OLLI Human Evolution
Scientific Update
July 2024

by

Charles J Vella, PhD

Einstein’s brain

Einstein’s brain

- When Einstein died in 1955 at Princeton Hospital in New Jersey, his brain was removed by a local pathologist named Thomas Harvey, who preserved, photographed, and measured it. A colleague of Harvey's cut most of the brain into 240 blocks and mounted them on microscope slides. From time to time, he sent the slides to various researchers, although few publications resulted. Harvey, who moved around the United States several times in the course of his career, kept the jar containing what remained of the brain in cardboard box. Finally, in 1998, Harvey--who died in 2007--gave the jar to the University Medical Center of Princeton, where it remains today.
- Einstein's parietal lobes--which are implicated in mathematical, visual, and spatial cognition--were 15% wider than normal parietal lobes.
- Size of his brain: At 1230 cc, it fell at the low end of average (1350 cc) for modern humans.

Einstein’s brain

- A pronounced knoblike structure in the part of the motor cortex that controls the left hand; associated with musical ability – he played violin
- More glial cells than normal
- A very rare pattern of grooves and ridges in the parietal regions of both sides of the brain that be related to Einstein's superior ability to conceptualize physics problems. Indeed, during his lifetime, Einstein often claimed that he thought in images and sensations rather than in words.
- Had superior school grades in Latin and the sciences and mediocre marks in art and geography.

Antikythera mechanism: 200 BCE

Antikythera mechanism

- The device is a geared astronomical calculation machine of immense complexity. Dated to 200 BCE.

- An ancient Greek hand-powered orrery (model of the Solar System), described as the oldest known example of an analogue computer used to predict astronomical positions and eclipses decades in advance.

- It could also be used to track the four-year cycle of athletic games similar to an Olympiad, the cycle of the ancient Olympic Games.

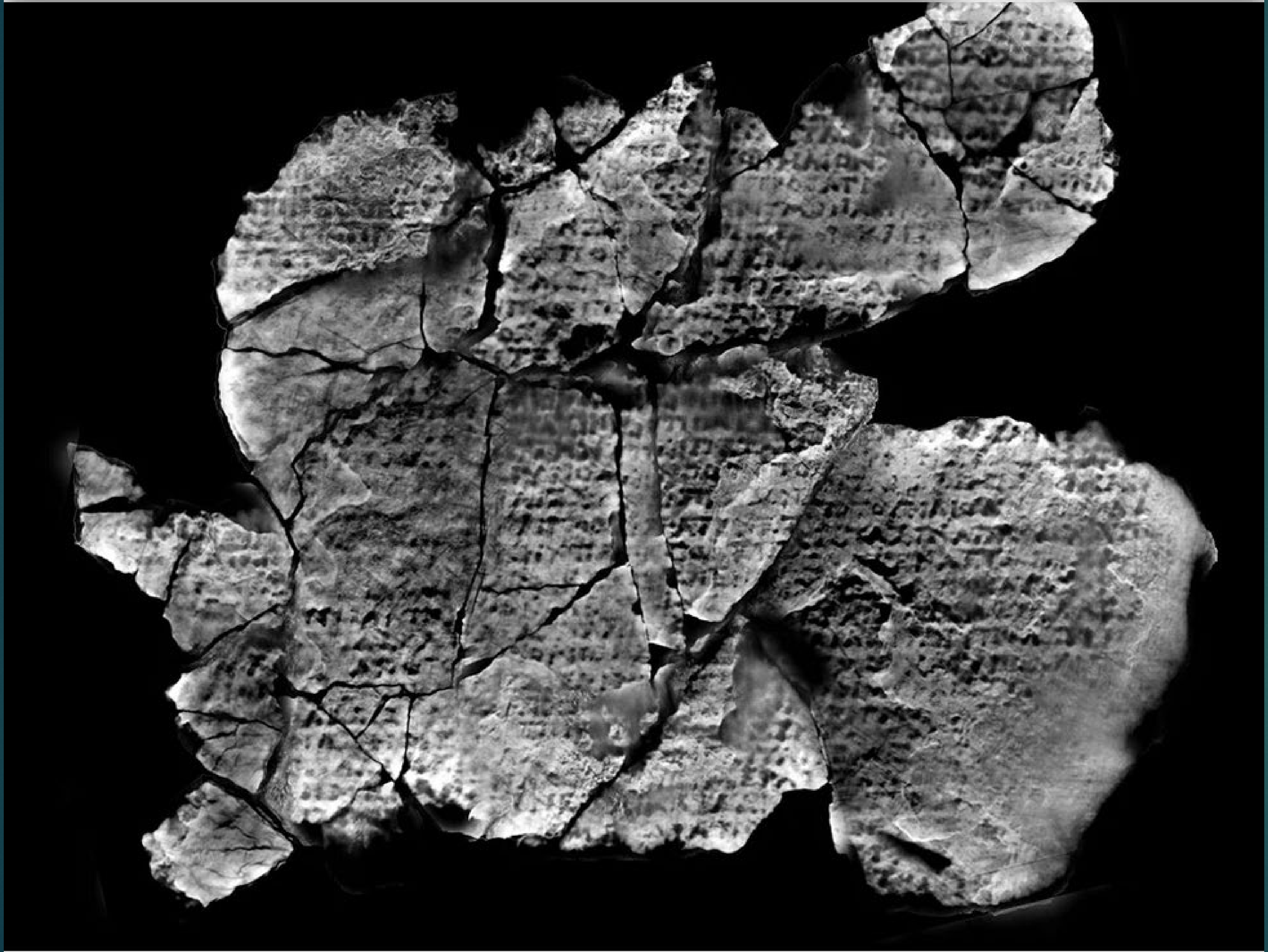
Antikythera mechanism

- Predicting the positions of the planets along its ecliptic route around the sun was very difficult for early astronomers. This task, it turns out, was one of the primary functions of the Antikythera mechanism.

- Another function was to track the positions of the sun and moon, which also have variable motions against the stars. And eclipses.

- Machines with similar complexity did not appear again until the astronomical clocks of Richard of Wallingford in the 14th century.

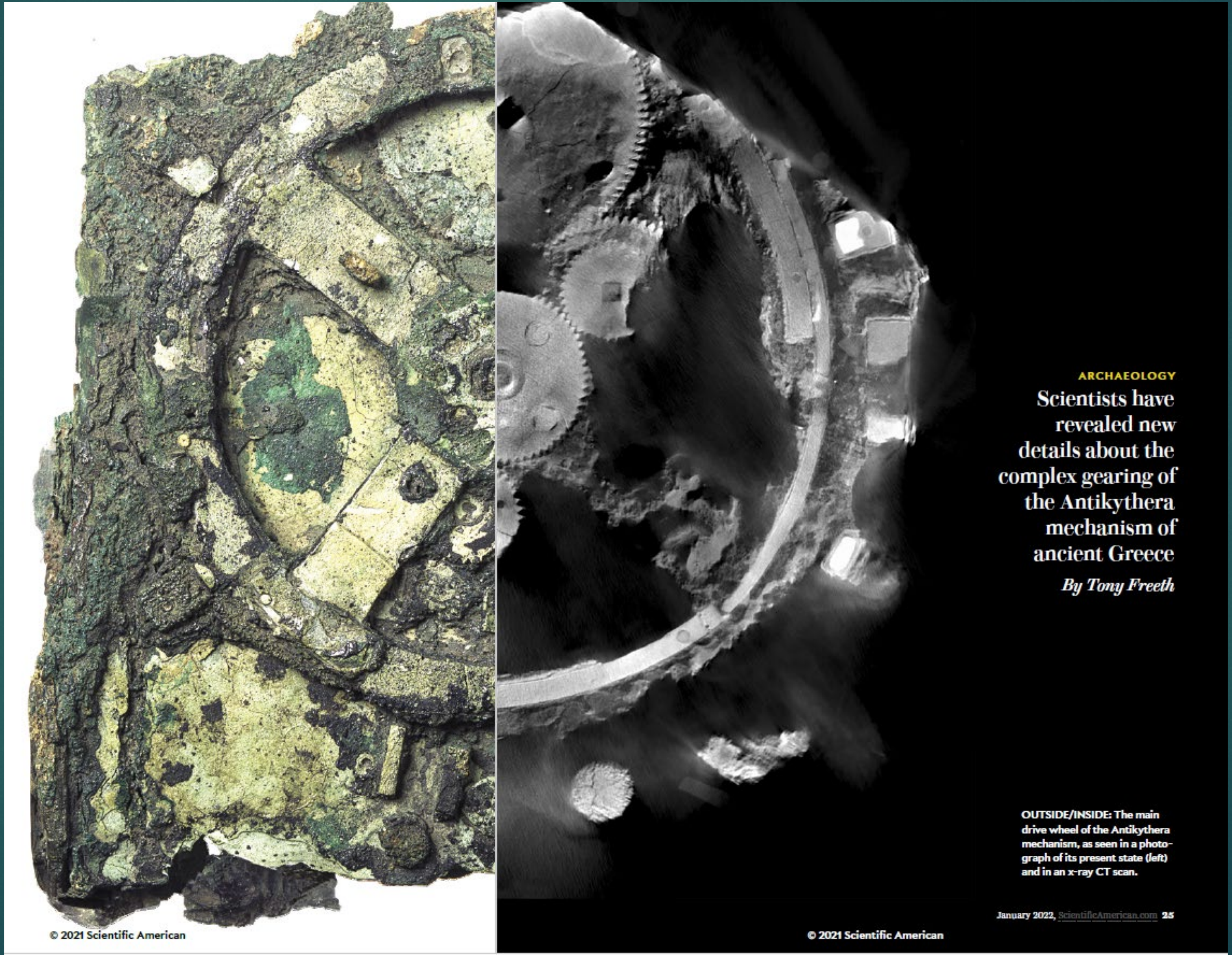
An Ancient Greek Astronomical Calculation Machine Reveals New Secrets



Hidden message: X-ray CT scans made in 2005 revealed previously unseen inscriptions on the Antikythera mechanism, including a list of planetary cycles on the front cover (*shown here*) and a “user's manual” on the back cover.

Fragments: Over the years the original mass of the Antikythera mechanism has split into 82 pieces. Figuring out how they all fit together has been a challenging puzzle for researchers. The largest fragment (*top left*) holds the main drive wheel.

CT Scan



ARCHAEOLOGY

Scientists have revealed new details about the complex gearing of the Antikythera mechanism of ancient Greece

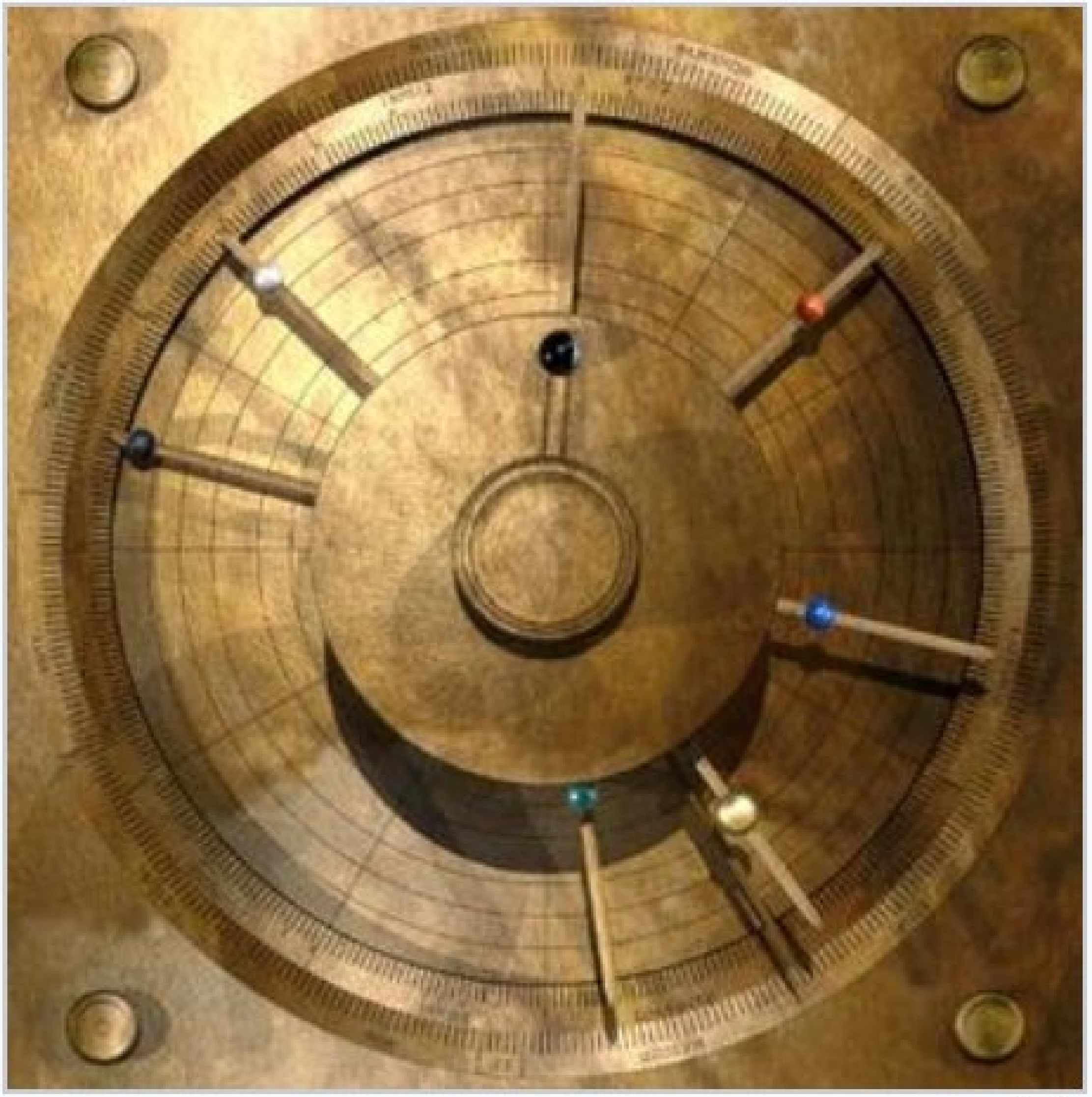
By Tony Freeth

OUTSIDE/INSIDE: The main drive wheel of the Antikythera mechanism, as seen in a photograph of its present state (left) and in an x-ray CT scan.

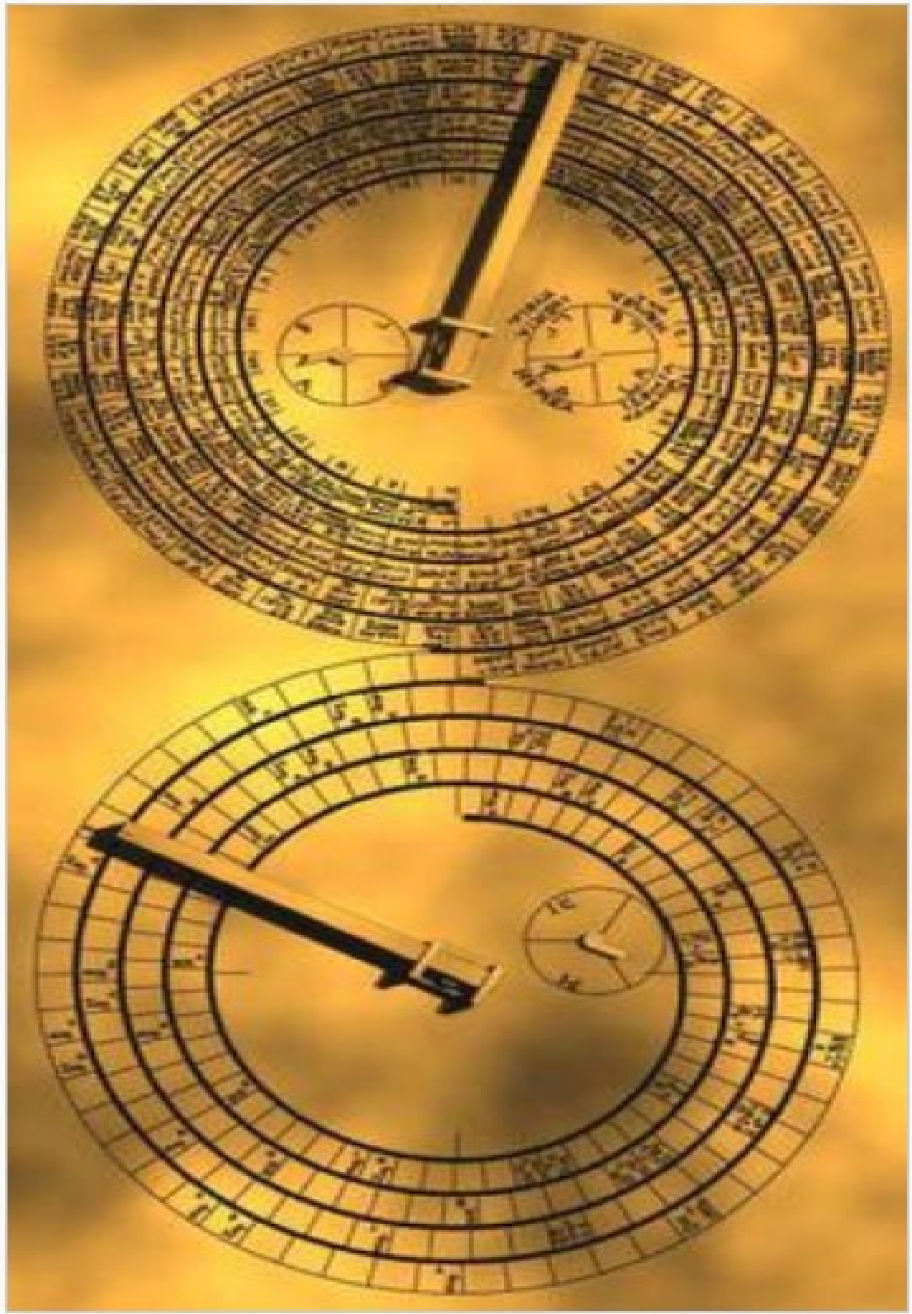
January 2022, ScientificAmerican.com 25

Front: Inside the device a "main drive wheel" turned all the gearing, which moved pointers and concentric rings displaying the positions of different celestial bodies. Small spheres showed the positions of the sun and moon and the phase of the moon. Colored beads marked the locations of the planets along the ecliptic, the plane of the solar system.

Back: The rear face contained two large dials, as well as some smaller ones. The large top dial was a calendar that represents the Metonic cycle, a 19-year period over which 235 moon phases recur. The large lower dial was the 223-month saros dial, which predicts the dates of solar and lunar eclipses.



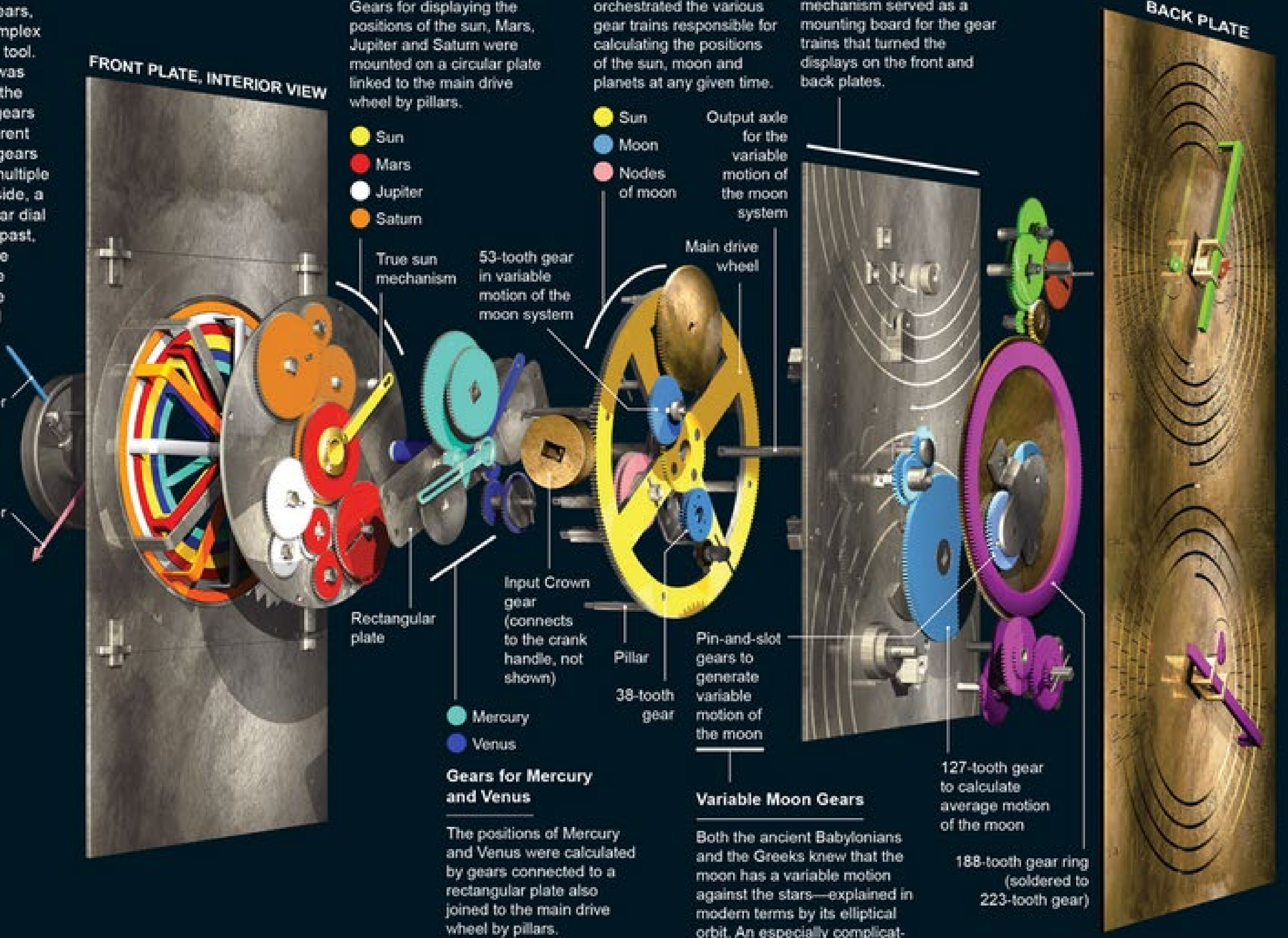
Computer-generated front panel of the Freeth model



Computer-generated back

INSIDE THE MACHINE

The new model of the Antikythera mechanism proposes a total of 69 gears, forming a shockingly complex astronomical calculation tool. Most of this complexity was hidden in the innards of the device, where trains of gears worked together on different calculations, and some gears served double duty for multiple purposes. From the outside, a user could turn a calendar dial to a desired point in the past, present or future, and the gears inside would move pointers and rings on the surface display to reveal celestial predictions.



Gears for True Sun, Mars, Jupiter and Saturn

Gears for displaying the positions of the sun, Mars, Jupiter and Saturn were mounted on a circular plate linked to the main drive wheel by pillars.

- ● Sun
- ● Mars
- ○ Jupiter
- ● Saturn

Main Drive Wheel

This central wheel orchestrated the various gear trains responsible for calculating the positions of the sun, moon and planets at any given time.

- ● Sun
- ● Moon
- ● Nodes of moon

Main Plate with Bearings

A central plate inside the mechanism served as a mounting board for the gear trains that turned the displays on the front and back plates.

- ● Mercury
- ● Venus

Gears for Mercury and Venus

The positions of Mercury and Venus were calculated by gears connected to a rectangular plate also joined to the main drive wheel by pillars.

Variable Moon Gears

Both the ancient Babylonians and the Greeks knew that the moon has a variable motion against the stars—explained in modern terms by its elliptical orbit. An especially complicated gear train calculated this variable motion of the moon in an extraordinary way.

- ● Metonic and Kallippic calendar
- ● Olympiad calendar
- ● Saros and exeligmos calendar

Back Dials

The upper back dial system was a Metonic/Kallippic calendar that reconciled the lunar month with the solar year. It also included a smaller dial showing the four-year Olympiad cycle of the Panhellenic Games, commonly used to mark time. The lower back dial system was a saros/exeligmos calendar that predicted solar and lunar eclipses according to the 223-month saros cycle. It was indexed to inscriptions on the back plate that describe the characteristics of the predicted eclipses.

Gears for True Sun, Mars, Jupiter and Saturn

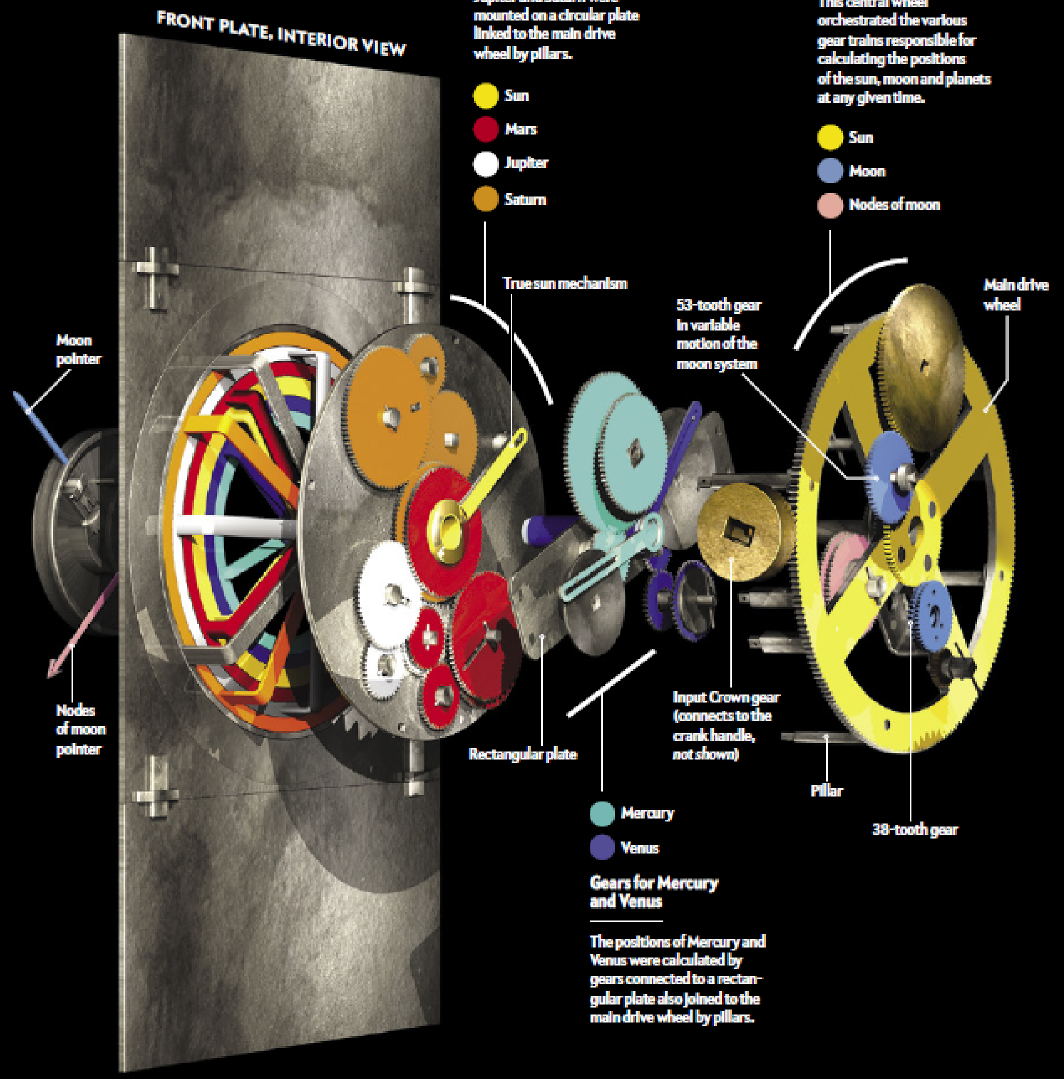
Gears for displaying the positions of the sun, Mars, Jupiter and Saturn were mounted on a circular plate linked to the main drive wheel by pillars.

● Sun
● Mars
● Jupiter
● Saturn

Main Drive Wheel

This central wheel orchestrated the various gear trains responsible for calculating the positions of the sun, moon and planets at any given time.

● Sun
● Moon
● Nodes of moon

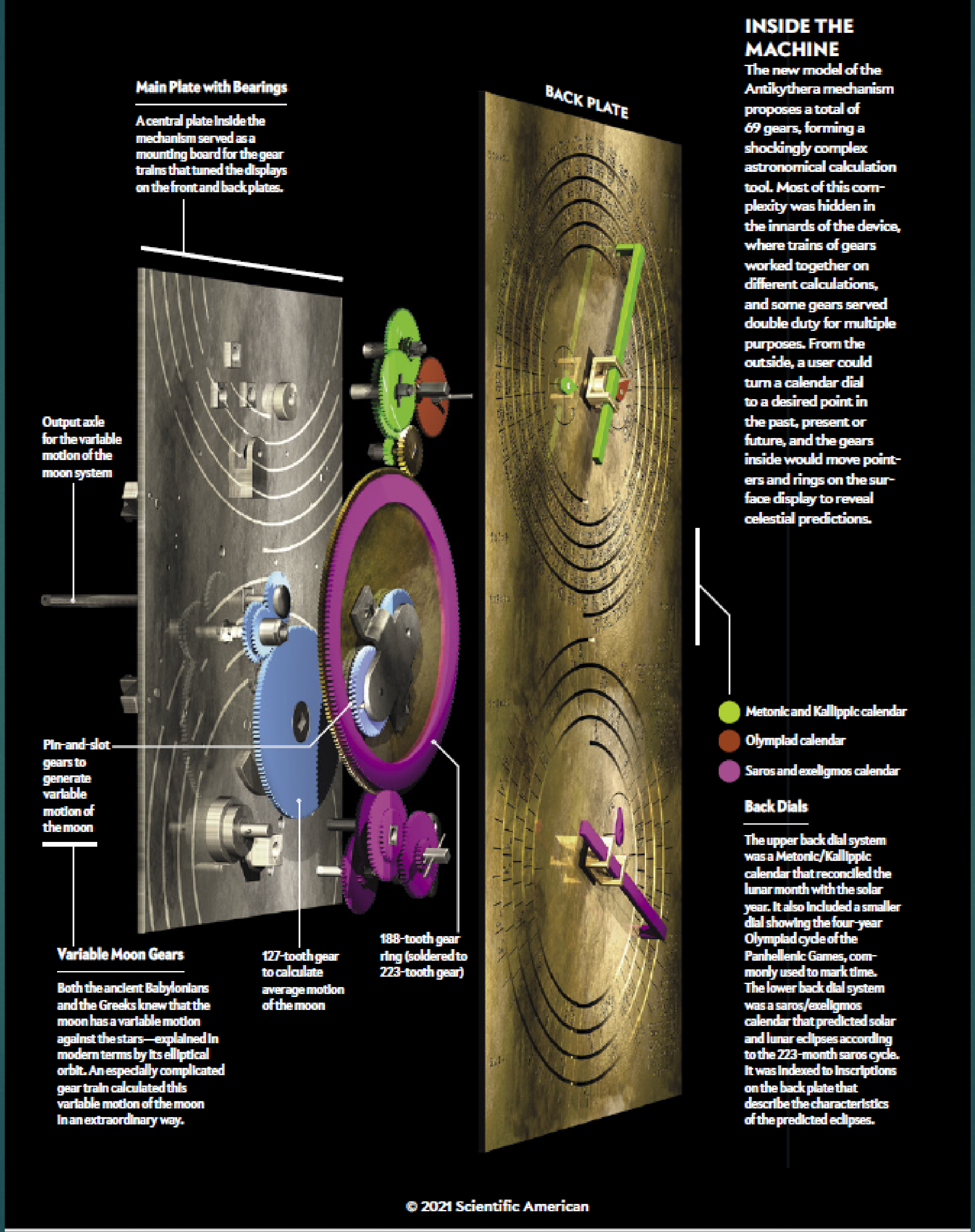


● Mercury
● Venus

Gears for Mercury and Venus

The positions of Mercury and Venus were calculated by gears connected to a rectangular plate also joined to the main drive wheel by pillars.

Graphic by Tony Freeth and Jen Christiansen, Model by UCL Antikythera Research Team



INSIDE THE MACHINE

The new model of the Antikythera mechanism proposes a total of 69 gears, forming a shockingly complex astronomical calculation tool. Most of this complexity was hidden in the innards of the device, where trains of gears worked together on different calculations, and some gears served double duty for multiple purposes. From the outside, a user could turn a calendar dial to a desired point in the past, present or future, and the gears inside would move pointers and rings on the surface display to reveal celestial predictions.

Main Plate with Bearings

A central plate inside the mechanism served as a mounting board for the gear trains that tuned the displays on the front and back plates.

Output axle for the variable motion of the moon system

Pin-and-slot gears to generate variable motion of the moon

Variable Moon Gears

Both the ancient Babylonians and the Greeks knew that the moon has a variable motion against the stars—explained in modern terms by its elliptical orbit. An especially complicated gear train calculated this variable motion of the moon in an extraordinary way.

127-tooth gear to calculate average motion of the moon

188-tooth gear ring (soldered to 223-tooth gear)

- 🟩 Metonic and Kallippic calendar
- 🟥 Olympiad calendar
- 🟪 Saros and exeligmos calendar

Back Dials

The upper back dial system was a Metonic/Kallippic calendar that reconciled the lunar month with the solar year. It also included a smaller dial showing the four-year Olympiad cycle of the Panhellenic Games, commonly used to mark time. The lower back dial system was a saros/exeligmos calendar that predicted solar and lunar eclipses according to the 223-month saros cycle. It was indexed to inscriptions on the back plate that describe the characteristics of the predicted eclipses.

Florida carpenter ants perform amputations on nestmates when their legs are injured. Only humans have been known to do it.

Florida carpenter ants perform amuptations on nestmates when their legs are injured. (Image credit: Bart

An innate ant ability: amputation

- In 2023, an African ant species, *Megaponera analis,* can treat infected wounds in their nestmates with an antimicrobial substance produced in their glands. Florida carpenter ants do not have any equivalent glands,
- Researchers looked at two types of leg wounds: lacerations on the femur (thigh) and those lower down on the tibia.
- The ants treated their nest members' femur injuries by cleaning the wound with their mouths before amputating the leg by repeatedly biting it, while the tibia wounds were treated with just cleaning.
- Survival rates for femur injuries improved from less than 40% to between 90 and 95% when amputations were performed, while survival rates for tibia injuries improved from 15% to 75% following cleaning.

T. rex: how many neurons dinosaurs like *T. rex* had

How smart was *T. rex*?

- How brainy was *Tyrannosaurus rex*? It depends on who you ask.

- Last year, Suzana Herculano-Houzel, a neuroscientist at Vanderbilt University in Nashville, calculated that the predator had 3.3 billion neurons in one part of the forebrain alone. The discovery put *T. rex*'s forebrain on par with modern baboons.

- The finding raised eyebrows — and doubts. "Having the same number of neurons as a primate does not make you a primate."

Criteria to use: reptiles or birds

- Now, Gutiérrez-Ibáñez and colleagues have come up with a much more conservative neuron count. The *T. rex* telencephalon, a part of the forebrain involved in sensory, cognitive and motor functions, had closer to 360 million neurons.
- The new estimate suggests that *T. rex*'s forebrain is more similar to that of modern crocodiles than of primates.

Modern proxies

- Used the neuron densities of modern relatives as proxies.
- Here lies the issue: *T. rex* is related to both reptiles and birds. But these two groups have vastly different neuron densities — reptiles have fewer neurons per square centimeter of brain than birds.
- When calculating the number of neurons in extinct theropods, the dinosaur group that includes *T. rex*, researchers must decide whether to use the neuron densities of birds, reptiles or some combination of the two.

Bird or crocodile brain comparison?

- In the 2023 study, Herculano-Houzel calculated the ratio between brain size and body mass of around 30 dinosaurs and then looked at how they stacked up against modern birds and reptiles.

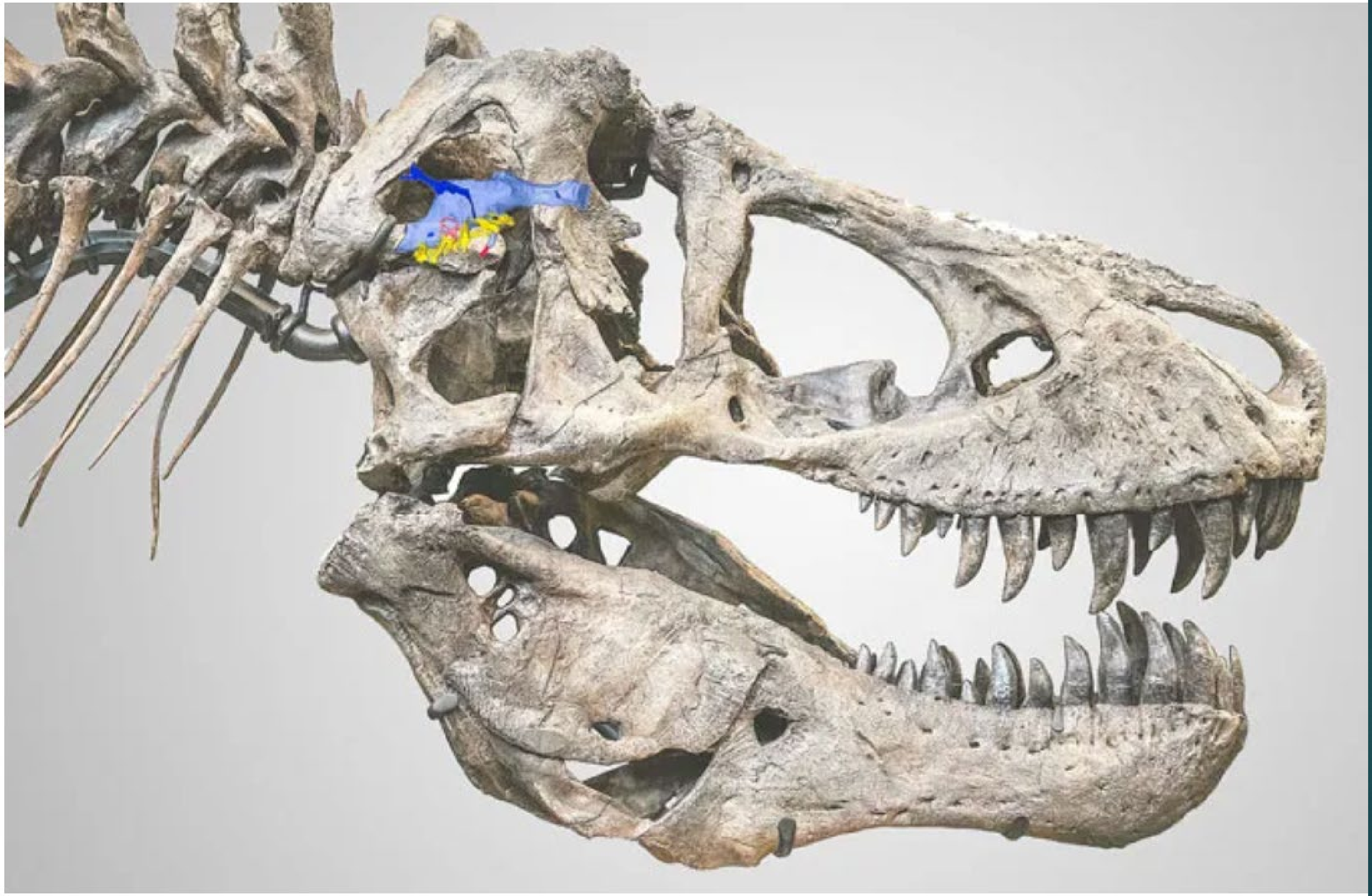
- Her calculations using ancient bird families (such as the group that includes pigeons) hinted that theropod brains were more like bird brains than that of other dinosaurs.

- Thus, she used the neuron densities of modern birds that are most closely related to theropods to calculate how many neurons T. rex had.

Bird or crocodile brain comparison?

- Gutiérrez-Ibáñez believes that even if birds are living dinosaurs, that assumption is flawed, Adding a broader range of living birds to the comparison of brain-to-body ratios brought T. rex's more in line with that of scaled reptiles.
- Herculano-Houzel's study also inflated the numbers of neurons by assuming that dinosaur brains occupied the whole braincase, like modern bird brains do, Gutiérrez-Ibáñez says. The brain of T. rex and many other dinosaurs floated in fluid — a trait found in modern crocodiles.

T. rex’s brain only occupied around 30-40 percent of its braincase



T. rex’s brain only occupied around 30-40 percent of its braincase (seen here in blue). How many neurons were

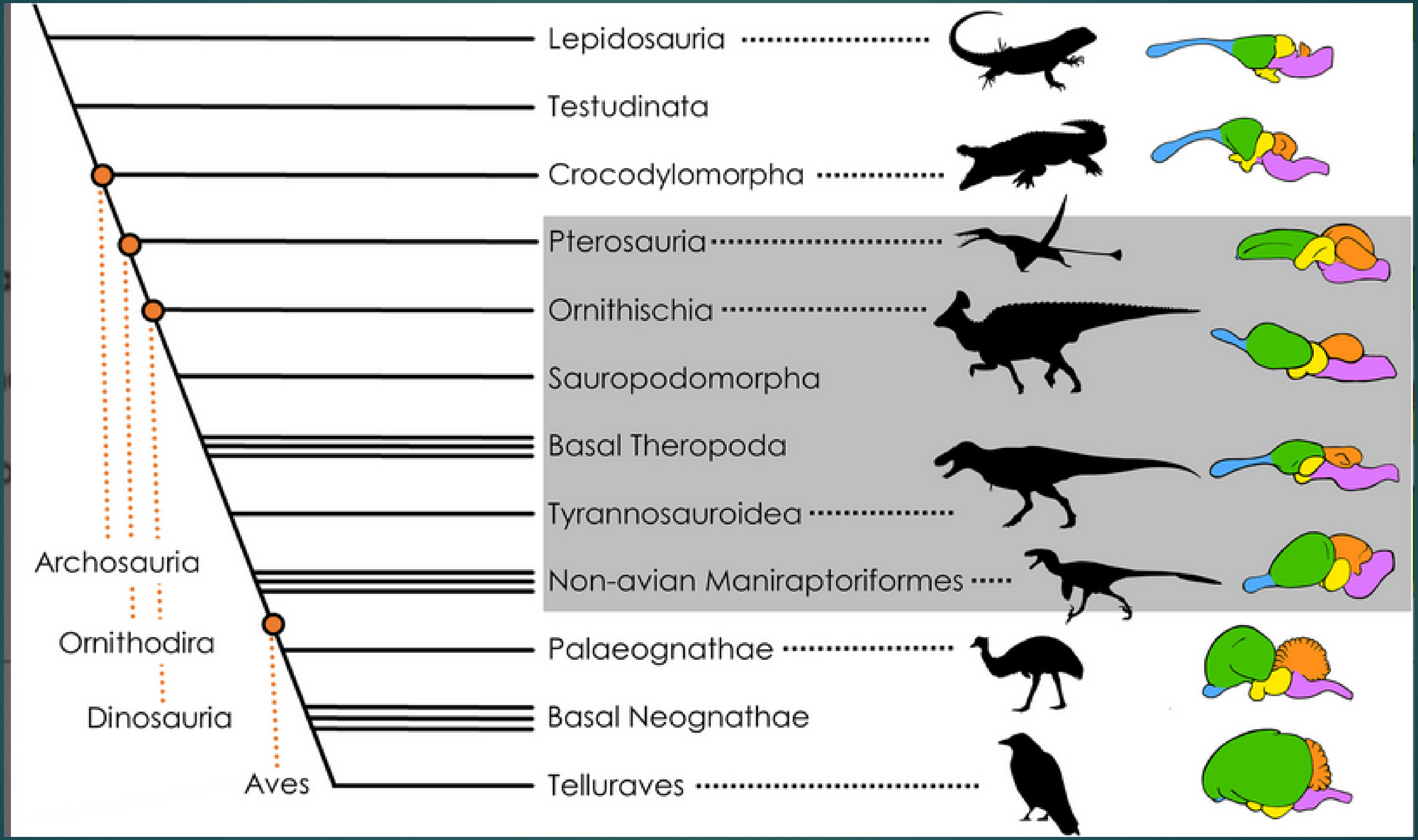
Recalculations

- Gutiérrez-Ibáñez's team recalculated *T. rex*'s brain size using a smaller brain volume, which cut down the amount of neurons in the telencephalon from 3.3 billion to 1.2 billion.

- Using reptile neuron density reduced the amount even further to between 245 million and 360 million.

- Herculano-Houzel says that her study did account for dinosaur brains not completely filling the braincase. She is also not convinced by the new findings.

Brain shapes



How smart was *T. rex*? Testing claims of exceptional cognition in dinosaurs and the application of neuron count estimates in palaeontological research

- Consider specific examples of complex behaviors, such as habitual tool use. Remarkably, Herculano-Houzel suggested that this might be within the realm of possibility for large theropods such as *T. rex*, as it is for primates and telluravian birds today.
- However, tool use even within these groups is rare, especially if the more rigorous definition of “tooling” (requiring the deliberate management of a mechanical interface) is employed: this occurs in only 9 avian and 20 primates.
- While it is true that telencephalon size in birds has an association with tool use, this correlation does not hold any predictive power in the sense that all birds with a certain-sized telencephalon exhibit this behavior. Even within corvids, which telencephalic neuron counts and sophisticated cognitive abilities overlap with those of anthropoid primates,

Kai R. Caspar, et al., 2024

Crows and parrots

- New Caledonian crows, and Hawaiian alalā crows are the only species known to employ and manufacture tools in the wild. Notably, both species inhabit remote islands, and they share unusually straight beaks and greater binocular overlap than other crows, which are thought to be specific morphological adaptations to enable tool use.
- A similar situation can be observed in parrots. These birds probably display the highest avian telencephalic neuron counts, and a greatly enlarged medial spiriform nucleus, which acts as an interface between the pallium and the cerebellum, enabling enhanced motor cognition. However, the Tanimbar corella is the only parrot known to be a sophisticated tool user in the wild

Beware of implications of neuron counts

- Considering these findings, it is unsurprising that taxa converging in neuronal counts often differ markedly in cognition and behavior.

- Herculano-Houzel ranked her neuronal count estimates for large theropods against those of anthropoid primates, but she might as well have done so for giraffes (1.7 B neurons), which exceed tool-proficient capuchins (1.1 B) and corvids (0.4–1.2 B) in telencephalic neuron numbers, rivaling macaques (0.8–1.7 B).

- We know little about giraffes' cognitive abilities, but it would be appropriate to be skeptical of any claim that they might exhibit "macaque-like" cognition based simply on that measure.

Beware of neuron counts

- Neuron counts corresponding to major brain regions, whether empirically determined or estimated, dramatically simplify neuronal tissue complexity, as do measures such as absolute brain size or EQ.
- Based on current evidence, they also whole brain, endocast based neuron counts represent flawed cognitive proxies that need to be viewed in the broader context of an animal's ecology, neuroanatomy, connectomics, and neurochemistry.
- All in all, we want to discourage attempts to predict cognitive performance in extinct species based on endocast-derived neuron count estimates.

*** Rapid volcanic ash entombment reveals the 3D anatomy of Cambrian trilobites

- Knowledge of Cambrian animal anatomy is limited by preservational processes that result in compaction, size bias, and incompleteness.
- Study documents pristine three-dimensional (3D) anatomy of trilobites fossilized through rapid ash burial from a pyroclastic flow entering a shallow marine environment.

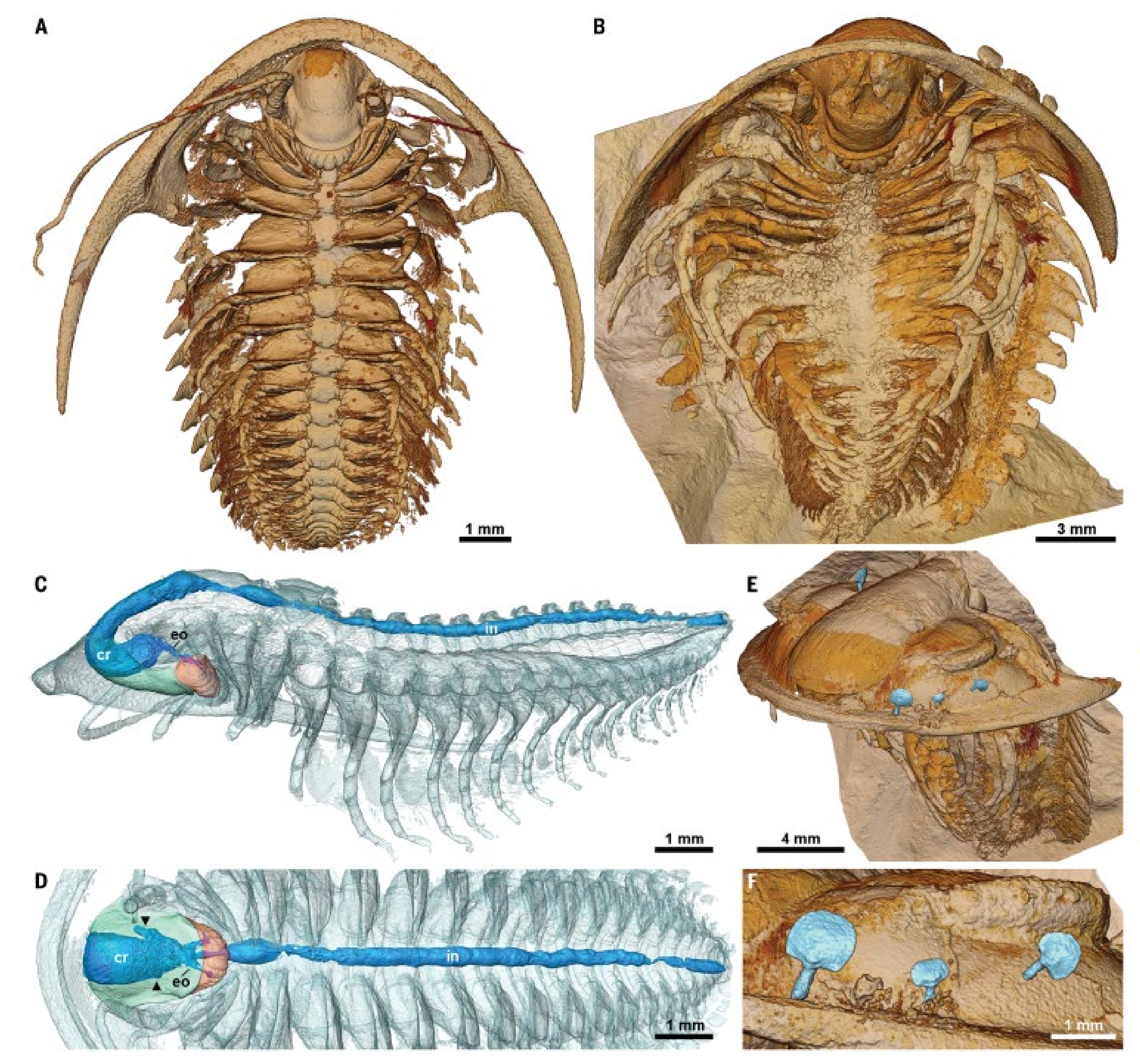
Trilobites

- Trilobites are arguably the most familiar of fossil invertebrates, known from over 22,000 species and millions of specimens spanning the Paleozoic. Their calcite exoskeleton confers high fossilization potential.
  .
- By contrast, the nonbiomineralized appendages and internal organs of trilobites are known for comparatively few species.
- Study documents trilobite anatomy captured with great fidelity by microtomographic (mCT) x-ray imaging of specimens of two species preserved as molds in volcanic ash from the Tatelt Formation (Cambrian Series 2, Stage 4) in the Lemdad Syncline of Morocco

Detailed look

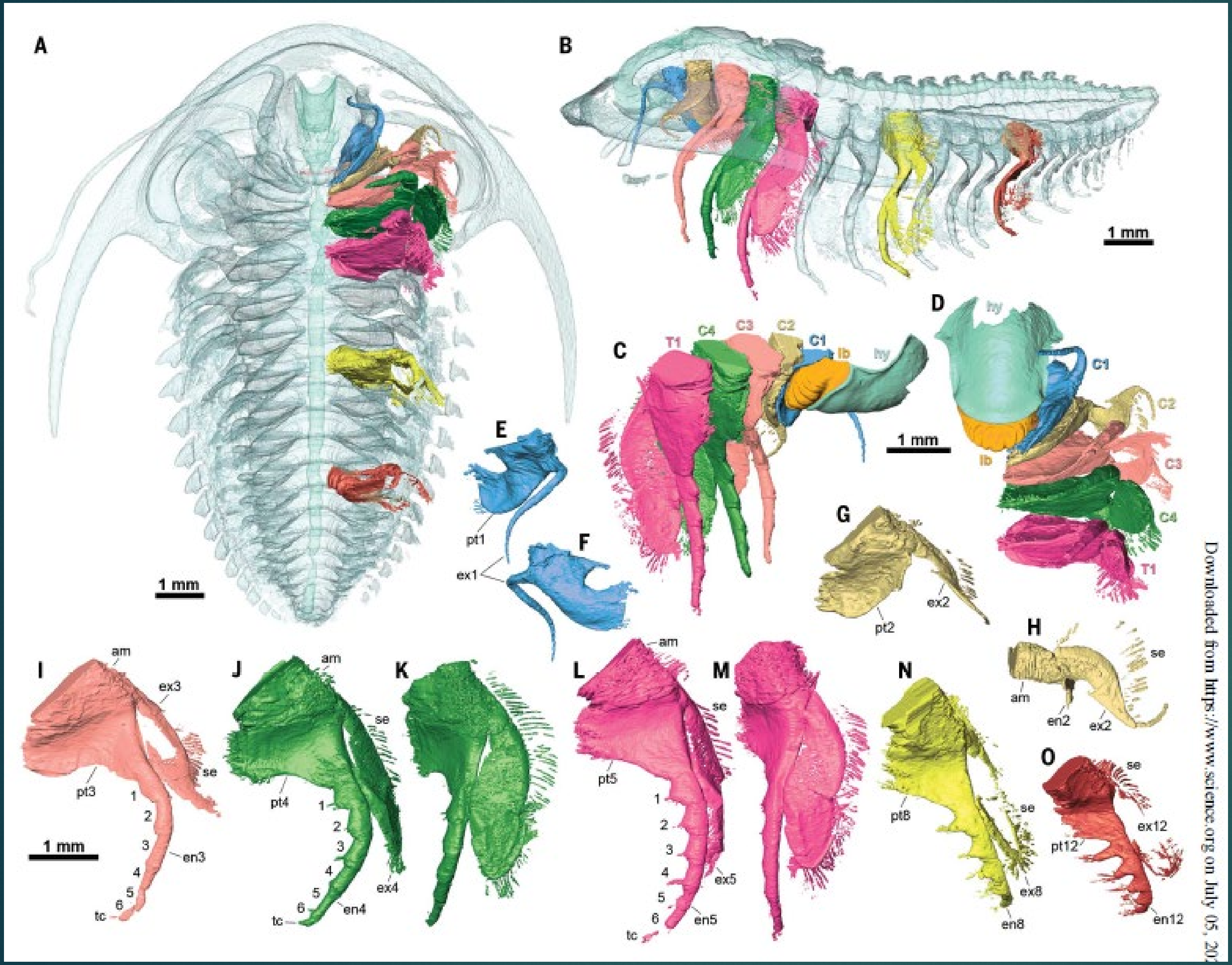
- Cambrian ellipsocephaloid trilobites from Morocco are articulated and undistorted, revealing exquisite details of the appendages and digestive system. Previously unknown anatomy includes a soft-tissue labrum attached to the hypostome, a slit-like mouth, and distinctive cephalic feeding appendages.

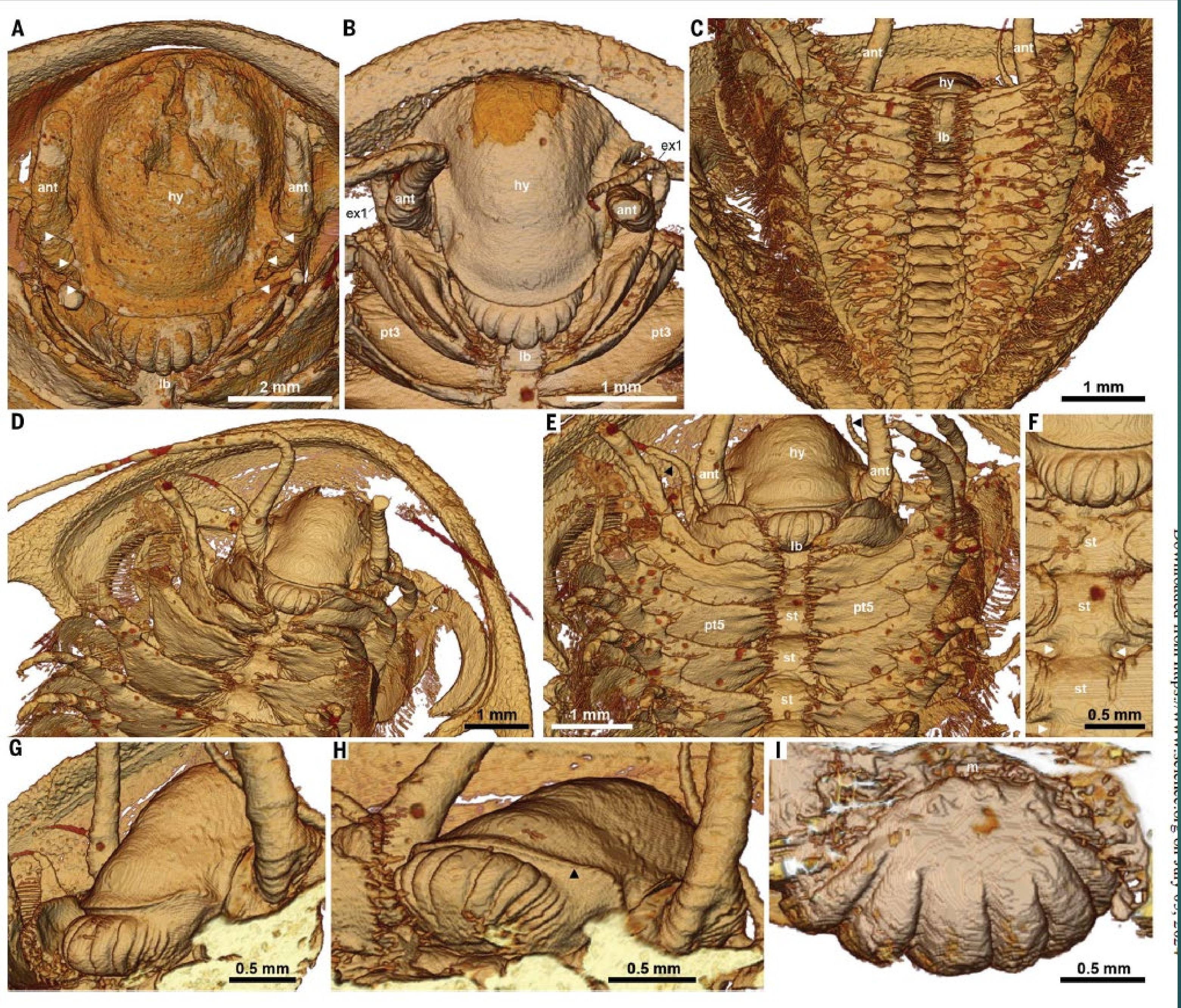
- This occurrence of moldic fossils with 3D soft parts highlights volcanic ash deposits in marine settings as an underexplored source for exceptionally preserved organisms.



Microtomographic reconstructions of the trilobites G. mauretanica and Protolenus (Hupeolenus) sp. from the lower Cambrian Tatelt Formation of Morocco

Postantennal appendages, hypostome, and labrum of Protolenus (Hupeolenus) sp.





Features of the hypostome, labrum, mouth, and appendages in G. mauretanica and Protolenus (Hupeolenus) sp.

Stingray sculpture

- In 2018, Emily Brink, spotted an intriguing rock east of Still Bay, about 330 km east of Cape Town. The rock was unusually symmetrical and was shaped uncannily like a stingray, minus the tail.
- They posit that it represents a sand-sculpture of a blue stingray (Dasyatis chrysonata). We believe that the sculpture might have begun with tracing a specimen in the sand.
- This would be the oldest known example of humans creating an image of a creature other than themselves—a form of representational art
- The rock was found about 30km east of the Blombos Cave, which is renowned for its paleoart. That includes an engraving on ochre dating back 77,000 years and a 73,000 year old drawing.

Charles W. Helm et al., 2024

Stingray sand 'sculpture' based on real stingray

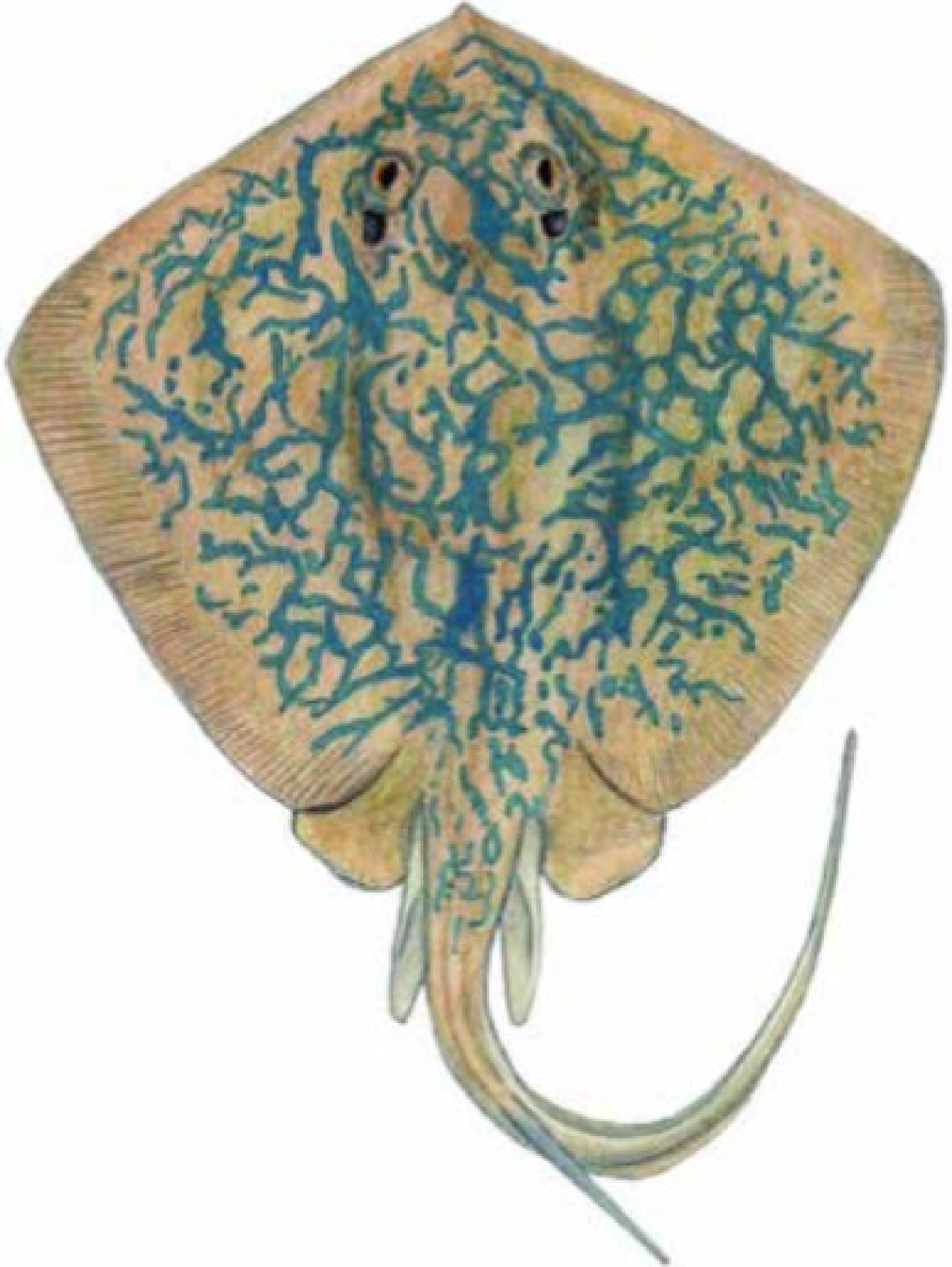
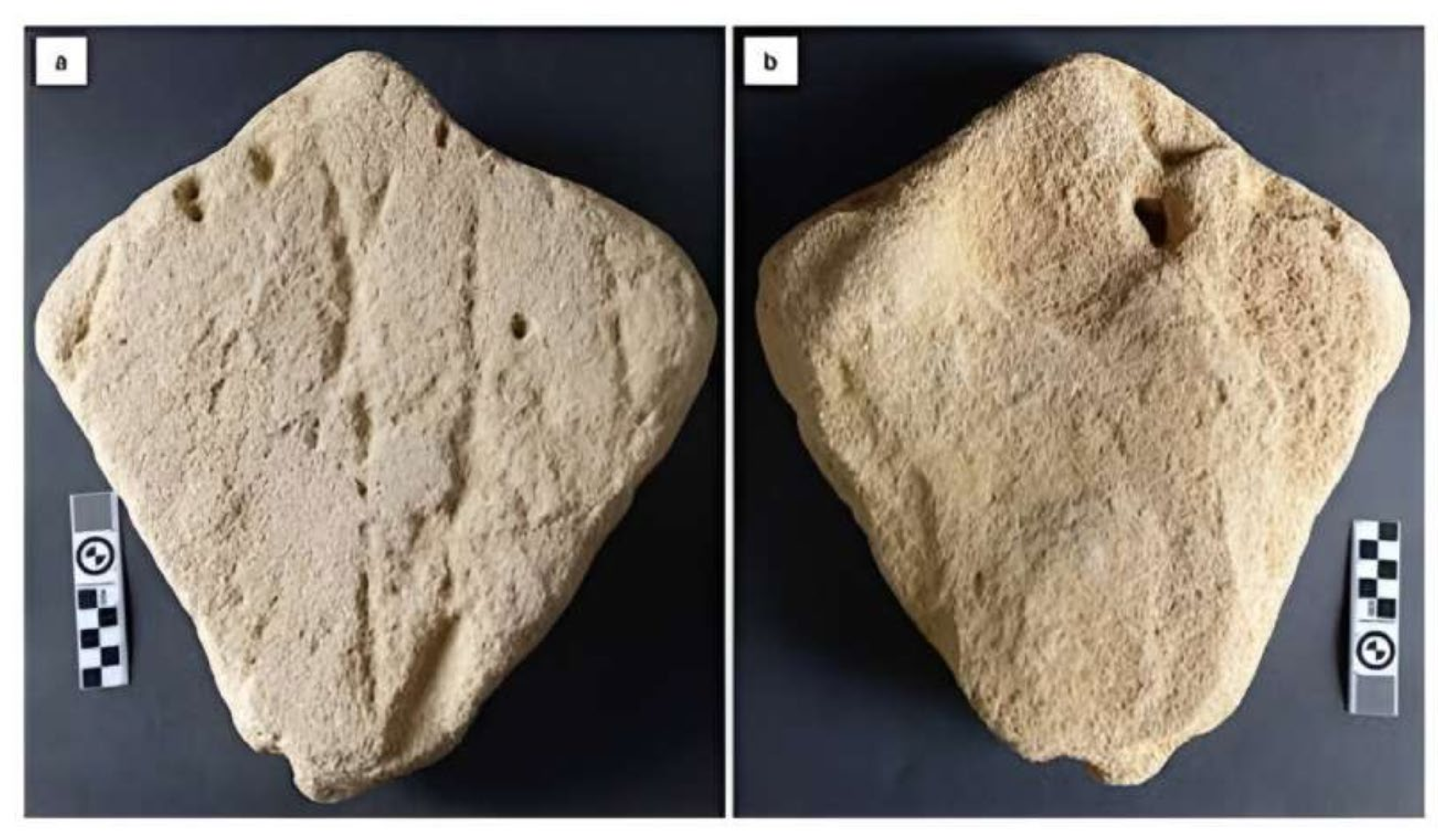
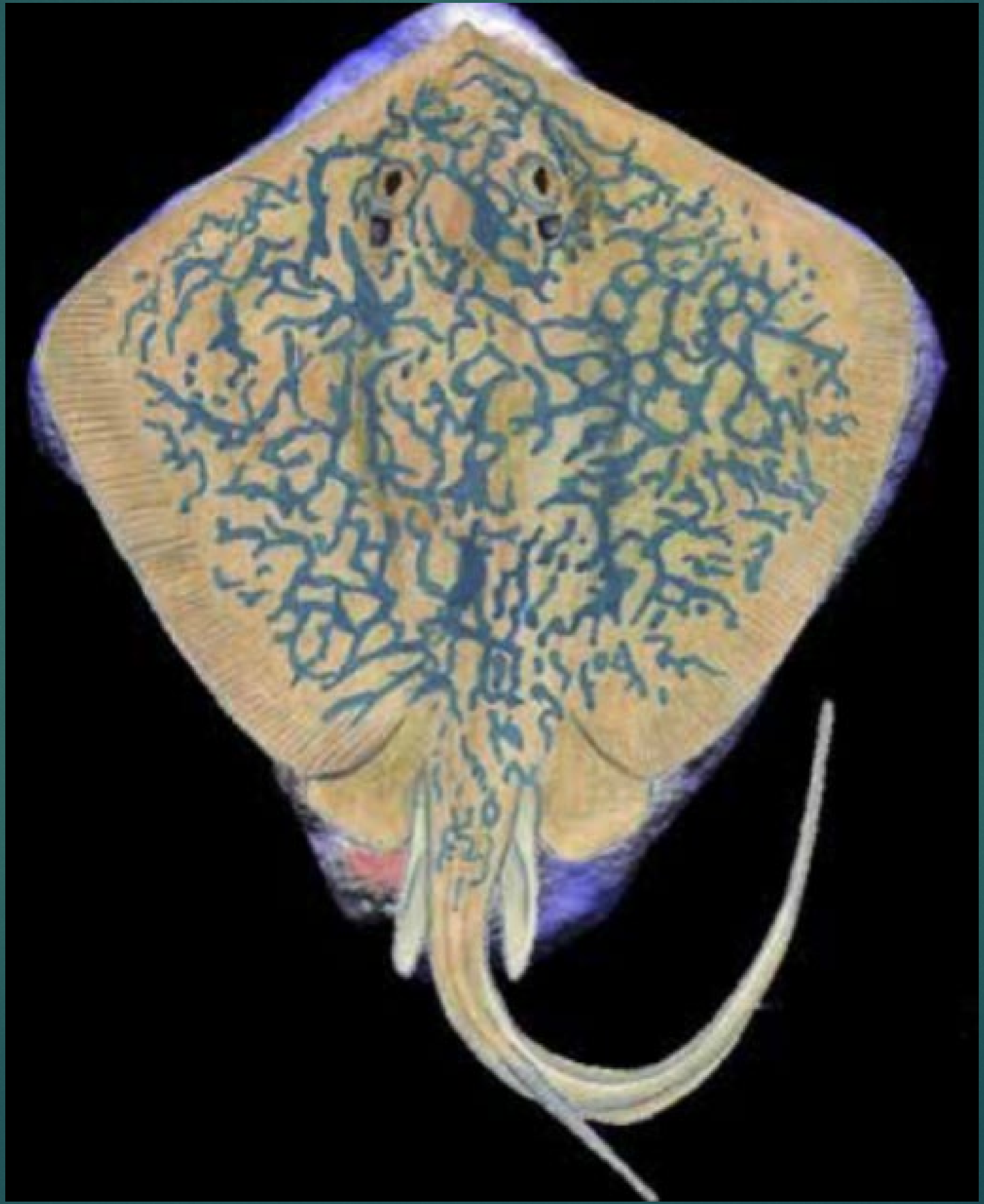


Figure 7. *The blue stingray (illustration by Elaine*

Stingray sand 'sculpture' in South Africa may be oldest example of humans creating an image of another creature



Stingray overlayed on sculpture



A Purported Pleistocene Sandscup from South Africa

- A purported cemented sand sculpture found in Pleistocene aeolianite deposits on the Cape south coast of South Africa resembles a stingray (minus a tail) in outline.
- Symmetry is evident in the rock's shape and the pattern of grooves on its surface. It is postulated that it may be a three-dimensional example of representational art of another species. Optically stimulated luminescence studies of rocks in the vicinity indicate that it dates to the Middle Stone Age, most probably during Marine Isotope Stage 5 (when high sea levels imply a nearby coastline).

Paleoart

- The correspondence in shape between the purported sand sculpture and the blue stingray (Dasyatis chrysonota) suggests that it may have been traced from a fresh specimen.
- Tracings on sand are postulated as a possible ‘stepping stone’ between abstract early paleoart and representational rock art.
- Features of the rock suggest that the creation of a stingray sand sculpture may conceivably have been followed by symbolically wounding it and amputating its lethal end.

130 Ka sculpture

- Optically stimulated luminescence suggests that it was created during the Middle Stone Age around 130,000 years ago.
- Indeed, ammoglyphs (patterns made in sand by ancestral hominins and now evident in rock) have only been reported from the Cape south coast.
- Suggest that tracing in sand might form a possible "stepping stone" between abstract images and images of creatures created "from scratch." A flattish animal such as a stingray would have provided a suitable model for tracing, compared with more three-dimensional varieties. We have tentatively suggested a sequence of progression of representational paleoart from initial tracing in sand, to the creation of images in sand (through copying or from memory), and then to rock art.

Sedimentary exposures from Lake Turkana in Kenya,

*** The Biogeographic Context of Human Evolution in the East African Rift System

- New study illuminates the environmental and climatic influences on mammalian and hominin evolution
- A groundbreaking study published in *Nature Ecology & Evolution*[1] sheds light on the biogeographic context of human evolution within the East African Rift System
- A comprehensive analysis of mammalian fossil records, revealing how climatic and environmental changes have shaped the evolution of mammals and hominins over the last six million years.
- The East African Rift System has long been recognized as a critical region for understanding human evolution.

Homogenization

- This new study emphasizes the significance of biotic homogenization—the process by which the faunas of different regions become increasingly similar in composition—as a key factor influencing the evolution of ecosystems and the species inhabiting them.
- The research delves into the Late Miocene and Pliocene epochs (approximately 3 to 6 million years ago), revealing that these periods were dominated by endemic species.
- However, around three million years ago, a significant shift towards biotic homogenization occurred. This transition was characterized by the loss of endemic species within functional groups and a rise in the number of grazing species shared between regions.

Rise of C4 grasses

- This biogeographic shift coincides with the regional expansion of ecosystems dominated by C4 grasses, which thrive in warm and dry climates. These environmental changes directly impacted the feeding and mobility patterns of both hominins and other faunas sharing their habitat.

eat, soybeans, and all

xamples of C_4 plants

*** Chimpanzee gestural exchanges share temporal structure with human language

- The ability to engage in fast-paced, conversational turn-taking is a core feature of human language
- When people are having a conversation, they rapidly take turns speaking and sometimes even interrupt. Now, researchers who have collected the largest ever dataset of chimpanzee "conversations" have found that they communicate back and forth using gestures following the same rapid-fire pattern.
- Human conversations are structured with fast-paced turns of just 200 milliseconds on average
- Found that the timing of chimpanzee gesture and human conversational turn-taking is similar and very fast, which suggests that similar evolutionary mechanisms are driving these social, communicative interactions

Chimp conversational turn taking

- Data on chimpanzee "conversations" across five wild communities in East Africa.

- Altogether, they collected data on more than 8,500 gestures for 252 individuals. They measured the timing of turn-taking and conversational patterns.

- They found that 14% of communicative interactions included an exchange of gestures between two interacting individuals.

Communicative turn-taking

- Report here that chimpanzees also engage in rapid signal-to-signal turn taking during face-to-face gestural exchanges with a similar average latency between turns to that of human conversation.
- This correspondence between human and chimpanzee face-to-face communication points to shared underlying rules in communication.

*** Animals with names

- Dolphins and parrots call one another by 'name' by imitating the signature call of the addressee.
- Elephant Study: approached 17 wild elephants and used a speaker to play calls specific to each of them. Although the elephants rarely reacted to the “names” of other animals, they quickly responded to their own.
- Elephants have been added to this name capacity list: using low, complex "rumbles”
- Dogs and cats respond to their names
- Elephants grieve for family members and friends, play throughout youth and into adulthood, and form close social networks.

*** Some of the first sewing needles, of various shapes and sizes, found at various sites in Eurasia.

The Role of Eyed Sewing Needles in the Expansion of Early Humans

- New book: *Climate, Clothing, and Agriculture in Prehistory: Linking Evidence, Causes, and Effects by Ian Gilligan*

- As humans expanded north, the fossil record shows how they became sheltered. No clothing has been preserved, but an increasing number of tools to make it have been found. At first, they were simple flakes to tear off and cut the hides, but later awls and burins emerged to make holes in them and sew them.
- But the truly great innovation, led by *Homo sapiens*, was eyed needles. With them, the first humans not only dressed to protect themselves even better from the cold; needles also allowed them to use the garments as a form of expression, as a culture.

Bone awls from Blombos Cave, southern Africa, discovered in Still Bay layers dated to approximately 73 to 70 Ka

Denisovan eyed needles

- Archaeological evidence indicates that eyed needles first appeared in southern Siberia about 40,000 years ago, followed by northern China between 35,000 and 30,000 years ago.

- At that time and in those latitudes, it was very cold. The Earth was going through the central portion of the last ice age.

- Three different species of humans lived at that time and were able to coexist: the Denisovans, the Neanderthals, and the Sapiens.

Denisovan needles

- It is in the Denisova cave complex, located in the Altai massif in Siberia, that the first needles were found.
- Opening a hole in a bone tool was a radical innovation: "Eyed needles made sewing more efficient, by combining two separate processes into one:
  - (i) the piercing of holes in hides and
  - (ii) the threading of sinew or fiber through the holes.

Ns: better thermal insulation.

- Original comparisons with current traditional societies suggest that Neanderthals used simpler garments, such as ponchos.
- However, the discovery of awls and burins in Neanderthal sites in southern Europe dating back more than 100,000 years suggests that they were also able to make garments by piercing and joining different hides, so that they fit the body better, thus achieving better thermal insulation.
- That is the key: adjusting clothing to the body as much as possible manages to better conserve human heat. And needles allowed humans to go further, with the construction of multiple garments: adding another layer almost doubles the insulation capacity.

Later in Africa

- There are no needles in previous human sites on the African continent, and there are hardly any at the time they appeared in Eurasia.

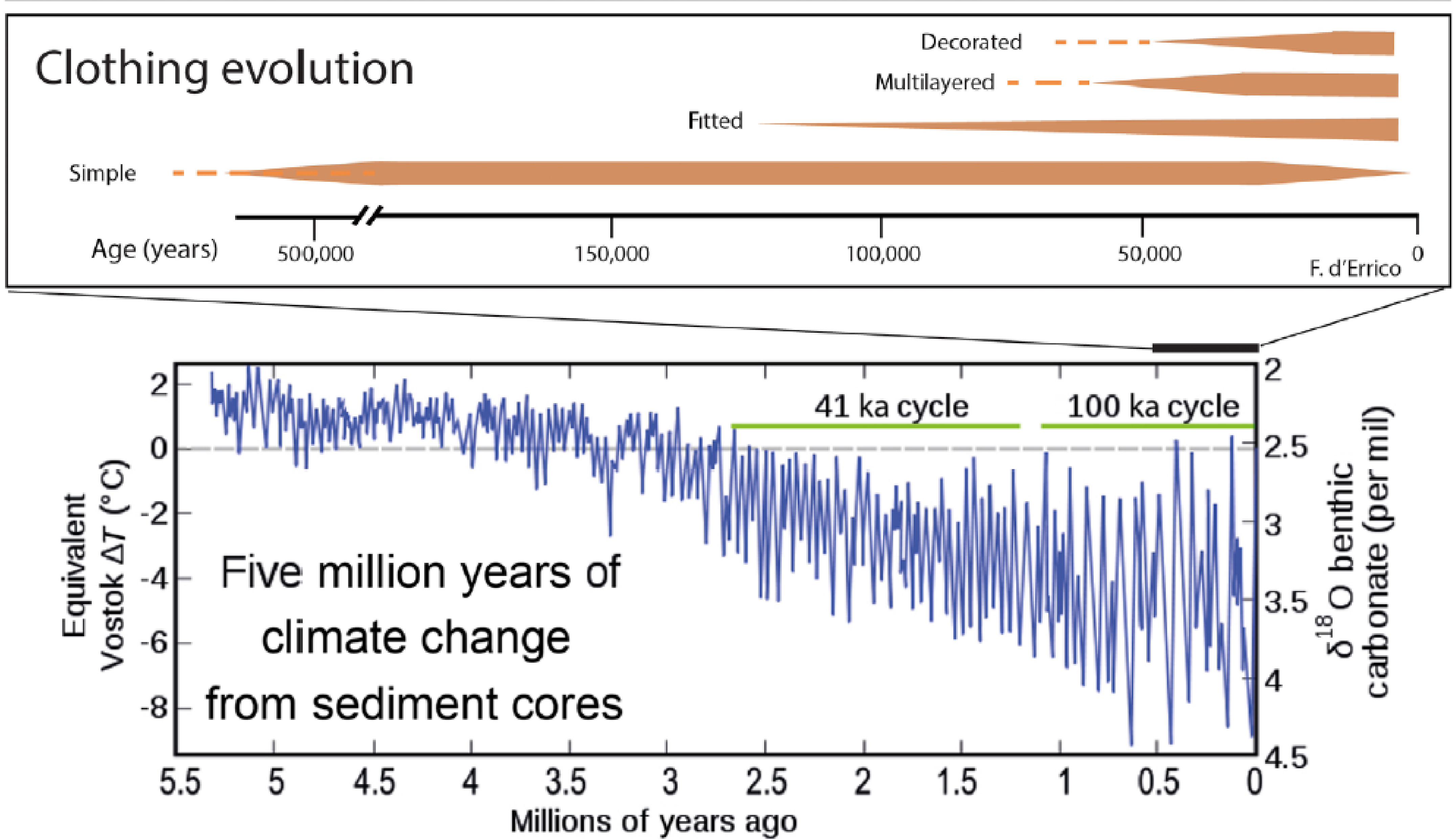
- Eyed needles did not reach Europe until several millennia later, with the emergence of the Solutrean culture in the south of present-day France and the north of the Iberian Peninsula, about 26,000 years ago. Again, the key must have been the climate.

- The main function of the earliest garments was thermal insulation. As early humans migrated from Africa and encountered colder climates, the need for protection from the elements became crucial for survival.

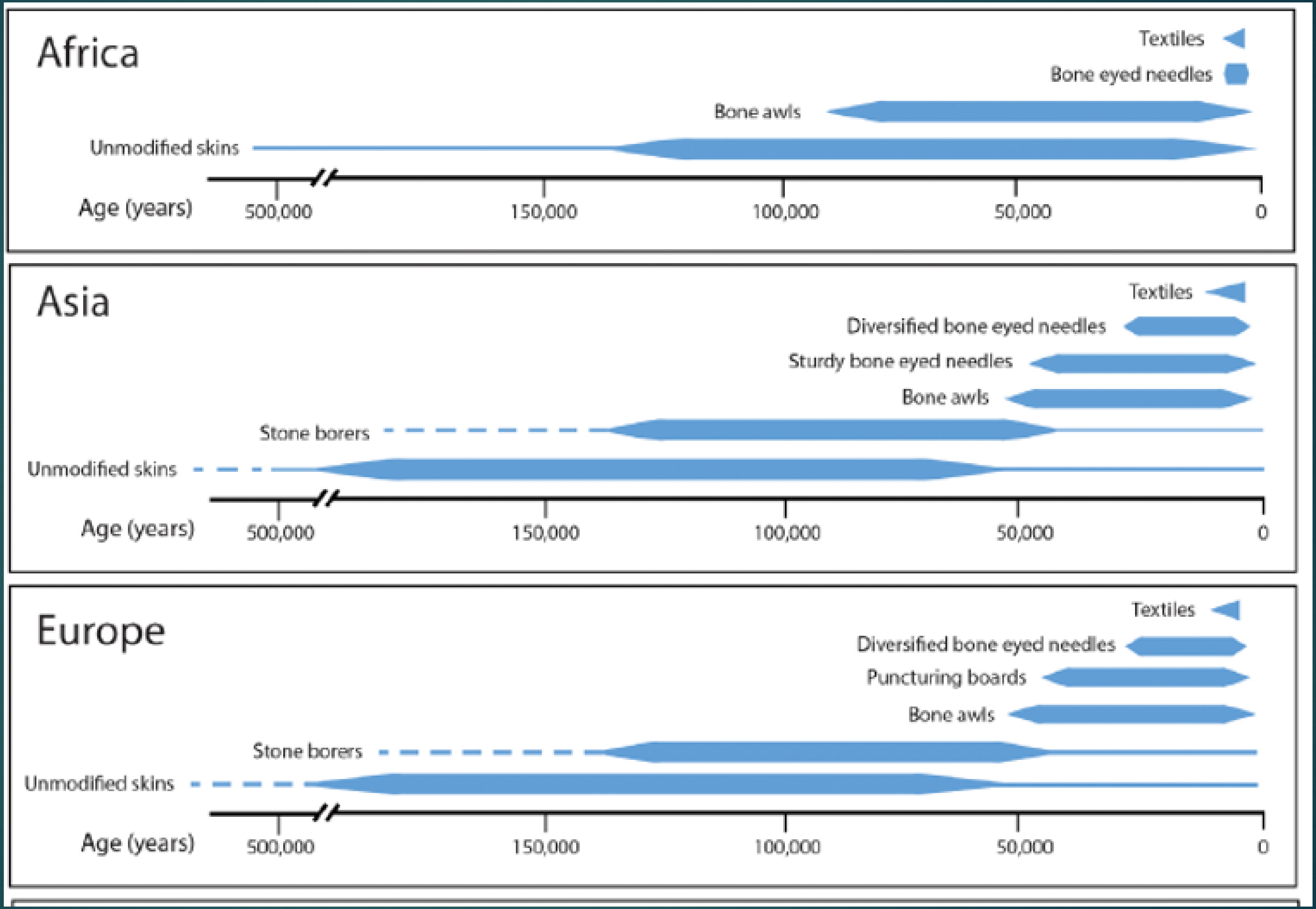
Underwear?

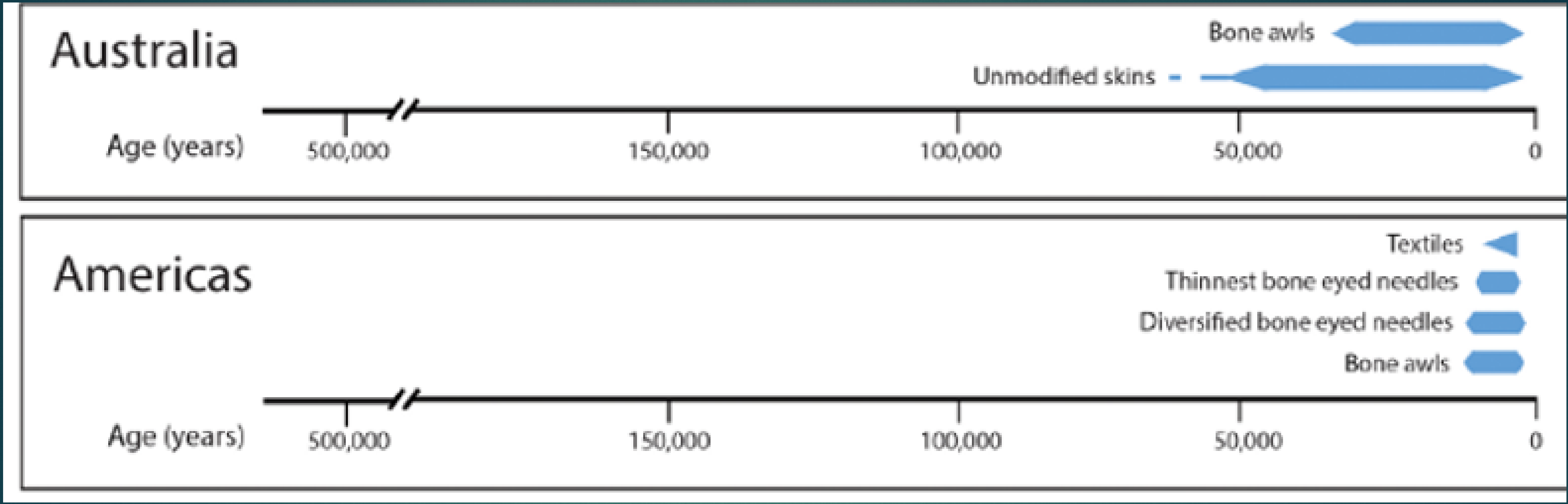
- Two major developments: the emergence of underwear in layered garment assemblages, and/or a transition in adornment from body modification to decorating clothes, as humans covered themselves more completely for thermal protection.
- Archaeological evidence for underwear is limited, but the Upper Paleolithic saw an increase in personal ornaments, some sewn onto clothing.
- Eyed needles may mark a pivotal shift as clothes acquired the social functions of dress, decoupling clothing from climate and ensuring its enduring presence.

Fig. 4. Puncture marks consistent with leather hole punching on a bone fragment at Canyars, Catalonia, dated to 39,600 cal B.P. Scale bars, 1 cm. Photos:


Clothing evolution
Decorated
Multilayered
Fitted
Simple
Age (years)
500,000
150,000
100,000
50,000
0
F. d'Errico
41 ka cycle
100 ka cycle
Five million years of
climate change
from sediment cores
Equivalent
Vostok ΔT (°C)
2
0
-2
-4
-6
-8
δ18O benthic
carbonate (per mil)
2
2.5
3
3.5
4
4.5
5.5
5
4.5
4
3.5
3
2.5
2
1.5
1
0.5
0
Millions of years ago

Evolution of Clothing




Australia
Bone awls
Unmodified skins
Age (years)
500,000
150,000
100,000
50,000
0
Americas
Textiles
Thinnest bone eyed needles
Diversified bone eyed needles
Bone awls
Age (years)
500,000
150,000
100,000
50,000
0

*** The archaeology of orality: Dating Tasmanian Aboriginal oral traditions to the Late Pleistocene = > 12,000 years of oral tradition

- Aboriginal people have lived in Australia, continuously, for tens of thousands of years. Over that time, they developed complex knowledge systems that were committed to memory and passed to successive generations through oral tradition. In recent years, scientists have weighed into the debate by studying traditions that describe natural events, such as volcanic eruptions and meteorite impacts, which can be dated using scientific techniques.

Duane Hamacher , et al., 2023

Orality

- Tasmanian Aboriginal (palawa) oral traditions that were recorded in the early nineteenth century. These traditions describe
  - the flooding of the Bassian Land Bridge connecting Tasmania to mainland Australia and the
  - presence of a culturally significant "Great South Star", identified as Canopus (α Carinae).

- 1 - Estimate the Bassian Land Bridge was finally submerged approximately 12,000 years ago.

Orality of 2 historical events

- 2 - Calculated the declination of the star Canopus over the last precessional cycle (26,000 years) to show that it was at a far southerly declination between 16,300 and 11,800 years ago, reaching its minimum declination approximately 14,000 years ago.

- These lines of evidence provide a terminus ante quem (latest possible date for something) of the Tasmanian traditions to the end of the Late Pleistocene (11,7 Ka).

- This paper supports arguments that the longevity of orality can exceed ten millennia,

Oral traditions can survive for an immense time period

- Estimate the antiquity of Aboriginal oral traditions, calculating a terminus ante quem to the end of the Late Pleistocene, some 11,960 years BP, with a more general age range of between 12 and 14 millennia BP.

- Conclude that these oral traditions, if they are accurate representations of experienced natural events, originated before 11,800 years BP.. This analysis indicates that Tasmanian oral traditions as some of the oldest recorded narratives in the world, supporting arguments that oral traditions can be passed to successive generations on timescales exceeding ten millennia while maintaining vitality.

*** Archaeological evidence of an ethnographically documented Australian Aboriginal ritual dated to the last ice age

- In societies without writing, ethnographically known rituals have rarely been tracked back archaeologically more than a few hundred years.

- At the invitation of GunaiKurnai Aboriginal Elders, we undertook archaeological excavations at Cloggs Cave in the foothills of the Australian Alps. In GunaiKurnai Country, caves were not used as residential places during the early colonial period (mid-nineteenth century CE), but as secluded retreats for the performance of rituals by Aboriginal medicine men and women known as 'mulla-mullung', as documented by ethnographers.

Bruno David, et al., 2024

11-12 Ka fireplaces with wooden stick

- Here we report the discovery of buried 11,000- and 12,000-year-old miniature fireplaces with protruding trimmed wooden artefacts made of Casuarina wood smeared with animal or human fat, matching the configuration and contents of GunaiKurnai ritual installations described in nineteenth-century ethnography.

- These findings represent 500 generations of cultural transmission of an Ethnographically documented ritual practice that dates back to the end of the last ice age and that contains Australia's oldest known wooden artefacts.

12,000-Year-Old Cultural Practices Discovered in Australia

- A remarkable discovery in southeastern Australia has unveiled archaeological evidence of what may be the oldest known culturally transmitted human ritual.
- Sticks found preserved in fireplaces within a cave, dating back to the end of the Last Ice Age, suggest that a ritual intended to cure or harm has been passed down through approximately 500 generations.

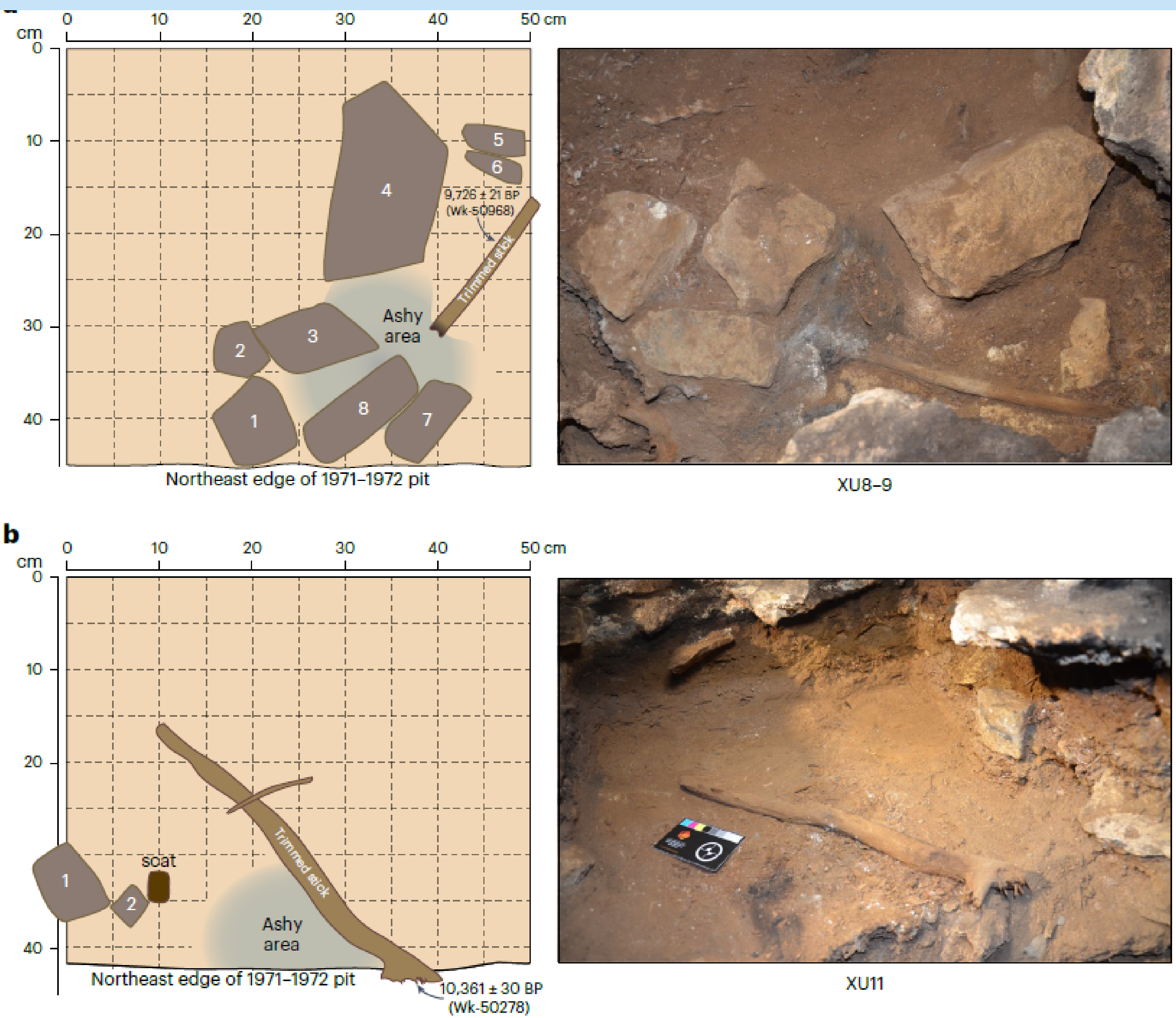


Fig. 2 | The two miniature fireplaces with trimmed sticks immediately after they were exposed by excavation in Cloggs Cave square R31, with the sticks' bases not yet separated from the sediments in which they sit. **a**, The installation from XU8–9 (SU4D) dates to 10,720–12,420 cal BP (Bayesian-modelled age). **b**, The installation from XU11 (SU4E) dates to 11,420–12,950 cal BP (Bayesian-modelled age).

Unique fireplaces and sticks

- The absence of animal food remains in or near each of the two fireplaces at Cloggs Cave square R31, their small size, the presence in each of a single straight, trimmed Casuarina stick only fleetingly burnt at a low temperature, and each stick having come into contact with animal or human fatty tissue and all indicate a peculiar design.
- These shared features suggest that each fireplace installation was uniquely crafted for purposes other than cooking or heating.

Aboriginal men and women ‘of High Degree’

- Nineteenth-century ethnography provides a good description of the function of such fireplaces.
- Published details of the ritual practices of the GunaiKurnai and neighboring groups from southeastern Australia. He documented the activities of individuals referred to as ‘sorcerers’, ‘wizards’ or medicine men and women, who performed magic on their victims or healed the dying—what anthropologist Adolphous P. Elkin later called Aboriginal men and women ‘of High Degree’.

Ritual spells

- Ritual spells cast on victims were conducted in secluded places, away from prying eyes.

- Howitt described how magic was employed to harm a victim using a ritual fire and a wooden object smeared or attached with a piece of human or animal fat (major sources of lipids).

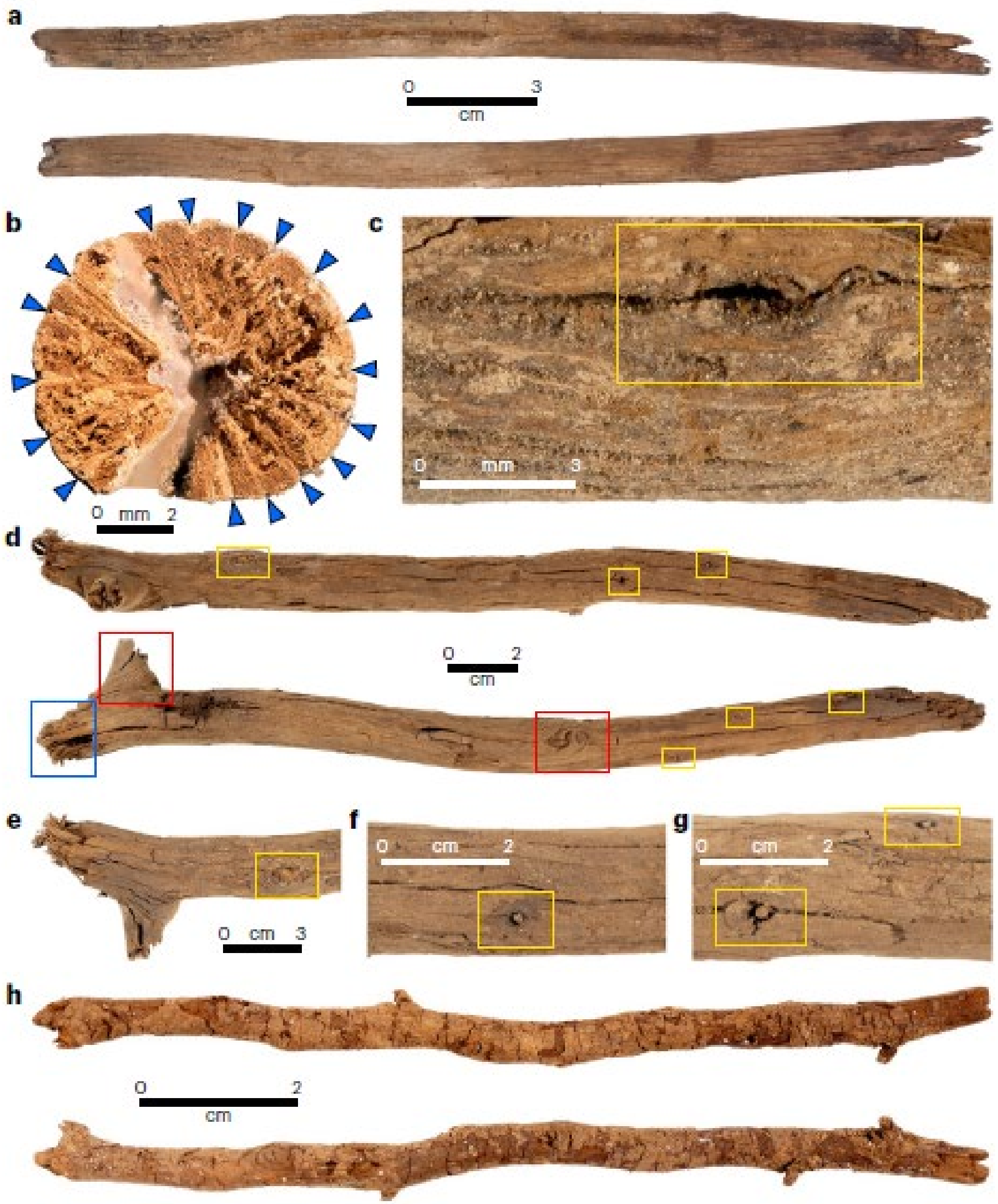


Fig. 4 | The three largest pieces of wood from the two miniature fireplaces at Cloggs Cave, showing details of the two trimmed sticks. a, The trimmed stick from the XU8–9 fireplace. **b**, End view of the XU8–9 trimmed stick, showing the

fibrous end was broken from the tree. The red rectangles show larger twigs that were trimmed or broken off. The yellow rectangles show small twig junctions cut or scraped off flush with the stem, creating a smooth shaft on the stick. **e**, Torn fibrous

Conclusion

- The wooden artefacts reported here are Australia's oldest, joining a unique array of wooden artefacts from a peat layer at Wyrie Swamp (South Australia).
- The close similarities between the Cloggs Cave miniature fires and their trimmed, lipid (animal or human fat)-smeared wooden sticks and mid-nineteenth-century ethnographic descriptions,
  - signal the continuity of ethnographically known practices from parallel antecedents dating back some 12,000 years to the end of the last ice age

12,000 years of transmitted knowledge

- In this light, we have found an exceptional convergence of factors—t
  - he rare preservation of wooden items, both of Casuarina and
  - juxtaposed or smeared with animal or human fatty substances;
  - the repeated construction of near-identical miniature fireplace installations built and used circa 1,000 years apart;
  - the extraordinary preservation of the final state of a ritual act;
  - and GunaiKurnai ethnographies that describe ritual installations akin to those found in the archaeology.

- This unique combination indicates the transmission of a very specific local cultural practice over 12,000 years. These findings are not about the memory of ancestral practices, but of the passing down of knowledge in virtually unchanged form, from one generation to the next, over some 500 generations.

*** Neandertal DNA and autism

- Certain genetic traits inherited from Neanderthals may significantly contribute to the development of autism.

- Specific Neanderthal genetic variants can influence autism susceptibility, suggesting a link between Ns and modern neurodevelopmental conditions.

- The researchers found that autistic individuals had a higher prevalence of rare Neanderthal-derived genetic variants compared to non-autistic controls.

Pauly, R., Johnson, L., Feltus, F. A., & Casanova, E. L. (2024).

Autism and N genes

- Ethnic differences: These rare variants, which occur in less than 1% of the population, were significantly enriched in the genomes of autistic individuals across three major ethnic groups: Black non-Hispanic, white Hispanic, and white non-Hispanic.
- "Our results are a little more nuanced than 'autistic people are just more Neanderthal.' We've found that autistic people, on average, have more rare Neanderthal variants, not that they have more Neanderthal DNA in general."
- These Neanderthal-derived variants are also occurring in people, especially family members, without autism.

N genes

- Also links certain Neanderthal variants to traits such as epilepsy, intellectual disability, language delay, and language regression

- It suggests that our tendency to 'whitewash' genetics and ignore variants that aren’t implicated across all genetic backgrounds means that we’re missing out on a lot of important genetic factors.

- Only looked at protein-coding genes (known as the exome), Need to do autosome next.

*** Wild Chimpanzees Found To Treat Illnesses With Medicinal Plants

- Chimpanzees consume plants with medicinal properties to treat their ailments, suggesting self-medication behaviors.
- Chimpanzees afflicted with illness consume tree bark, dead wood, and ferns known for their antibiotic and anti-inflammatory properties.
- The authors of the present study combined behavioral observations of wild chimpanzees (*Pan troglodytes*) with pharmacological testing of the potentially medicinal plants they eat.

Chimp medicines

- They monitored the behavior and health of 51 chimpanzees from two habituated communities in the Budongo Central Forest Reserve in Uganda.
- Next, they collected plant extracts from 13 species of trees and herbs in the reserve that they suspected the chimpanzees might be using to self-medicate, and tested them for their anti-inflammatory and antibiotic properties.
- These included plants that they observed sick or injured chimpanzees eating, but were not part of their normal diet, and plants that previous research has suggested chimpanzees might consume for their medicinal properties

Pharmacological and behavioral investigation of putative self-medicative plants in Budongo chimpanzee diets

- The researchers discovered that 88% of the plant extracts inhibited bacterial growth, while 33% had anti-inflammatory properties.

- Dead wood from a tree in the Dogbane family showed the strongest antibacterial activity and also had anti-inflammatory properties, suggesting that it could be used to treat wounds. Bark and resin from the East African mahogany tree and leaves from a fern exhibited potent anti-inflammatory effects.

Elodie Freymann,, et al., 2024

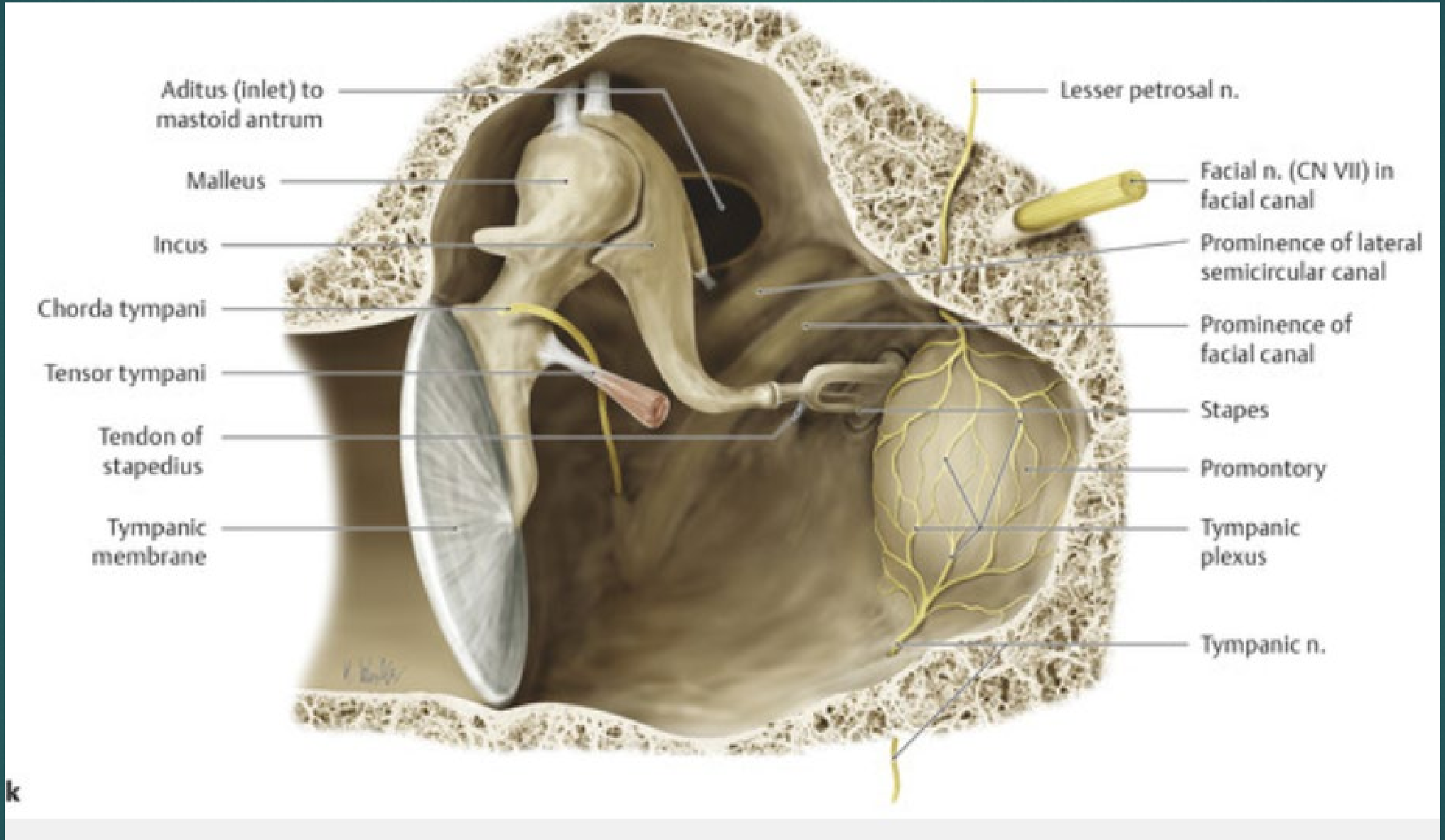
Self medication

- The researchers observed a male Chimpanzee with an injured hand seek out and eat leaves of the fern, which may have helped to reduce pain and swelling. They also recorded an individual with a parasitic infection consuming the bark of the cat-thorn tree.

- The results suggest that chimpanzees seek out specific plants for their medicinal effects.

- The study is one of the first to provide both behavioral and pharmacological evidence of the medicinal benefits to wild chimpanzees of feeding on bark and dead wood.

*** Inner ear in petreous bone of temporal bone: evidence of N caregiving



Neandertal Caregiving

The child who lived: Down syndrome among Neanderthals?

- Caregiving for disabled individuals among Neanderthals has been known for a long time.
- Study: presents the case of a Neanderthal child who suffered from a congenital pathology of the inner ear, probably debilitating, and associated with Down syndrome. This child would have required care for at least 6 years, likely necessitating other group members to assist the mother in childcare.
- When a CT scan of the small fragment of the temporal lobe , the bone where the inner ear is located, was done, they reconstructed the inner ear that showed five abnormalities associated with Down syndrome, which had never been detected before in a Neanderthal,

Mercedes Conde-Valverde, et al., 2024

Fossil CN-46700: right petromastoid portion of a temporal bone.

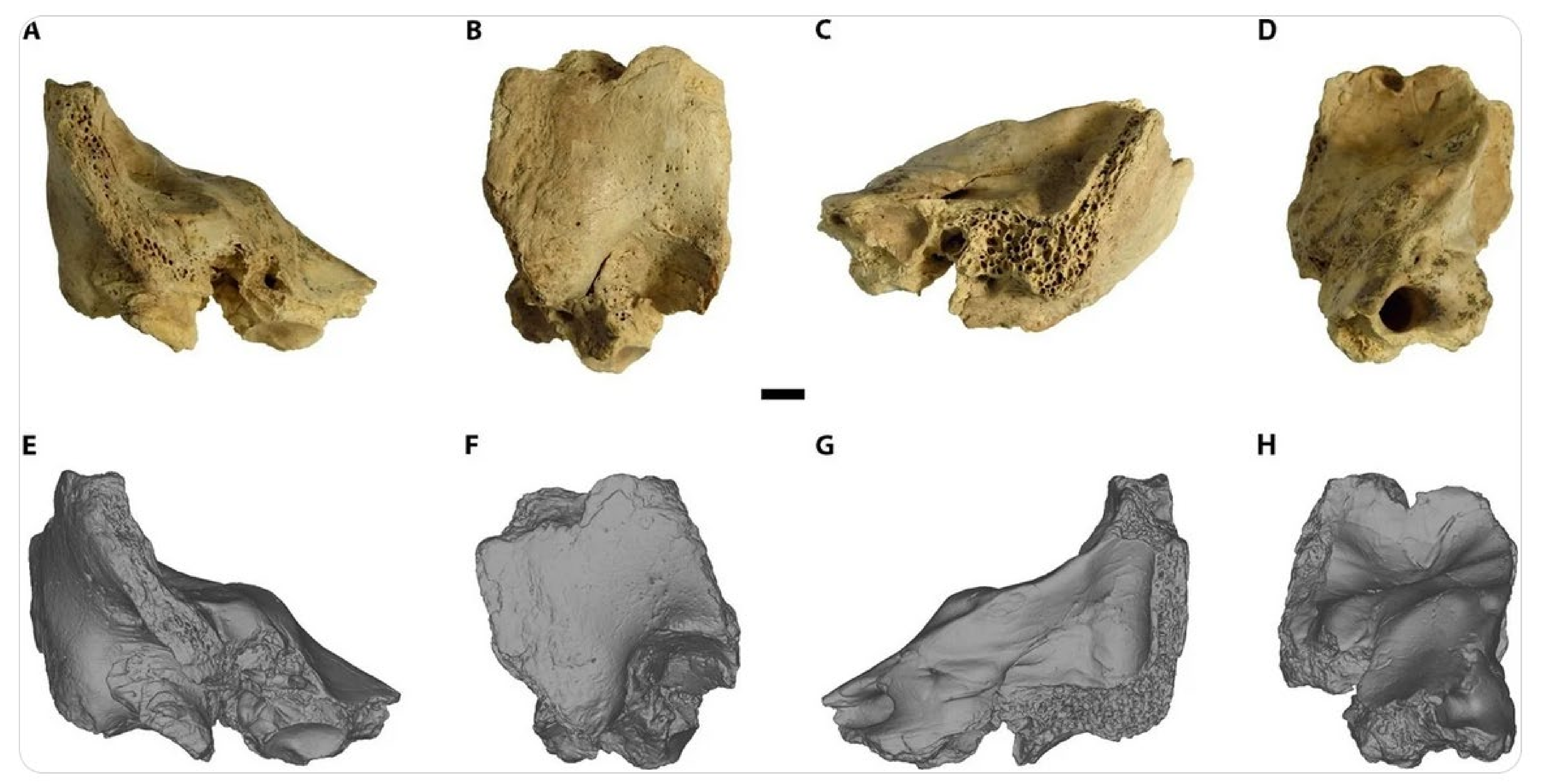
Severe inner ear pathology

- New fossil evidence of a Neanderthal child suffering from a severe inner ear pathology, most likely associated with the presence of Down syndrome.
- The symptoms produced by this pathology would have included, at a minimum, severe hearing loss and markedly reduced sense of balance and equilibrium.

Ear pathology

- Lateral Semicircular Canal (LSC) dysplasia is most commonly associated with sensorineural or mixed (sensorineural and conductive) hearing loss in addition to vestibular symptoms such as loss of balance and severe vertigo.
- In summary, the set of pathologies present in CN-46700 produced a lifelong symptomatology that would include severe hearing loss, and frequent crises of acute disabling vertigo and imbalance.

Original fossil and 3D model of CN-46700



Down syndrome

- The only syndrome that is compatible with the entire set of malformations present in CN-46700 is Down syndrome, where Lateral Semicircular Canal (LSC) dysplasia is common,

- Other malformations present in CN-46700 are also common in Down syndrome, such as a hypoplastic ASC and a small cochlea. The association between LSC dysplasia and the presence of a reduced vestibule has only been reported in individuals with Down syndrome

New case of Neanderthal care: a N child with Down syndrome

- Thus, the care necessary for their survival over a period of several years likely exceeded the capabilities of the mother and would have required the help of other members of the social group. This is a known case in Neanderthals of social care for a child with a severe pathology.
- As a reference, keep in mind that life expectancy at birth for children with Down syndrome was 9 years at the beginning of the 20th century. That individual required continuous care from other members of the group, in addition to that provided by his mother. And he did not have the possibility of returning the assistance received, or perhaps he did, in the form of affection and love.

Prosocial behaviors in N

- Debate: Some authors believe that caregiving took place between individuals able to reciprocate the favor, while others argue that caregiving was produced by a feeling of compassion related to other highly adaptive prosocial behaviors. Children have a very limited possibility to reciprocate the assistance. This may be a form of evidence.

- The recent study of the El Sidrón skeleton of a Neanderthal individual aged 6 to 7 years at death indicates an overall growth rate in Neanderthals similar to that of modern human children

CN-46700 from Cova Negra, Spain, 276-243 Ka

- The fossil analyzed is CN-46700, a fragment of the right petromastoid portion of a temporal bone.
- It comes from Cova Negra (Xàtiva, Spain), is dated between 276-143 ka, and identified as *Homo neanderthalensis* . The combination of the different malformations that the bone presents indicates that the individual had Down syndrome.
- This child would have problems in his physical and cognitive growth. Psychomotor development would be affected due to generalized hypotonia, ligamentous hypermobility, and poor postural control, balance, and locomotion. He would have had problems in speech acquisition, exploratory learning, and the development of communication and social skills.

"Tina"

- The ear problems would have caused deafness, vertigo and imbalance. Additionally, generalized hypotonia causes more than 80% of babies with Down syndrome to have sucking problems during breastfeeding.
- The dimensions of the petromastoid canal also vary with age, and the value in CN-46700 (0.29 mm wide) corresponds to an age of death of older than 6 years according to recent human standards
- In his more than 6 years of life, that Neanderthal child would probably require other members of the group to help the mother in caring for him. This child was nicknamed Tina, although her sex cannot be determined.

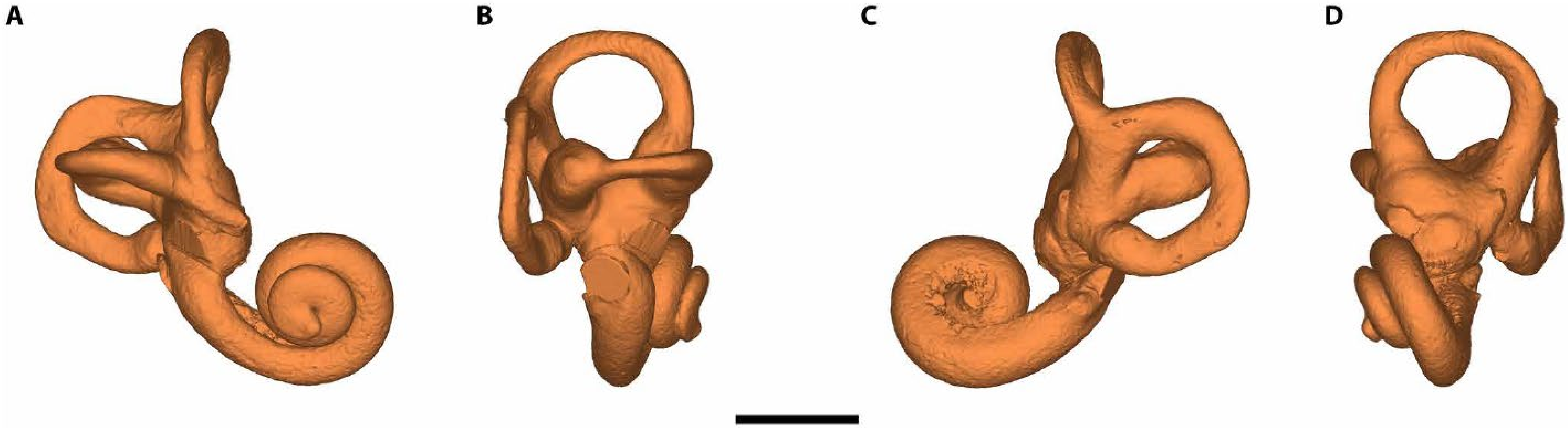


Fig. 2. 3D model of the inner ear of CN-46700. (**A**) Anterior view. (**B**) Lateral view. (**C**) Posterior view. (**D**) Medial view. Scale bar, 5 mm.

Prior burials of Down’s Syndrome ancients

- Genetic evidence of six cases of trisomy 21 (Down syndrome) in childhood or perinatal individuals among 9,855 prehistoric and historical human genomes from around the world had previously been published.

- All of these individuals received funerary rituals and careful burials, in some cases with exceptional objects, indicating recognition as members of the community, in contrast to the most common funerary practices of their time, which were cremation.

Altruism

- Consequently, all available evidence suggests that the CN-46700 individual probably had Down syndrome. Their survival appears to be based purely on the altruism of the adults around them.

- It is therefore notable that the individual represented by fossil CN-46700 lived to at least 6 years of age, which far exceeds the usual life expectancy of children with Down syndrome in prehistoric population. All other known MH Down's fossils were less than 16 months. A case is known of a chimpanzee with Down syndrome that survived to 23 months of age.

Down life expectancy

- In 1929, the life expectancy of children with Down syndrome, which was only 9 years, increased to 12 years in the 1940s and now exceeds 60 years in developed countries.

- Given the chronic nature of their impairments, the individual represented by CN-46700 would have required continuous and important care, beyond the normal care when child is helpless, throughout their life.

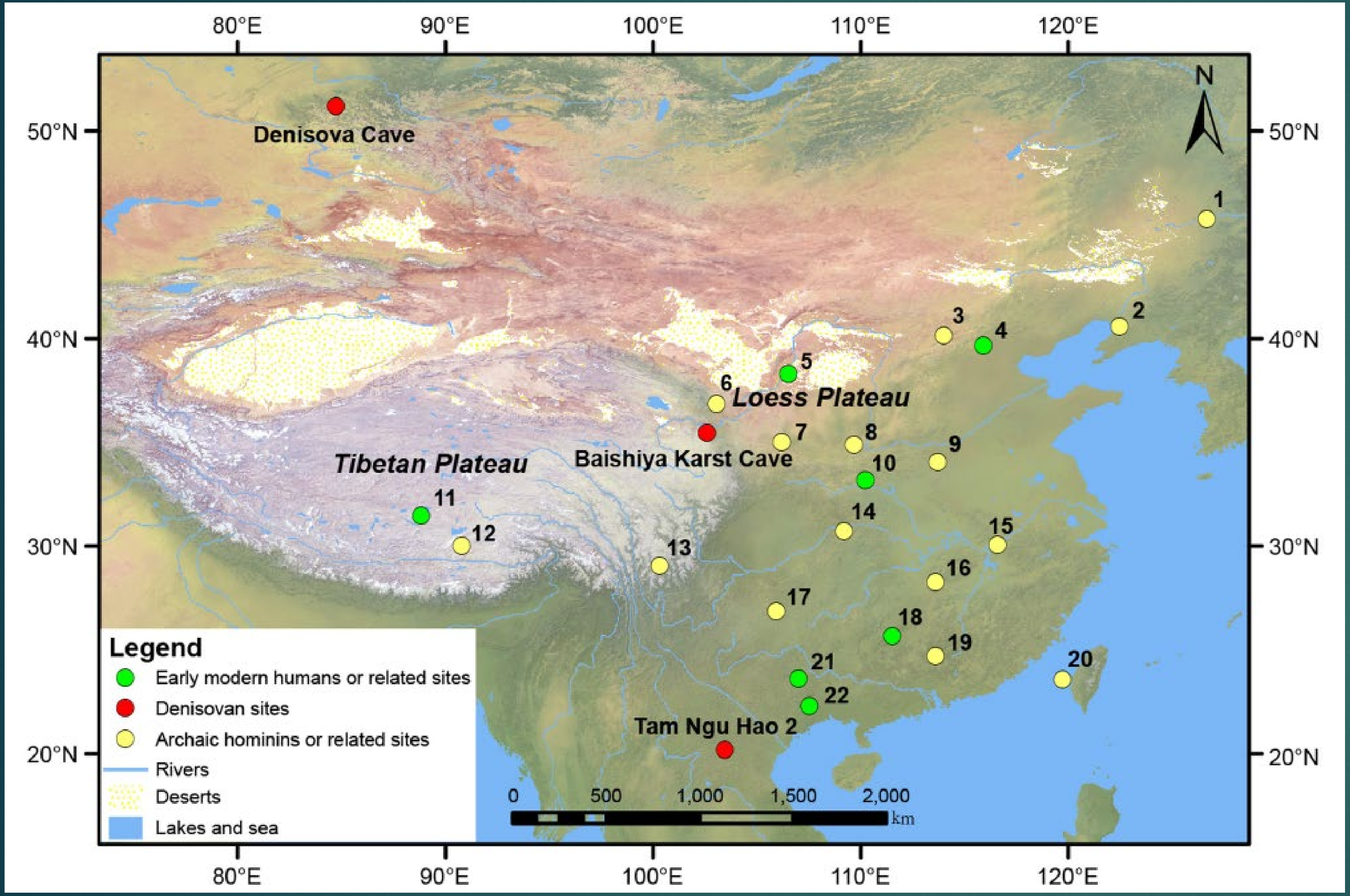
Caregiving pattern

- Because of the demanding lifestyle of Neanderthals, including high levels of mobility, it is difficult to think that the mother of the individual would have been able to provide such care alone and also carry out normal daily activities over a prolonged period of time.

- It is likely, therefore, that the mother required the continuous help of other members of the social group, either for assistance in performing other daily tasks (or to relieve her from performing them) or to directly assist in providing the necessary care for the child, or both.

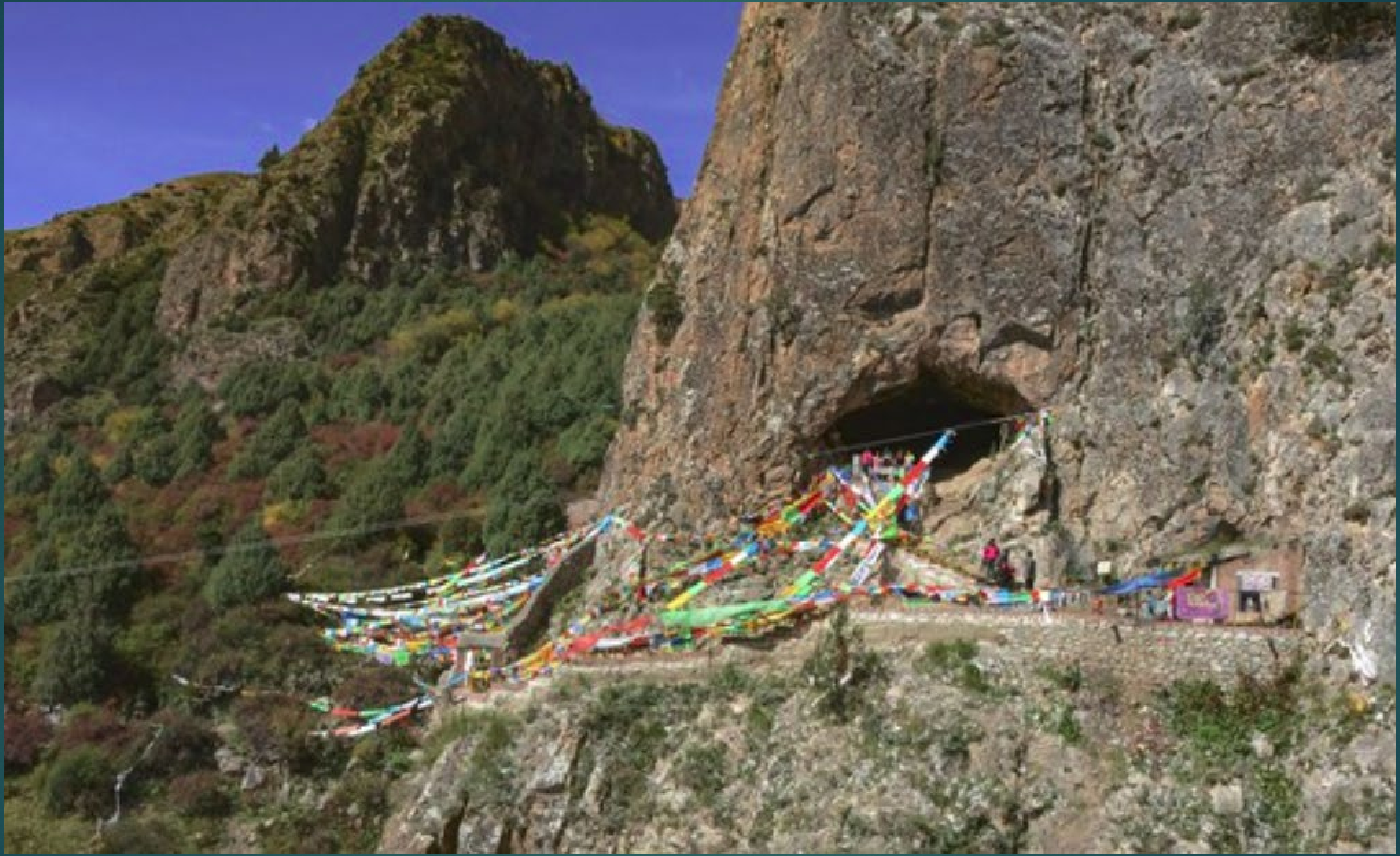
Caregiving as an ancestral trait

- Last, the evidence provided by CN-46700 is fully compatible with the idea previously advocated by other authors that caregiving and collaborative parenting occurred together in Neanderthals and that both prosocial behaviors were part of a broader social adaptation of high selective value that must have been very similar to that of our species.
- Moreover, the presence of this complex social adaptation in both Neanderthals and our own species suggests a very ancient origin within the genus Homo



Late Middle and Late Pleistocene sites in East Asia. The numbers represent archaeological sites and/or hominin fossils as follows: 1. Harbin cranium; 2. Jinniushan; 3. Xujiayao; 4. Tianyuan cave; 5. Shuidonggou Locality 1 and 2; 6. Jiangjunfu 01; 7. Yangshang; 8. Dali; 9. Lingjing; 10. Huanglong Cave; 11. Nwya Devu; 12. Quesang; 13. Piluo; 14. Xinglong Cave; 15. Hualongdong; 16. Tongzi; 17. Guanyindong; 18. Fuyan Cave; 19. Maba; 20. Penghu 1; 21. Lunadong; 22. Zhirendong (Zhiren Cave).

Karst Baishiya cave in Xiahe, China



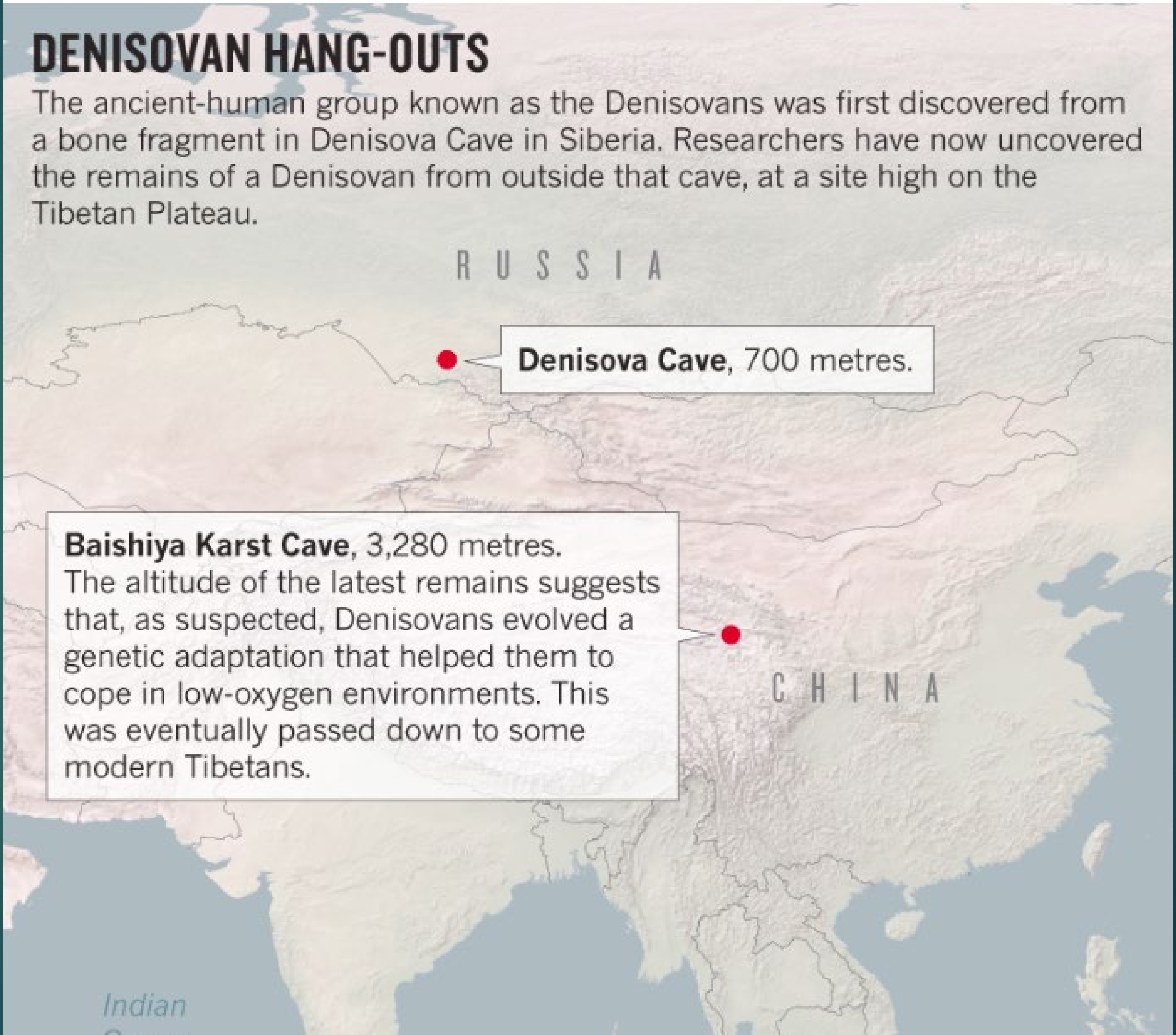
The Baishiya Karst Cave above the Jiangla riverbed in the Gansu province of China.
It is both a locally famous Buddhist cave and a tourist site.

Karst Baishiya cave

Baishiya Karst Cave is located on the cliffs bordering the Ganjia Basin.

Chen, et al., 2019

Finally, the mandible of a Denisovan!



DENISOVAN HANG-OUTS

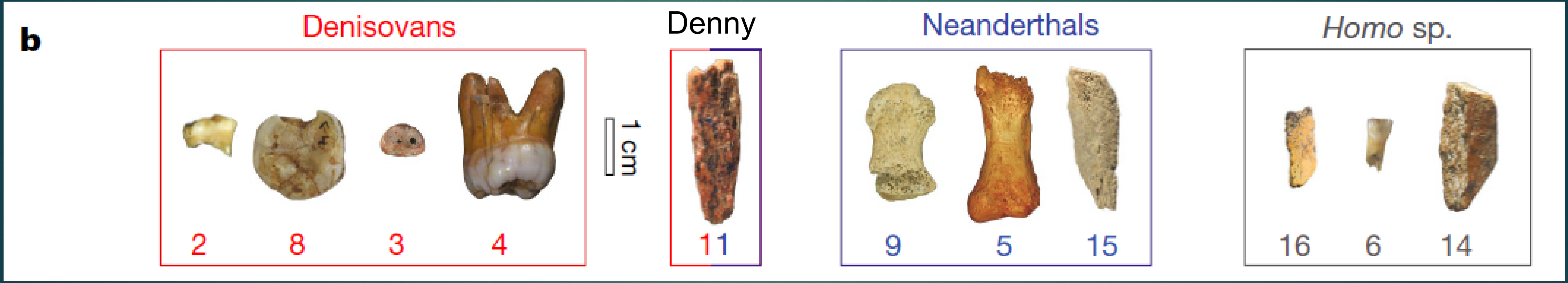
The ancient-human group known as the Denisovans was first discovered from a bone fragment in Denisova Cave in Siberia. Researchers have now uncovered the remains of a Denisovan from outside that cave, at a site high on the Tibetan Plateau.

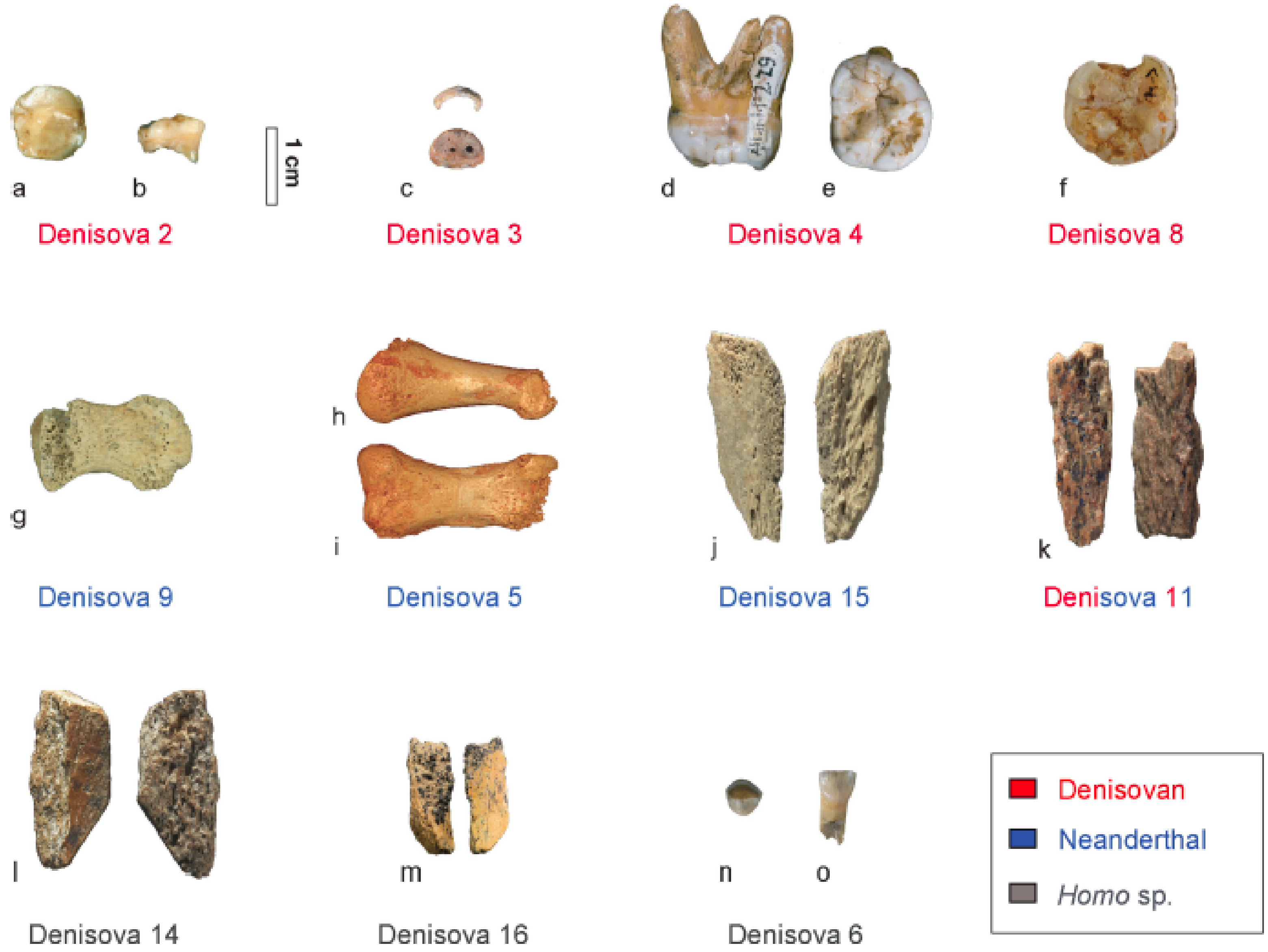
Denisova Cave, 700 metres.

Baishiya Karst Cave, 3,280 metres. The altitude of the latest remains suggests that, as suspected, Denisovans evolved a genetic adaptation that helped them to cope in low-oxygen environments. This was eventually passed down to some modern Tibetans.

Denisova Cave

Current 11 Denisova specimens numbering





Extended Data Fig. 1 | Human remains from Denisova Cave. Red labels indicate Denisovans; blue labels indicate Neanderthals; and grey labels indicate *Homo* sp. bones that have not been assigned to a group. Denisova 11 is shown in red and blue. A further, unpublished Denisovan specimen (Denisova 13) is mentioned in the Supplementary Information, section 3. **a**, **b**, Denisova 2 in occlusal (**a**) and lingual (**b**) views. **c**, Denisova 3 in proximal view. **d**, **e**, Denisova 4 in mesial (**d**) and occlusal (**e**) views. **f**, Denisova 8 in occlusal view. **g**, Denisova 9 in palmar view. **h**, **i**, Renderings based on micro-computed tomography of Denisova 5 in lateral (**h**) and plantar (**i**) views. **j**, Denisova 15. **k**, Denisova 11. **l**, Denisova 14. **m**, Denisova 16. **n**, **o**, Denisova 6 in occlusal (**n**) and lingual (**o**) views.

D #6 = Denisovan jaw, 160 Ka, Tibet, 10,000 feet

Xiahe half mandible

The Xiahe mandible (a, b, d, e, views after digital removal of the adhering carbonate matrix).

No chin

*** The Ancient Human Genome of Denisovans: A New D Genome

- A remarkable study has brought to light the most ancient human genome sequenced to date, belonging to a Denisovan male from 200,000 years ago. Based on a molar discovered at Denisova Cave; 24-fold coverage. The 2nd D genome.

- The unveiling of the Denisovan genome, the oldest high-quality human genome yet, surpasses the previous record held by a 120,000-year-old Neanderthal at Denisova. The first Denisovan genome was obtained from a girl's pinkie finger bone, dated between 60,000 to 80,000 years ago, found in Denisova Cave in the Altai Mountains of Siberia.

Stéphane Peyrégne at the annual meeting of the Society for Molecular Biology and Evolution in Puerto Vallarta, Mex

4th Denisovan lineage

- The newly sequenced male originates from a distinct population of early Denisovans that interbred multiple times with a previously undetected Neanderthal group.
- The DNA analysis revealed that the male Denisovan had inherited 5% of his genome from an ancient, previously unknown Neanderthal population.
- This male, labeled Denisova 25, came from a different D population than the girl, known as Denisova 3, whose DNA is more closely related to Denisovan sequences found in living modern humans

New N and D lineages

- These findings suggest that the older male's population was eventually replaced in the cave by later Denisovans. The data also indicate that the male Denisovan's ancestors interbred multiple times with Neanderthals.

- Evidence from a Neanderthal fossil dated to about 120,000 years ago supports the idea that Neanderthals temporarily replaced Denisovans in the cave, but by 60,000 years ago, Denisovans had returned.

Ns and Ds

- The Altai region appears to have been a significant crossroads for various human species. DNA from a bone fragment of a female over 50,000 years old shows her mother was a Neanderthal and her father a Denisovan. Later, both Denisovan and Neanderthal DNA and fossils indicate that modern humans occupied the cave, and Denisovans and Neanderthals eventually disappeared.

- Despite interbreeding, Denisovans and Neanderthals maintained distinct lineages. They diverged from a common ancestor at least 400,000 years ago, with Neanderthals settling in Europe and the Middle East, while Denisovans moved east into Asia.

- There, Denisovans evolved separately, acquiring roughly 300,000 genetic changes that differentiate them from Neanderthals.

Superarchaic DNA

- Issue of the potential presence of DNA from an even older, unidentified human species, possibly *Homo erectus*, in the Denisovan genome.
- Peyrégne confirmed that if any such "superarchaic" ancestry exists, it would be shared between Denisova 3 and Denisova 25.

Middle and Late Pleistocene Denisovan subsistence at Baishiya Karst Cave

- Denisovans were once widely distributed across eastern Eurasia. Despite limited archaeological evidence, this indicates that Denisovans were capable of adapting to a highly diverse range of environments.

- This study integrates zooarchaeological and proteomic analyses of the late Middle to Late Pleistocene faunal assemblage from Baishiya Karst Cave on the Tibetan Plateau, where previously a Denisovan mandible and Denisovan sedimentary mitochondrial DNA were found.

Huan Xia, et al, 2024

New D rib at 48-32 Ka

- Examined a pair of holes six feet down into the cave floor.
- Using zooarchaeology by mass spectrometry, we identify a new hominin rib specimen that dates to approximately 48–32 thousand years ago (layer 3).
- Shotgun proteomic analysis taxonomically assigns this specimen to the Denisovan lineage, extending their presence at Baishiya Karst Cave well into the Late Pleistocene.

Excavations at Baishiya Karst Cave on the Tibetan Plateau, where Denisovans lived for over 100,000 years, hunting or scavenging a wide range of animals that continue to live in the area.

Denisovans from 48 to 32 Ka

- Throughout the stratigraphic sequence, the faunal assemblage is dominated by Caprinae/goats, together with megaherbivores, carnivores, small mammals and birds.

- The high proportion of anthropogenic modifications on the bone surfaces suggests that Denisovans were the primary agent of faunal accumulation.

- The chaîne opératoire of carcass processing indicates that animal taxa were exploited for their meat, marrow and hides, while bone was also used as raw material for the production of tools.

The Denisovans and Baishiya Karst Cave (BKC)

- On the basis of the Denisovan genetic ancestry present in several East, South and Southeast Asian populations, it is inferred that Denisovans were widespread in eastern Eurasia during the Late Pleistocene.
  - The Xiahe mandible (named Xiahe 1) and
  - Denisovan sedimentary mitochondrial DNA (mtDNA) samples
  - from Baishiya Karst Cave (hereafter, BKC; 10,700 feet above sea level) in Ganjia Basin on the northeastern Tibetan Plateau

- Together, they show that Denisovans occupied BKC from at least 160 thousand years ago (ka) to around 60 ka, and possibly up to around 45 ka.

BKC

- Archaeological excavations at BKC have revealed a well-preserved stratigraphy containing a rich lithic and faunal assemblage, which provides evidence of hominin occupation from at least around 190 ka to about 30 ka

- Study: zooarchaeology by mass spectrometry (ZooMS) analysis of 1,857 bone and dental specimens from BKC. By combining morphological and ZooMS identifications, we taxonomically identify 2,005 (78.1%) of the analyzed 2,567 faunal specimens

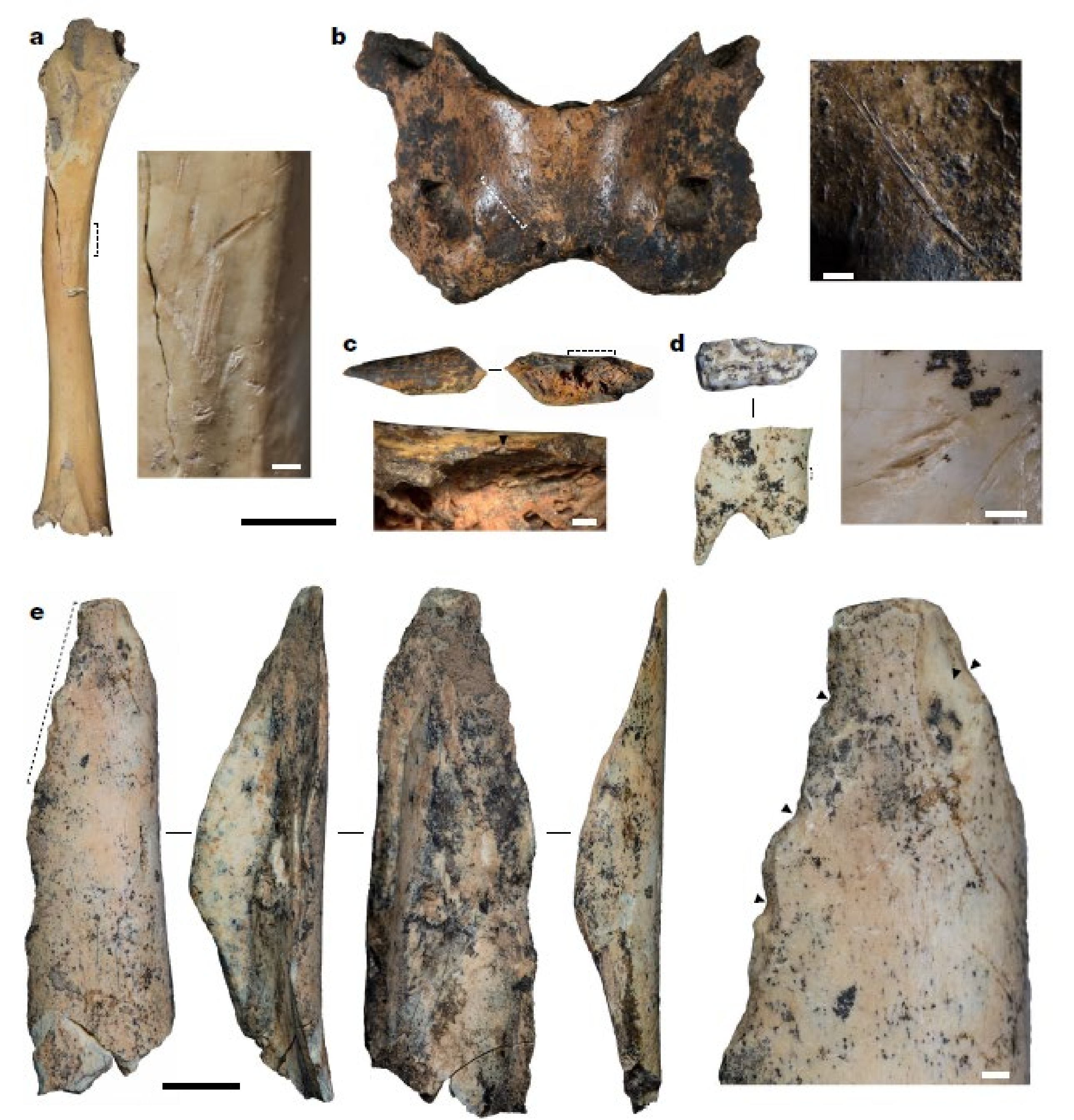
Lots of goats

- Results show that goats dominate the faunal assemblage. The high proportion of bovids—goats, blue sheep, wild yak and Tibetan gazelle and horses throughout the stratigraphy reveals a grass-dominated landscape in the Ganjia Basin during the late Middle and Late Pleistocene.

- Also small-scale mosaic forest-shrub habitats.– red and musk deer, porcupine; and carnivores: hyena, wolf, fox, snow leopard, eagle

Hominins were the primary accumulators

- A larger proportion of the faunal assemblage exhibits evidence of anthropogenic modifications (n = 386, 19.3%). Most of these specimens were identified through ZooMS. Cut marks and percussion notches were identified on both herbivore and some large carnivore bones.
- The higher proportion of anthropogenically modified bones and the presence of stone artefacts in each layer suggests that the BKC faunal assemblage accumulated mainly through hominin activities
-
- Denisovans used a wide range of species, including large herbivores and, to a lesser extent, carnivores, small mammals and birds.



Examples of anthropogenically modified faunal specimens and bone tools. a, Aquila right humerus (layer 4) with superficial and straight cut mark clusters, associated with the removal of feathers. b, Crocuta (layer 10a), with an oblique cut mark. c, Marmota sp. radius diaphysis (layer 9), with a flake scar (black triangle) d, A possible retoucher (layer 11). Equus sp. Right lower P2 with a set of scrape marks. e, Expedient bone tool. This humerus diaphysis is deliberately shaped by continuous direct percussion.

Hyena vertebra with cutmarks

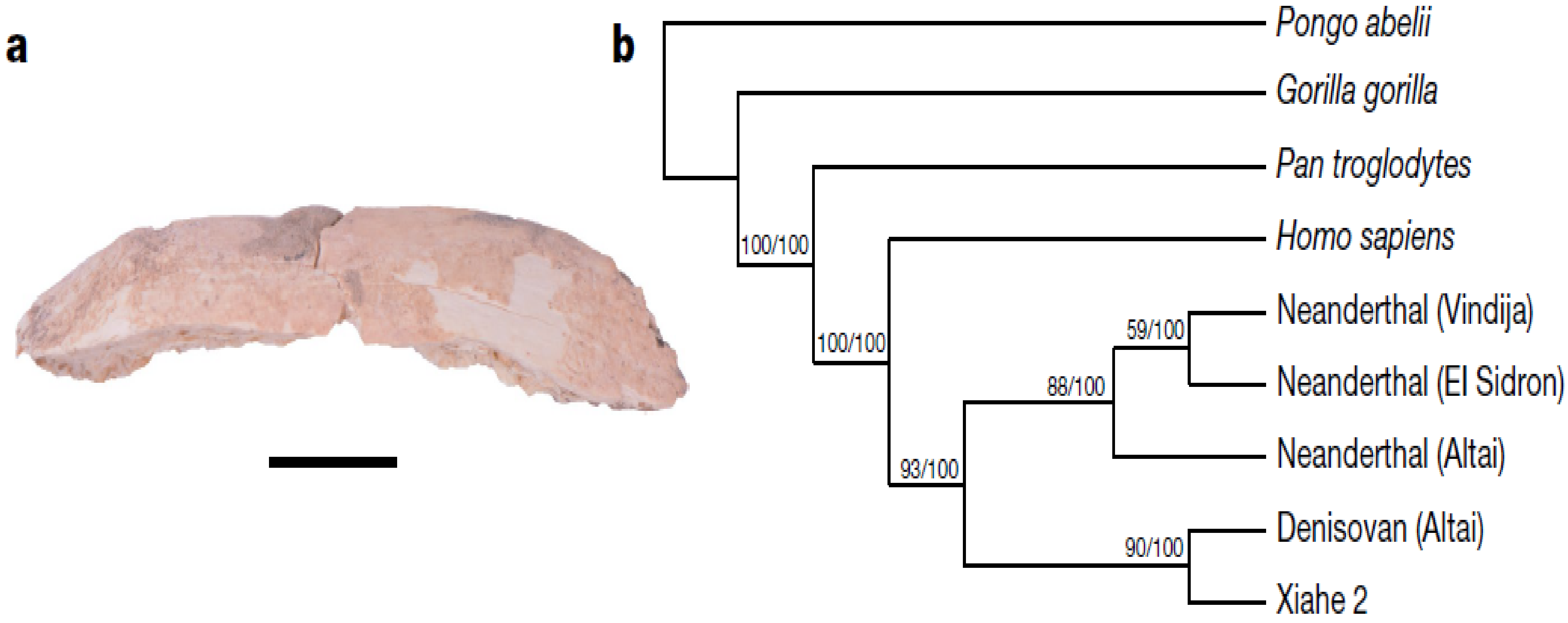
Xiahe 2: A new Denisovan individual: 48-32 Ka

- Proteinomic study: One rib specimen was identified as Homininae. The specimen contains 14 peptide markers of collagen type I matching Homininae, as well as one peptide marker unique to Hominoidea. This specimen could be confirmed as Homo sp.

- We therefore named this hominin specimen Xiahe 2. Xiahe 2 was broken into two pieces during excavation and belongs to the distal part of a rib (52 mm in length). The Xiahe 2 specimen comes from layer 3, which has been dated to 48–32 ka

D#7 = The 2-inch Xiahe 2 specimen, a. Homo sp. rib specimen discovered through ZooMS screening.

b. Phylogenetic tree for the Xiahe 2 specimen and reference proteomes.



Proteomic analysis: Xiahe 2 is Denisovan

- We reconstructed 4,597 amino acid positions for the Xiahe 2 specimen across the 21 protein sequences used for phylogenetic analysis. This is a considerably larger proteome than the six endogenous proteins that were used for the phylogenetic analysis of the Xiahe 1 mandible.
- Xiahe 2 consistently falling together with the published high-coverage Denisovan genome. As such, it can be determined that the Xiahe 2 individual is most closely related to the D3 Denisovan high-coverage individual.

160, 100, 60 Ka occupations

- The discovery of the Xiahe 2 Denisovan extends the fossil evidence for the presence of Denisovans well into the Late Pleistocene at BKC,

- Previous studies show that BKC is currently the only well-preserved cave site on the Tibetan Plateau that spans the late Middle to Late Pleistocene.

- The Xiahe 1 mandible and sedimentary mtDNA analyses reveal that Denisovans occupied the cave at least around 160 ka, 100 ka (layer 7) and 60 ka (layer 4), and possibly as late as 45 ka (end layer 4).

Conclusions

- The Xiahe 2 rib identified here, and Denisovan sedimentary mtDNA discovered from layer 3, show that Denisovan occupation occurred at the site until at least 48–32 ka.
- In addition, Xiahe 1 mandible has a minimum U-series age of around 160 ka, which also corresponds to the chronological age of layer 10 or below at BKC.

Xiahe Denisovans: Denisovans were adaptable survivalists

- The Xiahe Denisovans were the most likely occupants during the formation of these layers. So far, there is no evidence for the presence of other hominins at BKC for layers 3–11, nor is there evidence for other archaic hominin occupation elsewhere on the northeastern Tibetan Plateau during the same period.

- It is therefore reasonable to assume that Denisovans occupied BKC at least from around 167 ka (level 10) to around 40 ka (layer 3), and possibly from more than 224 ka

- Denisovans exploited a wide range of animal taxa that were present in the grass-dominated landscape around Ganjia Basin.

Goats and fauna at high attitude

- This reveals that Denisovans made full use of the animal resources available to them in order to survive on the high-altitude Tibetan Plateau during the last glacial–interglacial–glacial cycle.
- During both glacial and interglacial periods, the Ganjia Basin might have provided a suitable refugium with relatively stable resource availability despite its altitude.
- Showed an adaptability to harsh, high-altitude environments over two glacial periods.

*** Magnetostratigraphic dating of earliest hominin sites in Europe

- When did early hominins arrive in Europe?
- Three superposed hominin sites are dated between the Olduvai and Jaramillo magnetic subchrons (1.78–1.07 Myr) for the first time in Europe. Using Magnetostratigraphic dating
- A Bayesian age-stratigraphic model provides Europe's oldest and most accurate early Pleistocene hominin ages.

Site dating

- Hominins with Oldowan tools entered Europe for the first time ~ 0.5 Ma after first leaving Africa.
- This migration occurred ~0.5 Ma before the arrival of Acheulian technology in Europe.
- Both African migrations are first reported in Spain, suggesting that the Strait of Gibraltar was a permeable barrier for early Pleistocene hominins

*** New geological dating techniques place first European hominids in Iberian Peninsula 1.3 million years ago

- Question of when and by what route the first hominins arrived in Europe from the African continent. Now, geological dating techniques at the Orce sites (Baza basin, Granada) place the human remains found in this area as the oldest in Europe, at approximately 1.3 million years old.

- These results reinforce the hypothesis that humans arrived in Europe through the south of the Iberian Peninsula, through the Strait of Gibraltar, instead of returning to the Mediterranean via the Asian route based on the analysis of the paleomagnetism of an area of the Orce region

Luis Gibert, et al., 2024

3 sites

- Were able to identify a magnetic polarity sequence "with five magnetic events that allow them to place the three Orce sites with human presence between the Olduvai and Jaramillo subchron, that is, between 1.77 and 1.07 million years ago (Ma),

Magnetostratigraphic dating of earliest hominin sites in Europe

- The result of this innovative methodology is that the oldest site with human presence in Europe would be:
  - Venta Micena with an age of 1.32 Ma,
  - followed by Barranco León, with an age of 1.28 and
  - finally Fuente Nueva 3, with an age of 1.23 Ma.
- With these data, the other major site on the peninsula, the Sima del Elefante in Atapuerca, would be relegated to second place, far behind Orce, between 0.2 and 0.4 Ma more modern
- Paper presents a detailed analysis of the micromammals and large mammals from all the Orce sites

Key dated sites showing the world distribution of hominins before 1 Ma (orange color) and potential dispersion routes.

The figure shows sites with Oldowan technology (black dots) older than 2 Ma in Africa and older than 1 Ma in Eurasia

Colonization of Europe through Gibraltar

- Finding tips the balance in favor of the colonization of Europe through the Strait of Gibraltar, rather than the alternative route: the return to the Mediterranean via Asia,
- There is the existence of a lithic industry with similarities to that found in the north of the African continent and also the presence of remains of African fauna in the south of the peninsula, such as those of Hippopotamus, found in the sites of Orce, and those of Theropithecus oswaldi, an African primate similar to a baboon, found in the Victoria cave, a site near Cartagena (Murcia), non-existent anywhere else in Europe.
- No older evidence has been found at any other site along the alternative route

SW Europe

- With these results, the researchers point to a "diachronism" between the
  - oldest occupation of Asia, measuring 1.8 Ma,
  - and the oldest occupation of Europe, which would be 1.3 Ma ago,
  - so that African hominins would have arrived in southwestern Europe more than 0.5 Ma after leaving Africa for the first time about 2 Ma ago.

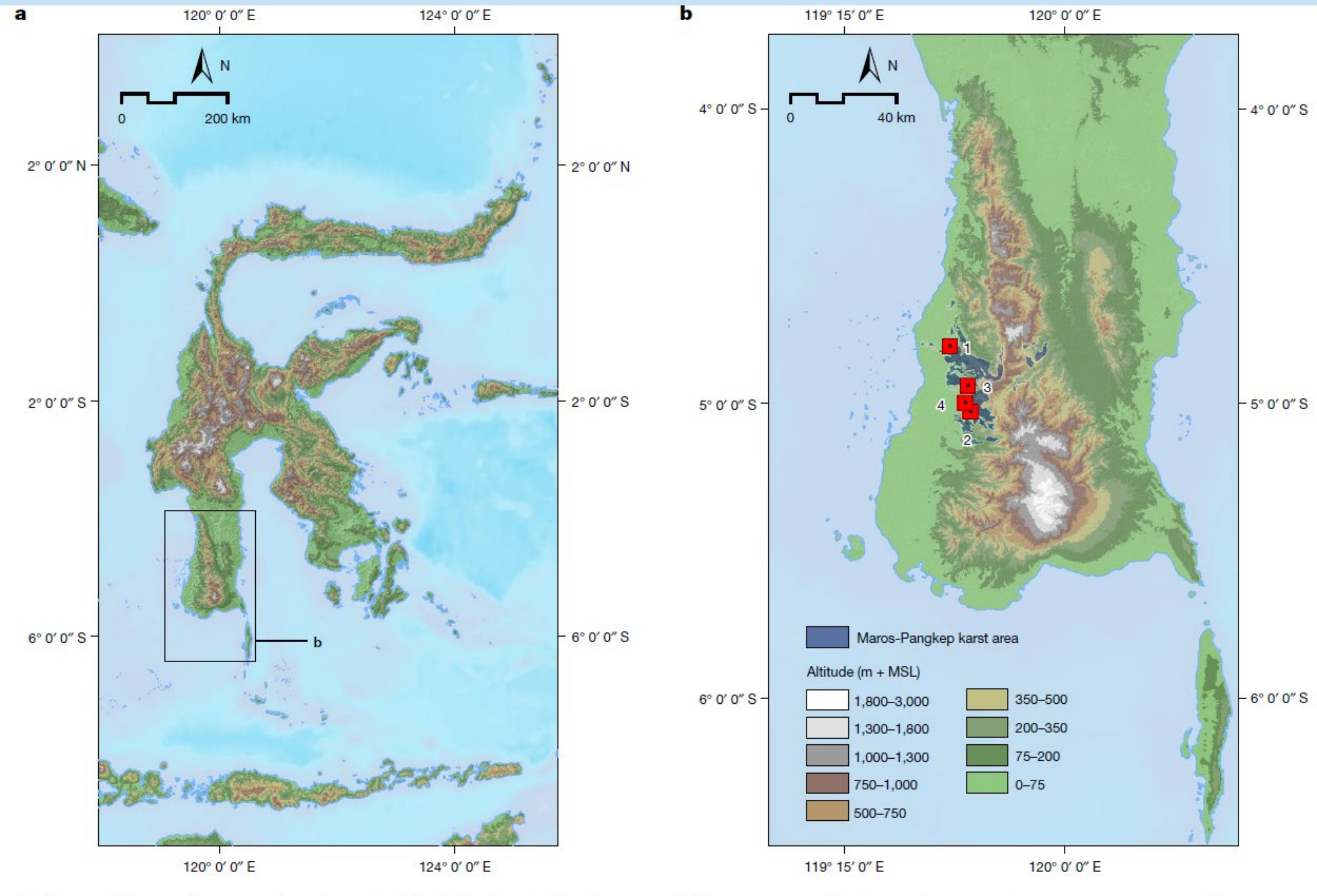
- These differences in human expansion can be explained by the fact that Europe is isolated from Asia and Africa by biogeographical barriers that are difficult to overcome, both to the east (Bosphorus Strait, Dardanelles, Sea of Marmara) and to the west (Strait of Gibraltar).

- Humanity arrived in Europe when it had the necessary technology to cross maritime barriers, as happened before a million years ago on the island of Flores (Indonesia),

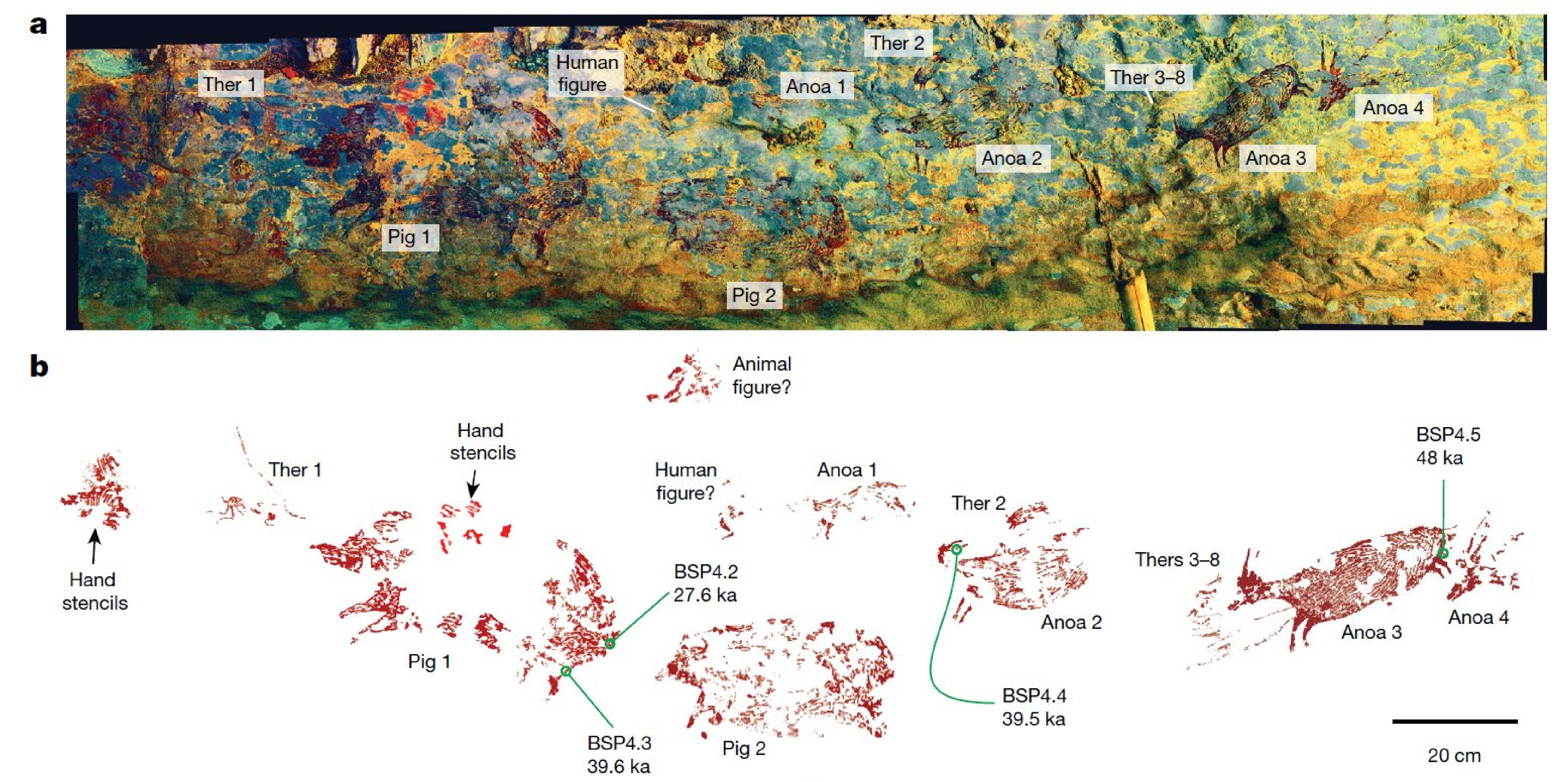
5 hominin remains

- A total of five human remains were found at the Orce sites since excavations began in 1982 by the paleoanthropologist Josep Gibert. Firstly, two fragments of humerus bitten by hyenas were found at Venta Micena, as well as parts of a cranial fragment consisting of two parietals and an occipital, associated with an abundant Early Pleistocene fauna.
- The subsequent discovery at the nearby sites of Barranco León and Fuente Nueva 3 of two human molar teeth and thousands of Oldowan lithic tools as well as cut marks on bones "served to consolidate the evidence of the presence of hominins in the Early Pleistocene at Orce,

*** The Indonesian island of Sulawesi, showing the location of the southwestern peninsula: Earliest H. sapiens art



Art world of Sulawasi: Leang Bulu' Sipong 4: now 51.2 Ka



Narrative cave art in Indonesia by 51,200 years ago

- Indonesian island of Sulawesi is host to some of the oldest known rock art.

- That work was based on solution uranium-series (U-series) analysis of calcite deposits overlying rock art in the limestone caves of Maros-Pangkep, South Sulawesi.

- Here we use a novel application of this approach—laser-ablation U-series imaging—to re-date some of the earliest cave art in this karst area. This method provides enhanced spatial accuracy, resulting in older minimum ages for previously dated art.

Adhi Agus Oktaviana, et al., 2024,

Leang Bulu’ Sipong 4 = 51 Ka

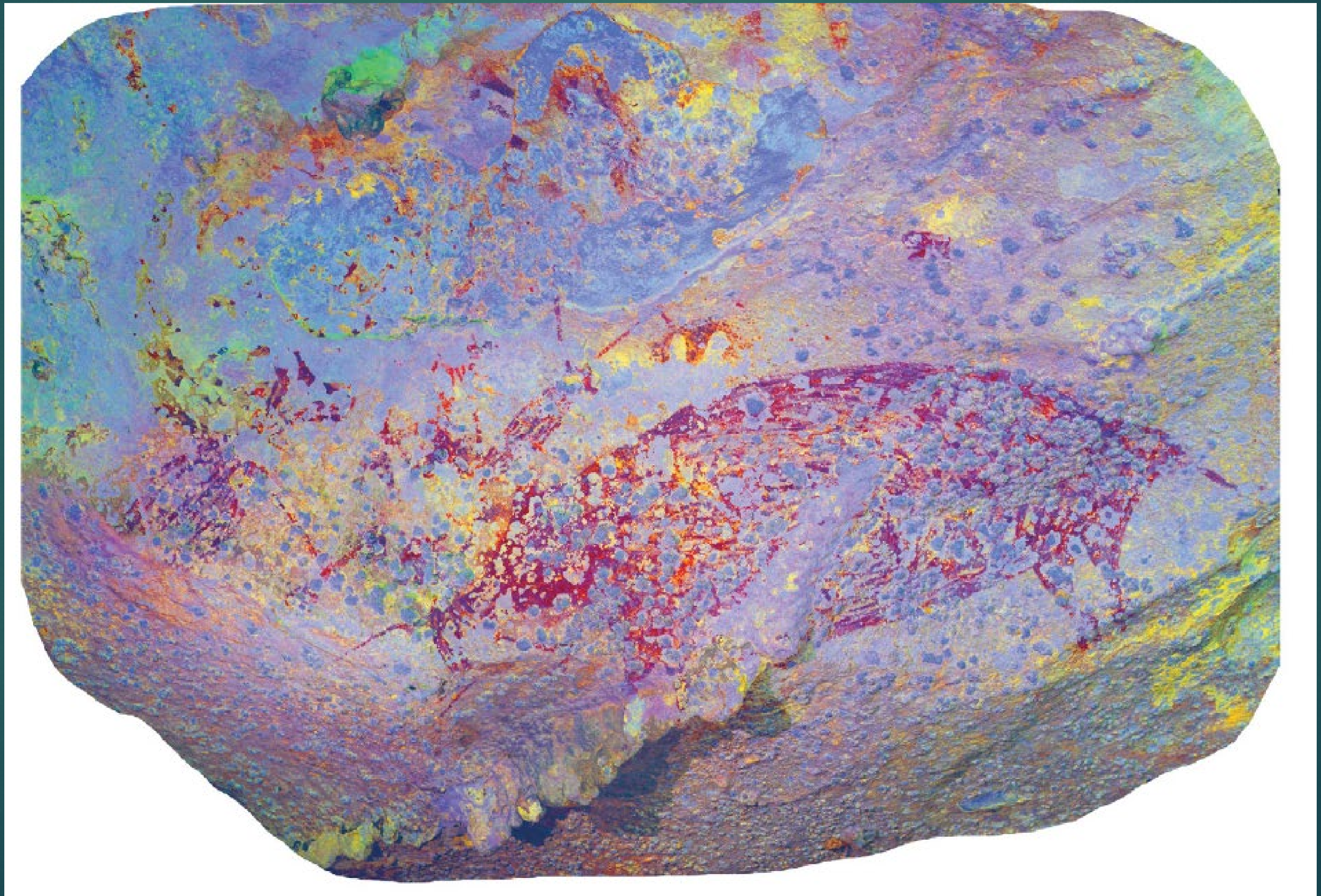
- We show that a hunting scene from Leang Bulu’ Sipong 4, which was originally dated using the previous approach to a minimum of 43,900 thousand years ago (ka), has a minimum age of 50.2 ± 2.2 ka, and so is at least 4,040 years older than thought.
- Using the imaging approach, we also assign a minimum age of 53.5 ± 2.3 ka to a newly described cave art scene at Leang Karampuang.

Hunting scene from Leang Karampuang, 51.2 Ka

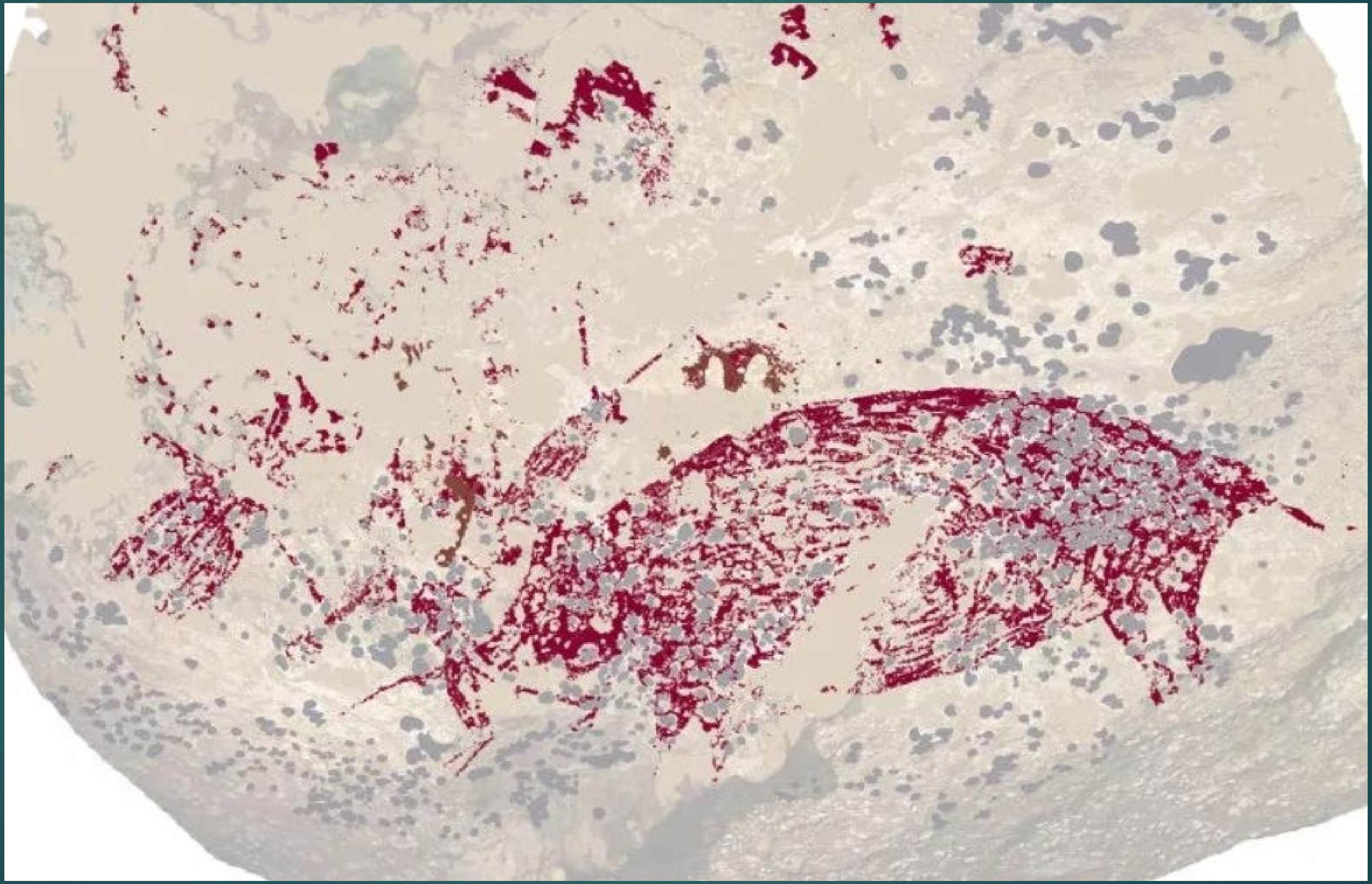
- *** Painted at least 51,200 years ago, this narrative composition, which depicts human-like figures interacting with a pig, is now the earliest known surviving example of representational art, and visual storytelling, in the world.

- Our findings show that figurative portrayals of anthropomorphic figures and animals have a deeper origin in the history of modern human (*Homo sapiens*) image-making than recognized to date, as does their representation in composed scenes.

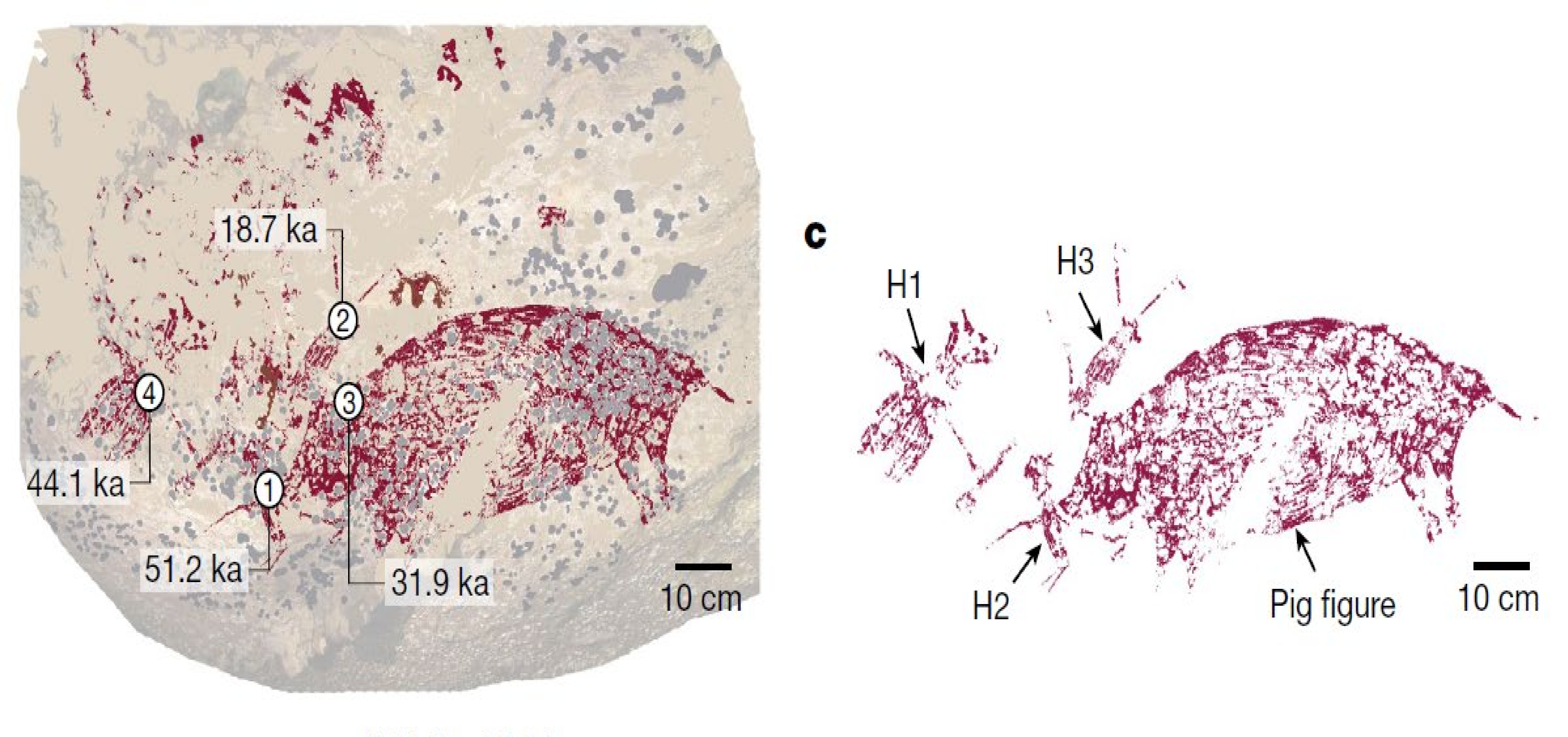
Scene from Leang Karampuang, 51.2 Ka: oldest found figurative depiction in a painting



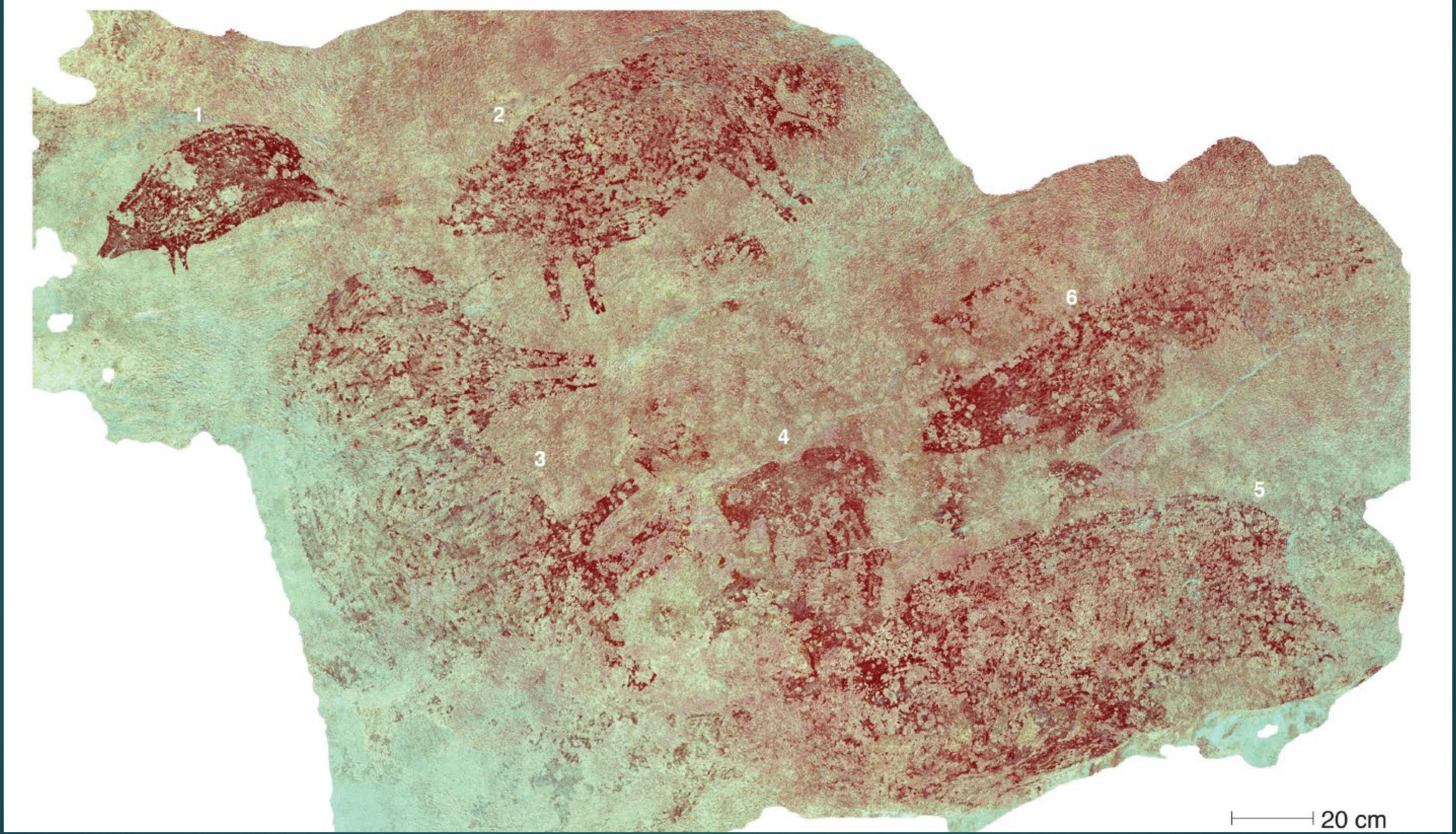
Leang Karampuang



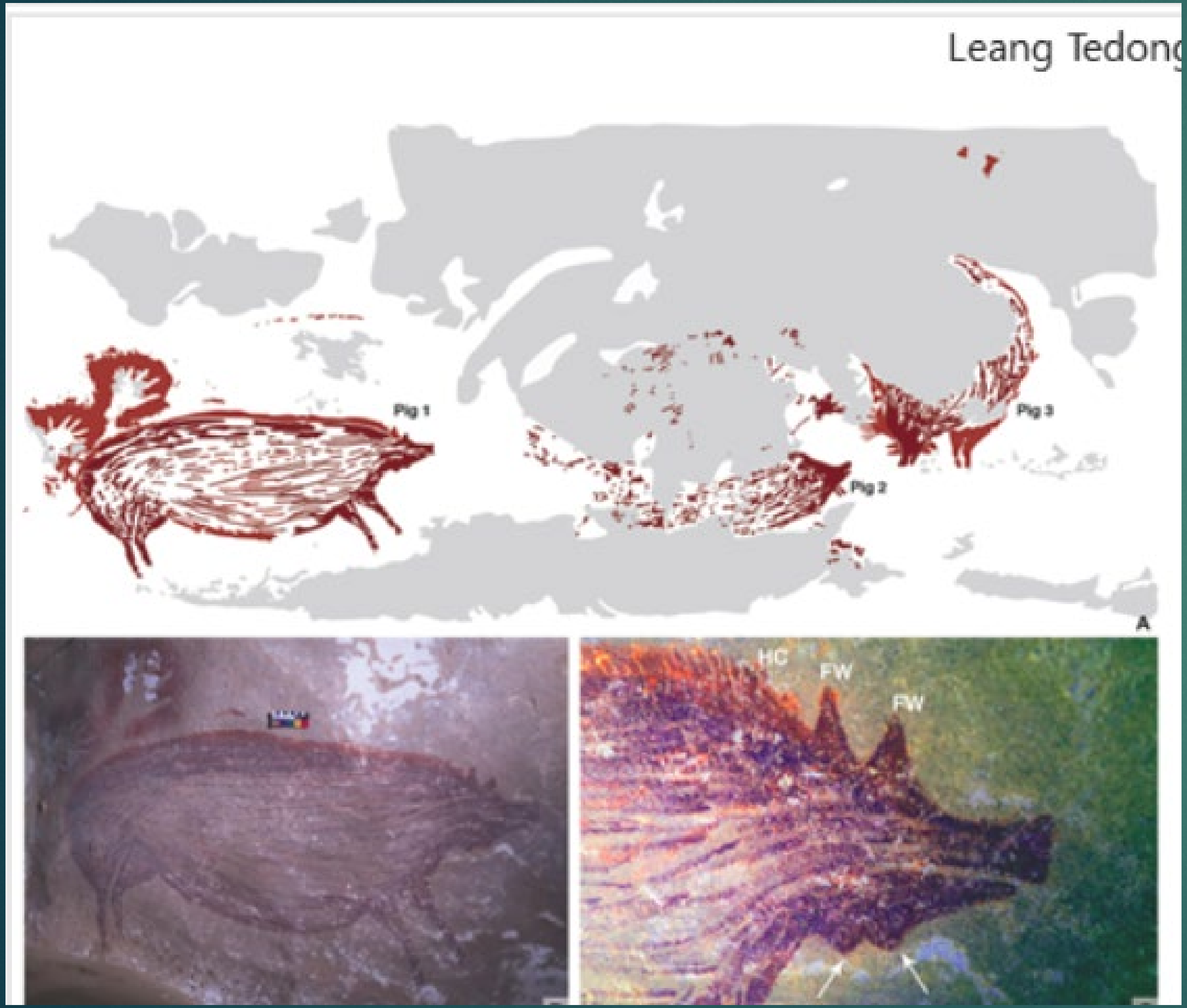
3 humans and a local pig

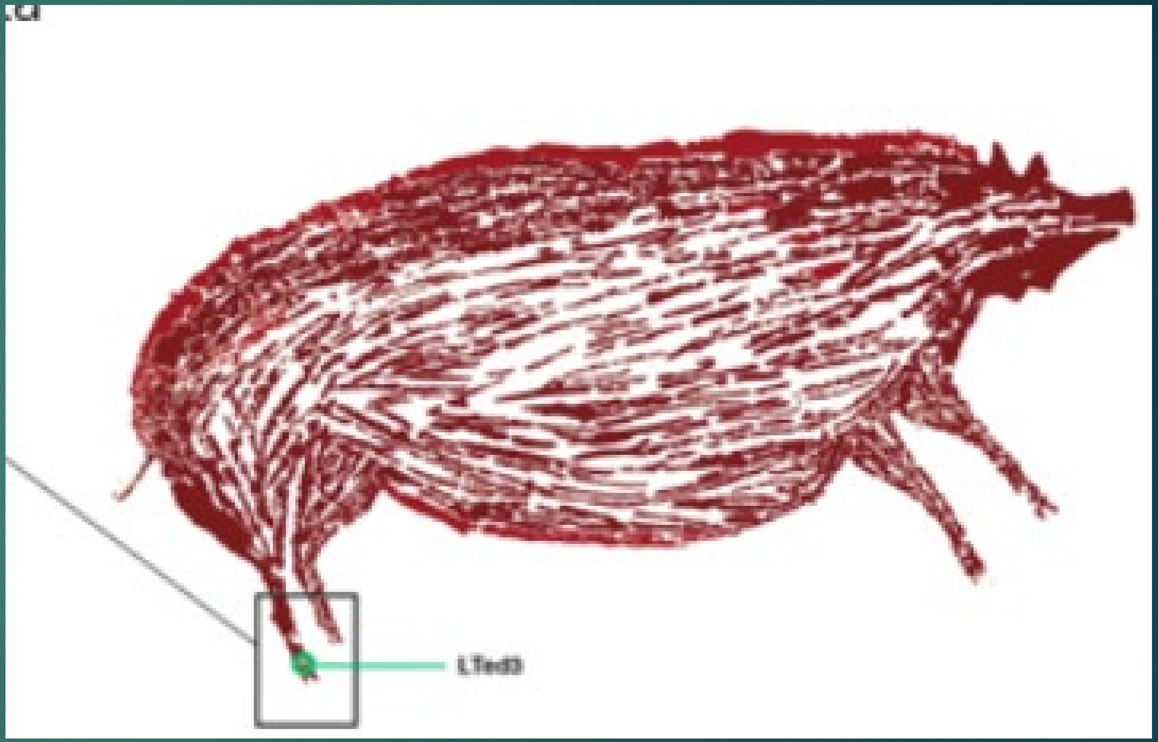


Other pigs from Leang Karampuang

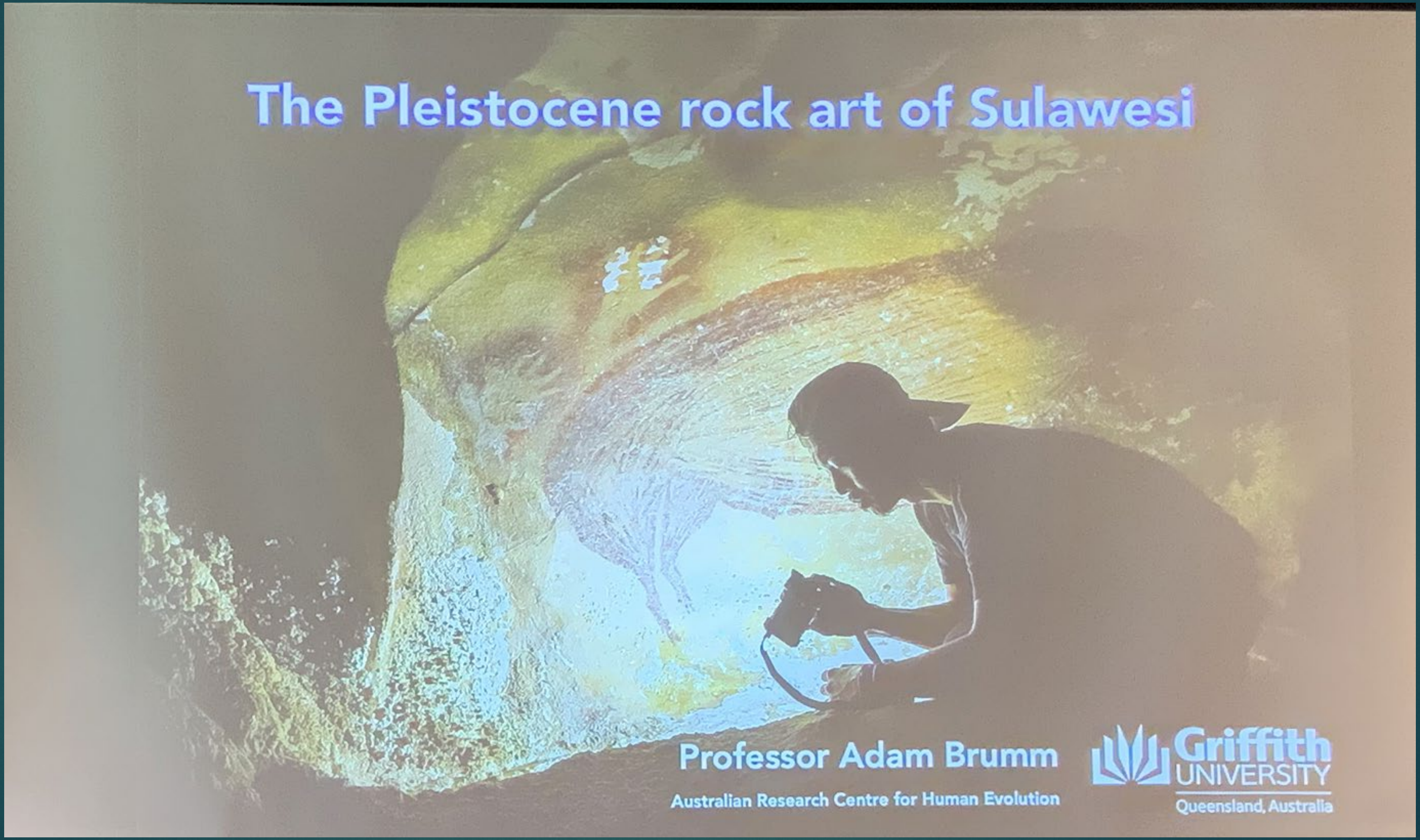


Leang Tedongnge: 45,500 year





Pleistocene rock art of Sulawesi by Adam Brumm



The Pleistocene rock art of Sulawesi

Professor Adam Brumm

Australian Research Centre for Human Evolution

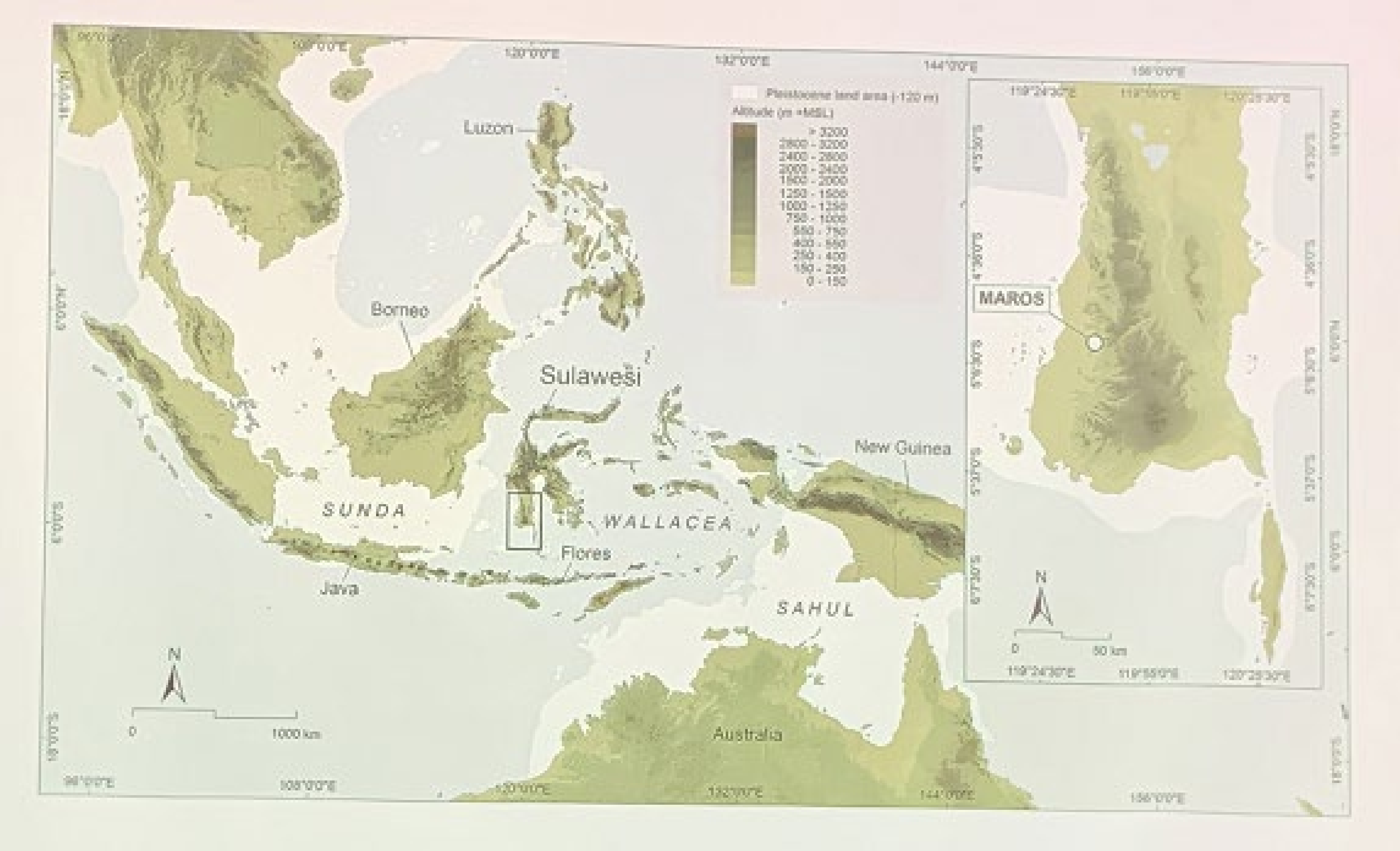
Griffith UNIVERSITY

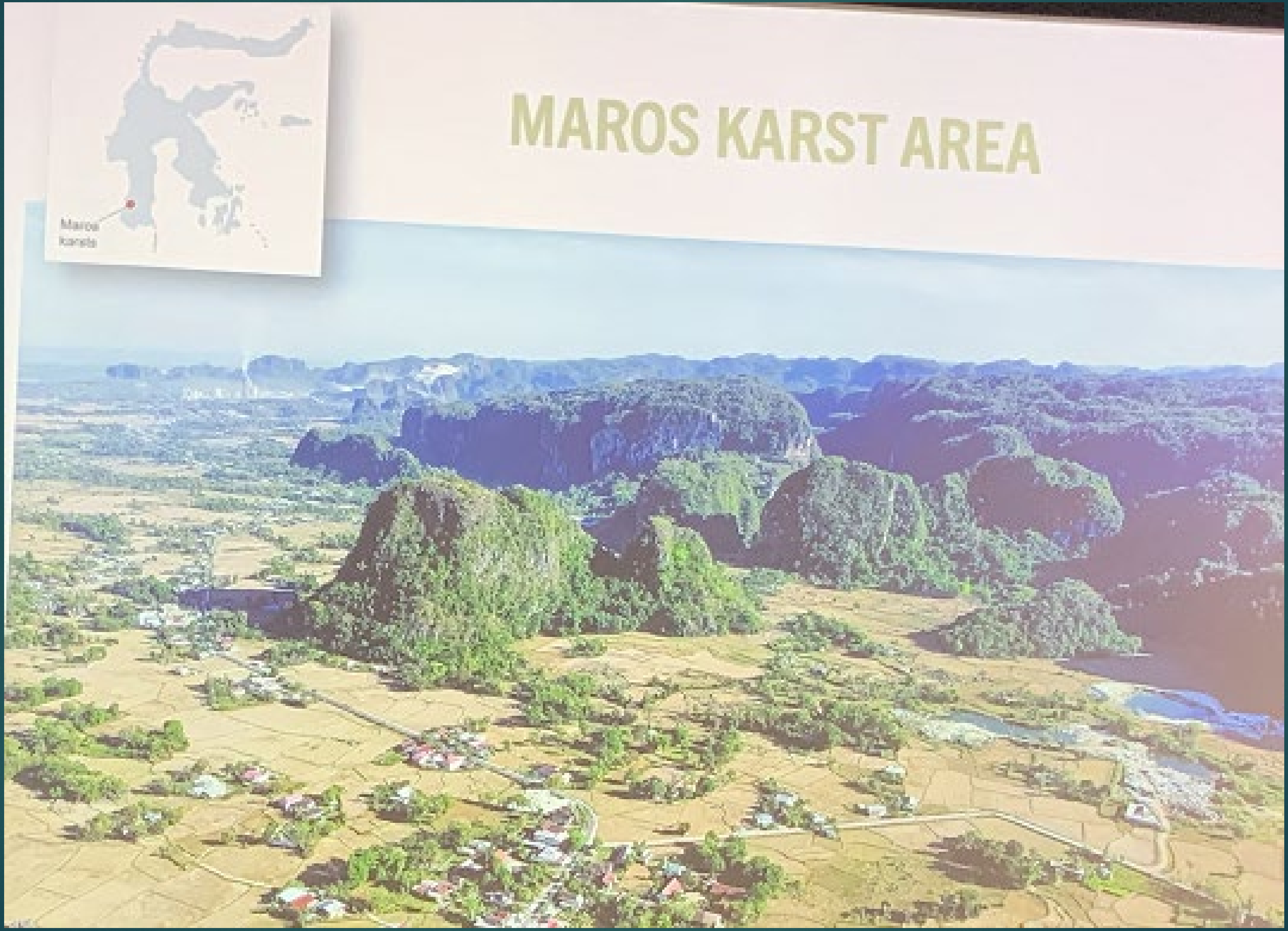
Queensland, Australia

Adam Brumm:
Australian
Paleontologist

Worked 10 Years
on Flores with
H. floresiensis

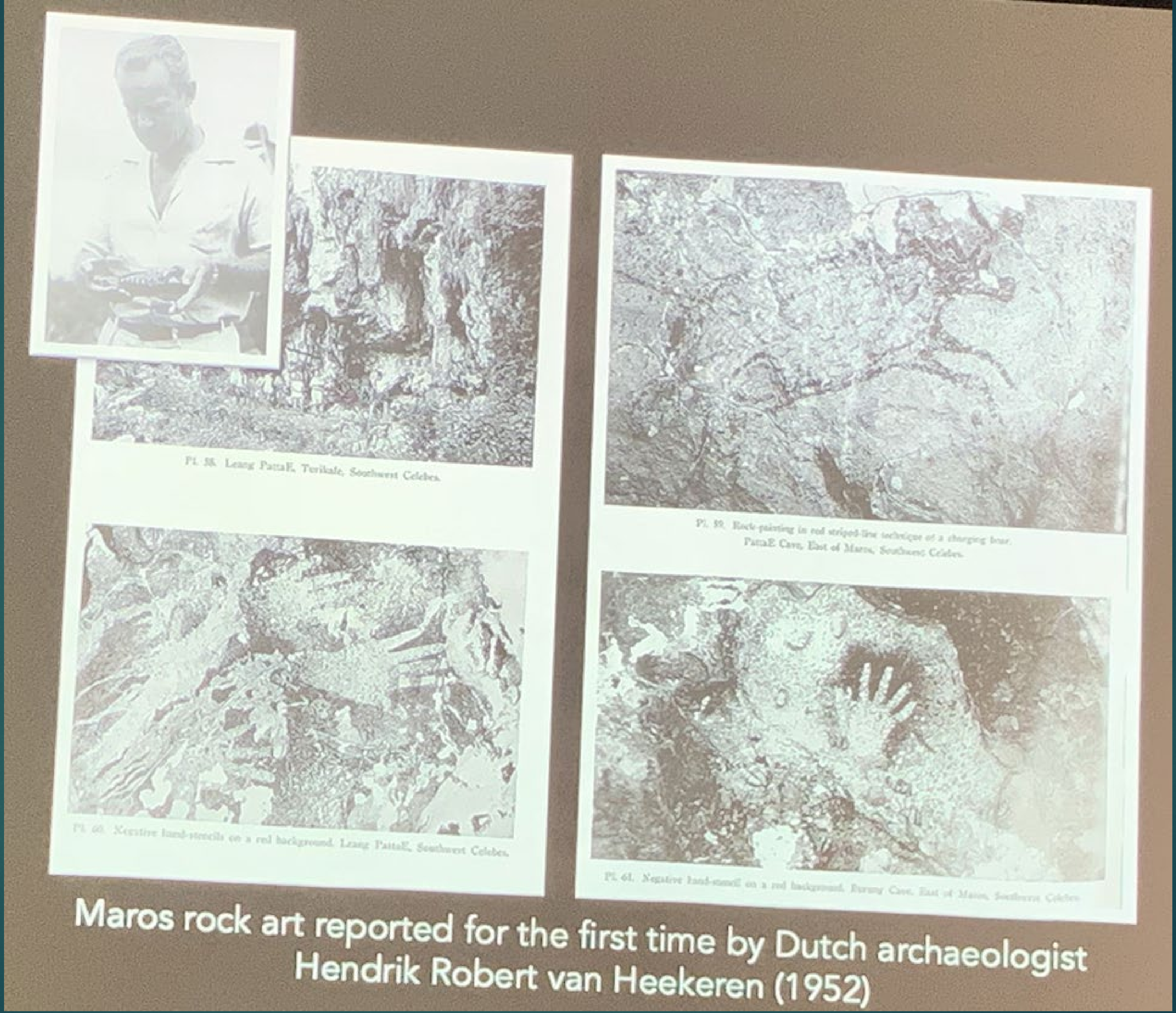
Indonesia & island of Sulawesi





MAROS KARST AREA

1952 art discovery



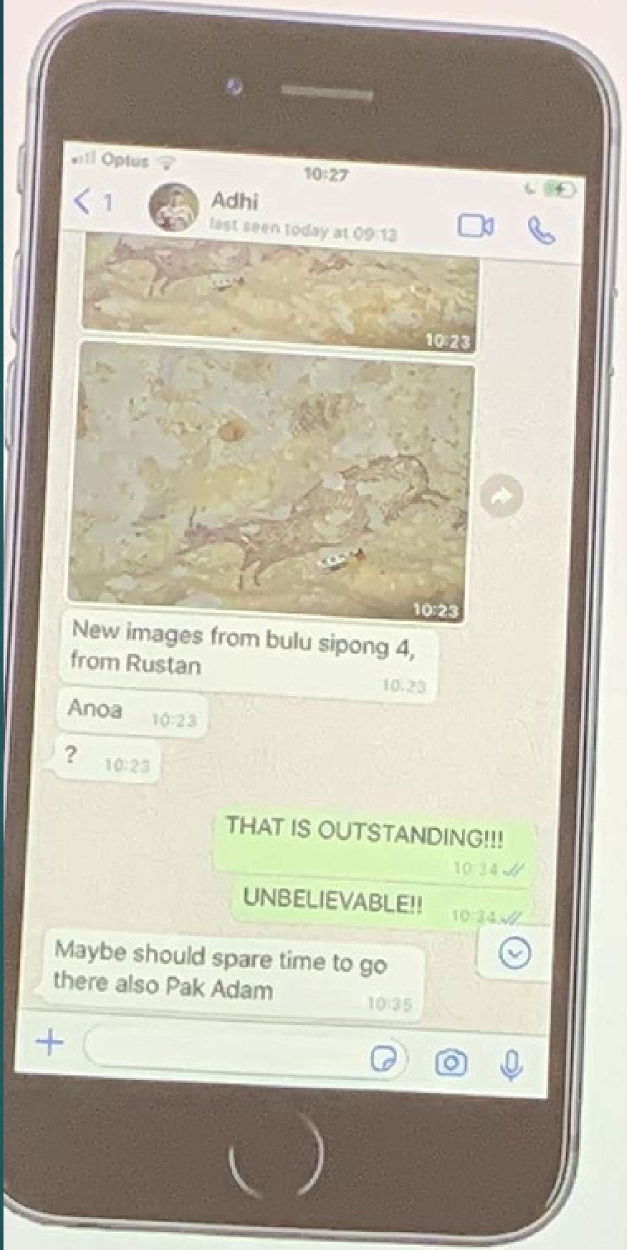
Pl. 58. Leang PattaE, Turikale, Southwest Celebes.

Pl. 59. Rock-painting in red striped-line technique of a charging boar. PattaE Cave, East of Maros, Southwest Celebes.

Pl. 60. Negative hand-stencils on a red background. Leang PattaE, Southwest Celebes.

Pl. 61. Negative hand-stencil on a red background. Burung Cave, East of Maros, Southwest Celebes.

Maros rock art reported for the first time by Dutch archaeologist Hendrik Robert van Heekeren (1952)



10:23

10:23

New images from bulu sipong 4, from Rustan 10:23

Anoa 10:23

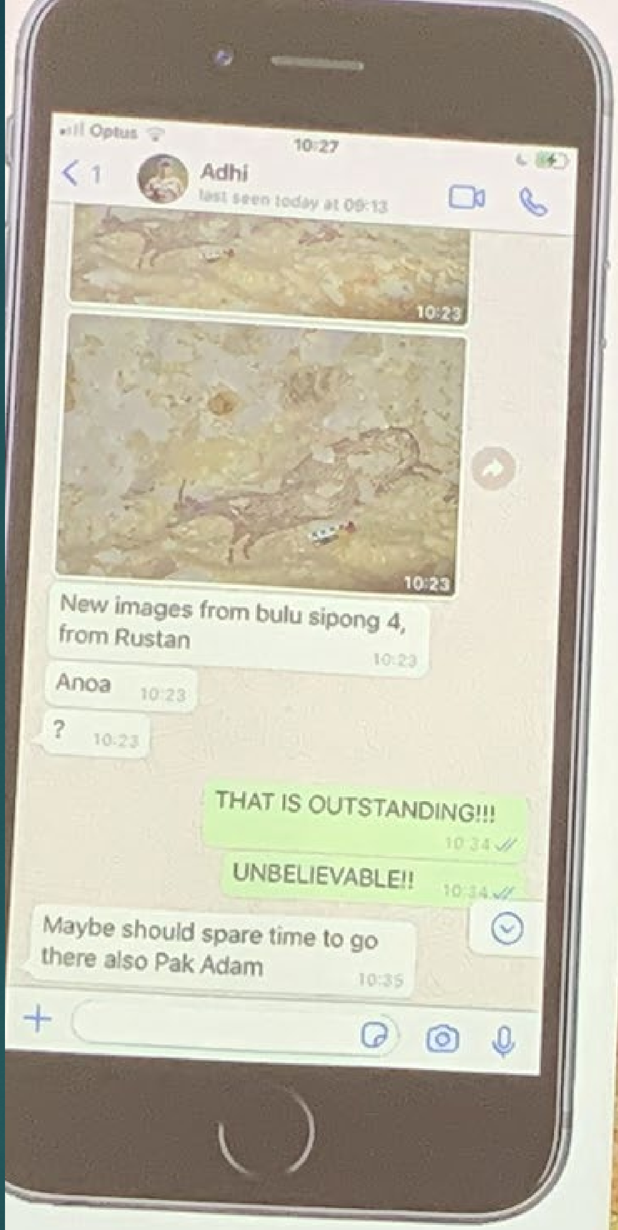
? 10:23

THAT IS OUTSTANDING!!! 10:34

UNBELIEVABLE!! 10:34

Maybe should spare time to go there also Pak Adam 10:35

18 January 2018, Leang Bulu' Sipong 4
(Maros karsts, South Sulawesi)



Adhi
last seen today at 09:13

New images from bulu sipong 4, from Rustan 10:23

Anoa 10:23

? 10:23

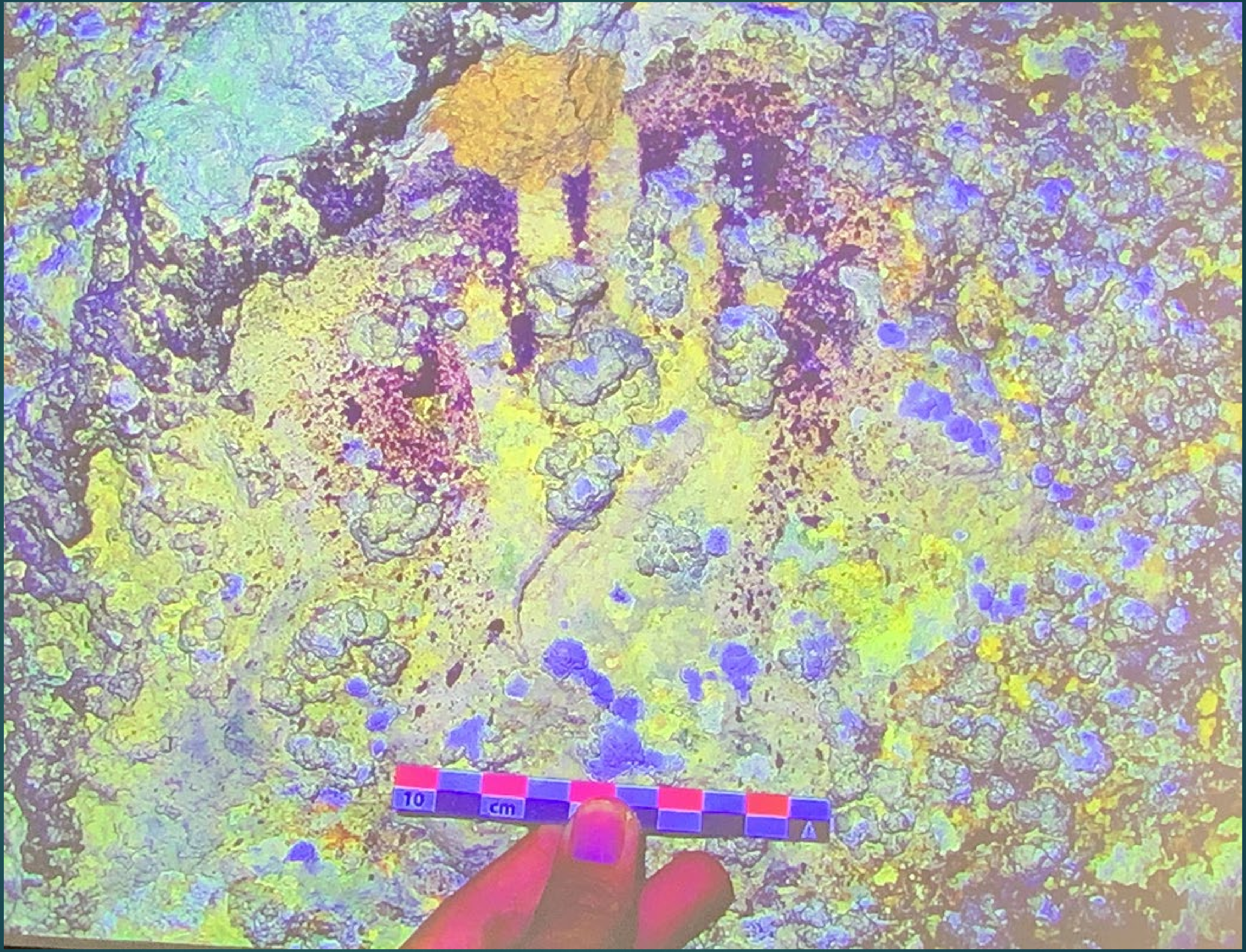
THAT IS OUTSTANDING!!! 10:34

UNBELIEVABLE!! 10:34

Maybe should spare time to go there also Pak Adam 10:35

18 January 2018, Leang Bulu' Sipong 4
(Maros karsts, South Sulawesi)

Hand Print



nature

THE INTERNATIONAL WEEKLY JOURNAL OF SCIENCE

ICE AGE ART IN THE TROPICS

Indonesian cave paintings show figurative art present at opposite ends of the late Pleistocene world

PAGES 170 & 223

PARTICLE PHYSICS

LHC PRIMED FOR ACTION

Physicists get ready for particle-collider reboot

PAGE 158

EVOLUTION

SURVIVAL OF THE BEST FIT

Theorists battle over what's in and what's out

PAGE 161

GUT MICROBIOTA

BITTER HARVEST

How artificial sweeteners disrupt glucose metabolism

PAGES 175 & 181

NATURE.COM/NATURE

9 October 2014 £10

Vol. 514, No. 7521

LETTER

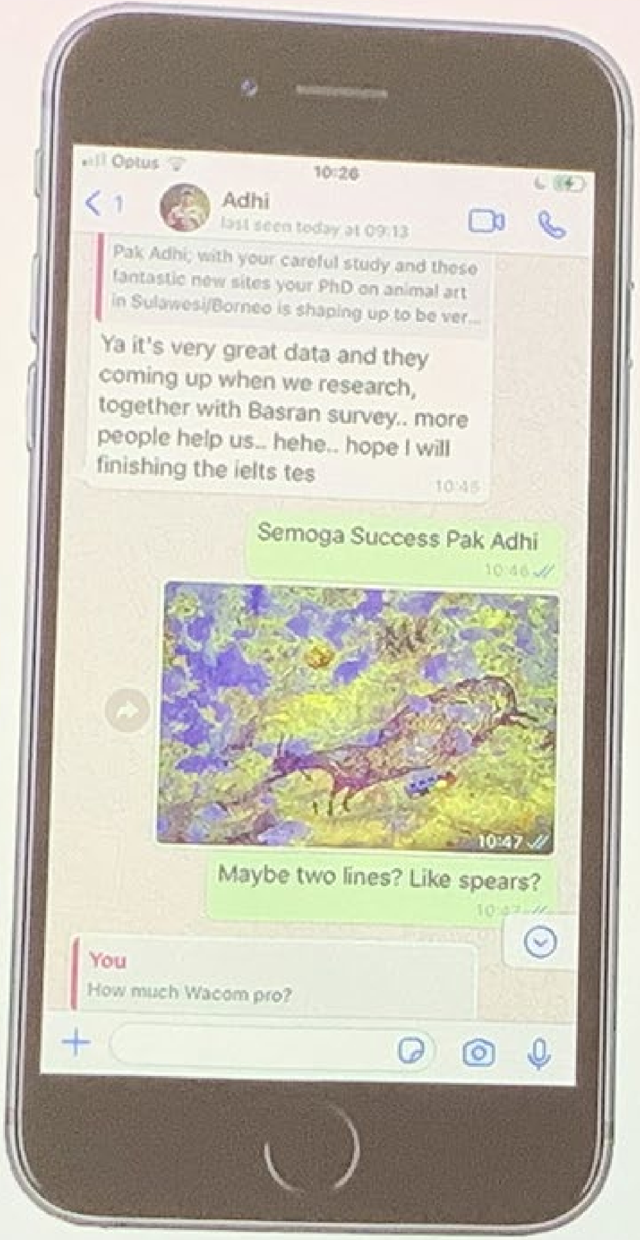
Pleistocene cave art from Sulawesi, Indonesia

M. Aubert, A. Brumm, M. Ramli, T. Sutikna, E. W. Saptomo, B. Hakim, M. J. Morwood, G. D. van den Bergh, L. Kinsley & A. Dosseto

40,000
years ago


Ireland
Britain
Germany
France
Lascaux
174,000 km²
Spain
Altamira
Chauvet
AFRICA

Early German figurines
40,000 to 30,000 years ago



Pak Adhi; with your careful study and these fantastic new sites your PhD on animal art in Sulawesi/Borneo is shaping up to be ver...

Ya it's very great data and they coming up when we research, together with Basran survey.. more people help us.. hehe.. hope I will finishing the ielts tes 10:45

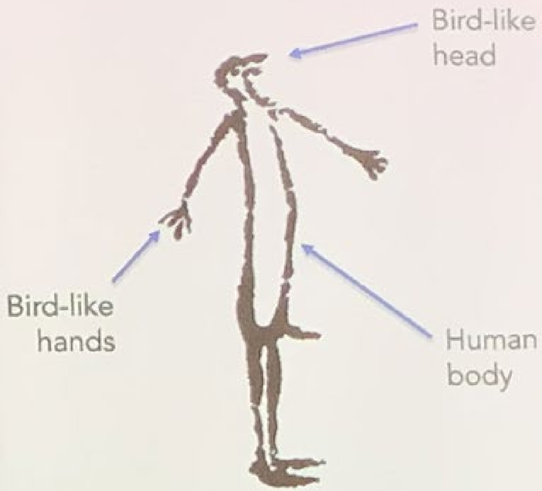
Semoga Success Pak Adhi 10:46

10:47

Maybe two lines? Like spears?

You
How much Wacom pro?

18 January 2018, Leang Bulu' Sipong 4
(Maros karsts, South Sulawesi)



This ancient **masterpiece** is one of the world's most iconic rock art images.

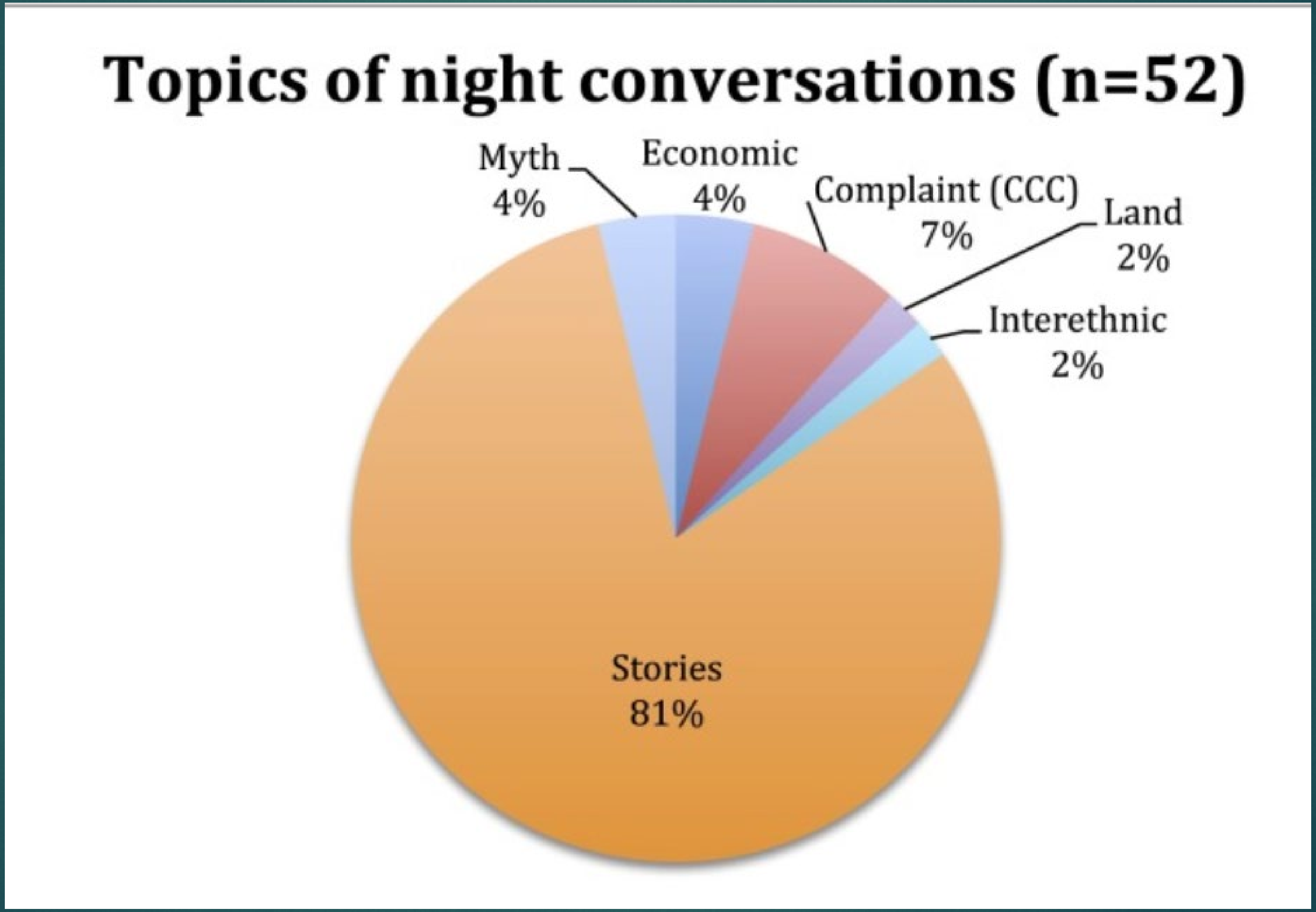
Created ~21,000 to 14,000 years ago at Lascaux Cave in France, it is a hunting scene depicting a 'man' with a bird-like head being charged by a bison that the former has wounded with a spear.

It has two features rarely seen in the Palaeolithic cave art of Europe:
1) A therianthrope (part-human, part-animal being);
2) A narrative composition or 'scene' in the modern western sense.

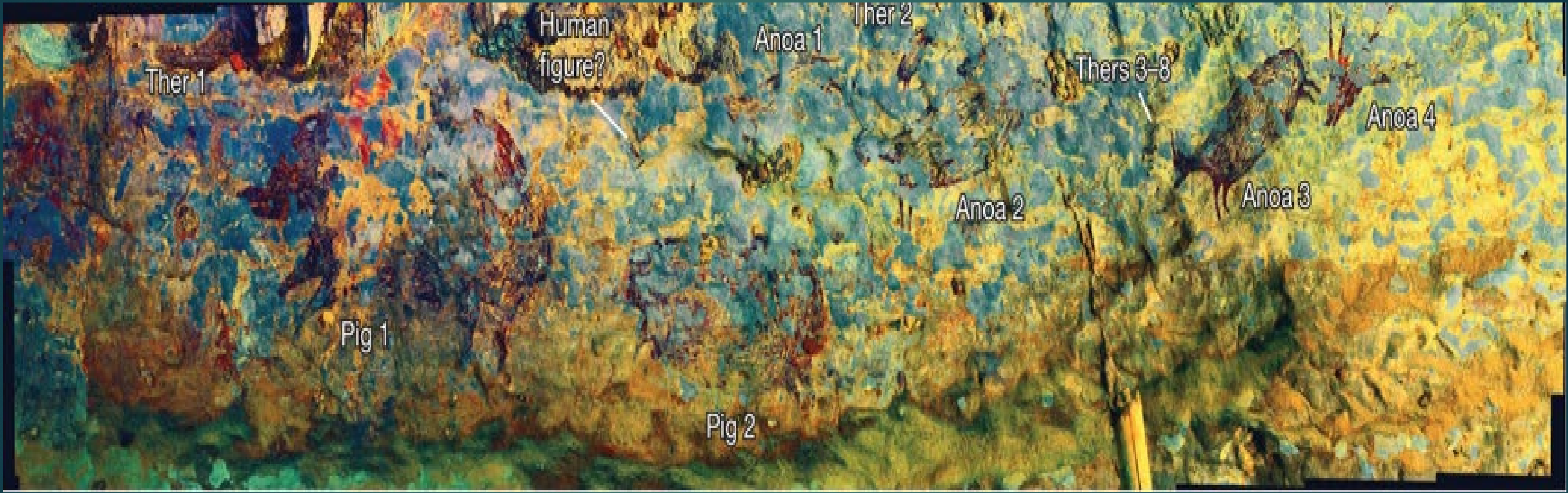
Embers of society. Firelight talk among the Bushmen

- Images of therianthropes in Palaeolithic cave art could represent many things: spirits, supernatural beings, monsters, gods or other deities, to name a few - but at minimum, they seem to comprise evidence for imaginative storytelling (myths, folk tales etc.) of some kind.

What do Ju/’hoansi/San of Kalahari people talk about:

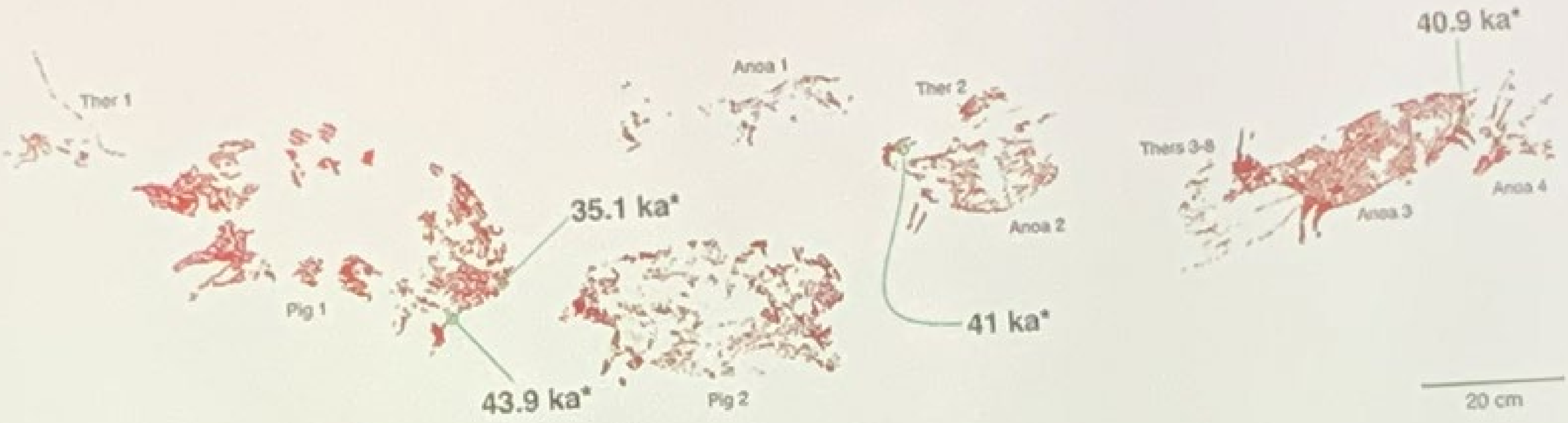


3rd oldest MH artwork: Indonesian, not Europe - 43,900 years old; 5-meter-long panel: in Sulawesi, Indonesia



M. Aubert *et al*., 2019

Image credit: Ratno Sardi / Adhi Agus



*Minimum Uranium-series age for art
(ka = thousand years ago)

Local animals and human-animal creatures

World’s 2nd oldest painted hunting scene: 44 Ka

Lascaux
'bird-man'

The Leang Bulu’ Sipong 4 art work is the oldest example of human story telling

Article

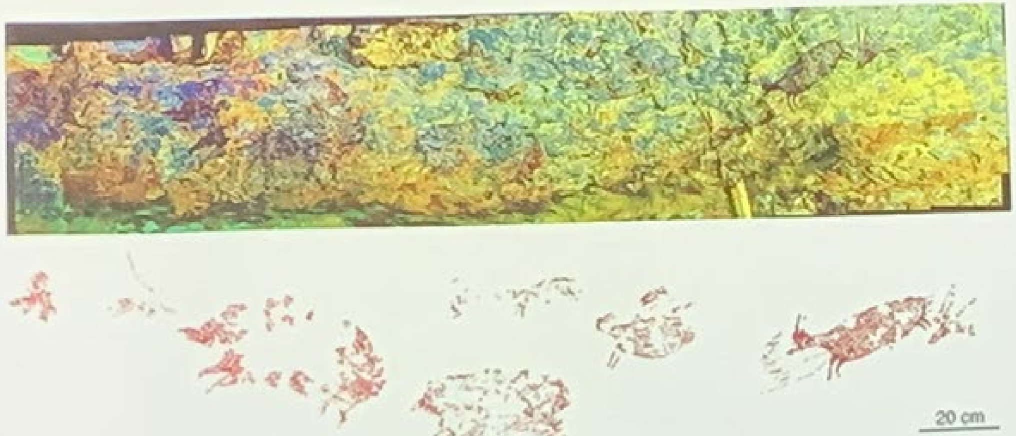
Earliest hunting scene in prehistoric art

nature

https://doi.org/10.1038/s41586-019-1806-y
Received: 9 May 2019
Accepted: 18 October 2019

Maxime Aubert[1,2,8], Rustan Lebe[3], Adhi Agus Oktaviana[1,4,8], Muhammad Tang[3], Basran Burhan[1], Hamrullah[1], Andi Jusdi[3], Abdullah[3], Budianto Hakim[5], Jian-xin Zhao[6], I. Made Geria[4], Priyatno Hadi Sulistyarto[4], Ratno Sardi[7] & Adam Brumm[2,8]*

Humans seem to have an adaptive predisposition for inventing, telling and consuming stories[1]. Prehistoric cave art provides the most direct insight that we have into the earliest storytelling[2–4], in the form of narrative compositions or 'scenes'[2,3] that feature clear figurative depictions of sets of figures in spatial proximity to each other, and from which one can infer actions taking place among the figures[5]. The Upper Palaeolithic cave art of Europe hosts the oldest previously known images of humans and animals interacting in recognizable scenes[2,3], and of therianthropes[6,7]—abstract beings that combine qualities of both people and animals, and which arguably communicated narrative fiction of some kind (folklore, religious myths, spiritual beliefs and so on). In this record of creative expression (spanning from about 40 thousand years ago (ka) until the beginning of the Holocene epoch at around 10 ka), scenes in cave art are generally rare and chronologically late (dating to about 21–14 ka)[7], and clear representations of therianthropes are uncommon[6]—the oldest such image is a carved figurine from Germany of a human with a feline head (dated to about 40–39 ka)[8]. Here we describe an elaborate rock art panel from the limestone cave of Leang Bulu' Sipong 4 (Sulawesi, Indonesia) that portrays several figures that appear to represent therianthropes hunting wild pigs and dwarf bovids; this painting has been dated to at least 43.9 ka on the basis of uranium-series analysis of overlying speleothems. This hunting scene is—to our knowledge—currently the oldest pictorial record of storytelling and the earliest figurative artwork in the world.



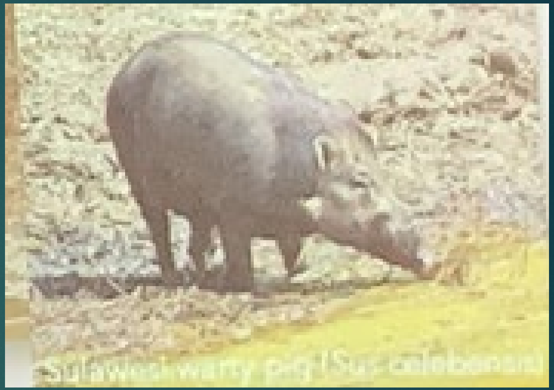
Leang Bulu' Sipong 4

The Three Little Pigs

Image: A.A. Oktaviana

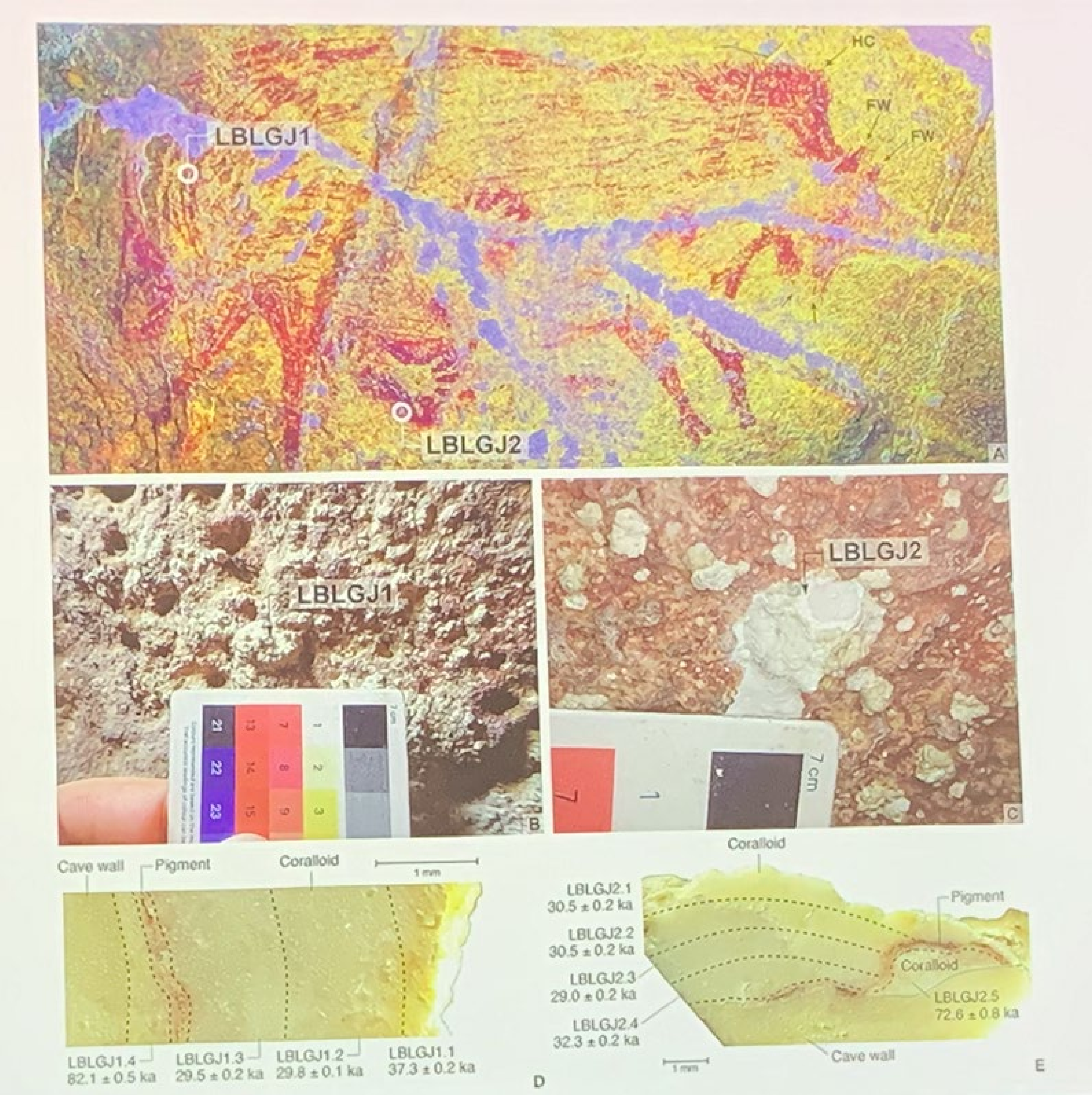
45,500 Ka


10 cm
LTed3
Image: A.A. Oktaviana
LTed3
Image: A.A. Oktaviana


Sulawesi warty pig (Sus celebensis)

32,000 years ago

via overlaying
“popcorn”
calcite



There is broad agreement that modern human symbolic behavior had emerged in Africa by at least 100,000 years ago

Blombos Cave,
South Africa
~100,000 years old

Diepkloof Shelter,
South Africa
~100,000 years old

Were there two Explosions in Human Creative potential in widely separated parts of the Late Pleistocene Old World?

*** The Widespread Exploitation of Straight-Tusked Elephants by Neanderthals

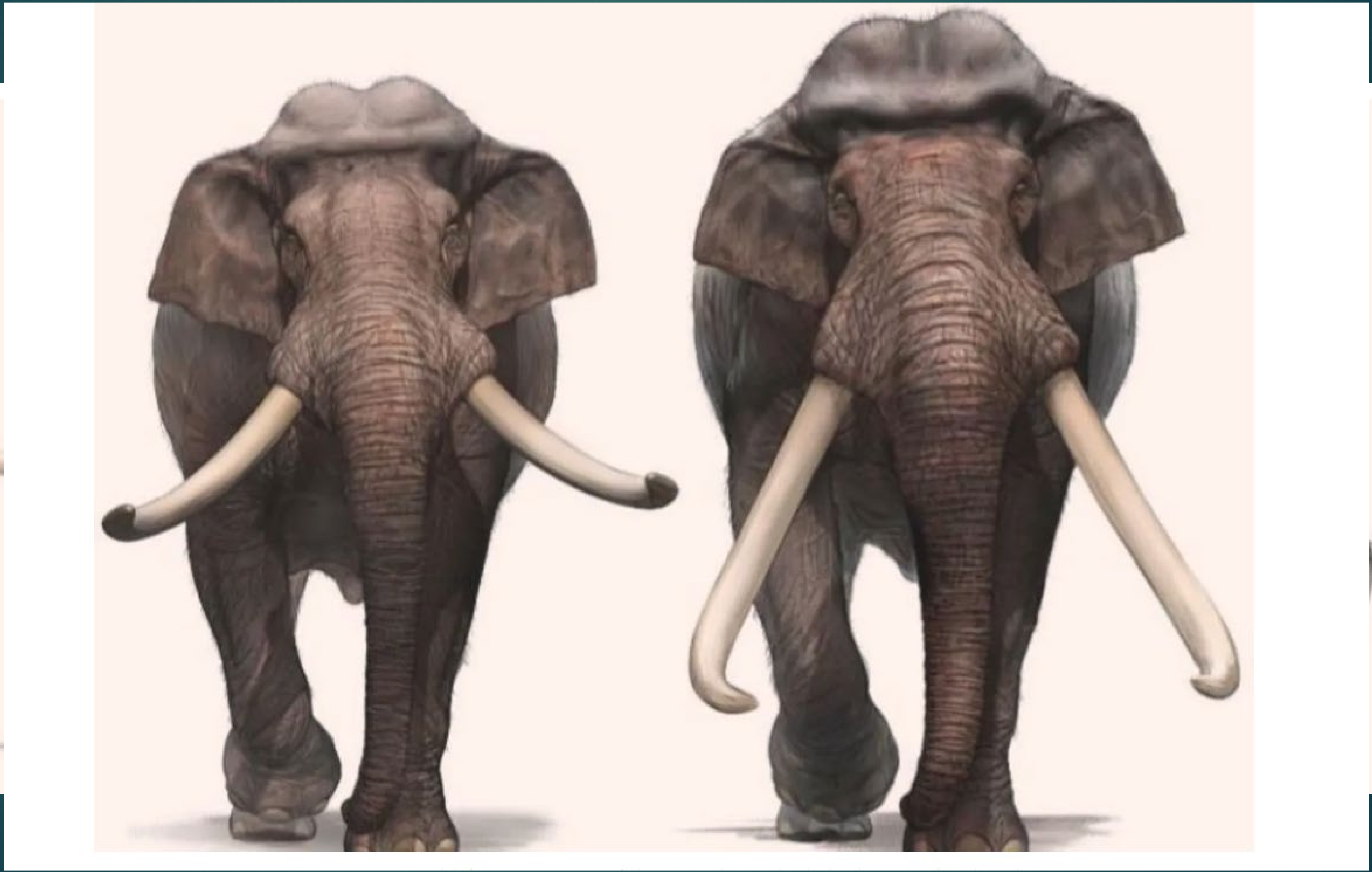
- Expanding beyond the Neumark-Nord site, comprehensive research explored two contemporaneous locations, Gröbern and Taubach, illuminating a widespread practice among Neanderthals in the North European plain.

- The consistency in butchering patterns observed across these sites solidified the assertion that straight-tusked elephant exploitation was not an isolated occurrence but rather a recurring and widespread behavior among Neanderthals.

Sabine Gaudzinski-Windheuser *et al*. 2023

Straight-Tusked Elephants

- The straight-tusked elephants (*Palaeoloxodon antiquus*), the largest land mammals of all time, were colossal creatures.
- With a head width and tusk length far surpassing living elephants, these creatures reached an astounding three times the size of Asian elephants, twice the size of African elephants, and even dwarfed woolly mammoths.
- Estimates suggest shoulder heights of 10 to 14 feet and body masses ranging from 4.5 to 13 tons for females and males, respectively

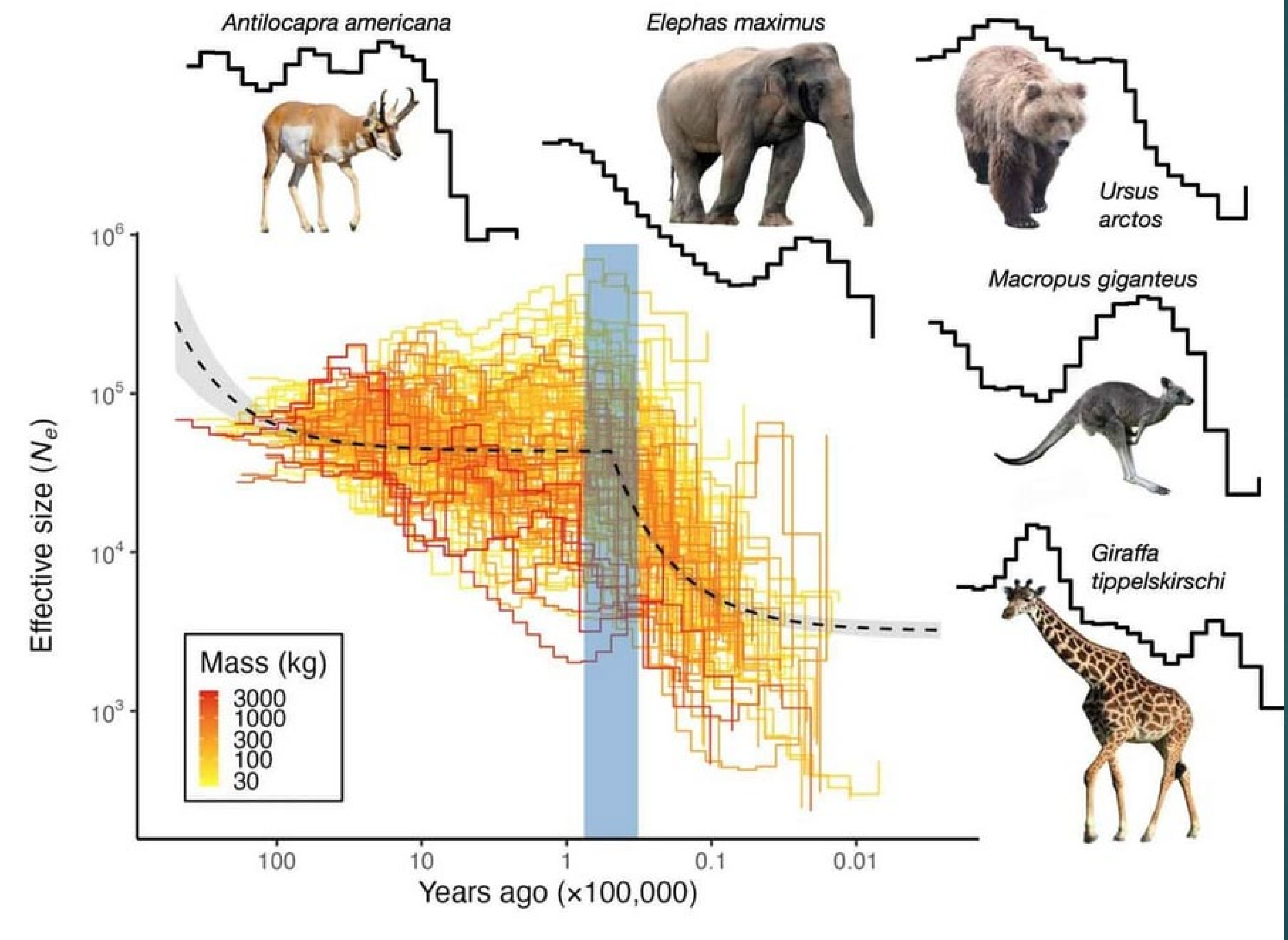


Ns in Germany hunted 13-foot-tall straight-tusked elephant; (28,000 lbs).

Twice as big as today's African elephant

Credit: Lutz Kindler, LEIZA

Megafauna decline



Plot showing effective population size histories for 139 species of living large mammals. The line for each species is coded by body size, with the largest-bodied mammals red and medium-sized ones yellow. The breakpoint analysis identified a range between 76,000 and 32,000 years ago in different geographic regions.

Pleistocene overkill hypothesis

- Going back to the nineteenth century, naturalists thought that the Ice Age megafauna became extinct when the climate changed to the much warmer conditions of the present day.
- During the 1960s, the paleontologist Paul Martin proposed an alternative: Ancient humans had hunted the prehistoric beasts to extinction. Martin built this "Pleistocene overkill hypothesis" from the observation extinctions across different continents and islands did not correspond with the global end of the last glaciation.
- In some regions, especially the Americas, Australia, and Madagascar, extinctions seemed to follow the first arrival of humans. In defense of the climate-induced extinction hypothesis, many researchers have focused upon lesser-known climate events that preceded the Last Glacial Maximum but may nonetheless have made survival harder for megafauna.

Megafauna collapse 76-32 Ka

- Not only extinct species but also surviving large mammals suffered population declines during the Late Pleistocene.
- This year, Juraj Bergman and collaborators used DNA from more than 100 species of Pleistocene survivors to examine when each species declined in numbers.

- These species show substantial disruptions in their demographic histories during the Late Pleistocene.

- Bergman and coworkers found a shared pattern: a collapse in numbers between 76,000 and 32,000 years ago. That timeframe is earlier than the Last Glacial Maximum around 18,000 years ago, and also much earlier than the end of the Pleistocene 10,000 years ago.

Humans involved in collapse

- The timeline of known climate events does not match up well with these demographic reconstructions.
- The species did not share any consistent pattern across previous glacial cycles, giving weight to the often-heard argument that so many species survived every Pleistocene glaciation but the last one.
- Bergman and coworkers found that the shared pattern of collapses could be explained by considering a model that includes the times of human habitation for regions where each species lives.

*** Neandertal ancestry through time: Insights from genomes of ancient and present-day humans – L. N. M. Iasi, et al. 2024

- We identify the location and size of introgressed Neandertal ancestry segments in more than 300 genomes spanning the last 50,000 years.
- Study of the time and duration of the original Neandertal gene flow.
- Found the correlation of Neandertal segment locations across individuals and their divergence to sequenced Neandertals, both support a model of a single major Neandertal gene flow.

Fast natural selection effects

- Our catalog of introgressed segments through time confirms that most natural selection, both positive and negative, on Neandertal ancestry variants occurred immediately after the gene flow,

- The sequencing of the Neandertal and Denisovan genomes has revealed extensive gene flow between the ancestors of modern humans and archaic hominins.

- As a result, most non-Africans harbor 1–2% of Neandertal ancestry, with East Asians exhibiting ~20% more Neandertal ancestry compared to West Eurasians.

N ancestry

- The distribution of Neandertal ancestry is not uniform across the MH genome:
  - some regions are significantly depleted of Neanderthal ancestry (referred as “archaic deserts”),
  - while other regions contain variants at unusually high frequency possibly because they harbor beneficial mutations (“candidates of adaptive introgression”).
- Sample: used genomic data from 59 ancient modern human individuals ranging between 45,000–2,200 yBP, including 33 individuals that are older than 10,000 years. We also include the genomes from 275 diverse present-day individuals from worldwide populations

Divergences

- In contrast, secondary Neandertal gene flow events (private to some populations) would introduce ancestry at new genomic locations, and would thus lead to populations with largely uncorrelated ancestry patterns and increased level of unique ancestry.

- Furthermore, gene flow events from genetically differentiated Neandertal populations would result in differences in divergence estimates between the introgressing segments and the reference Neandertal genomes.

*** New estimate of N gene flow into MHs at 47 Ka

- The Early Out of Africa cluster has large amounts of unique Neandertal ancestry.

- Some Neandertal ancestry in these older individuals is not shared with modern humans after 40,000 years

- *** Neandertal gene flow occurred between 321 and 950 generations before these individuals lived. Infer the average generation interval as 28.4 years and the time of the shared pulse of Neandertal gene flow as 46,364 yBP [45,682-47,045 yBP].

Conclusions

- *** In summary, the sharing of Neandertal segments supports
  - a single major Neandertal gene flow event into the common ancestors of all surviving lineages of non-Africans
  - that occurred ~47,000 years ago
  - with a duration of ~6,800 years.
- This gene flow continued, to some extent, as early modern humans spread throughout Eurasia but did not leave detectable traces in later populations.

Frequency of N variants has changed through time

- Using Neandertal segments in ancient and present-day individuals, recovered Neandertal ancestry in 61.7% (1,551 Mb) of the autosomal genome.
- On the X-chromosome, we find Neandertal ancestry only in 18.7% (29Mb / 154.84 Mb) of the genome.
- The distribution of Neandertal ancestry segments on X chromosome is non-uniform and non-random distribution, with large regions devoid of any Neandertal segments.

Amount of N DNA: 347 N genes survived

- Regions under constraint (related to viability) consistently harbor less Neandertal ancestry compared to the rest of the genome.

- For instance, in individuals older than 30,000 yBP, initial gene flow may have been >5% in modern humans

- To identify candidate regions of natural selection, we examined how the frequency of Neandertal segments changed with time.

N genes

- Segments that harbor beneficial alleles may increase in frequency as a result of positive selection or adaptive introgression, while segments carrying deleterious alleles are predicted to be purged quickly, leading to Neandertal deserts.
- Identified 86 regions (347 genes) that are at high-frequency (99.9th percentile) in both present-day and ancient individuals
- Find these candidate regions are enriched for pathways related to skin pigmentation, metabolism and immunity; many of these N genes were immediately beneficial to modern humans as they encountered new environmental pressures outside Africa.

Beneficial N genes

- 91 candidate regions (169 genes) that are present at high frequency in present-day individuals but not in ancient individuals, indicating that these regions may contain variants that became adaptive later on.

- We also find 32 candidate regions (102 genes) that were at high frequency in ancient DNA individuals but not in present-day individuals. Many of these regions (~44%) are located within 1Mb of candidate regions at high frequency, suggesting that these haplotypes hitchhiked with beneficial mutations and decreased in frequency as recombination occurred.

Gene flow effects and N deserts

- The most significant is a 2 Mb region on chromosome 2 where the highest Neandertal ancestry in ancient individuals is 64% and in present-day individuals is 67%.
- This region contains 12 genes that have been associated with intellectual disability and autism disorders. Another example is BNC2, a gene that plays a role in skin pigmentation, that is at ~25% frequency in Early OOA and ~65% in present-day individuals, indicating that variants at this locus may have been immediately beneficial and increased over time in modern humans

Deserts

- Notably, we find almost no introgressed Neandertal segments within the boundaries of four out of five deserts in ancient or present-day individuals. This indicates that the deserts formed rapidly after the initial gene flow,.

- We find that Neandertal ancestry on the X chromosome is already depleted in Early OoA individuals, and the X-to-autosome ratio of Neandertal ancestry remains stable over time.

Consistencies

- Concordantly, we find large regions that are depleted of Neandertal ancestry in our earliest time intervals.

- *** In summary, the majority of positive and negative selection on Neandertal ancestry happened very quickly, and left clear signals in the genetic diversity of the first modern humans outside Africa. Only a smaller proportion of variants became adaptive later on.

Neanderthal–human baby-making was recent — and brief

- Analysis of dozens of ancient genomes reveals that close encounters between the two species took place in a narrow time window.
- Found that the genetic intermingling lasted for only a short time, at least on an evolutionary scale.
- The high-resolution analysis also allowed the authors to track when certain Neanderthal DNA sequences appeared in the *H. sapiens* genome and determine whether they were retained
- Previous estimates indicated that this mixing occurred over a broad period between 50,000 and 60,000 years ago, but the actual timing of this ‘gene flow’ and its long-term consequences remain poorly understood.

Negative selection

- *** Many of the Neanderthals’ genomic contributions were subsequently removed with remarkable speed from the *H. sapiens* genome.

- *** Modern human genomes contain vast ‘deserts’ that have been fully cleared of Neanderthal remnants — but the authors detected these deserts even in ancient genomes from the latest stages of human–Neanderthal interaction

- *** Many Neanderthal sequences could have been detrimental to humans, and were therefore actively and rapidly selected against by evolution.

Responses

- Rajiv McCoy, a population geneticist at Johns Hopkins University, noted that other instances of interbreeding might have occurred without leaving lasting genetic traces. For example, a modern human jaw from 37,000 to 42,000 years ago found in Romania contains Neanderthal DNA not present in other modern genomes, suggesting isolated interbreeding events.

- Chris Stringer emphasized that this new estimate of 47,000 years ago for Neanderthal interbreeding influences our understanding of human dispersal from Africa. This timeframe constrains the dispersal of modern human ancestors to less than 47,000 years ago. However, evidence of human occupation in northern Australia around 65,000 years ago poses questions.

-

Stringer

- Stringer suggested that either this evidence is incorrect, those early populations went extinct or were overwhelmed by later dispersals, or they were not *Homo sapiens*, which is less likely given the complex behavior implied by the evidence.

- Curiously, the exchange of DNA appears to have been one-way—modern human DNA does not seem to have entered Neanderthal genomes. Stringer noted,

One-way DNA: N into MH only, Not MH into N

- "There is little evidence of gene flow in the reverse direction at this time—that is, Homo sapiens to Neanderthal."
- This absence of reciprocal gene flow could imply behavioral differences between the two populations or possible disadvantages for hybrids, such as reduced health or fertility.

*** But see the next ingenious new study, Harris et al. 2024, about MH DNA into N DNA.

*** Diverse African genomes reveal selection on ancient modern human introgressions in Neanderthals

- Anatomically modern human-to-Neanderthal introgression occurred ~250,000 years ago
- ~6% of the Altai Neanderthal genome was inherited from anatomically MH
- Recent non-African admixture brought Neanderthal ancestry to some African groups

D. N. Harris, … S. Tishkoff, et al., 2023

N DNA in Africans

- Modern human alleles were deleterious to Neanderthals
- Dr. Tishkoff and her colleagues compared the genome of a 122,000-year-old Neanderthal fossil with the genomes of 180 people from 12 populations across Africa.
- Previous studies had found no sign of Neanderthal DNA in African genomes. But Dr. Tishkoff's group detected tiny pieces of Neanderthal-like DNA scattered across all 12 of the populations they studied.

N DNA in Africans

- *** Also concluded that Neanderthals inherited DNA from early Africans. That meant an early wave of Africans expanded into Europe or Asia about 250,000 years ago and interbred with Neanderthals.

- *** Comparisons of Neanderthal genomes to anatomically modern human (AMH) genomes show a history of Neanderthal-to-AMH introgression stemming from interbreeding after the migration of AMHs from Africa to Eurasia.

- All non-sub-Saharan African AMHs have genomic regions genetically similar to Neanderthals that descend from this introgression. Regions of the genome with Neanderthal similarities have also been identified in sub-Saharan African populations, but their origins have been unclear

N DNA in sub-Saharan Africa & 6% MH DNA in Ns

- Analyzed a dataset of whole-genome sequences from 180 individuals from 12 diverse sub-Saharan African populations.
- *** In sub-Saharan African populations with non-sub-Saharan African ancestry, as much as 1% of their genomes can be attributed to Neanderthal sequence introduced by recent migration, and subsequent admixture, of AMH populations originating from the Levant and North Africa.
- *** However, most Neanderthal homologous regions in sub-Saharan African populations originate from migration of AMH populations from Africa to Eurasia ~250 kya, and subsequent admixture with Neanderthals, resulting in ~6% AMH ancestry in Neanderthals.

Speciation hallmark

- These results indicate that there have been multiple migration events of AMHs out of Africa and that Neanderthal and AMH gene flow has been bi-directional.
- Observing that genomic regions where AMHs show a depletion of Neanderthal introgression are also regions where Neanderthal genomes show a depletion of AMH introgression points to deleterious interactions between introgressed variants and background genomes in both groups—a hallmark of incipient speciation.
- Joshua Akey has reached same conclusion.

*** Akey Lab: Neandertals and H. sapiens comingled

- Modern human and Neanderthal populations "shared a long history of exchanging individuals.”
- Now, a study of ancient DNA turns the tables on Neanderthals and asks: What did they (Ns) get from us (MHs)?
- *** A paper this week in Science (L. Li, et al., 2024) concludes Neanderthals inherited as much as 10% of their genome from modern humans, including several genes involved in brain development.
- The Neanderthal-eye view allowed the researchers to date when the two groups mingled: more than 200,000 years ago. These introgressions were repeated 105,000 to 120,000 years ago, and 45,000 to 60,000 years ago, the ancient Neanderthal DNA suggest.

New method finds heterozygosity

- This study relied on the fact that both modern humans and Neanderthals generally possess two versions of every gene, one inherited from the father, the other from the mother.

- *** Because the two groups were more different from each other than they were from others of their own kind, interbreeding between Neanderthals and humans would lead to offspring that had a higher chance of possessing two different versions of each gene — a situation known as heterozygosity — than children that did not result from such interbreeding.

Used an ingenious method

- *** They reasoned that:
  - in the Neanderthal genome, segments of DNA inherited from MHs should stand out by having more genetic diversity, or heterozygosity, than surrounding DNA.
  - That's because genetic diversity reflects population size,
  - and previous genomic work showed modern humans long outnumbered Neanderthals.

- The researchers scanned the published genomes of three Neanderthals from Croatia and Siberia to see whether they actually had such regions of high heterozygosity from MHs—and they did.

Segments of heterozygosity

- To confirm that the variable DNA segments originated in ancient modern humans, the researchers searched for the segments in the genomes of living Africans, whose ancestors rarely encountered the Eurasia-based Neanderthals
- *** The segments of heterozygosity were present, implying they originated in ancient modern humans in Africa, not in Neanderthals.
- Some of those people stayed in Africa and passed the segments to living Africans; others left and bequeathed the diverse alleles to Neanderthals.

Hunting for DNA segments

- "The method's ingenious—it uses very small bits of modern human DNA in Africans to learn about what Neanderthals got from us," says Chris Stringer of the Natural History Museum in London.

- *** By analyzing the length and other features of the diverse segments of modern human DNA, Akey and Li could calculate when and how often these ancient hookups happened. The smaller the stretches of DNA, the earlier Neanderthals got them, because inherited segments get shorter over generations.

Early mating of Ns and MHs

- The first mating episode the team spotted was very ancient—200,000 to 250,000 years ago, around the time anatomically modern humans first show up in the fossil record in Africa.

- The team speculates that perhaps some early modern humans crossed the Sahara Desert when the climate was humid, on the trail of antelope, ostrich, and other game, and eventually wandered to the Middle East, where they met the Neanderthals.

Other introgression dates of MH into N

- Akey’s team dated another round of Neanderthal-modern mating to about 105,000 to 120,000 years ago. Researchers speculate those encounters, too, could have happened in the Middle East, because modern humans and Neanderthals are known to have lived in nearby caves at that time.
- A recent, not-yet peer-reviewed study suggests that most Neanderthal DNA seen in the modern human genome resulted from a single major period of interbreeding about 47,000 years ago that lasted about 6,800 years.
- Interbreeding that occurred at other times, such as the earlier events that impacted the Neanderthal genome, likely did not leave a detectable trace in our genome.

Ns had even smaller populations: less than 3000

- The third bout of mixing is the familiar one, about 50,000 to 60,000 years ago, likely in the Middle East or Europe, where Neanderthals and modern humans overlapped for thousands of years.

- If some of the diverse DNA in Neanderthals came from modern humans, then our cousins had even less genetic diversity than previously thought—and therefore even smaller populations.

- The study implies Neanderthal numbers dwindled between 250,000 years and 40,000 years ago, and that by the end of their time on the planet, their breeding population was less than 3000, compared with at least 10,000 breeding modern humans, Akey says.

Ns were absorbed by MH population

- Stringer says Neanderthal numbers may have been so small because they mostly lived in northern regions where they were vulnerable to climate change and glaciation.
- People with Neanderthal genes didn’t abruptly vanish, Akey says—their offspring just acquired more and more modern human DNA. They were overwhelmed by waves of modern humans extending out of Africa. The modern human population eventually absorbed the Neanderthals.

Ns were absorbed by MH population

- "Recurrent waves of modern human migrations out of Africa eventually overwhelmed the ability of Neanderthals to remain a distinct population, and they were ultimately just assimilated into the modern human gene pool."
- “This paper closes the loop in terms of us thinking about ‘us’ versus ‘them”.

*** Recurrent gene flow between Neanderthals and modern humans over the past 200,000 years – L. Li, et al., 2024

- A number of methods have been developed to identify Neanderthal-introgressed sequences in the DNA of modern humans; the consequences of admixture on the Neanderthal genome have received comparatively less attention.
- *** Developed a simple method to investigate introgressed human sequences in Neanderthals that is predicated on the expectation that sequences inherited from modern human ancestors would be, on average, more genetically diverse and would result in local increases in heterozygosity across the Neanderthal genome.

Liming Li, Troy J. Comi, Rob F. Bierman, Joshua M. Akey, 2024

What we currently know about MH-N-D gene flow

- There was gene flow/introgression:
  - between modern humans and Neanderthals,
  - between modern humans and two distinct Denisovan populations
  - between Neanderthals and Denisovans,
  - including Denny, an F1 hybrid who had a Neanderthal mother and Denisovan father.
  - in modern humans, non-African individuals derive ~2% of their genome from Neanderthal ancestors
  - individuals of Melanesian and Australian aboriginal ancestry can trace an additional 2 to 5% of their genome to Denisovan ancestors, with the highest levels in certain Philippine groups

MH gene flow into Ns

- In contrast to the detailed studies of how admixture with Neanderthals affected the genomes of modern humans, comparatively little is known about the consequences that admixture had on the Neanderthal genome.

- Several studies have shown evidence of modern human ancestry in the Neanderthal genome as a result of admixture that predates the out-of-Africa dispersal of ~60 thousand years ago, to which contemporary non-Africans can trace the majority of their ancestry.

MH DNA in Ns

- Thus, admixture between modern humans and Neanderthals has occurred at least twice, with one admixture resulting in modern human–to-Neanderthal (H→N) gene flow ~250 to 200 ka and the other admixture resulting in Neanderthal-to–modern human (N→H) gene flow ~60 to 50 ka.

- The signal of modern human–to-Neanderthal gene flow was initially detected in the Altai Neanderthal but was also subsequently found in the Vindija, which suggests that admixture occurred before the divergence of these two lineages

MH DNA in Ns

- Questions about the dynamics and significance of introgressed modern human sequence in the Neanderthal genome:
  - Neanderthals had a substantially lower effective population size (denoted as Ne)
  - and, thus, less genetic diversity compared with modern humans.

- Therefore, modern human–introgressed sequences in Neanderthals may affect inferences of Neanderthal genetic diversity and population genetics parameters. MH DNA in Ns may confound inferences about how such Neanderthal ancestry exists in modern human individuals.

H→N and N→H gene flow

- Their model: takes advantage of the well-known differences in Ne between modern humans and Neanderthals.

- Our approach derives power from the fact that
  - both H→N and N→H gene flow make substantial contributions identified in African individuals,
  - whereas the signal of Neanderthal-introgressed sequences detected in non-African individuals is primarily the result of N→H admixture

- Study identified 92.4, 85.5, and 84.3 gigabases (Gb) of introgressed Neanderthal sequence across all 2000 MH individuals using the Vindija Neanderthal, Altai Neanderthal, and Chagyrskaya Neanderthal as the archaic reference genome, respectively

Regions of high heterozygosity in Neanderthal genomes are enriched for introgressed MH sequences

- Demonstrates that regions of high heterozygosity in the Neanderthal genome are enriched for modern human–introgressed sequences.
- In summary, these data provide additional evidence that introgressed modern human sequences contribute to regions of high heterozygosity in the Neanderthal genome.
- This method can be leveraged to quantitatively identify the proportion of introgressed sequences in modern humans due to H→N and N→H gene flow.

Estimating the proportion of modern human ancestry in Neanderthals: Ns had 2.5 to 3.7% MH DNA

- Estimate that Vindija and Altai N genomes contain 53.9 and 80.0 Mb of modern human–introgressed sequence, respectively. this corresponds to ~2.5 and 3.7% modern human ancestry in Vindija and Altai, respectively, which is higher than the estimated amount of Neanderthal ancestry in present-day modern humans. That is akin to 1 in 30 modern human parents in the ancestral Neanderthal population.
- Revising estimates of Neanderthal ancestry in modern humans: When using Vindija as the Neanderthal reference genome, IBDmix identified a total of 62.3, 60.1, and 55.8 Mb of Neanderthal sequence per individual in East Asians, South Asians, and Europeans, respectively.

H→N and N→H gene flow

- The percentage of total IBDmix identified Neanderthal sequence attributable to N→H gene flow is 91.1% (56.8 Mb), 92.3% (55.5 Mb), and 91.8% (51.2Mb) in East Asians, South Asians, and Europeans, respectively.

- These data show that Neanderthal-introgressed sequences in Africans and non-Africans are influenced by both H→N and N→H gene flow but their relative contributions differ among populations.

Neanderthals had significantly smaller population sizes than previously thought

- The presence of MH sequences in Neanderthal genomes could potentially influence estimates of their population size.
- Without accounting for H→N gene flow, the estimated long-term Ne of Altai, Chagyrskaya, and Vindija were 3369, 2964, and 3408 individuals, respectively, which is similar to previous estimates.
- The estimated long-term Ne significantly decreased in all three Neanderthal lineages. Specifically, the estimated Ne in Altai, Chagyrskaya, and Vindija decreased to 2484, 2379 and 2807 individuals, respectively. This constitutes a reduction in the long-term Ne of 26.3% in Altai, 19.7% in Chagyrskaya, and 17.5% in Vindija.
- Observed amount of human to Neanderthal gene flow can inflate estimates of Ne in Neanderthals

20% Smaller N population size (Ne)

- However, when accounting for modern human–introgressed sequences, we found that the Ne of Vindija is 13% higher than that of Altai, which suggests that Altai had a smaller Ne after it split with other Neanderthal lineages.
- Estimate that the Ne of the Altai and Chagyrskaya lineages are 45 and 27%, respectively, the size relative to the Vindija lineage
- *** These data show that Neanderthals had smaller and more variable population sizes among lineages than previously thought. The ~20% lower estimate of long-term Ne has important implications for the cost of introgression to modern humans because it potentially allowed more deleterious mutations to accumulate in Neanderthals that were subsequently Altai, which inherited by the ancestors of predominantly non-African populations

Evidence for two distinct pulses of modern human–to-Neanderthal gene flow

- Although previous studies have found evidence for gene flow from modern humans to Neanderthals, they assumed a single period of admixture.

- *** Found that our data are most consistent with models where the H→N admixture fraction was 5% and the time of admixture was 200 ka or where the admixture fraction was 10% and the time of admixture was 250 ka,

.

Evidence for two distinct pulses of modern human–to-Neanderthal gene flow

- Asked whether Vindija, Chagyrskaya, or both Vindija and Chagyrskaya received an additional wave of H→N admixture relative to Altai

- Two distinct pulses of MH to N gene flow: Results are broadly concordant between Vindija and Chagyrskaya and are consistent with a second pulse of modern human–to-Neanderthal gene flow ~120 to 100 ka of substantially smaller magnitude relative to the first wave of H→N admixture

*** Abstract

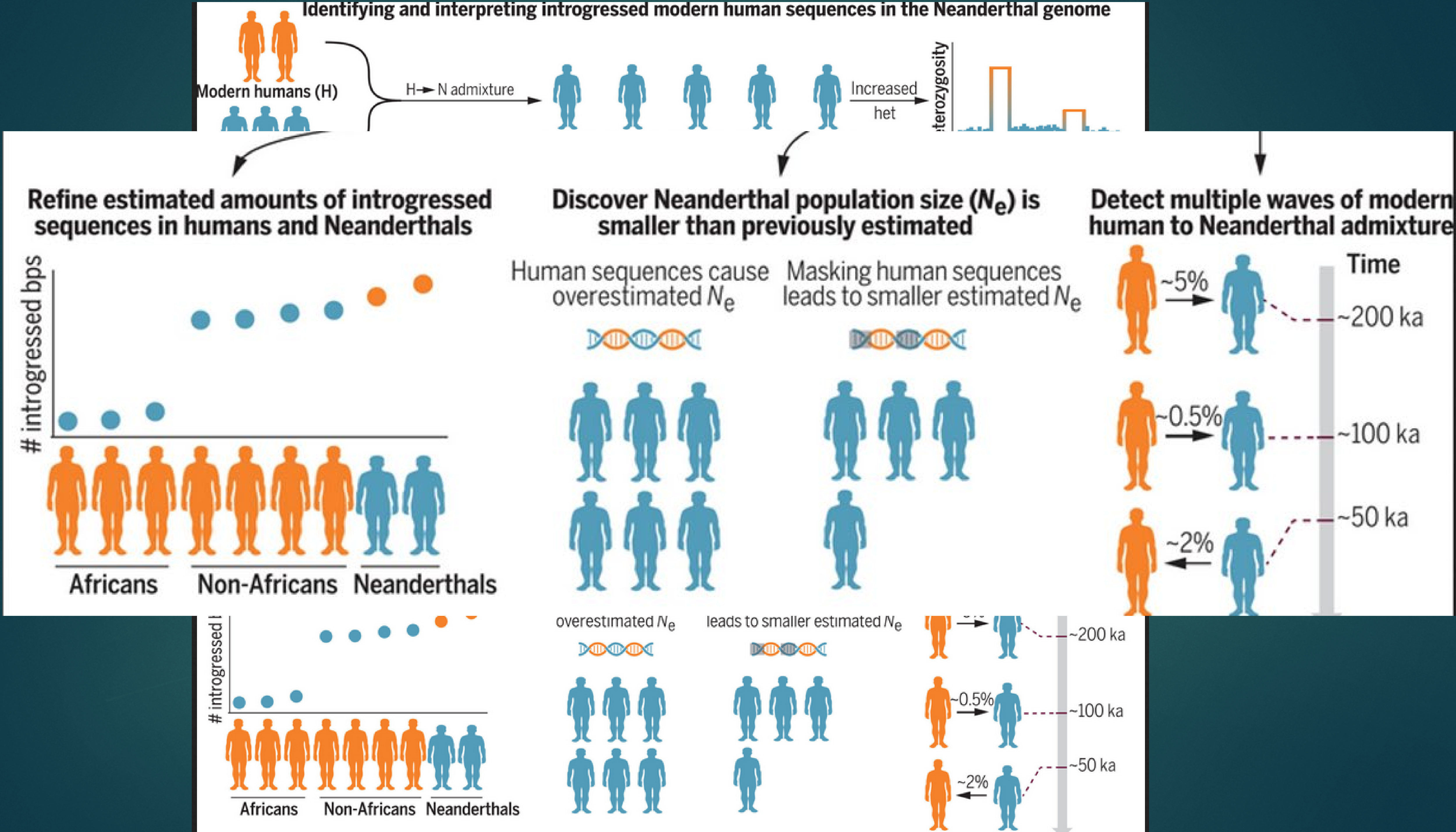
- *** Developed methods to estimate the amount of human-introgressed sequences in Neanderthals and apply it to whole-genome sequence data from 2000 modern humans and three Neanderthals.
  - estimate that Neanderthals have 2.5 to 3.7% human ancestry,
  - leverage human-introgressed sequences in Neanderthals to revise estimates of Neanderthal ancestry in modern humans,
  - show that Neanderthal population sizes were significantly smaller than previously estimated
  - identify two distinct waves of modern human gene flow into Neanderthals

IBDmix method: find MH heterozygote basepairs in Ns

- Used a method referred to as IBDmix to identify introgressed Neanderthal sequences in 2000 modern humans sequenced by the 1000 Genomes Project.
- We found that sequences identified by IBDmix as Neanderthal in African individuals are significantly enriched in regions of high heterozygosity in the Neanderthal genome, whereas no such enrichment is observed with sequences detected as introgressed in non-African individuals.
- We show that these patterns are caused by gene flow from modern humans to Neanderthals and estimate that the Vindija and Altai Neanderthal genomes have 53.9 Mb (2.5%) and 80.0 Mb (3.7%) of human introgressed sequences, respectively.

Reduced N population size

- We leverage human-introgressed sequences in Neanderthals to revise estimates of the amount of Neanderthal introgressed sequences in modern humans.
- Additionally, we show that human-introgressed séquences cause Neanderthal population size to be overestimated and that accounting for their effects decrease estimates of Neanderthal population size by ~20%. The smaller estimated population size and inferred admixture dynamics are consistent with a Neanderthal population that was decreasing in size over time and was ultimately being absorbed into the modern human gene pool
- Finally, we found evidence for two distinct epochs of human gene flow into Neanderthals.


Identifying and interpreting introgressed modern human sequences in the Neanderthal genome
Modern humans (H)
H→N admixture
Increased het
Heterozygosity
Refine estimated amounts of introgressed sequences in humans and Neanderthals
introgressed bps
Africans
Non-Africans
Neanderthals
Discover Neanderthal population size (N_e) is smaller than previously estimated
Human sequences cause overestimated N_e
Masking human sequences leads to smaller estimated N_e
Detect multiple waves of modern human to Neanderthal admixture
Time
~5%
~200 ka
~0.5%
~100 ka
~2%
~50 ka

Prior slide

- Detecting modern human–to-Neanderthal gene flow (H→N) and its consequences.

- Modern human–to-Neanderthal admixture causes a local increase in heterozygosity in the Neanderthal genome, a characteristic that enabled approaches to quantify and detect introgressed sequences.

- We also used modern human–introgressed sequences to discover that:
  - Neanderthals had a smaller effective population size (N_e) than previously estimated and that
  - a second wave of modern human–to-Neanderthal gene flow occurred ~100 to 120 thousand years ago (ka). bps, base pairs.

Conclusions

- There is a now well-characterized admixture that occurred between these lineages ~60 to 50 ka, which resulted in the introgression of 1-2% Neanderthal sequences into modern human genomes.
- In this work, we provide insights into the long admixture history and dynamics of gene flow between modern humans and Neanderthals.
- Our data, along with previous studies, show that recurrent episodes of gene flow, beginning ~250 to 200 ka, resulting in modern human gene flow into Neanderthals.

H→N and N→H gene flow

- find that both H→N and N→H gene flow of Neanderthal-introgressed sequence in the 1000 Genomes Project populations.
- In the non-African populations studied, N→H gene flow accounts for ~90% of detected introgressed sequences, whereas in the African populations studied, H→N gene flow explained 61 to 82% of the signal depending on the specific population and Neanderthal reference genome used.
- Similarly, Harris et al. recently used IBDmix to identify Neanderthal-introgressed sequences in 12 sub-Saharan African populations.

H→N and N→H gene flow

- Nonetheless, it seems clear that:
  - although all contemporary human populations harbor the signal of a shared historical dispersal that led to H→N gene flow,
  - the amount of introgressed segments attributable to N→H admixture is unevenly distributed across the African continent.
- More studies needed in Africa.

OLLI Science Update
August 2024

C3 vs C4 dates and types

N→H gene flow

- The initial wave of H→N admixture occurred ~250 to 200 ka and represents an early dispersal of modern humans from Africa. For example, the first morphological features of anatomically modern humans emerged in Africa ~300 ka, and fully anatomically modern fossil remains discovered in southern Ethiopia date to a minimum age of 233 ka.
- Thus, early to fully anatomically modern humans existed in this time frame. Additionally, the fossil record shows that early modern humans had dispersed out of Africa by at least ~200 ka.
- Of particular relevance is the Apidima 1 fossil from the Apidima Cave in southern Greece that dates to ~210 ka, which shows that these early out-of-Africa diasporas were not confined to the Levant

MH to D gene flow?

- Where the first wave of H→N admixture occurred is unknown.

- Need future studies that look for evidence of modern human–to-Denisovan gene flow

Hx of earlier migrations

- Found evidence for an additional pulse of modern human–to-Neanderthal gene flow ~120 to 100 ka. This timing is consistent with the presence of the Nile-Sinai land bridge between 130 and 96 ka and fossil and archeological data showing that modern humans reached the Levant and Arabian Peninsula in this time frame.

- Data demonstrate that although contemporary non-African populations can trace much of their ancestry to a single out-of-Africa dispersal 50 to 60 ka, these early, effectively extinct dispersals of modern humans out of Africa nonetheless played an important role in hominin evolutionary history.

Admixture history & N extinction

- This new data offers a perspective on factors possibly related to the disappearance of Neanderthals.
- *** Specifically, we show that the magnitude of H→N gene flow decreased through time, from 5 to 10% at 250 to 200 ka, to 0.5% at 120 to 100 ka, to 0% for late Neanderthals who lived between 47 and 39 ka.
- *** Conversely, as H→N gene flow ceased, numerous examples of N→H admixture began to appear. These include:
  - N→H gene flow ~60 to 50 ka with an initial Neanderthal admixture proportion as high as 10%,
  - possible additional waves of N→H admixture in specific modern human populations such as East Asians,
  - ancient DNA from several early modern humans who lived ~39 to 45 ka that show evidence of more-recent N→H gene flow.

Pattern lead to N extinction

- *** This asymmetric admixture pattern, where gene flow is primarily detected in one direction, initially from H→N but then from N→H, suggests a Neanderthal population that was decreasing in size over time, eventually reaching a point where it was not large enough to absorb modern humans into their gene pool.
-
- *** At this time, gene flow reverses direction (N→H), and the one-way flow of Neanderthal genes into modern humans may have contributed to the extinction of Neanderthals.

N extinction: YDNA and mitochondrial replacement

- *** Specifically, the assimilation of Neanderthals into modern human populations as they spread throughout Eurasia would have effectively increased the size of modern human populations while simultaneously decreasing the size of an already at-risk Neanderthal population.
- Our finding that the effective population size of Neanderthals was likely even smaller than previously estimated would only hasten the assimilation process, and the replacement of the Y chromosome and mitochondrial DNA in late Neanderthals by modern humans may have marked an irrevocable path toward the disappearance of one of the few remaining hominin lineages that coexisted with modern humans.