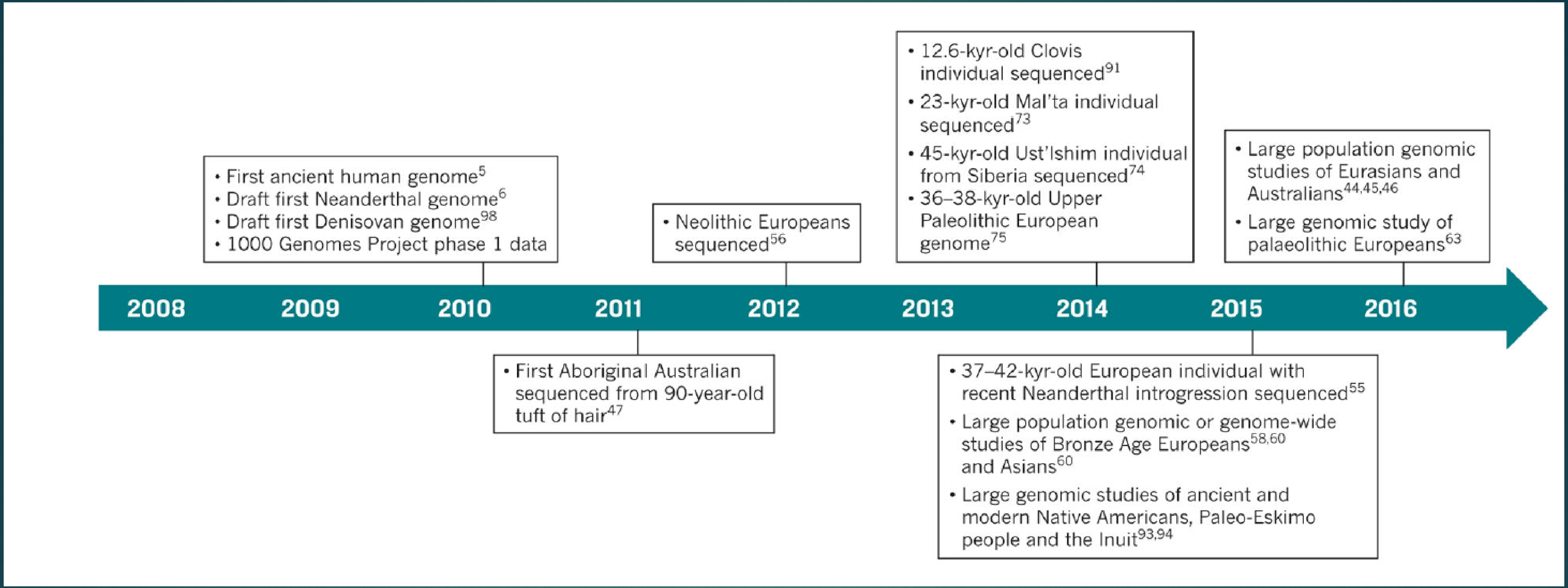
- Will review when we get to Reich's Asia discussion

Who We Are and How We Got Here

- Part II, “How We Got to Where We Are Today,” is about
- · how the genome revolution and ancient DNA have transformed our understanding of MHs,
- age of modern humans, and it takes readers on
- a tour around the world with population mixture as a unifying theme.

Chapter 4, “Humanity’s Ghosts,” introduces the idea that we can reconstruct populations that no longer exist in unmixed form in genetic material they have left behind in present-day people.

Peopling of the world through genetics



- First ancient human genome[5]
- Draft first Neanderthal genome[6]
- Draft first Denisovan genome[98]
- 1000 Genomes Project phase 1 data

- First Aboriginal Australian sequenced from 90-year-old tuft of hair[47]

- Neolithic Europeans sequenced[56]

- 12.6-kyr-old Clovis individual sequenced[91]
- 23-kyr-old Mal'ta individual sequenced[73]
- 45-kyr-old Ust'Ishim individual from Siberia sequenced[74]
- 36–38-kyr-old Upper Paleolithic European genome[75]

- 37–42-kyr-old European individual with recent Neanderthal introgression sequenced[55]
- Large population genomic or genome-wide studies of Bronze Age Europeans[58,60] and Asians[60]
- Large genomic studies of ancient and modern Native Americans, Paleo-Eskimo people and the Inuit[93,94]

- Large population genomic studies of Eurasians and Australians[44,45,46]
- Large genomic study of palaeolithic Europeans[63]

Multiple Major Genomic Studies: 2010-2016

- 2010: First ancient human genome
    - Draft first Neanderthal genome
    - Draft first Denisovan genome
    - 1000 Genomes Project
- 2011: First Aboriginal Australian sequenced from 90-year-old tuft of hair
- 2012: Neolithic Europeans sequenced
- 2014: 12.6-kyr-old Clovis individual sequenced
    - 23-kyr-old Mal'ta individual sequenced
    - 45-kyr-old Ust’Ishim individual from Siberia sequenced
    - 36-38-kyr-old Upper Paleolithic European genome

Genomic Studies: 2008-2016

- 2015: 37-42-kyr-old European Oase 1 individual with recent Neanderthal introgression sequenced
    - Bronze Age Europeans and Asians (3000-1000 BC)
    - Ancient and modern Native Americans, Paleo-Eskimo people and the Inuit
- 2016:
    - Large population genomic studies of Eurasians and Australians
    - Large genomic study of palaeolithic Europeans

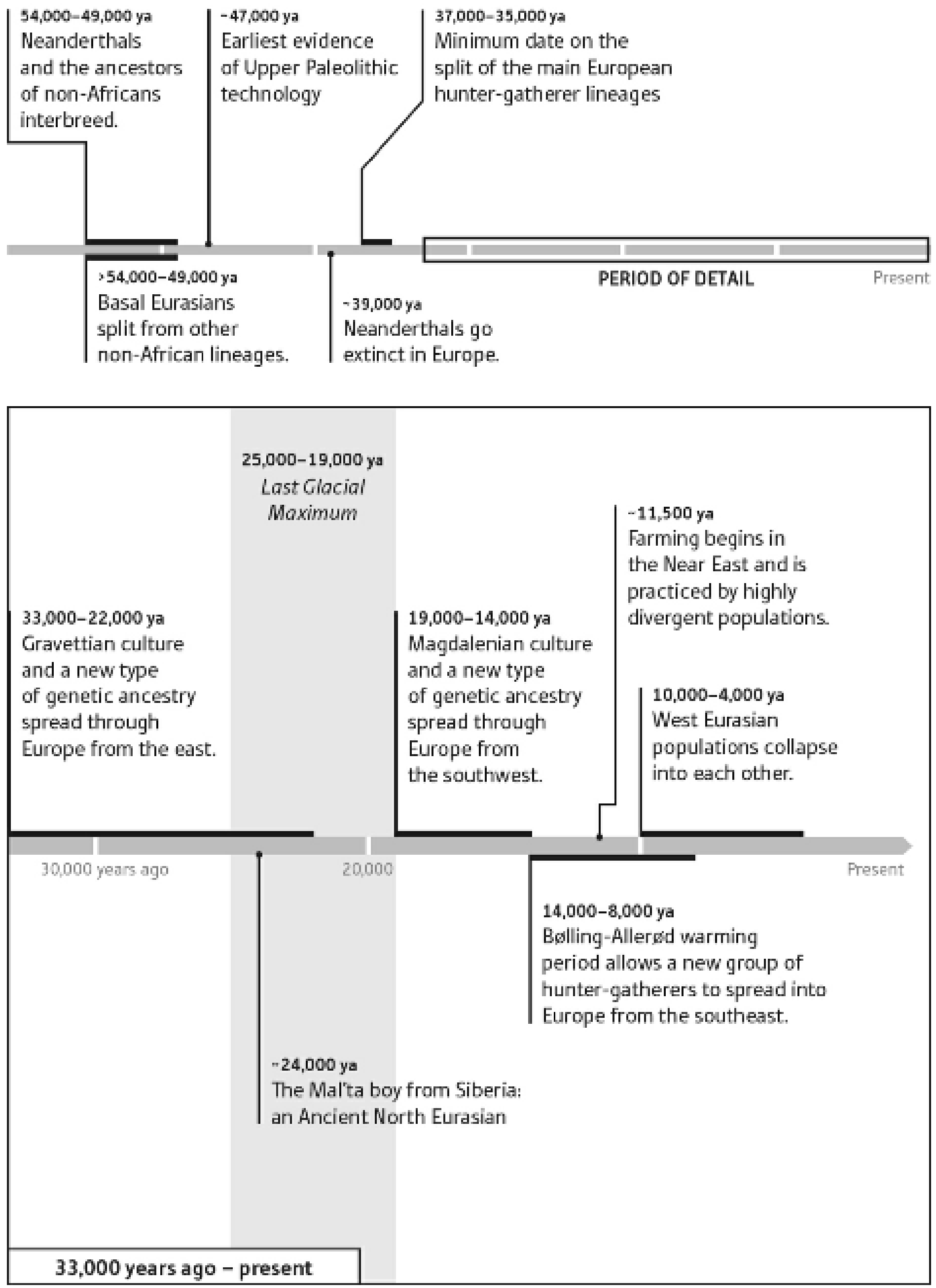
How to discover a ghost species

- Ghost Population: Extinct group that explains the current genetic variance in modern population
- Evidence for a previously unknown species of archaic hominin can be found in the genes of a modern-day population
- Historically, archeologists and genetic researchers have required the use of reference DNA in order to compare and draw conclusions from fossilized genetic material.

Ghost populations

- Can now use statistics rather than a reference DNA, computational biologists can identify a ghost population, formed from an extinct relative of humans, to which a modern population can trace a percentage of their genetic ancestry.
- Can identify sections of DNA that are different from MH, N, and D genes, indicating they come from a different ancient relative.
- Can conclude that they come from a heretofore unknown, or ghost, population.

Modern Humans in Eurasia



Modern Humans in Eurasia

54,000–49,000 ya
Neanderthals and the ancestors of non-Africans interbreed.

~47,000 ya
Earliest evidence of Upper Paleolithic technology

37,000–35,000 ya
Minimum date on the split of the main European hunter-gatherer lineages

>54,000–49,000 ya
Basal Eurasians split from other non-African lineages.

~39,000 ya
Neanderthals go extinct in Europe.

25,000–19,000 ya
Last Glacial Maximum

33,000–22,000 ya
Gravettian culture and a new type of genetic ancestry spread through Europe from the east.

19,000–14,000 ya
Magdalenian culture and a new type of genetic ancestry spread through Europe from the southwest.

~11,500 ya
Farming begins in the Near East and is practiced by highly divergent populations.

10,000–4,000 ya
West Eurasian populations collapse into each other.

14,000–8,000 ya
Bølling-Allerød warming period allows a new group of hunter-gatherers to spread into Europe from the southeast.

~24,000 ya
The Mal'ta boy from Siberia: an Ancient North Eurasian

33,000 years ago – present

Modem Humans in Eurasia: 33,000 years ago - present

- 33 to 22 Ka: Gravettian culture: a new type of genetic ancestry spread through Europe from the east.
- 25 to 19 Ka: *Last Glacial Maximum*
- -24 Ka: The Mal'ta boy from Siberia: an Ancient North Eurasian
- 19 to 14 Ka: Magdalenian culture: a new type of genetic ancestry spread through Europe from the southwest,

Modem Humans in Eurasia: 33,000 years ago - present

- 14 to 8 Ka: Bolling-Allergd warming period allows a new group of hunter gatherers to spread into Europe from the southeast.
- -11.5 Ka: Farming begins in the Near East and is practiced by highly divergent populations.
- 10 to 4 Ka: West Eurasian populations collapse into each other. Finalization of current European genetics profile

Modem Humans in Eurasia

- 54 to 40 Ka: Neanderthals and the ancestors of non-African MH interbreed
- 54 to 40 Ka: Basal Eurasians split from other non-African lineages
- -47 Ka: Earliest evidence of Upper Paleolithic technology
- 39 Ka: Neanderthals go extinct in Europe
- 37 to 35 Ka: Minimum date of the split of the main European hunter-gatherer lineages

The Discovery of the Ancient North Eurasians

- Reich's laboratory's first major discovery using the Four Population Test came when they tested the widely held view that
    - Native Americans and East Asians were "sister populations"
- But Europeans turned out to be more closely related to Native Americans than they are to the geographically closer East Asians.

Native Americans related to northern Europeans

- Evidence that people in northern Europe are descended from a mixture of populations, one of which shared more ancestry with present-day Native Americans than with any other population living today.

- Theory:
  - More than 15 Ka, there was a population living in northern Eurasia that was not the primary ancestral population of the present-day inhabitants of that region.
  - Some people from this population migrated east across Siberia and contributed to the population that crossed the Bering land bridge and gave rise to Native Americans.
  - Others migrated west and contributed to Europeans.

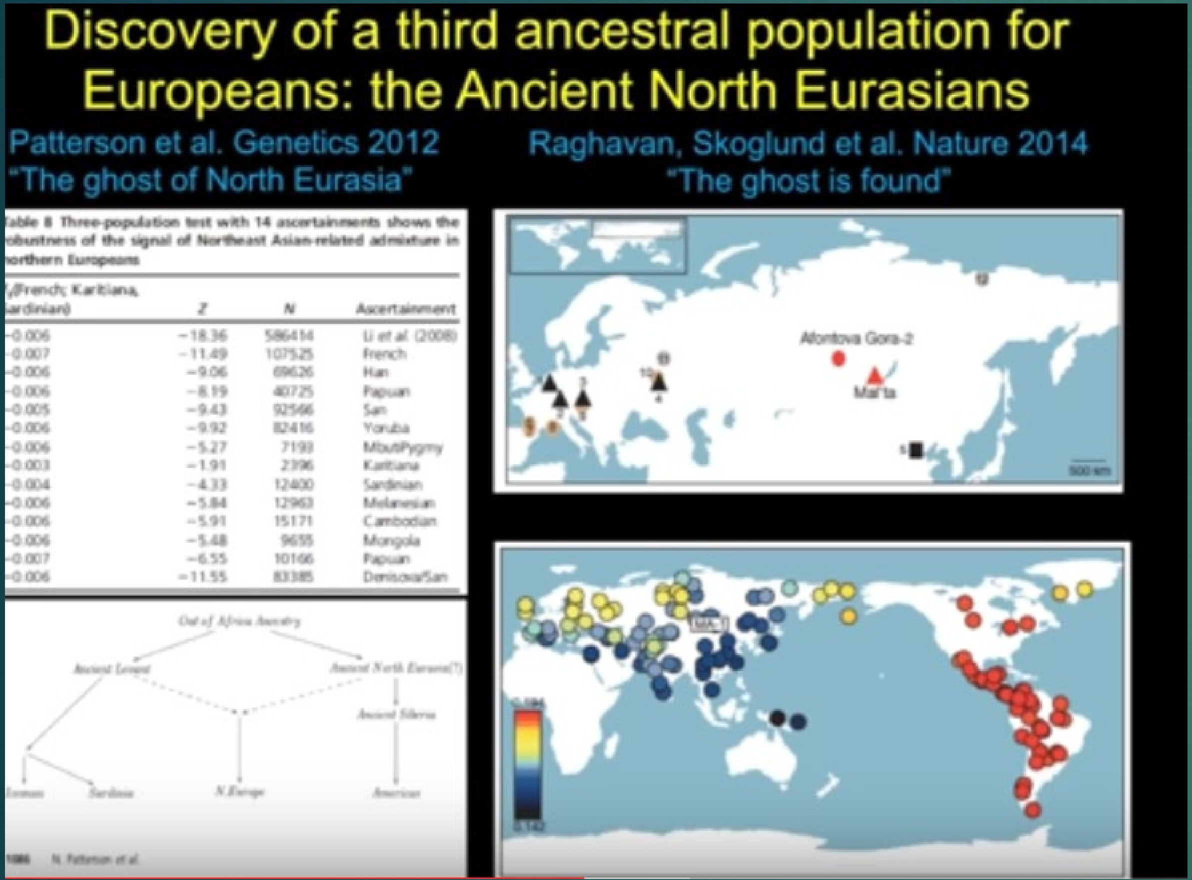
Ancient North Eurasians (ANE)

- This would explain why today, the evidence of mixture in Europeans is
  - strong when using Native Americans as a surrogate for the ancestral population and
  - not as strong in indigenous Siberians, who plausibly descend from more recent, post–ice age migrations into Siberia from more southern parts of East Asia.

- Proposed new population name: the "Ancient North Eurasians" (ANE). Originally, they were a "ghost"—a population that we can infer existed in the past based on statistical reconstruction but that no longer exists in unmixed form.

- Patterson group (2012) finds this ANE population: contributed 30% of Native American DNA & also to European (Sardinian) population

Ancient North Eurasian population (ANE)



Discovery of a third ancestral population for Europeans: the Ancient North Eurasians

Patterson et al. Genetics 2012
"The ghost of North Eurasia"

Raghavan, Skoglund et al. Nature 2014
"The ghost is found"

able 8 Three-population test with 14 ascertainments shows the obustness of the signal of Northeast Asian-related admixture in orthern Europeans

(French; Karitiana, ardinian)	Z	N	Ascertainment
−0.006	−18.36	586414	Li et al. (2008)
−0.007	−11.49	107525	French
−0.006	−9.06	69626	Han
−0.006	−8.19	40725	Papuan
−0.005	−9.43	92566	San
−0.006	−9.92	82416	Yoruba
−0.006	−5.27	7193	MbutiPygmy
−0.003	−1.91	2396	Karitiana
−0.004	−4.33	12400	Sardinian
−0.006	−5.84	12963	Melanesian
−0.006	−5.91	15171	Cambodian
−0.006	−5.48	9655	Mongola
−0.007	−6.55	10166	Papuan
−0.006	−11.55	83385	Denisova/San

1086 N. Patterson et al.

- Test of modern populations discovers a 3^{rd} ancestral population for Europeans.
- Found Sardinian group (S farmers from Middle Eastern agriculturists); other is strongest signal from Native Americans from Brazil
- A ghost sample arising in East Eurasia that splits, one migrating into N America and other becomes Sardinian farmers from Middle East

Ancient North Eurasians: many modern descendants

- The Ancient North Eurasians would without a doubt have been called a genetic “race” had they lived today, as we could show that they must have been genetically about as differentiated from all other Eurasian populations who lived at the time as today’s “West Eurasians,” “Native Americans,” and “East Asians” are from one another.

- While they have not left unmixed descendants, the Ancient North Eurasians have in fact been extraordinarily successful.

- All told, more than 50% of the world’s population derives between 5 to 40 percent of their genomes from the Ancient North Eurasians.

Ghost of Ancient North Eurasians Is found

4 The ghost is found: The genome of the Mal'ta boy from ~24,000 years ago matches the predicted Ancient North Eurasian population.

In 1927, skeleton o f Mal’ta Boy, near Lake Baikal in eastern Siberia

Mal’ta Boy, 24 Ka

- A boy whose remains were found near Mal’ta, Siberia is usually known by the abbreviation **MA-1** (or MA1).
- Discovered in the 1927, the remains have been dated to 24 Ka.
- 2013 genome: MA-1 belonged to a population related to the genetic ancestors of Siberians, American Indians, Bronze Age Yamnaya people of the Eurasian steppe, and Europeans

Mal’ta boy, 24 Ka = prototype of Ancient North Eurasians

- At the end of 2013, Eske Willerslev published genome-wide data from the bones of a boy who had lived at the Mal’ta site in south-central Siberia, dated to 24 Ka.

- The Mal’ta genome had its strongest genetic affinity to Europeans and Native Americans, and far less affinity to the Siberians who live in the region today—just as predicted for the ghost population of the Ancient North Eurasians.

- The Mal’ta genome has now become the prototype sample for the Ancient North Eurasians. Paleontologists would call it a “type specimen”

Mal’ta child, 17 Ka: Origin of Native Americans

- Eske Willerslev : The origins of the First Americans remain contentious Native Americans are more closely related to Europeans than to East Asians
- Sequenced the draft genome of an approximately 24,000-year-old individual (MA-1), from Mal’ta in south-central Siberia.
- The MA-1 mitochondrial genome belongs to haplogroup U, which has also been found at high frequency among Upper Palaeolithic and Mesolithic European hunter-gatherers, and the Y chromosome of MA-1 is basal to modern-day western Eurasians and near the root of most Native American lineages.

M. Raghavan, et al., 2014

Siberia: Mal’ta boy

- The 24 Ka Mal’ta genome showed surprisingly strong affinities to both western Eurasian and Native American populations

- Populations related to Mal’ta contributed 10–20% of the ancestry of present-day Europeans and 30–40% of the ancestry of Native Americans.

- Gene flow from the MA-1 lineage into Native American ancestors could explain why several crania from the First Americans have been reported as bearing morphological characteristics that do not resemble those of east Asians.

Mal’ta genome: model ghost lineage to explain migration

- What became possible with the Mal’ta genome is the best example Reich knows of the power of ancient DNA to uncover history that until then was only a statistic in present-day data.
- It was no longer necessary to reconstruct from present-day populations what had happened long ago.
- Instead, with a genome sampled directly from the ghost population, it is possible to understand migrations and population admixtures from tens of thousands of years ago as if we were analyzing recent history.

Native American mixtures

- The analysis of the Mal'ta genome made it clear that Native Americans derive 30% of their ancestry from the Ancient North Eurasians, and the remainder from East Asians.

- It is this major mixture that explains why Europeans are genetically closer to Native Americans than they are to East Asians.

Mixtures all along

- The Willerslev team not only proved that Native Americans issued from population mixture, but they also showed that the mixture was part of a larger story.
- There was never a single trunk population in the human past. It has been mixtures all the way down.
- Even for *H. sapiens* in Africa

The Ghost of the Near East

- Ghost of the Near East: Conflicting data
- Iosef Lazaridis: Four Population Test aDNA result showed that East Asians, present-day Europeans, and pre-farming European hunter-gatherers from around 8 Ka are not related to one another.
- His analysis showed that East Asians today are genetically more closely related to the ancestors of ancient European hunter-gatherers than they are to the ancestors of present Europeans.

The Ghost of the Near East

- aDNA studies: present-day Europeans derive some of their ancestry from migrations of farmers from the Near East, who Reich had assumed were derived from the same ancestral population as European hunter-gatherers.

- Lazaridis now realized that the ancestry of the first European farmers was distinct from European hunter-gatherers in some way.

New Ghost Population: Basal Eurasians

- Mal’ta and the pre-farming European hunter-gatherers appeared to descend from a common ancestral population that arose after the separation from East Asians and sub-Saharan Africans.
- Present-day Europeans and Near Easterners are mixed: they carry within them ancestry from a divergent Eurasian lineage that branched from Mal’ta, European hunter-gatherers, and East Asians before those three lineages separated from one another.

Basal Eurasians: 25% of European ancestry

- Lazaridis called this lineage "Basal Eurasian" to denote its position as the deepest split in the radiation of lineages contributing to non-Africans.
- The Basal Eurasians were a new ghost population, one as important as the Ancient North Eurasians, measured by the sheer number of descendant genomes they have left behind
- This ghost population contributed about 25% of the ancestry of present-day Europeans and Near Easterners. It also contributed comparable proportions of ancestry to Iranians and Indians.

aDNA of Basal Eurasians = current Holy Grail of aDNA

- No one has yet collected ancient DNA from the Basal Eurasians.
- Finding such a sample is at present one of the holy grails in the field of ancient DNA, just as finding the Ancient North Eurasians had been before the Mal’ta discovery.
- But we know that Basal Eurasians existed.
- Basal Eurasians had No Neandertal DNA:
  - An extraordinary feature of the Basal Eurasians is that they harbored little or no Neanderthal ancestry.

1st Ghost - Basal Europeans: Origin of farming in the near East

- Lazaridis, 2016: reported genome-wide ancient DNA from 44 ancient Near Easterners ranging in time between ~12,000 and 1,400 bc, from Natufian hunter–gatherers to Bronze Age farmers.
- Their DNA held genetic markers indicative of a distinct group of ancient *H. sapiens* based in the region more than 45,000 years ago.
- Show that the earliest populations of the Near East derived ~50% of their ancestry from a 'Basal Eurasian' lineage that had little if any Neanderthal admixture and that separated from other non-African lineages before their separation from each other.
- Soon after that migration, a group of humans became isolated while the rest bumped into and mated with Neanderthals.

Iosif Lazaridis, Dani Nadel, David Reich, 2016

1st Ghost - Basal Europeans – spread of farmer groups

- The impact of the Near Eastern farmers extended beyond the Near East:
  - farmers related to those of Anatolia spread westward into Europe;
  - farmers related to those of the Levant spread southward into East Africa;
  - farmers related to those of Iran spread northward into the Eurasian steppe;
  - and people related to both the early farmers of Iran and to the pastoralists of the Eurasian steppe spread eastward into South Asia.

Basal Eurasians

- In 2016, analyzed ancient DNA from the Near East to show that people who lived in the region 14 to 10 Ka had ~50 percent Basal Eurasian ancestry, about twice the proportion in Europeans today.

- The less Basal Eurasian ancestry a non-African person has, the more Neanderthal ancestry they have.

- Thus non-Africans who have zero percent Basal Eurasian ancestry have twice as much Neanderthal DNA as ones with 50 percent Basal Eurasian ancestry.

- By extrapolation, we might expect 100 percent Basal Eurasians to have no Neanderthal ancestry at all.

Basal Eurasians

- Peoples who lived 10 Ka+ in what are now Iran and Israel each had around 50 %t Basal Eurasian ancestry, despite the clear genetic evidence that these two populations had been isolated from one another for tens of thousands of years.
- This suggests the possibility that there were multiple highly divergent Basal Eurasian lineages coexisting in the ancient Near East, not exchanging many migrants until farming expanded.
- The Basal Eurasians were a major and distinctive source of human genetic variation, with multiple subpopulations persisting for a long period of time.

Basal Eurasians: where was their origin?

- Where could the Basal Eurasians have lived, isolated as they seem to have been for tens of thousands of years from other non-African lineages?

- In the absence of ancient DNA, we can only speculate.

- It is possible that they may have sojourned in North Africa, which is difficult to reach from southern parts of the African continent because of the barrier of the Sahara Desert, and which is more ecologically linked to West Eurasia.

Basal Eurasians

- Today, the peoples of North Africa owe most of their ancestry to West Eurasian migrants, making the deep genetic past in that region difficult to discern.
- However, archaeological studies have revealed ancient cultures there that could potentially have corresponded to the Basal Eurasians.
- The Nile Valley, for example, has been occupied by humans for the entire period since present-day Eurasians diverged from their closest relatives in sub-Saharan Africa.

Basal Eurasians: Natufians?

- A hint about the possible homeland of the Basal Eurasians comes from the Natufians, hunter-gatherers who lived after ~14 Ka in the Near East.
- They were the first people known to have lived in permanent dwellings—they did not migrate from place to place searching for food despite being hunter-gatherers
- They built large stone structures and actively managed local wild plants before their successors became full-fledged farmers. Thought that Natufians migrated to the Near East from North Africa.

Origins of Basal Eurasians: Natufians?

- In 2016, Reich's lab published ancient DNA from six Natufians from Israel, and we found that they share with early Iranian hunter-gatherers the highest proportions of Basal Eurasian ancestry in the Near East.
- However, our ancient DNA data cannot determine where the ancestors of the Natufians lived; there is no other aDNA data from any other populations that lived at this time or earlier in North Africa, Arabia, or the southwestern Near East.
- And even if a genetic connection between Natufians and North Africa is established, it will not be the whole story, as it cannot explain the equally high proportions of Basal Eurasian ancestry in the ancient hunter-gatherers and farmers of Iran and the Caucasus.

The Ghosts of Early Europeans

- In 2016, the lid of Pandora’s box opened wide, and a whole mob of ancient ghosts whirled out.
- Reich lab assembled genome-wide data from fifty-one ancient modern humans in Eurasia, most of them from Europe, who lived between 45 to 7 Ka.
- These samples spanned the entire period of the Last Glacial Maximum—which occurred between 25 to 19 Ka—when glaciers covered the northern and middle latitudes of Europe so that all humans there lived in refuges in its southern peninsulas.
- Showed that repeated population transformations, replacements, migrations, and mixtures had taken place over this vast stretch of time.

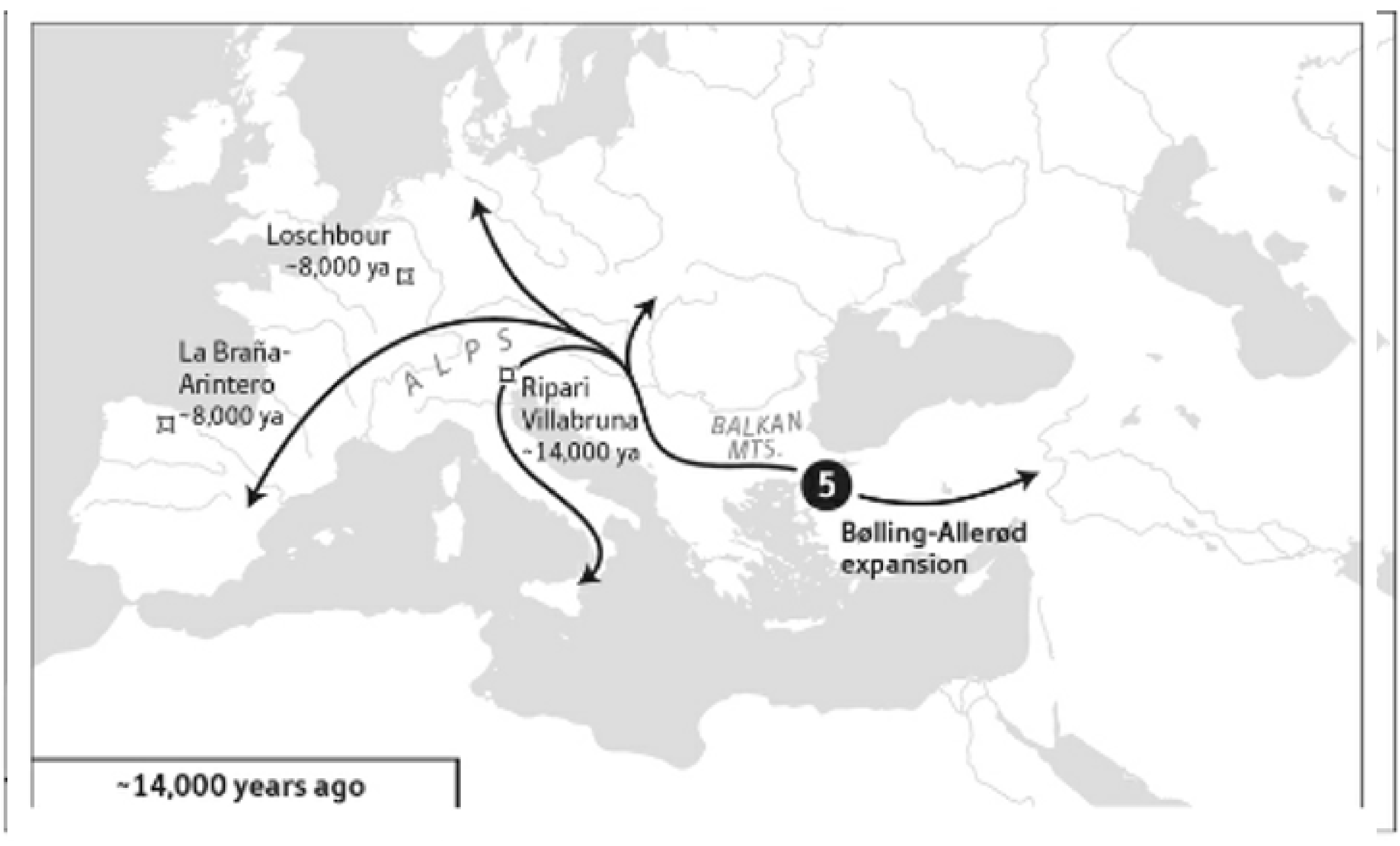
The Ghosts of Early Europeans – Hunter Gatherers

- Qiaomei Fu, of Reich’s lab, compared the ancient individuals to one another.

- She grouped them in four clusters that contained many samples that were similar both genetically and with respect to their archaeologically determined dates.

- Fu was able to break down the story of the first thirty-five thousand years of modern humans in West Eurasia into at least five key events, based on multiple skeletons and their aDNA.

5 Great Events in History of Hunter-Gatherers



Event 1: First Hunter Gatherers

Hunter-gatherer Hx: Migration into Western Eurasia

- Event One was the spread of modern human hunter gatherers into western Eurasia and is evident in the two most ancient aDNA samples -
  - ~45 Ka individual in western Siberia (Ust'Ishim), and the
  - ~ 40 Ka lower jaw from Oase, Romania.
- This Migration left no descendants:
  - Both were no more closely related to later European hunter-gatherers than they were to present-day East Asians.
  - They flourished, but descendants largely disappeared.

Hunter-gatherer Hx: Genetic dead ends

- The existence of these pioneer populations makes it clear that the past is not an inevitable march toward the present.

- Human history is full of dead ends, and we should not expect the people who lived in any one place in the past to be the direct ancestors of those who live there today.

Hunter-gatherer Hx: Disappearance of both Ns and MHs

- Around 39 Ka, a super volcano near present-day Naples in Italy dropped an estimated three hundred cubic kilometers of ash across Europe, separating archaeological layers preceding it from those that succeeded it.
- Almost no Neanderthal fossils or tools are found above this volcanic rock layer
- Most modern human archaeological cultures that left remains below the ash layer left none above it.
- So many MHs disappeared as dramatically as their Neanderthal contemporaries.

Event 2: Aurignacian Hunter Gatherers

Aurignacian lineage of HGs -- with descendants

- Event Two was the spread of the lineage that gave rise to all later hunter-gatherers in Europe.

- By 35 Ka, one group founded a lineage of European hunter-gatherers that persisted largely uninterrupted for more than twenty thousand years.
  - Both ~37 Ka individual from eastern Europe (Kostenki 14, Russia) and a
  - ~35 Ka from western Europe (Goyet Q116-1, present-day Belgium)
  - were part of a Aurignacian population that contributed to all later Europeans.

- During the entire period from around 37 to 14 Ka, almost all the individuals from Europe could be described as descending from a single common ancestral population that had not experienced mixture with non-European populations.

Hunter-gatherer Hx: a long lineage of HGs

- Archaeologists have shown that after the volcanic eruption 39 Ka,
  - a modern human culture spread across Europe making Aurignacian stone tools, and that
  - this replaced the diverse stone toolmaking styles that existed before.
- Multiple independent migrations of early modern human pioneers into Europe, some of which went extinct and were replaced by a more homogeneous population and culture

Event 3: Gravettian expansion

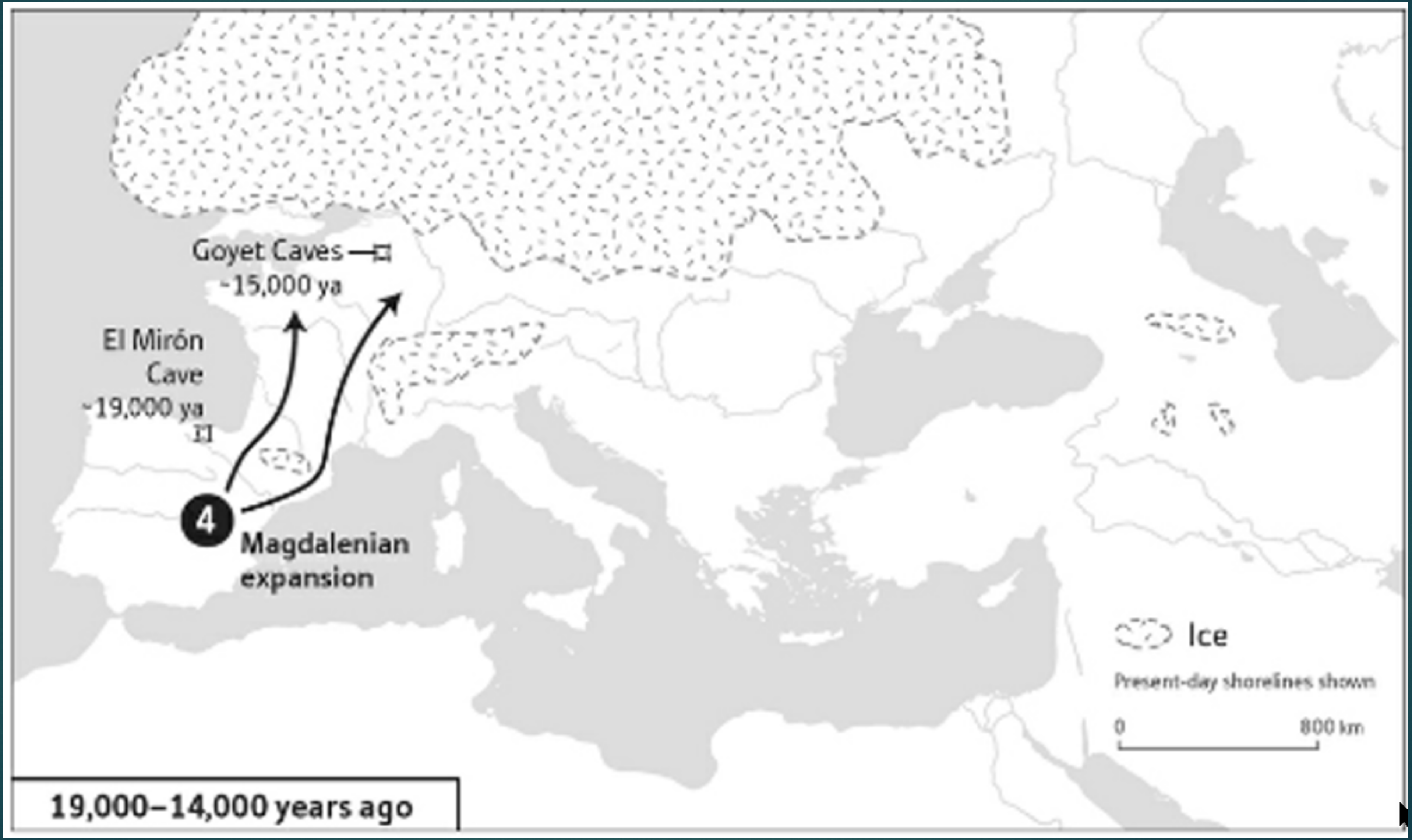
Hunter-gatherer Hx: Gravettians for next 10 Ka

- Event Three was the coming of the people who made Gravettian tools, who dominated most of Europe between around 33 to 22 Ka.
- Eventually, groups derived from an eastern branch of this founding population of European hunter-gatherers spread west, displaced previous groups, and were eventually themselves pushed out of northern Europe by the spread of glacial ice.
- The material remains they left behind include voluptuous female statuettes, as well as musical instruments and dazzling cave art.
- More deliberate about burying their dead; more skeletons from this period than we do from the earlier Aurignacian period.

Hunter-gatherer Hx: Gravettians

- DNA from Gravettian-era individuals buried in present-day Belgium, Italy, France, Germany, and the Czech Republic. They were all genetically very similar despite their extraordinary geographic dispersal.
- Most of their ancestry derived from the same sublineage of European hunter-gatherers as the 37 Ka individual from far eastern Europe, and that they then spread west, displacing the sublineage associated with Aurignacian tools and represented in the 35 Ka Belgian individual.
- The changes in artifact styles associated with the rise of the Gravettian culture were thus driven by the spread of new people.

Event 4: Magdalenian expansion



Hunter-gatherer Hx: Magdalenian culture

- Event Four was heralded by a skeleton from present-day Spain dating to 19 Ka -- associated with the Magdalenian culture, whose members over the next five thousand years migrated to the northeast out of their warm-weather Spanish refuge, chasing the retreating ice sheets into present-day France and Germany.
- As the glaciers receded, western Europe was repeopled from the southwest by a population that had managed to persist for tens of thousands of years and was related to an approximately thirty-five-thousand-year-old individual from far western Europe.

- There was a spread of a new group of people into central Europe who were not directly descended from the Gravettians who had preceded them.

Hunter-gatherer Hx: Magdalenian culture

- There was also a surprise: most of the ancestry of individuals associated with the Magdalenian culture came from the sublineage represented by the 35 Ka man from Belgium who was associated with Aurignacian tools (43-26 Ka) but who was later succeeded at the same site by people who used Gravettian tools and carried DNA similar to others in Europe associated with that culture of eastern European origin.
- Here was yet another ghost population that contributed to later groups in mixed form.
- The Aurignacian lineage had not died out, but instead had persisted in some geographic pocket, possibly in western Europe, before its resurgence at the end of the ice age.

Event 5: from Near East

Hunter-gatherer Hx: HGs spread from the southeast

- Event Five happened ~ 14 Ka, during the first strong warming period after the last ice age, a major climatic change known as the Bolling- Allerod.
- The Alpine glacial wall that extended down to the Mediterranean Sea near present-day Nice finally melted after about ten thousand years of dividing the west and east of Europe.
- Plants and animals from southeastern Europe (the Italian and Balkan peninsulas) migrated in abundance into southwestern Europe. So did the humans.
- After ~14 Ka, a group of hunter-gatherers spread across Europe with ancestry quite different from that of the people associated with the preceding Magdalenian culture, whom they largely displaced.

Hunter-gatherer Hx: HGs spread from the southeast

- This migration had an even larger impact, with a spread from the southeast that not only transformed the population of western Europe but also homogenized the populations of Europe and the Near East.
- After ~14 Ka, western European hunter-gatherers became much more closely related to present-day Near Easterners.
- This proved that new migration occurred between the Near East and Europe around this time.

SE Europe and Near East

- We do not yet have ancient DNA from the period before 14 Ka from southeastern Europe and the Near East. We can only surmise.

- The people who had waited out the ice age in southern Europe became dominant across the entire European continent following the melting of the Alpine glacial wall.

- Perhaps these same people also expanded east into Anatolia, and their descendants spread farther to the Near East,

The Genetic Formation of Present-Day West Eurasians

- Today, the peoples of West Eurasia—the vast region spanning Europe, the Near East, and much of central Asia—are genetically highly similar.
- Reich: The physical similarity of West Eurasian populations was recognized in the eighteenth century by scholars who classified the people of West Eurasia as "Caucasoids" to differentiate them from East Asian "Mongoloids," sub-Saharan African "Negroids," and "Australoids" of Australia and New Guinea. (CJV: race issue)
- In the 2000s, whole-genome data emerged as a more powerful way to cluster present-day human populations than using physical features.

Statistics of genetic affinity

- The whole-genome data at first seem to validate some of the old cultural “racial” categories.
- The most common statistical way to measure the genetic similarity between two populations is by taking the square of the difference in mutation frequencies between them, and then averaging across thousands of independent mutations across the genome to get a precisely determined number.

The Genetic Formation of Present-Day West Eurasians

- Measured in this way, populations within West Eurasia are typically around seven times more similar to one another than West Eurasians are to East Asians.

- When frequencies of mutations are plotted on a map, West Eurasia appears homogeneous, from the Atlantic end of Europe to the steppes of central Asia.

- East Asia is another region of an alternate genetic homogeneity.

West Eurasian Genetics : Farmers

- How did the present-day European genetic population structure emerge from the one that existed in the deep past?

- Several labs in 2016: formation of the present-day West Eurasian population was propelled by the spread of farmers.

- Farming began between 12 and 16 Ka in southeastern Turkey and northern Syria, where local hunter-gatherers began domesticating most of the plants and animals many West Eurasians still depend upon today, including wheat, barley, rye, peas, cows, pigs, and sheep.

The Genetic Formation of Present-Day West Eurasians

- After 9 Ka, farming began spreading west to present-day Greece and roughly at the same time began spreading east, reaching the Indus Valley in present-day Pakistan.

- Within Europe, farming spread west along the Mediterranean coast to Spain, and northwest to Germany through the Danube River valley, until it reached Scandinavia in the north and the British Isles in the west.

The Genetic Formation of Present-Day West Eurasians

- Until 2016, getting genome-wide ancient DNA from the Near East had failed.
- Ancient DNA analysis of petrous bones in 2015 and 2016 made it possible for the first time to get ancient DNA from the warm Near East.
- Obtained aDNA from 44 ancient Near Easterners across much of the geographic cradle of farming.
- Around 10 Ka, at the time that farming was beginning to spread, the population structure of West Eurasia was far from the genetic monoculture we observe today.

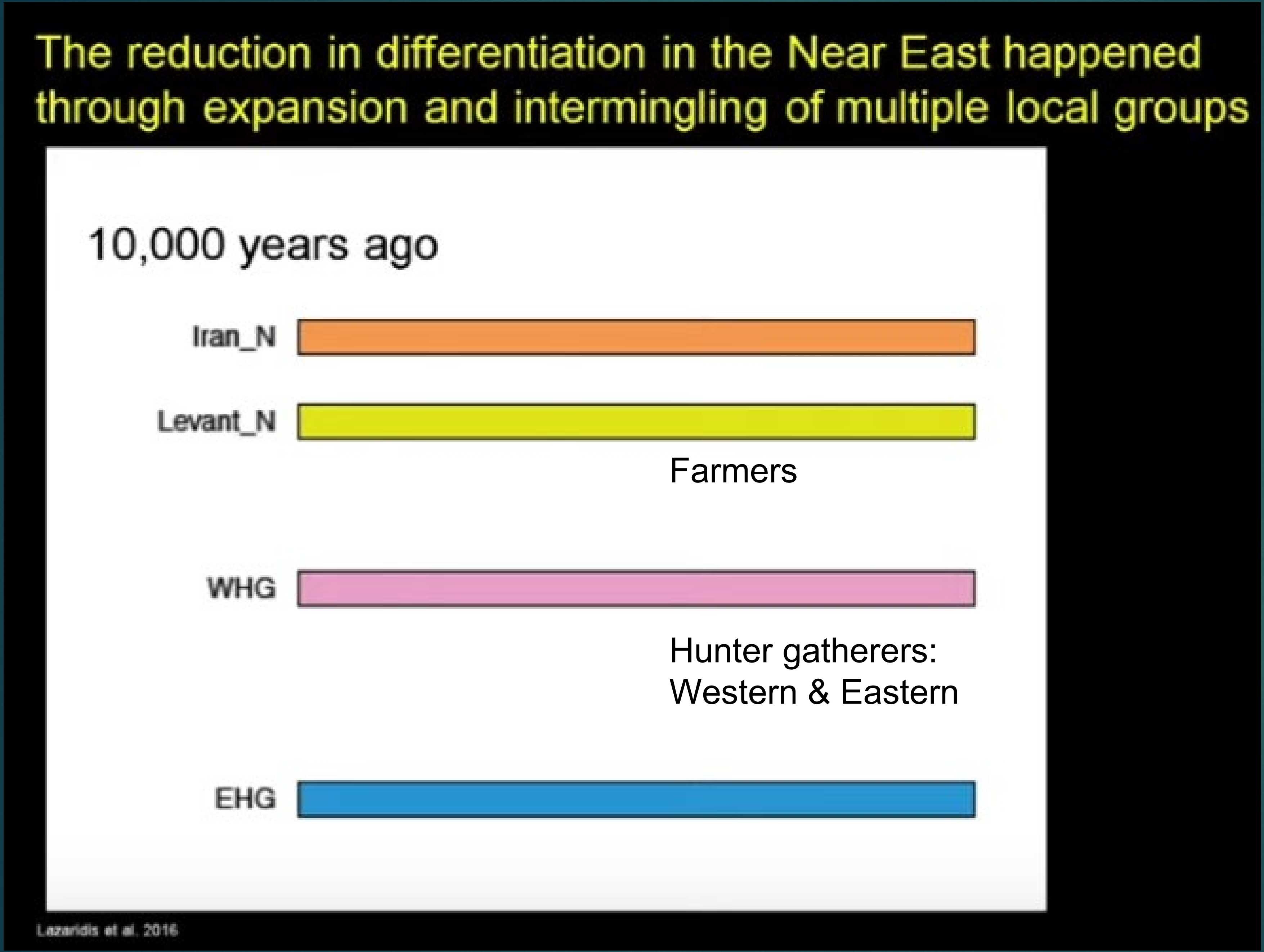
The Genetic Formation of Present-Day West Eurasians

- The farmers of the western mountains of Iran, who may have been the first to domesticate goats, were genetically directly derived from the hunter- gatherers who preceded them.
- Similarly, the first farmers of present-day Israel and Jordan were descended largely from the Natufian hunter-gatherers who preceded them.
- But these two populations were also very genetically different from each other.

The Genetic Formation of Present-Day West Eurasians

- The first farmers of the western part of the Near East (the Fertile Crescent, including Anatolia and the Levant) and the first farmers of the eastern part (Iran) were genetically very different.

- In the Near East, the expansion of farming was accomplished not just by the movement of people, as happened in Europe, but also by the spread of common ideas across genetically very different groups.



The reduction in differentiation in the Near East happened through expansion and intermingling of multiple local groups

Lazaridis et al. 2016

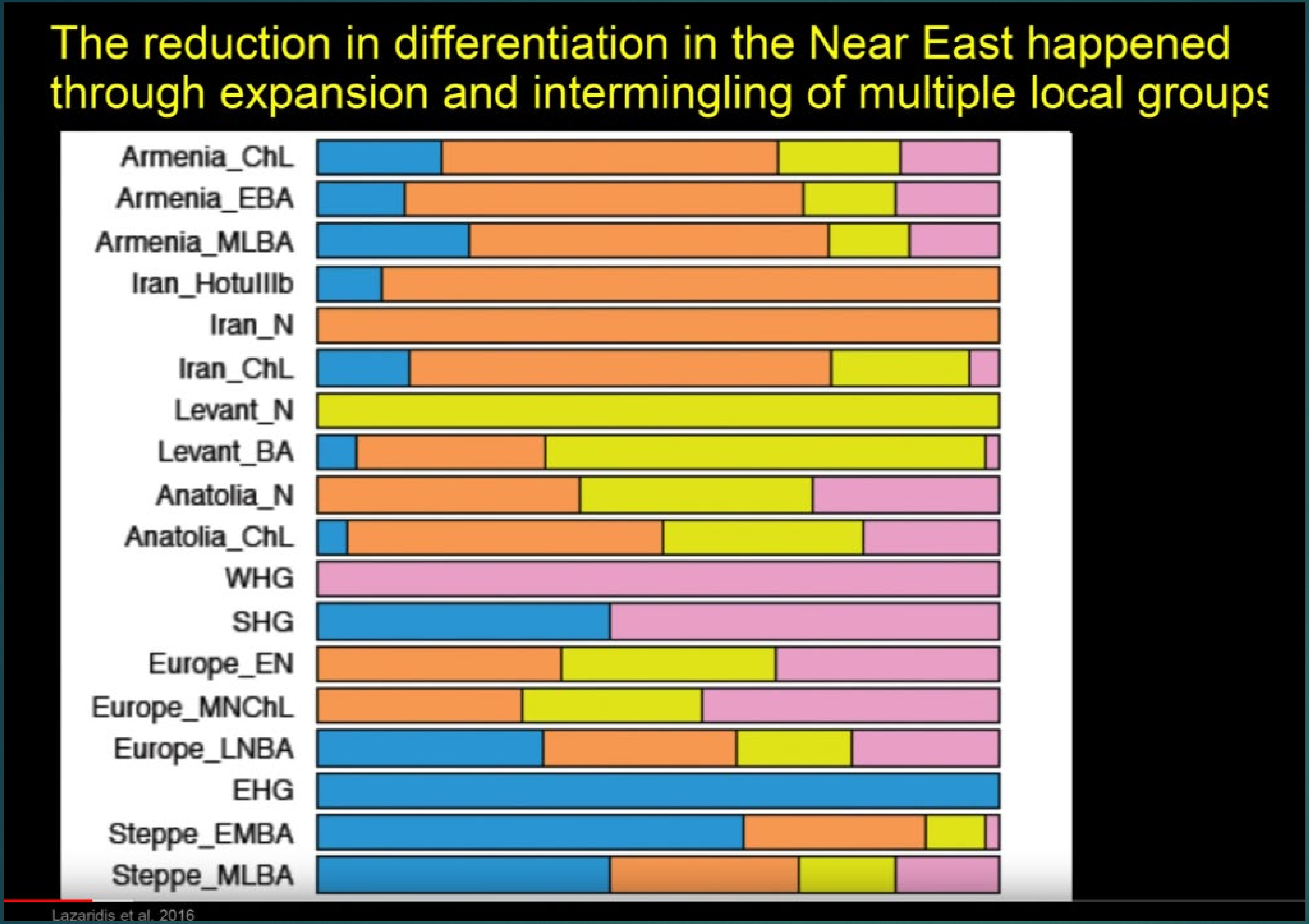
Not just 1 group expanding and taking over another group at 10 Ka

At 10 Ka, West Eurasia was composed of 4 groups:

1 - Iranian farmers
2 - Levantine farmers

3 - Western European hunter gatherers &
4 - Eastern European hunter gatherers

These 4 mixed



The reduction in differentiation in the Near East happened through expansion and intermingling of multiple local groups

Lazaridis et al. 2016

Near Eastern farming expansion eventually homogenized West Eurasia via profound mixing

Population structure of past is very different than it is today

Genetic variation today is 1/10th of what it was at 10 Ka;
At 4000 ya, present day variation achieved

The Genetic Formation of Present-Day West Eurasians

- The farmers of the Near East began migrating and mixing with their neighbors.
- But instead of one group displacing all the others and pushing them to extinction, as had occurred in some of the previous spreads of hunter-gatherers in Europe, in the Near East all the expanding groups contributed to later populations.
- The farmers in present-day Turkey expanded into Europe.

The Genetic Formation of Present-Day West Eurasians

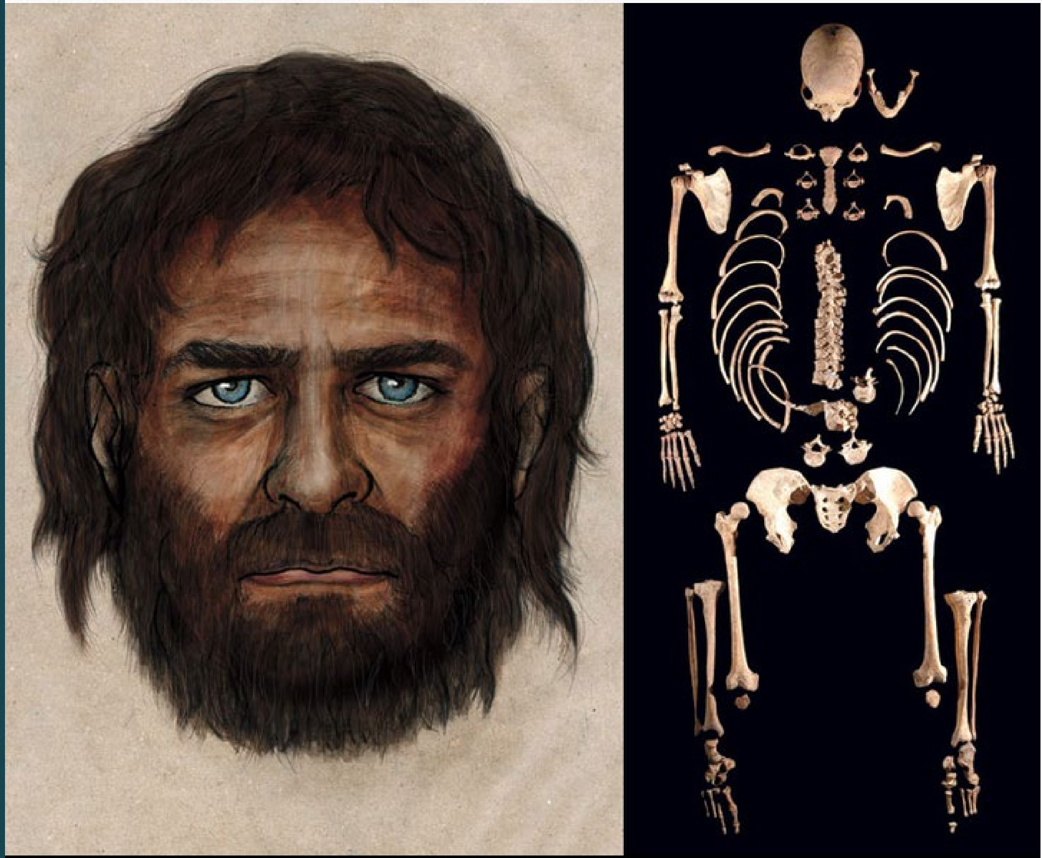
- Headed south: The farmers in present-day Israel and Jordan expanded into East Africa, and their genetic legacy is greatest in present-day Ethiopia.

- Farmers related to those in present-day Iran expanded into India.

- Today's West Eurasians: classic northern European look:
  - blue eyes, light skin, and blond hair.

- But Western European hunter-gatherers around 8 Ka had
  - blue eyes but dark skin and dark hair, a combination that is rare today.

La Brana-1: 7,000-year-old Spanish hunter-gatherer: blue eyes and dark skin

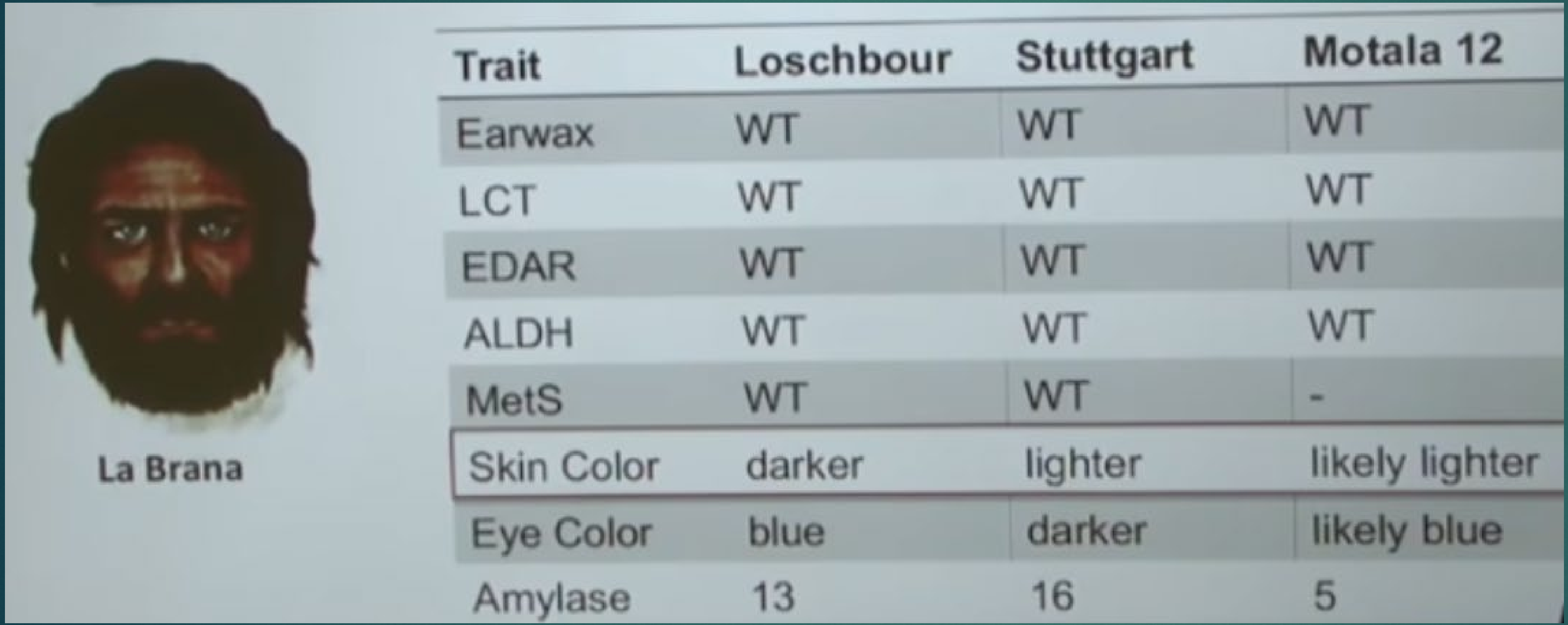


DNA from the tooth of a 7,000-year-old Spanish hunter-gatherer revealed that he had blue eyes and dark skin (left), details that couldn't be discerned by looking at his skeleton (right).

- La Braña-1 7,000-year-old Mesolithic skeleton discovered at the La Braña-Arintero site in León, Spain;
- existence of a common ancient genomic signature across western and central Eurasia from the Upper Paleolithic to the Mesolithic;
- spread from Luxembourg & Hungary to Spain;
- already resistant to some diseases carried by domestic animals;
- pale skin came later

I. Olalde et al., *Nature*, 2014

HG Phenotypes: 8 Ka Spanish HG at La Brana = dark skin, blue eyes; same as 8 Ka Luxemburg HG; but 7 Ka Stuttgart farmer had light skin, darker eyes



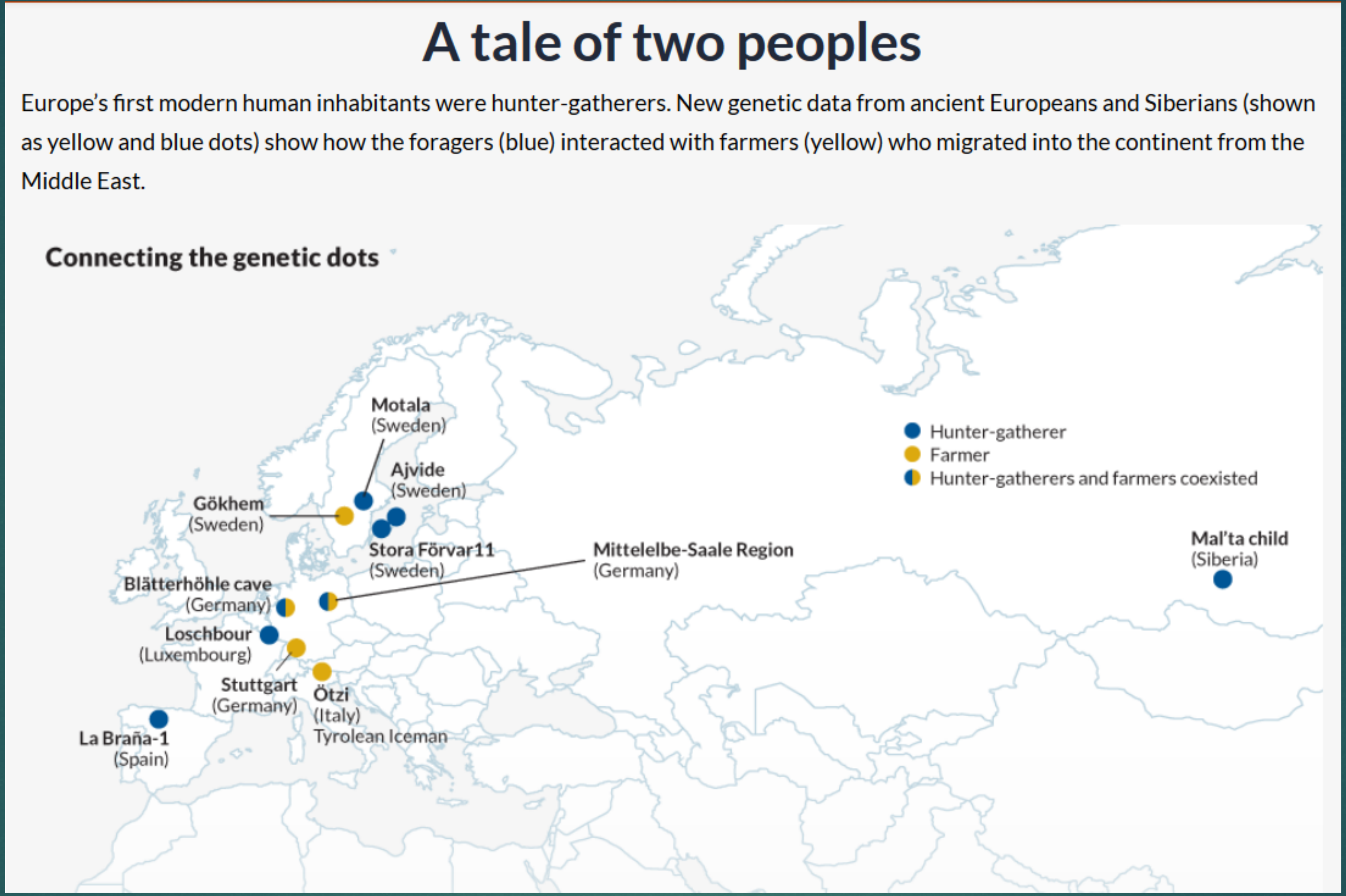
La Brana

Trait	Loschbour	Stuttgart	Motala 12
Earwax	WT	WT	WT
LCT	WT	WT	WT
EDAR	WT	WT	WT
ALDH	WT	WT	WT
MetS	WT	WT	-
Skin Color	darker	lighter	likely lighter
Eye Color	blue	darker	likely blue
Amylase	13	16	5

Krause: All European HGs had blue eyes

Amylase (starch digestion): chimps have 2 copies, MHs up to 20 copies (esp. East Asians); these farmers had 16 copies, but HGs had 13 (the ave of current MHs)

Northern Foragers vs. Southern Farmers in Europe



A tale of two peoples

Europe's first modern human inhabitants were hunter-gatherers. New genetic data from ancient Europeans and Siberians (shown as yellow and blue dots) show how the foragers (blue) interacted with farmers (yellow) who migrated into the continent from the Middle East.

Hunter-gatherers and farmers led parallel lives for roughly 2,000 years; More HGs in Northern Europe. Southern Europe had more farmer DNA and fewer hunter-gatherer ancestors.

The Genetic Formation of Present-Day West Eurasians

- The first farmers of Europe mostly had light skin but dark hair and brown eyes—thus light skin in current Europe largely owes its origins to migrating farmers.
- The earliest known example of the classic European blond hair mutation is in an Ancient North Eurasian from the Lake Baikal region of eastern Siberia from17 Ka.
- The hundreds of millions of copies of this mutation in central and western Europe today likely derive from a massive migration into the region of people bearing Ancient North Eurasian ancestry,

Second Lesson in humility: No one is “pure”.

2nd lesson in humility No one is “pure”

Hundreds of West Eurasian ancient genomes show that the “Caucasian” grouping simply didn’t exist ~10,000 years ago

*** Early genetic foundation of Europe: Hunter Gathers, Early Farmers, Pastoralists

2014: Ancient human genomes suggest three ancestral populations for present-day Europeans

- Iosif Lazaridis: Sequenced the genomes of a ~7,000 year old farmer from Germany and eight ~8 Ka hunter-gatherers from Luxembourg and Sweden; and 2345 current humans

- Most present Europeans derive from at least three highly differentiated populations:

Iosif Lazaridis, et al., 2014

Hunter-Gatherers

- 1 - West European Hunter-Gatherers (WHG), who contributed ancestry to all current Europeans but not to Near Easterners; no current Europeans look like this today
- West European Hunter-Gatherers (WHG), arriving 45 Ka, related to La Braña-1, had Europe alone for 30 K years.

Early Farmers

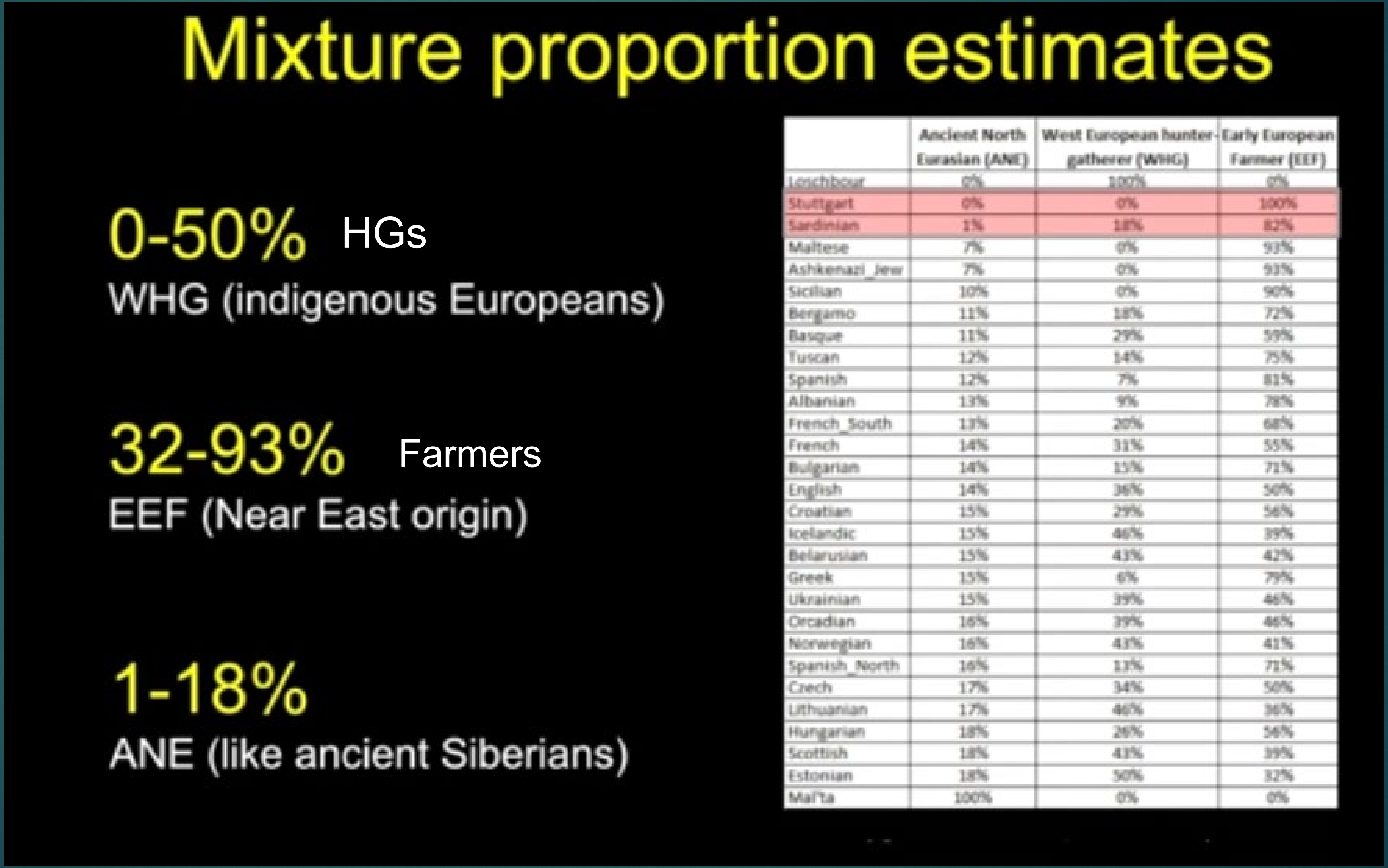
- 2 - Early European Farmers (EEF), who were mainly of Near Eastern origin but also harbored WHG-related ancestry
- Early European Farmers, arriving 9 K; spread to South & central Europe; gene for light skin spreads
- EEF had ~44% ancestry from a “Basal Eurasian” population that split prior to the diversification of other non-African lineages.

Ancient North Eurasians

- 3 - Ancient North Eurasians (ANE) related to Upper Paleolithic Siberians, who contributed to both Europeans and Near Easterners; related to Mal’ta child & Native Americans

- Ancient North Eurasians: massive Yamnaya migration arriving 4.5 Ka, Corded Ware culture; cattle herders, used wheel and horses; brought Proto-Indo-European language

3 European Groups: profoundly different



Mixture proportion estimates

0-50% HGs
WHG (indigenous Europeans)

32-93% Farmers
EEF (Near East origin)

1-18%
ANE (like ancient Siberians)

	Ancient North Eurasian (ANE)	West European hunter-gatherer (WHG)	Early European Farmer (EEF)
Loschbour	0%	100%	0%
Stuttgart	0%	0%	100%
Sardinian	1%	18%	82%
Maltese	7%	0%	93%
Ashkenazi_Jew	7%	0%	93%
Sicilian	10%	0%	90%
Bergamo	11%	18%	72%
Basque	11%	29%	59%
Tuscan	12%	14%	75%
Spanish	12%	7%	81%
Albanian	13%	9%	78%
French_South	13%	20%	68%
French	14%	31%	55%
Bulgarian	14%	15%	71%
English	14%	36%	50%
Croatian	15%	29%	56%
Icelandic	15%	46%	39%
Belarusian	15%	43%	42%
Greek	15%	6%	79%
Ukrainian	15%	39%	46%
Orcadian	16%	39%	46%
Norwegian	16%	43%	41%
Spanish_North	16%	13%	71%
Czech	17%	34%	50%
Lithuanian	17%	46%	36%
Hungarian	18%	26%	56%
Scottish	18%	43%	39%
Estonian	18%	50%	32%
Mal'ta	100%	0%	0%

Modern-day Europeans are a mix of 3 ancient groups

- Myths of Origin: There was no separate, unmixed origin of Basques, or Black Irish, or Aryans or Philistines or Native Americans

Josif Lazaridis, et al., 2014

Early European genetics

- European early farmers (EFs) were genetically distinct from the early hunter-gatherers (HGs) inhabiting the continent.
- Genetic exchange between EFs and HGs appears to have been limited in the early phases of the agricultural expansion, with more intense exchange taking place in the later stages
- World's first farmers were genetically very different from European HGs.

Early European genetics

- Strong genetic drift during EF’s expansion through Anatolia contributed to making western EFs look more dissimilar than they actually were and somehow concealed their hybrid nature.

- The earlier theory of a single cultural and genetic origin of all farmers in the Fertile Crescent, without significant initial contribution of European like HGs, is no longer tenable

Neolithic revolution: The genomic origins of the world’s first farmers

- Europe’s first farming populations descend mostly from farmers in the Anatolian peninsula, in what is now Turkey.

- Sometime before 12,000 years ago, nomadic hunter-gatherers in the Middle East made one of the most important transitions in human history: they began staying put and took to farming.

- This transition is known as the Neolithic revolution, and is linked to the first domestic plants and animals.

- Ancient Anatolian farmers descended from repeated mixing between distinct hunter-gather groups from Europe and the Middle East.

Nina Marchi, et al., 2022

The genomic origins of the world’s first farmers

- HG groups first split around the height of the last Ice Age, some 25,000 years ago.
- Modelling suggests that the western hunter-gatherer groups nearly died out, before rebounding as the climate warmed.
- Once established in Anatolia, early farming populations moved west into Europe in a stepping-stone-like fashion, beginning around 8,000 years ago.
- They mixed occasionally — but not extensively — with local hunter-gatherers. It’s really the spread of people, of farming communities, that brought farming further west

The genomic origins of the world's first farmers

- European HGs diverged from SW Asian HGs during the LGM (~20 Ka)
- Low genetic diversity of European HGs is due to a strong LGM demographic bottlenecks.
- Ancestors of western early farmers emerged after repeated post-LGM admixtures
- Early Farmers strongly diverged from SW Asians during their expansion through Anatolia

The genomic origins of the world's first farmers

- After the last glacial maximum, early farmers of Anatolia and Europe emerged from a staggered mixing of a Southwest Asian population with a strongly bottlenecked western hunter-gatherer population

- Moreover, the ancestors of the first farmers of Europe and Anatolia went through a period of extreme genetic drift during their westward range expansion, contributing highly to their genetic distinctiveness.

The genomic origins of the world’s first farmers

- The genetic origins of the first agriculturalists in the Neolithic period long seemed to lie in the Near East. "Fertile Crescent," a region in the Near East where people began to settle down and domesticate animals and plants about 11,000 years ago.
- 2022 study: first farmers actually represented a mixture of Ice Age hunter-gatherer groups, spread from the Near East all the way to south-eastern Europe.
- Europe's first farmers were descended from hunter-gatherer populations in Anatolia. The Neolithic genetic origins cannot clearly be attributed to a single region.

Nina Marchi, et al., Cell, 2022

First Farmers: demographic modeling based on ancient DNA

- First farmers did not originate from a single group as was previously thought but from the mixing of two groups of hunter-gatherers. The mixing process started around 14,000 years ago, which was followed by a period of extreme genetic differentiation lasting several thousand years.
- Two study techniques: the production of high-quality ancient genomes from prehistoric skeletons, coupled with demographic modeling on the resulting data.

European HGs

- About 25,000 years ago, a large initial HG population split into two groups. One moved to Western Europe, while the other stayed in Southwest Asia.
- Later, due to a drop in global temperature, the Western group experienced an extreme reduction in its population, where some came close to extinction.
- This model explains why descendants of European hunter-gatherers have lower genetic diversity.
- Researchers have thought the groups' small population size was what contributed to their low genetic diversity, but the new evidence showed that their populations were much larger than previously thought.

First Farmers

- As the temperature fell and rose, the population ebbed and flowed. During warm periods, the populations dispersed, resulting in overlapping territories and admixtures, where individuals from previously isolated groups interbred.
- The model revealed that some of the first farmers emerged from the admixture of hunter-gatherers from a Western group and an already mixed group living in the east around 12,900 years ago.
- These farmers who domesticated plants and animals then migrated west, eventually bringing their culture to central Europe. Today, many people from all over Europe have descended from them.

HGs and Early Farmers

- European Hunter Gatherers (HGs) diverged from SW Asian HGs during the Last Glacial Maximum.
- Early farmers of Anatolia and Europe emerged from a mixing of a Southwest Asian population with a strongly bottlenecked western hunter-gatherer population after the last glacial maximum.
- Low genetic diversity of European HGs is due to a strong LGM demographic bottleneck
- Ancestors of western early farmers emerged after repeated post-LGM admixtures.

First Farmers

- The ancestors of the first farmers of Europe and Anatolia went through a period of extreme genetic drift (random gene freq. change) during their westward range expansion, contributing highly to their genetic distinctiveness.
- European Early Farmers strongly diverged from SW Asians during their expansion through Anatolia
- All western EFs share a remote common ancestry with Caucasus HGs

2022 study: HGs and EFs

- A team co-led by paleogeneticist Eske Willerslev at the University of Copenhagen sequenced the genomes of 317 hunter-gatherers and early farmers from across Eurasia, the largest-yet ancient genome study from this period.
- Found an ancient split between eastern and western hunter-gatherer groups, and traces the arrival of Anatolian farmers in Europe, beginning around 8,700 years ago in the Balkans.

Allentoft, M. E. *et al., 2022*

The transitions from foraging to farming and later to pastoralism

- The transitions from foraging to farming and later to pastoralism in Stone Age Eurasia (c. 11 to 3 thousand years ago) represent some of the most dramatic lifestyle changes in human evolution.
- 1) Hunter-gatherer groups were more genetically diverse than previously known, and deeply divergent between western and eastern Eurasia.
- 2) Hunter-gatherers from the Middle Don river region contributed ancestry to the later Yamnaya steppe pastoralists

East & West farmers

- 3) The genetic impact of the Neolithic transition was highly distinct, east and west of a boundary zone extending from the Black Sea to the Baltic
- Large-scale shifts in genetic ancestry occurred to the west of this "Great Divide", while no substantial ancestry shifts to the east.
- Genetic relatedness decreased substantially in the western group but not in the east where it remained high until c. 4,000 BP

Steppe Pastoralists

- 4) The second major genetic transformation around 5,000 BP happened at a much faster pace with Steppe-related ancestry reaching most parts of Europe within 1,000-years.
- Local Neolithic farmers admixed with incoming pastoralists in eastern, western, and southern Europe
- 5) Extensive regional differences in the ancestry components involved in these early events remain visible to this day, even within countries.
- Neolithic farmer ancestry is highest in southern and eastern England while Steppe-related ancestry is highest in the Celtic populations of Scotland, Wales, and Cornwall

Genetic effects

- 6) Shifts in diet, lifestyle and environment introduced new selection pressures involving at least 21 genomic regions.

- Selection on the FADS regions, associated with fatty acid metabolism, began before the Neolithization of Europe.

- Light skin pigmentation in Europeans was already present at high frequency in the Bronze Age (5300-2100 ya)

- Similarly, the lactase persistence allele, started increasing in frequency with arrival of Steppe-related groups into Europe

Ancestry of present-day Europeans

- The geographic structure of these population transformations gave rise to the population structure of present-day Europe.

- For example, Anatolian Neolithic ancestry is highest in southern European populations such as Sardinians and lowest in northern European populations.

- Steppe ancestry is at high frequency in north-central Europeans and at low frequency in the south.

- In much of Europe, extreme population discontinuity was the norm.

History of European Migrations: Are there pure lineages?

- The idea that there were once “pure” populations of ancestral Europeans, there since the days of woolly mammoths, has inspired ideologues since well before the Nazis.
- It has long nourished white racism, and in recent years it has stoked fears about the impact of immigrants: fears that have threatened to rip apart the European Union and roiled politics in the United States.
- New research answers: who Europeans really are and where they came from. The continent has been a melting pot since the Ice Age.
- Europeans living today, in whatever country, are a varying mix of ancient bloodlines hailing from Africa, the Middle East, and the Russian steppe.

Andrew Curry, Nat. Geog., 2019

Migrations

- The evidence comes from archaeological artifacts, from the analysis of ancient teeth and bones, and from linguistics. But above all it comes from the new field of paleogenetics.

- The result has been an explosion of new information that is transforming archaeology.

- In 2018 alone, the genomes of more than a thousand prehistoric humans were determined, mostly from bones dug up years ago and preserved in museums and archaeological labs.

- In the process any notion of European genetic purity has been swept away on a tide of powdered bone.

Europe is a continent of immigrants

- Three major movements of people shaped the course of European prehistory.

- Europe is a continent of immigrants and always has been.

- “The people who live in a place today are not the descendants of people who lived there long ago,” says David Reich. “There are no indigenous people—anyone who hearkens back to racial purity is confronted with the meaninglessness of the concept.”

First Europeans

- All people outside Africa descend from ancestors who left that continent 60,000 years ago.
- 1 -Those first modern human hunter gatherers (HG) ventured into Europe about 45,000 years ago, having made their way up through the Middle East. Their own DNA suggests they had dark skin and light eyes. These early settlers were widely scattered. They kept their distance when Neolithic farmers first arrived.
- The first modern Europeans lived as hunters and gatherers in small, nomadic bands. They followed the rivers, edging along the Danube from its mouth on the Black Sea deep into western and central Europe.

First Europeans

- As Europe was gripped by the Ice Age, the modern humans hung on in the ice-free south, adapting to the cold climate.
- Around 27,000 years ago, there may have been as few as a 1000 of them, according to some population estimates.
- 2 - From 9500-4000 B.C. Neolithic farmers from present-day Turkey had joined them in southern Europe before pushing deeper into the continent. Brought wheat, sheep, cattle—and their own DNA—to rest of Europe by 4000 B.C.

Prehistoric Melting Pot

- 3 - Yamnaya from Russia arrive ca 3300-2200 B.C. Their mastery of horses and wagons introduced a new mobile lifestyle to Europe.
- Most Europeans today have DNA from all three groups. Yamnaya bloodlines are strongest in the north, those of Neolithic farmers in the south.
- DNA Legacy: Before the arrival of the Yamnaya, Neolithic farmer DNA had largely replaced that of hunter-gatherers. By 1000 B.C. Yamnaya DNA could be found all across Europe

1 Hunter-Gatherers (white)

2 Neolithic Farmers' DNA (blue) became slightly less dominant by 4500 B.C. as they began to mix with hunter-gatherers.

3 Yamnaya (orange)

First immigrants

- 1 - Post Ice Age: About 14,500 years ago, as Europe began to warm, humans followed the retreating glaciers north. In the ensuing millennia, they developed more sophisticated stone tools and settled in small villages. Archaeologists call this period the Mesolithic, or Middle Stone Age.
- 2 - Second wave: Out of Anatolia
- People began planting small plots of emmer and einkorn, two ancient forms of wheat, and probably herding small flocks of sheep and goats, some 10,300 years ago, near the dawn of the Neolithic period.
- Within a thousand years the Neolithic revolution, spread north through Anatolia and into southeastern Europe.
- By about 6,000 years ago, there were farmers and herders all across Europe.

Demic and cultural diffusion propagated the Neolithic transition across different regions of Europe

- It has long been clear that Europe acquired the practice of farming from Turkey or the Levant, but did it acquire farmers from the same places?

- The Neolithic transition is the shift from hunting-gathering into farming. About 9000 years ago, the Neolithic transition began to spread from the Near East into Europe, until it reached Northern Europe about 5500 years ago.

- There are two main models of this spread. The cultural model assumes that European hunter-gatherers become farmers by acquiring domestic plants and animals, as well as knowledge, from neighboring farmers. The demic model assumes that it was mainly due to the migration of farmers

Demic vs Cultural

- The answer isn't obvious.
- For decades, many archaeologists thought a whole suite of innovations—farming, but also ceramic pottery, polished stone axes capable of clearing forests, and complicated settlements—was carried into Europe not by migrants but by trade and word of mouth, from one valley to the next, as hunter-gatherers who already lived there adopted the new tools and way of life.
- But DNA evidence from Boncuklu (Anatolia, Turkey) has helped show that migration had a lot more to do with it.

Migration, not cultural exchange

- Early Anatolian farmers had migrated, spreading their genes as well as their lifestyle. DNA of Europe's first farmers still dominates the genes of modern Sardinians.
- They didn't stop in southeastern Europe. Over the centuries their descendants pushed along the Danube and deep into the heart of the continent.
- Others traveled along the Mediterranean by boat, colonizing islands such as Sardinia and Sicily and settling southern Europe as far as Portugal. From Boncuklu to Britain, the Anatolian genetic signature is found wherever farming first appears.
- Those Neolithic farmers mostly had light skin and dark eyes—the opposite of many of the hunter-gatherers with whom they now lived side by side.

Hunter gatherer-Farmer mix; then change

- Across Europe, this creeping first contact was standoffish, sometimes for centuries. There’s little evidence of one group taking up the tools or traditions of the other. Even where the two populations did mingle, intermarriage was rare. There’s no question they were in contact with each other, but they weren’t exchanging wives or husbands.

- About 5,400 years ago, everything changed. All across Europe, thriving Neolithic settlements shrank or disappeared altogether. The dramatic decline has puzzled archaeologists for decades. There’s less stuff, less material, less people, less sites