Scientific Update

August 2023

by

Charles J Vella, PhD

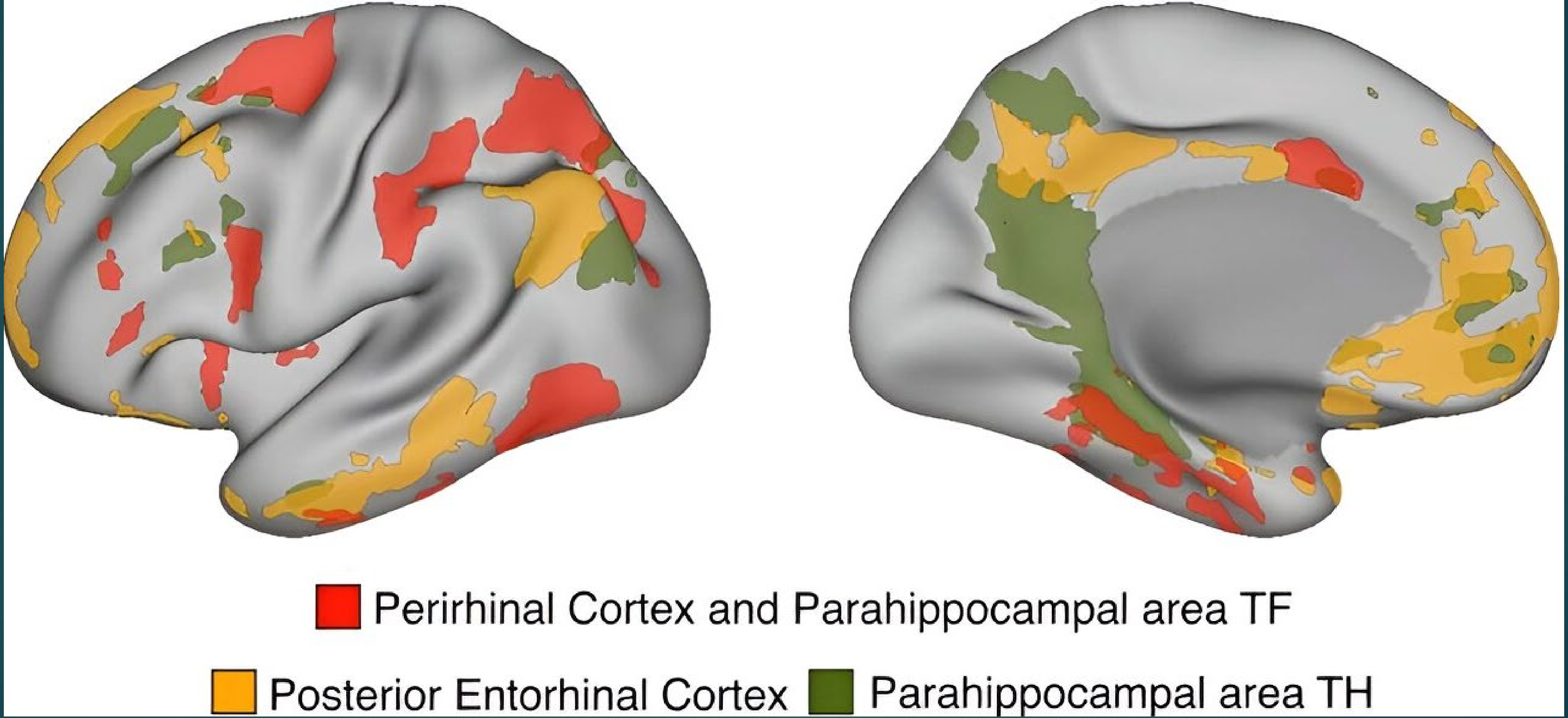
AR15 assault rifle for children – only 2 lbs

Succulent Gibbaeum heathii is endemic to a valley in South Africa; nicknamed “baby’s bum”; 2 inches high

Keep on walking! Number of steps a day

- New metaanalysis of 226,889 people from 17 different studies around the world has shown that the more you walk, the greater the health benefits.
- The risk of dying from any cause or from cardiovascular disease decreases significantly with every 500 to 1000 extra steps you walk.
- An increase of 1000 steps a day was associated with a 15% reduction in the risk of dying from any cause, and an increase of 500 steps a day was associated with a 7% reduction in dying from cardiovascular disease.

Cortical networks associated with the human medial temporal lobe that were unknown to previous memory research.



MTL and brain networks

- Human MTL is associated with at least three distributed cortical networks

- Discovered three biologically meaningful networks associated with the entorhinal cortex, perirhinal cortex, and parahippocampal area TH, respectively.

Autopsied Alzheimer's brain deficient in antioxidants

- Concentrations of lutein, zeaxanthin, lycopene, retinol, and α-tocopherol are profoundly lower in brains with documented AD, that lycopene and zeaxanthin were the two most deficient antioxidants.
- Eat green, yellow and orange veggies: dark leafy greens/spinach, chard, kale, peas, summer squash, zucchini, pumpkin, brussels sprouts, broccoli, asparagus, lettuce, carrots, sweet potatos, pistachios, tomato products, fruits.
- Eat liver, fish, eggs, and dairy products

Heart-brain connections: Phenotypic and genetic insights from magnetic resonance images

- Cardiovascular disorders correlate with some neurological and psychiatric conditions.
- Examined imaging and genetic data from tens of thousands of participants in the UK Biobank and BioBank Japan.
- Analyzed 82 cardiac and aortic MRI-derived traits across six categories: left and right ventricles, left and right atria, and ascending and descending aortas, as well as 458 brain MRI traits that measured structure and function
- Uncovered correlations between structure and function of both the heart and the brain, such as links between specific features of cardiac imaging and neuropsychiatric disorders. Demonstrate shared genetic influences on both the brain and the heart

Bingxin Zhao , et al., 2023

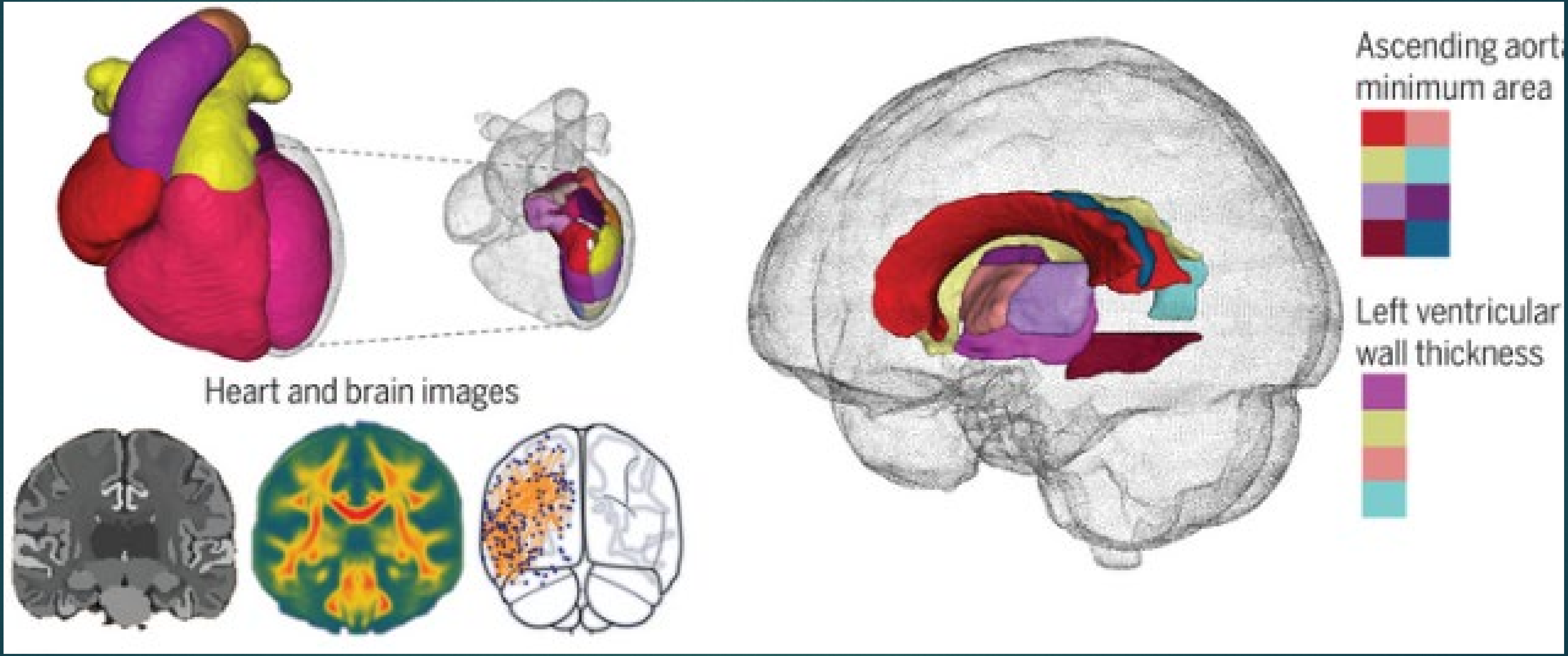
Know evidence of CV-Brain correlations

- Evidence suggests close interplays between heart health and brain health.
- CV diseases are associated with several brain diseases, including stroke, dementia, cerebral small vessel disease, and cognitive impairment.
- Atrial fibrillation to an increased incidence of dementia and silent cerebral damage even in stroke-free cohorts.
- Heart failure is associated with cognitive impairment and eventually dementia, likely because of the reduced cerebral perfusion caused by the failing heart.
- Conversely, mental disorders and negative psychological factors may contribute substantially to the initiation and progression of cardiovascular diseases. Patients with mental illnesses such as schizophrenia, bipolar disorder, epilepsy, or depression show an increased incidence of cardiovascular diseases.
- Acute mental stress may cause a higher risk of atherosclerosis because of stress-induced vascular inflammation and leukocyte migration.

Adverse heart metrics have implications for brain abnormalities and the risk of brain diseases

- Found that heart MRI traits were clearly associated with the brain across all imaging modalities studied. We observed multiple patterns of association for brain gray matter morphometry, white matter microstructure, and functional networks. For example, we found that the left ventricle of the heart showed the strongest correlations with microstructure metrics of cerebral white matter tracts, suggesting that adverse heart features were associated with poorer white matter microstructure.
- Identified genetic correlations between heart MRI traits and various brain complex traits and diseases such as stroke, eating disorders, schizophrenia, cognitive function, and mental health traits. For example, adverse myocardial wall thickness condition was positively genetically correlated with stroke. We further used two-sample Mendelian randomization to explore causal genetic links between the heart and brain, and our findings suggest that adverse heart features have genetic causal effects on several brain diseases such as psychiatric disorders and depression.

Corresponding heart and brain connections



Associations between multimodal MRI measurements of the heart and brain

- Aortic traits were associated with basal forebrain volumes in both the left and right hemispheres. The basal forebrain cholinergic system, which is the primary cholinergic output of the central nervous system, is crucial in cognitive decline and dementia
- Reduced basal forebrain volume and vascular dysregulation are early predictors of Alzheimer’s disease pathology. Moreover, several CV traits were associated with the somatomotor, auditory, and default mode networks in resting fMRI.
- Early intervention in heart conditions and the management of cardiac risk may have a positive impact on brain health. Numerous studies have examined the cognitive and neuropsychiatric effects of anti-hypertensive medications. in a meta-analysis of 209 studies, antihypertensive medications were found to reduce dementia risk by 21%. Brain-penetrant calcium channel blockers were associated with a lower incidence of neuropsychiatric disorders

Reconstruction of Shaihuludia shurikeni from the Spence Shale of Utah: new 500 Ma sea worm, Shai-Hulud is the indigenous name for the giant worms on the planet Arrakis in the "Dune" novels by Frank Herbert,

Epigenetics of Mammalian lifespan

- Mammals vary greatly in life span; for example, the bowhead whale (*Balaena mysticetus*) can live up to 200 years, whereas giant Sunda rats (*Sundamys muelleri*) only live for about 6 months in the wild.
- This disparity is encoded in the genomes of each species. Because mammals have approximately the same genes, variation in how these genes are regulated should be important in determining the timing of aging.
- Haghani *et al.* describe a large-scale study of DNA methylation (which has a role in gene regulation) in a diverse range of mammalian species. They identified genomic regions that might govern life-span variation among lineages, which could help uncover the molecular drivers of life span and other traits in mammals.

DNA methylation

- DNA methylation differences occur mostly at “enhancers,” stretches of DNA that dictate the expression of nearby genes. Thus, each cell type and tissue in the body has a precise DNA methylation signature, like a barcode. Although DNA methylation is frequently not the main factor that dictates gene regulation, it is a robust biomarker for gene activity and cell identity
- Study profiled the DNA methylation of 15,456 samples from 348 species, including up to 70 tissues per species. DNA methylation was profiled in species including the African elephant (*Loxodonta africana*, left), which lives for 70 years on average, and the lab mouse (*Mus musculus*, above), which lives for an average of 2 years.

Importance of stem cells

- Variation in DNA methylation in these genomic regions explained, to some extent, the differences in life span across species.
- This finding is linked to the discovery that as humans and mice age, DNA methylation changes in many genomic regions. This has allowed the construction of so-called “epigenetic clocks,” which are mathematical models that enable the prediction of biological age on the basis of methylation status
- Length of life correlated with availability of Yamanaka stem cell factors (creation of induced pluripotent stem cells). Inducing these factors affects aging in animals.
- The study of Haghani *et al.* shows that DNA methylation can be a powerful biomarker of age across mammals.

Epigenetic clock to determine age via a blood sample

- Aging is evolutionarily conserved and intertwined with developmental processes across all mammals.
- In a newly published study on aging, researchers studied 185 mammals via blood test.
- The epigenetic clock is made possible thanks to millions of small molecules called methyl groups that are bound to our DNA like Christmas lights on a wire. When a cell divides, the DNA in the two new cells typically ends up with the same, distinctive pattern of methyl groups.
- Adding methyl groups around a gene is a step in shutting it off, while removing them may be involved in turning the gene back on.
- In the 1960s, Soviet scientists noticed that as salmon grew old, their DNA became less methylated.

Universal DNA methylation age across mammalian tissues – A. T. Lu, et al., 2023

- Dr. Horvath reported in 2013 that a computer needed to examine just 353 spots in the DNA of a cell to make a guess that was within a few years of a person's chronological age. The research has shown, for example, that smoking, obesity and drinking can add years to the epigenetic clock, and that this acceleration in biological age predicts a greater risk of death.
- Trained a computer to create a new clock that could predict the age of animals based on a single epigenetic pattern across species. It was able to make good predictions about the ages of 185 species by looking at fewer than 1,000 spots in mammal DNA.
- Help to decipher why all mammals — including us — get old.
- No FDA approval for commercial epigenetic clock estimates

Age and methylation

- The consistent age-related alterations in DNA methylation profiles across mammalian species challenges the view that aging is simply due to the random accumulation of cellular damage.
- It is instead a pseudo-programmed process that is also intimately associated with mammalian development that begins to unfold from conception.
- The successful construction of universal clocks is a compelling mathematical demonstration of the deterministic element in the process of aging that transcends species barriers within the mammalian class; related to mortality risk

Methylation sites

- Found a set of methylation sites in DNA sequences conserved across mammals consistently changing with age, predominantly gaining methylation. These sites regulate the expression of genes involved in the process of development, which is one of the most conserved biological processes that threads through all mammalian species

- Progressive methylation loss is exploited as a mitotic (cell division) clock, which also correlates very well with chronological age.

- Opens the path to uncovering interventions that modulate conserved aging processes in mammals.

High-coverage genome of the Tyrolean Iceman reveals unusually high Anatolian farmer ancestry

- Ötzi’s new high coverage genome had an unusually high proportion of genes in common with those of early farmers from Anatolia, that his skin was darker than previously thought, and that he was likely bald or had little hair on his head when he died.
- Very low amount of hunter-gatherer genes in Ötzi's genome
- No steppe ancestry: original study contaminated with MH DNA. From a rather isolated Alpine population with limited gene flow from hunter-gatherer-ancestry-related populations
- Low European hunter-gatherer-related ancestry south of and within the eastern Italian Alps

Ke Wang, et al., 2023

Ötzi

- Darkest skin tone that has been recorded in contemporary European individuals
- Carried risk alleles associated with male-pattern baldness, type 2 diabetes, and obesity-related metabolic syndrome.
- Dated to 3350–3120 BCE

Platelet factor 4

- Platelets are behind the cognitive benefits of young blood, exercise and the longevity hormone klotho. In a remarkable convergence, scientists have discovered that the same blood factor is responsible for the cognitive enhancement that results from young blood transfusion, the longevity hormone klotho, and exercise.
- Trio of papers appearing in *Nature*: identify platelet factor 4 (PF4) as a common messenger of each of these interventions.
- PF4 = a type of blood cell that alerts the immune system when there is a wound and helps to form clots. It turns out that PF4 is also a cognitive enhancer. Under its influence, old mice recover the sharpness of middle age and young mice get smarter.

PF4 = rejuvenation

- Young blood, klotho, and exercise can somehow tell your brain, 'Hey, improve your function'
- When we realized we had independently and serendipitously found the same result about PF4, our jaws dropped
- Saul Villeda is an expert on parabiosis, an experiment in which two animals are linked together by their blood circulation. When a young, sprightly animal is connected to an aging animal, the aging animal becomes more youthful–its muscles more resilient, its brain more capable of learning.
- Platelets quell the inflammation of an aging brain and body: More PF4 in young animals. Just injecting PF4 into old animals was about as restorative as young plasma. Taking 22-month-old mice, equivalent to a human in their 70s, and PF4 is bringing them back to function close to their late 30s, early 40s.

PF4

- Platelet-derived chemokine PF4 is a pro-youthful factor that attenuates age-related neuroinflammation, elicits synaptic-plasticity-related molecular changes and rescues hippocampal-dependent learning and memory in aged mice. = potential therapeutic targets to abate inflammation and rescue cognition in old age.
- Systemic platelet factor 4 (PF4) permeates the brain and enhances cognition.
- Klotho may require platelets to enhance cognition. In young mice, PF4 enhanced synaptic plasticity and cognition. In old mice, PF4 decreased cognitive deficits and restored hippocampal function.

Klotho

- Klotho is a longevity factor that improves cognitive functions. It circulates as a hormone
- Longevity factor klotho increases systemic levels of platelet factors. Klotho induces platelet activation in the blood and increases circulating platelet factors.
- Klotho-mediated cognitive enhancement may require platelet activation
- PF4, but not klotho, crosses into the brain
- Direct PF4 application to hippocampus increases synaptic plasticity
- PF4 enhances cognition in young and aging mice

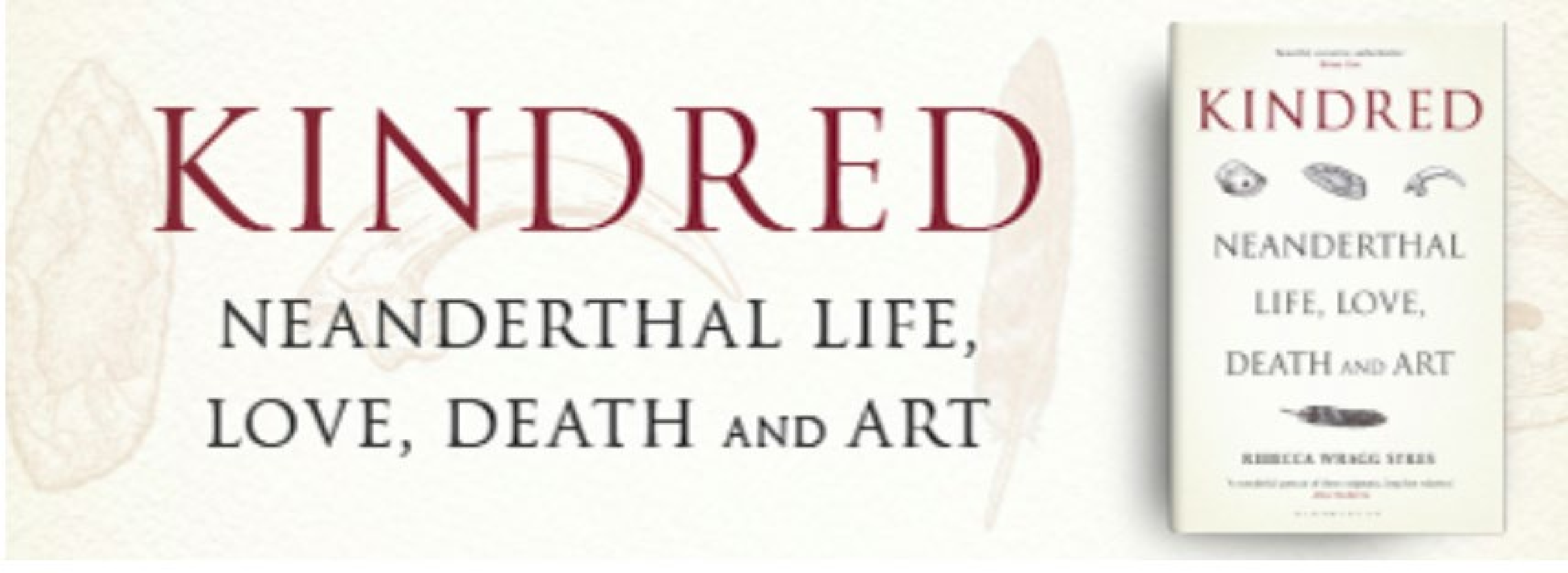
Platelets ferry klotho's signal for cognitive enhancement into the brain

- PF4 had a dramatic effect on the hippocampus, the brain region responsible for making memories, where it enhanced neurogenesis and increase in synaptic connections
- It also gave both old and young animals a brain boost in behavioral tests

- Exercise also improves brain health via platelets: platelets released PF4 into the bloodstream following exercise.
- Adam Schroer, et al., 2023
- Park, C. et al., 2023
- Odette Leiter et al, 2023

Get your vaccines!!

- Prior vaccination against tetanus and diphtheria, with or without pertussis (Tdap/Td); herpes zoster (HZ), better known as shingles; and pneumococcus are all associated with a reduced risk for developing Alzheimer's disease = 20-30 percent reduction in risk. Vaccines may change how the immune system responds to the build-up of toxic AD proteins, such as by enhancing the efficiency of immune cells at clearing the toxic proteins; reduces neuroinflammation.
- Another study in the journal, which found that people who received at least one influenza vaccine were 40% less likely than their unvaccinated peers to develop Alzheimer's disease.
- For comparison, the three new anti-amyloid antibodies used to treat Alzheimer's have shown they slow disease progression by 25%, 27%, and 35%.



KINDRED

NEANDERTHAL LIFE, LOVE, DEATH AND ART

Dr. Rebecca M. Wragg Sykes

An email to Rebecca Skaggs: Re: Your opinion about Châtelperronian material not being Neanderthal

On Sat, 25 Mar 2023, CHARLES VELLA wrote:
Rebecca
Kindred is a fantastic book. My only concern is your apparent opinion that the Châtelperronian material is not Neanderthal. I would like your analysis of the use of proteomics in this study which appears to conclude that Neanderthals did create the material at this site: Welker, F. Pääbo, & Hublin, J. , et al., 2016. Palaeoproteomic evidence identifies archaic hominins associated with the Châtelperronian at the Grotte du Renne.
Many thanks.
Charlie
Charles J Vella, PhD

Rebecca Wragg Sykes<rebeccawraggsykes@gmail.com> Aug. 21, 2023
To CHARLES VELLA

Dear Charlie,

Thank you for your email and kind words about my book, and apologies for the delay in my response.

I think I do go into a lot of detail in the book about my concerns with the Grotte du Renne, which is simply that lithic refitting has demonstrated some movement of objects within the CP layer, and therefore until there is a full investigation into the stratigraphic integrity of this site, the presence of fossils or DNA in the CP layer must be suspect as there may have been movement between layers.

Dr Rebecca M. Wragg Sykes

A new paper was recently published which reports such a fossil, but I think the most important point they make in their conclusion is this:

"Furthermore, additional analyses must be conducted to discuss the archaeological integrity of the Châtelperronian sequence of the GDR such as what has been done at Saint-Césaire[23]. Indeed, it incites to undertake taphonomic and spatial studies of the GDR remains since it is now the only site delivering human remains in Châtelperronian layers for which these kind of studies have not been carried out. "

https://www.nature.com/articles/s41598-023-39767-2

Dr Rebecca M. Wragg Sykes

In addition, the supposed mixed technological character of the CP lithic industry itself has been shown not to exist at sites where there is no possibility of stratigraphic mixing, instead it looks very much like it is embedded in a blade-focused, Upper Palaeolithic technological world.

I would also suggest this paper which for me places the CP in a framework which makes sense:
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0277444

Best wishes
Rebecca

Dr Rebecca M. Wragg Sykes
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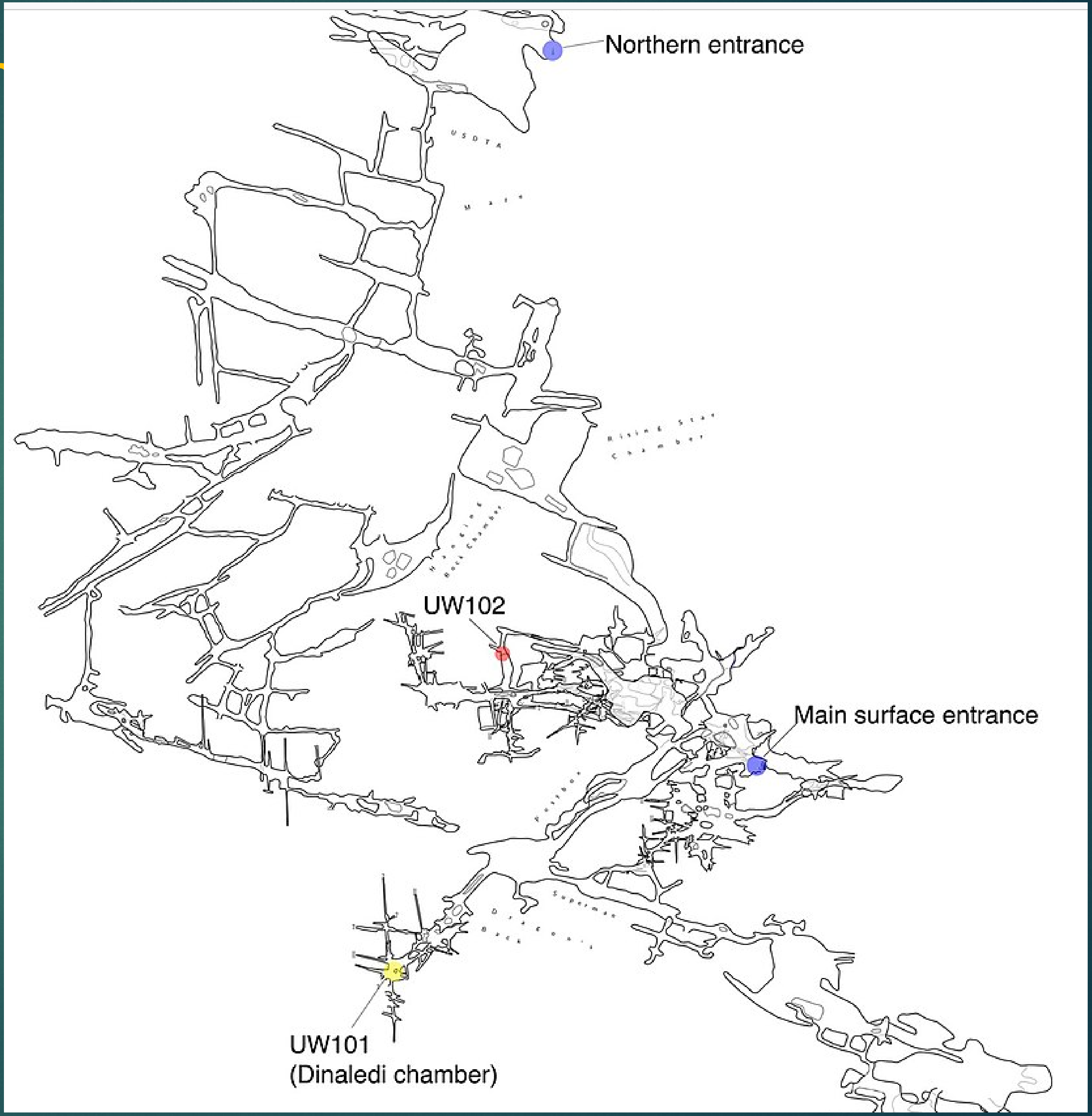
University of Liverpool; rebeccawraggsykes.com

Rising Star Cave Syster

49 people have entered Dinaledi chamber since 2013

Unknown number before then



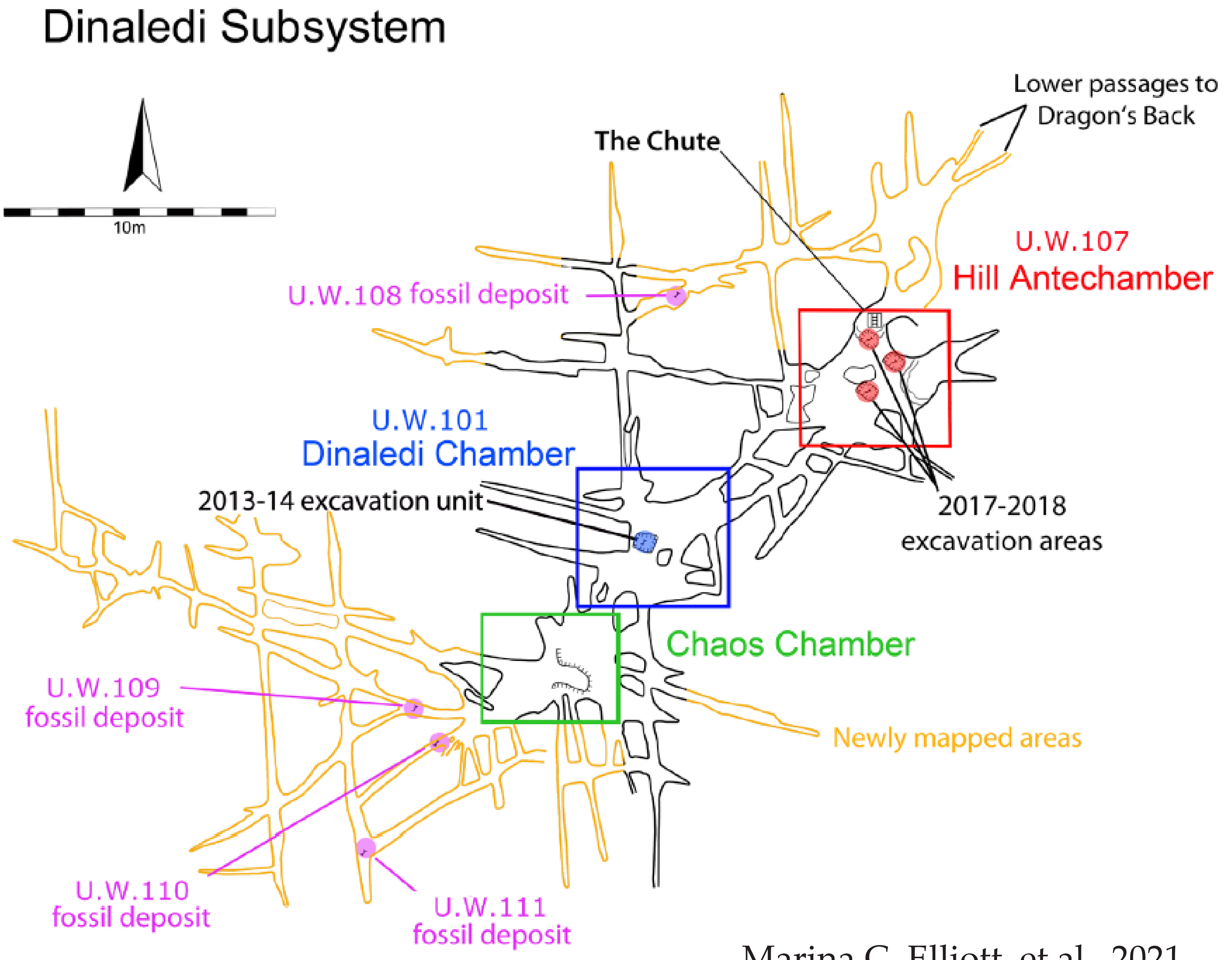
2017-1918 field season:
No other entrances

UW 108: 1 long bone – Naledi??

UW 109: 6 fossil fragments of juvenile baboon on floor

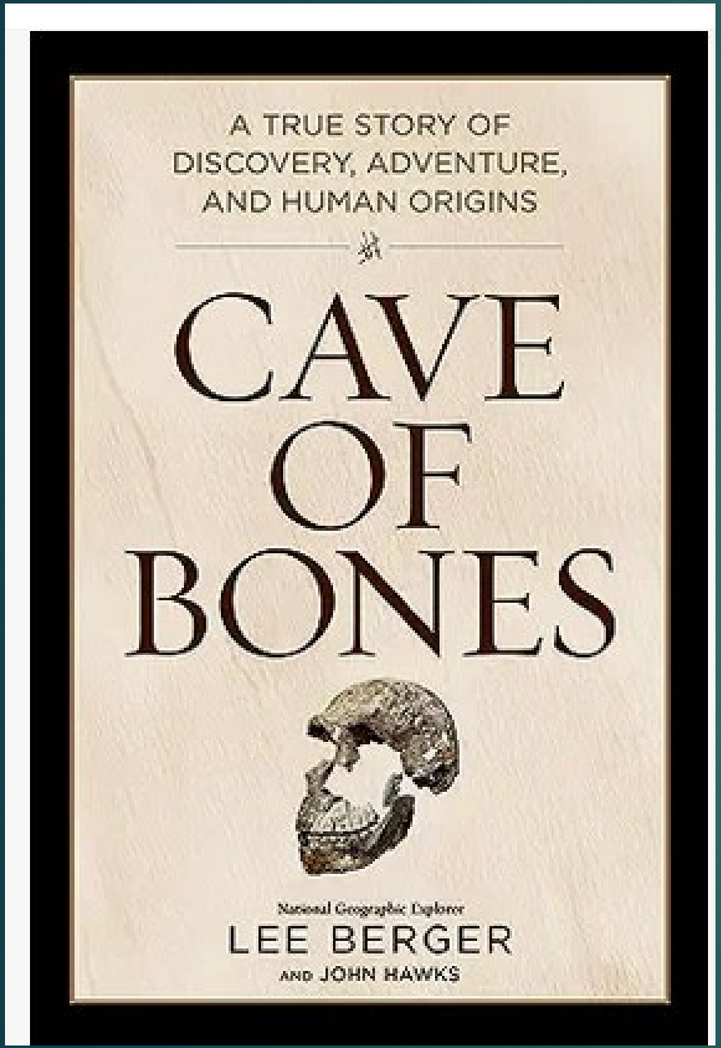
UW 110: fragments of juvenile Naledi

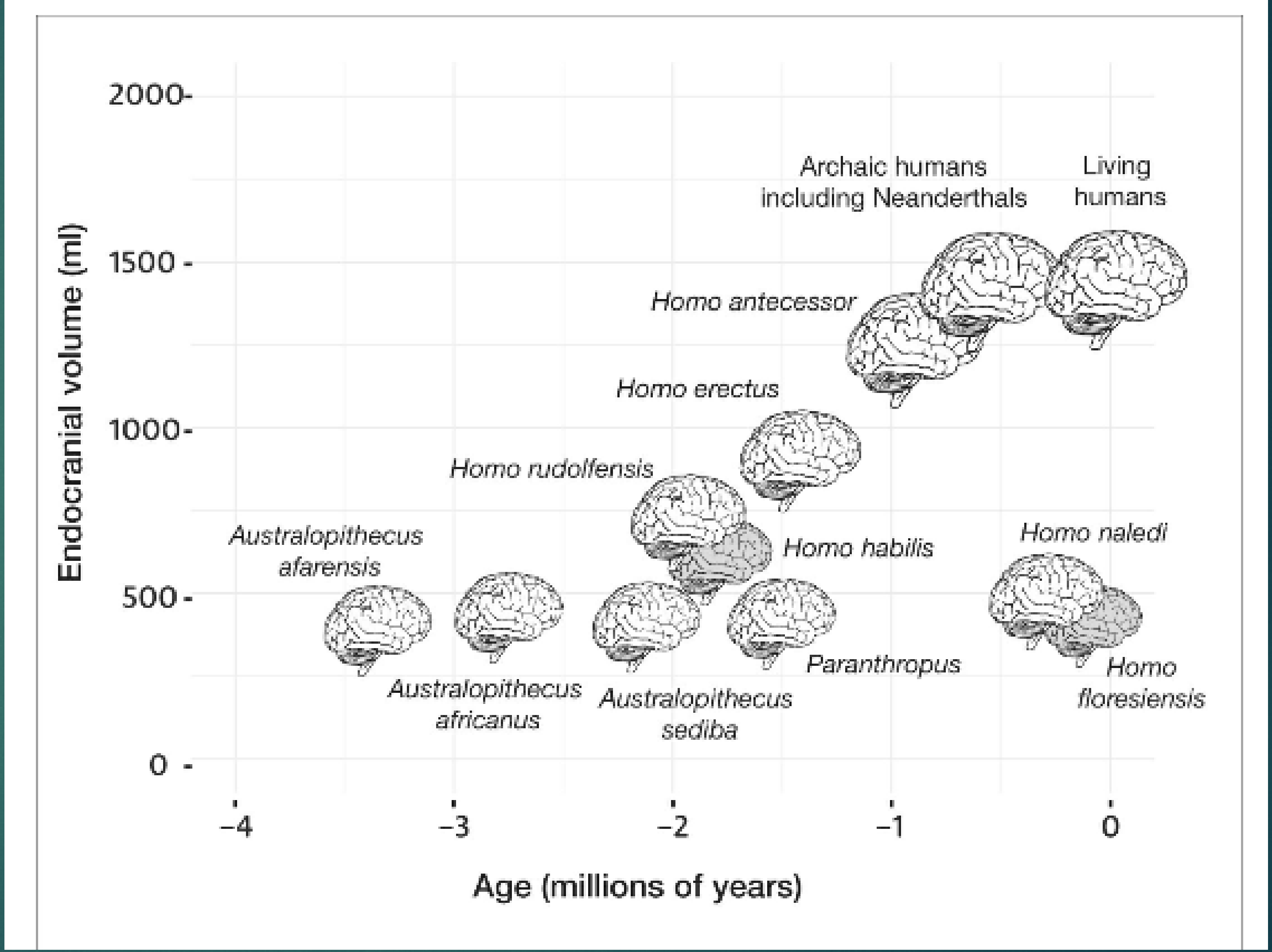
UW 111:
Several Naledi long bones



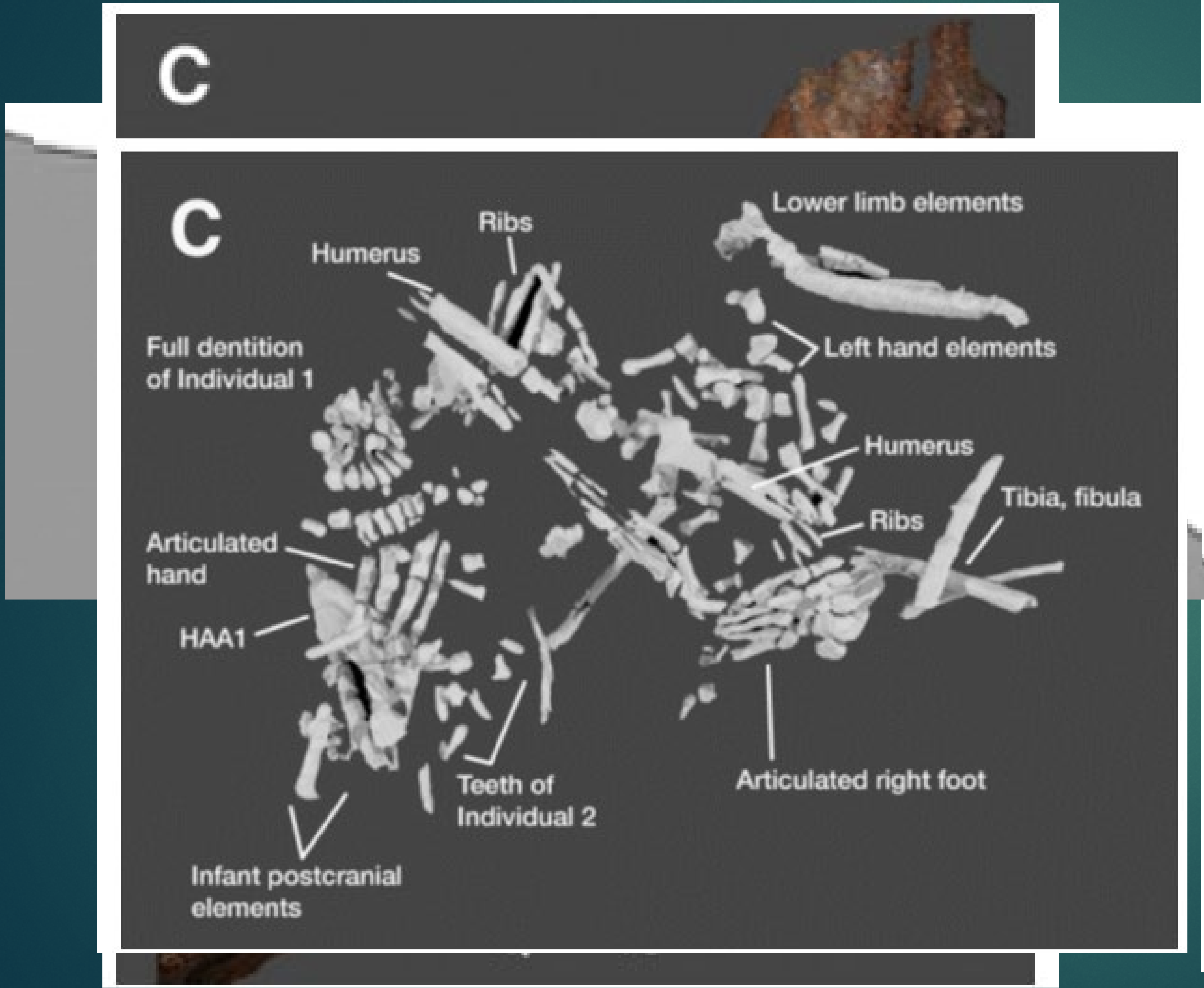
Marina C. Elliott, et al., 2021

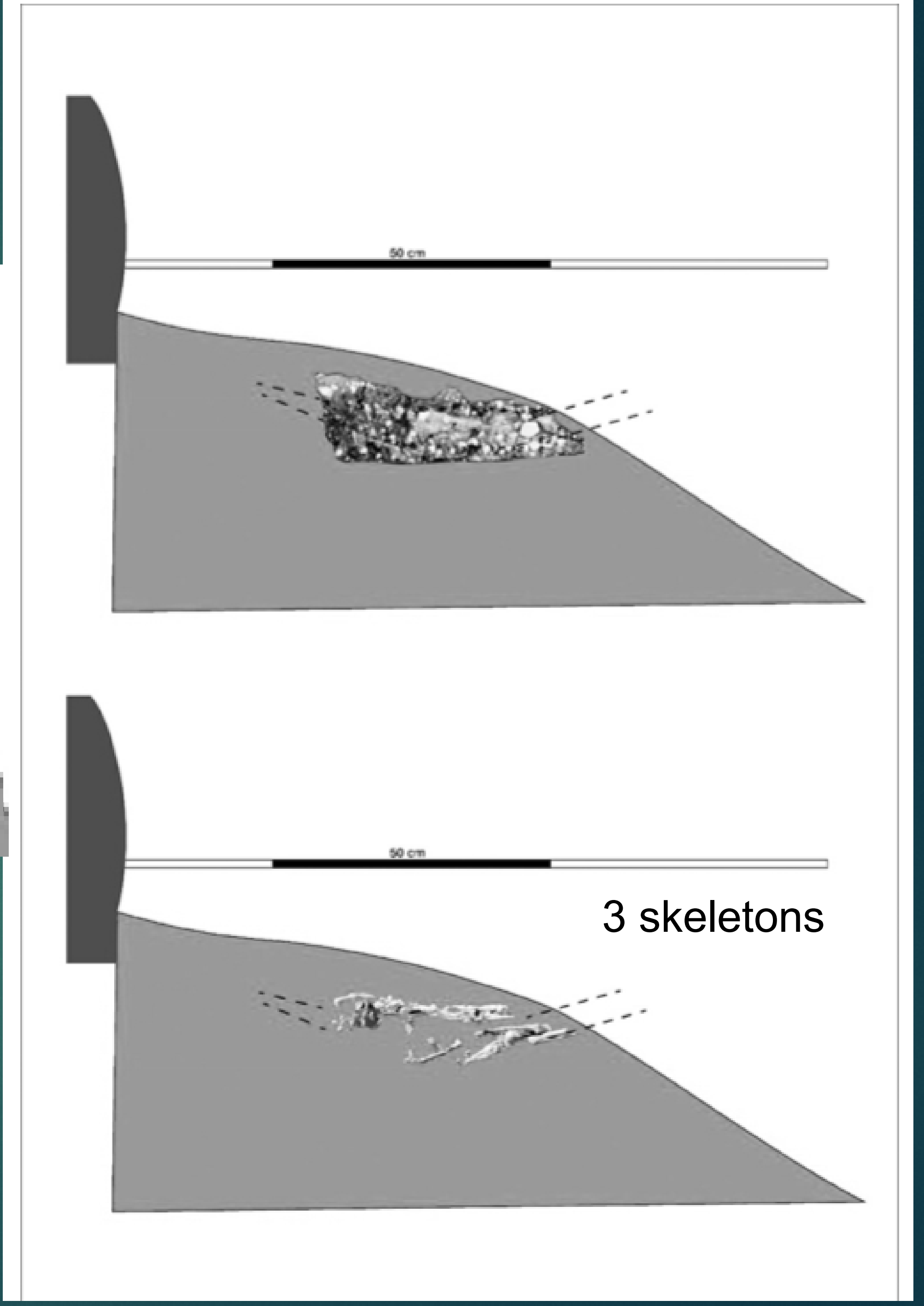
Cave of Bones, Berger & Hawks, 2023 publication



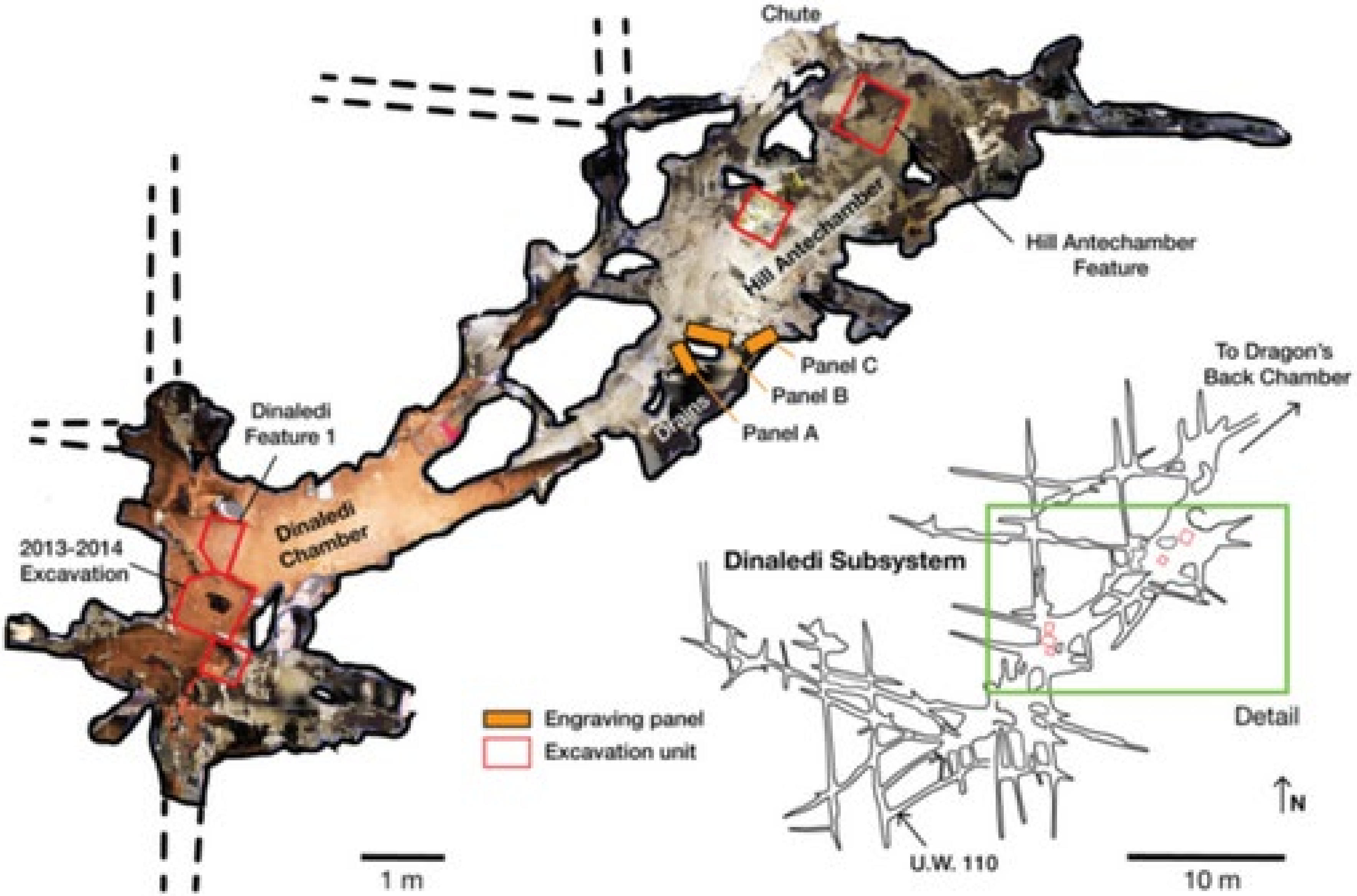


Skeletons in Hill Antechamber

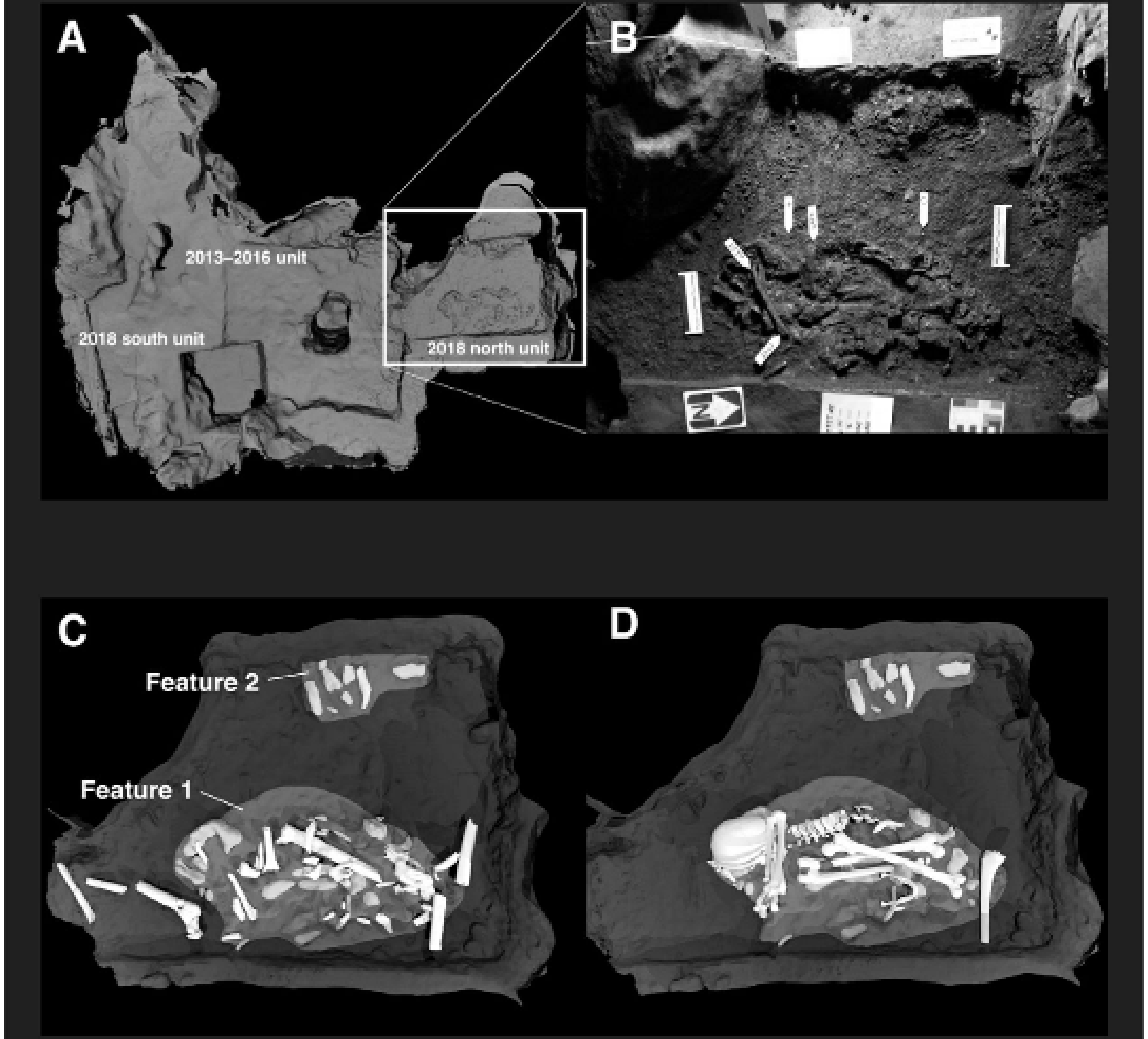




3 skeletons



A map of the Dinaledi Subsystem showing the placement of the various excavations


A
2013–2016 unit
2018 south unit
2018 north unit
B
C
Feature 2
Feature 1
D

Hearth with bones in Dragon’s Back area

Finding ancient fire use in the Rising Star cave system

- The team identified charcoal, burned bone, or other evidence of fire in at least four chambers, widespread from each other in deep parts of the system.

- Some of this evidence is from excavations led by Dr. Keneiloe Molopyane in the Dragon's Back Chamber, including concentrations of well-preserved charcoal, ash, and discolored clay that appear to be small hearths. The excavations also turned up many fragments of animal bone.

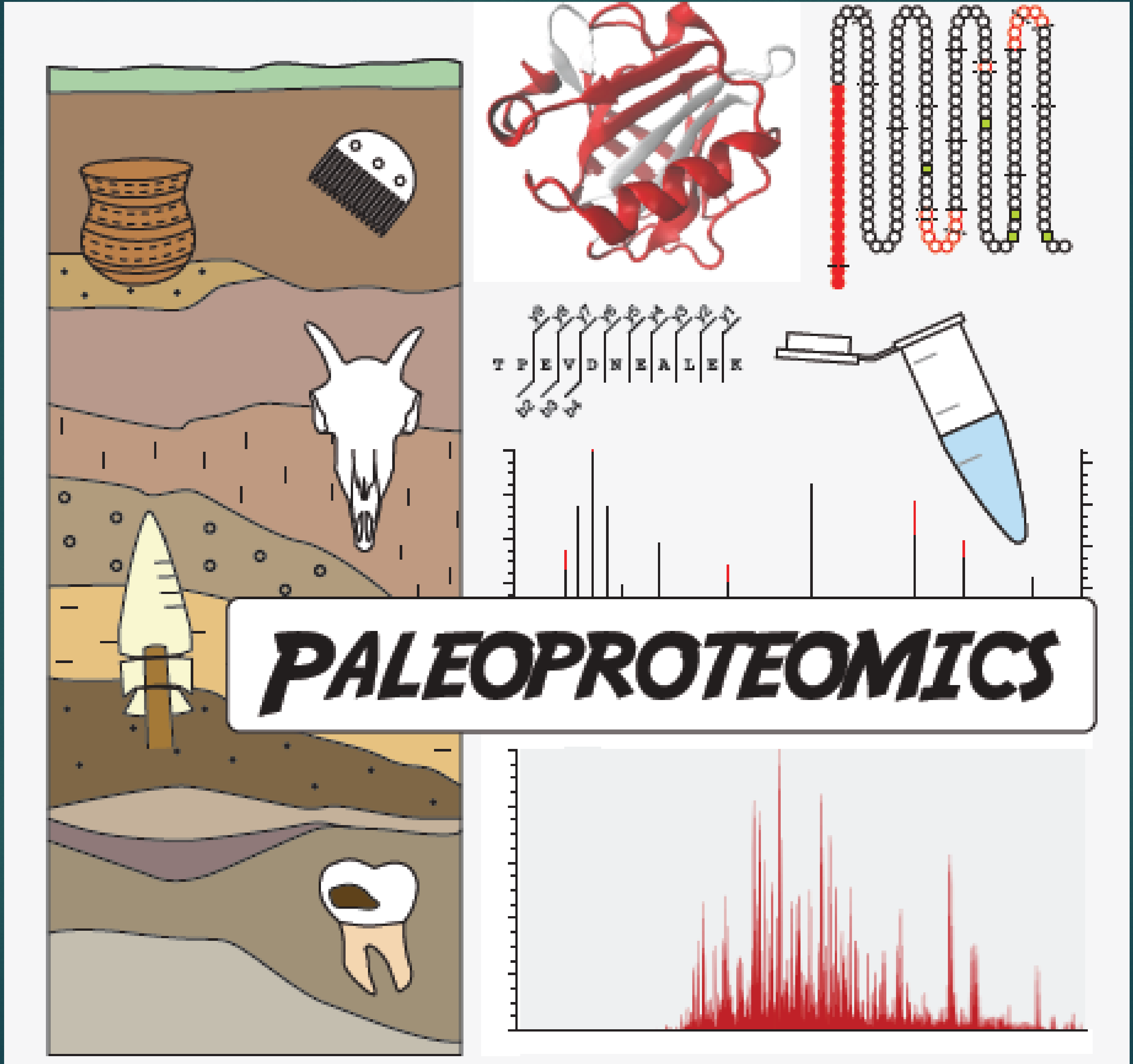
- In addition to Dragon's Back, in two other deep chambers our exploration has encountered concentrations of charcoal.

Rising Star Chamber: in western area of Rising Star Cave System

Charcoal in the Rising Star Chamber

APOe4 gene may have helped our ancestors have more kids

- The *APOE* gene encodes apolipoprotein E, a molecule that helps the body transport cholesterol in the blood.
- APOe4 gene triples your chance of heart disease and Alzheimer's disease in old age; 2 copies = 12x risk. 1 in 5 have 1 copy of it.
- Why has APOe4 persisted evolutionarily
- Now, a study of nearly 800 women in a traditional society in the Amazon finds that those with the disease-promoting variant had slightly more children. Such a fertility benefit may have allowed the gene to persist during human evolution despite its harmful effects for older people today.
- The women had nine children on average, but the 147 women who carried one copy of *APOE4* averaged about 9.5 children. The 12 women with two copies had two additional children on average,



PALEOPROTEOMICS

Paleoproteomics

- **Proteomics** is the large-scale study of proteins. Proteins are vital parts of living organisms

- After genomics and transcriptomics, proteomics is the next step in the study of biological systems. It is more complicated than genomics because an organism's genome is more or less constant, whereas proteomes differ from cell to cell and from time to time. Distinct genes are expressed in different cell types, which means that even the basic set of proteins produced in a cell must be identified

- In paleontology, identification of ancient proteins is done via mass spectrometry

Paleoproteomics - Christina Warinner, et al., 2022

Paleoproteomics

- Paleoproteomics research leverages the longevity and diversity of proteins to explore fundamental questions about the past.
- While its origins predate the characterization of DNA, it was only with the advent of soft ionization mass spectrometry that the study of ancient proteins became truly feasible.
- Technological gains over the past 20 years have allowed increasing opportunities to better understand preservation, degradation, and recovery of the rich bioarchive of ancient proteins found in the archaeological and paleontological records.

Species identification

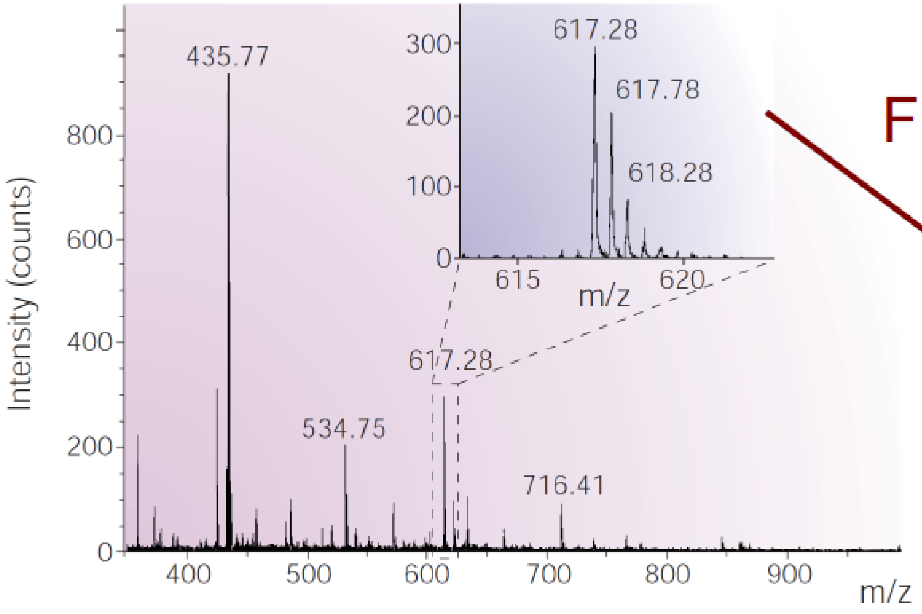
- Paleoproteomics today is an expanding field with diverse applications ranging from the
  - taxonomic identification of highly fragmented bones and shells and
  - the phylogenetic resolution of extinct species to
  - the exploration of past cuisines from dental calculus and pottery food crusts
  - the characterization of past diseases

- Analysis of the hominin fossil record through large scale screening of nondiagnostic bone fragments, and the phylogenetic resolution of the vertebrate fossil record

- Proteins can persist for millions of years or more. Protein fragments are recognizable in fossils (e.g., seeds, bone), worked biological remains, (e.g., wood, textiles, archaeological and art historical artifacts), as residues on cooking vessels, and also entrapped within soils and sediments

Mass spectra

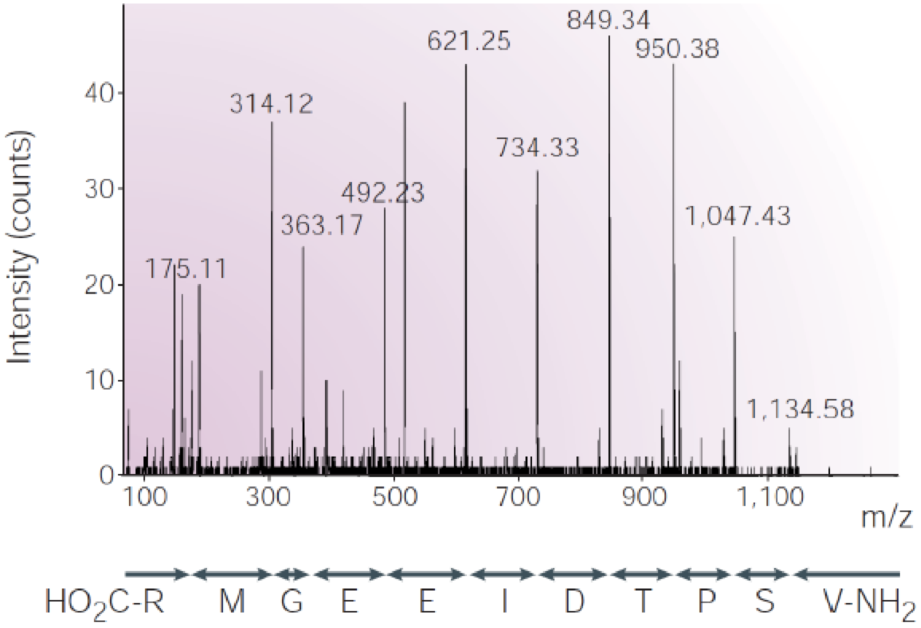
MS^1



Steen and Mann *Nat Rev Mol Cell Biol* 2004

Fragment and analyze one precursor ion

MS^2



Mass-to-charge ratio

Spectrum contains information about amino acid sequence, fragment at different bonds

Proteins as a Bioarchive of the Past

- Proteins are long-lived biomolecules capable of surviving over millions of years. They routinely outlast even the oldest surviving DNA, and their full longevity has yet to be determined. Although proteins do not persist into deep time as long as lipids, their sequence diversity makes them more informative, and consequently proteins represent one of our most valuable bioarchives of the past.
- The longevity and biological utility of proteins derive in large part from their structure. Proteins are large biomolecules built from linear sequences of amino acids folded into complex three-dimensional forms
- Only contain about 1% of the maximum information that you could get from a DNA sample. That means that we will need a lot to be able to generate enough data to carry out meaningful analyses.

Use for developing phylogenic trees

- Because proteins are derived from the genetic code, individual proteins preserve part of the heritable genetic signal of an organism, and therefore, protein sequences can be used to make taxonomic identifications and reconstruct phylogenies.
- In nearly all cases, mineralization is an important factor in protein long-term survival. Examples: enamel, bone (colagen), dental calculus, and shell. But proteins can be extracted from almost anything.
- In phylogenetic studies of taxa for which the exact protein sequence is unknown, software is available for de novo sequencing. This is especially valuable for determining sequences in extinct species for which genomic data cannot be obtained.

Taxonomic Discrimination

- Once peptides are identified to proteins, their sequences can be used to infer taxonomy and to discriminate between related taxa.
- Overall, protein sequences provide less taxonomic resolution than DNA sequences, but proteins can persist millions of years longer than DNA, they are biologically present in much higher amounts than DNA, and they are found even in acellular tissues (e.g., enamel, eggshell).
- As such, they are our most valuable form of molecular sequence data for providing successful and reliable taxonomic identifications in deep time fossils

Collagens: Bone, Dentine, Antler, Ivory, Parchment, Leather, Gut, and Scales

- ZooMS analysis of COL1 is the most frequently conducted type of paleoproteomic analysis, and it can be conducted on almost any collagenous tissue, including mineralized tissues such as bone, dentine, antler, ivory, and horn core, as well as nonmineralized tissues such as skin, parchment, leather, gut, scales, and other soft tissues.
- It has contributed to the reconstruction of past ecologies and to the study of extinct megafauna.
- ZooMS has also been notably used as a low-cost, high-throughput screening tool of bone fragments in large Pleistocene cave sequences, leading to the discovery of otherwise nondiagnostic hominid remains, including Denny, the offspring of a Neanderthal mother and Denisovan father.

Amelogenin: Sex Typing of Humans and Other Mammals

- Use for sex typing independent of morphology

- Amelogenin (gene AMEL) plays an important role in enamel formation and mineralization in newly secreted enamel.

- AMELY is expressed, protein analysis can allow sex discrimination. These species include humans (& archaic humans), cattle, bison, sheep, goats, deer, pigs, horses, and bears.

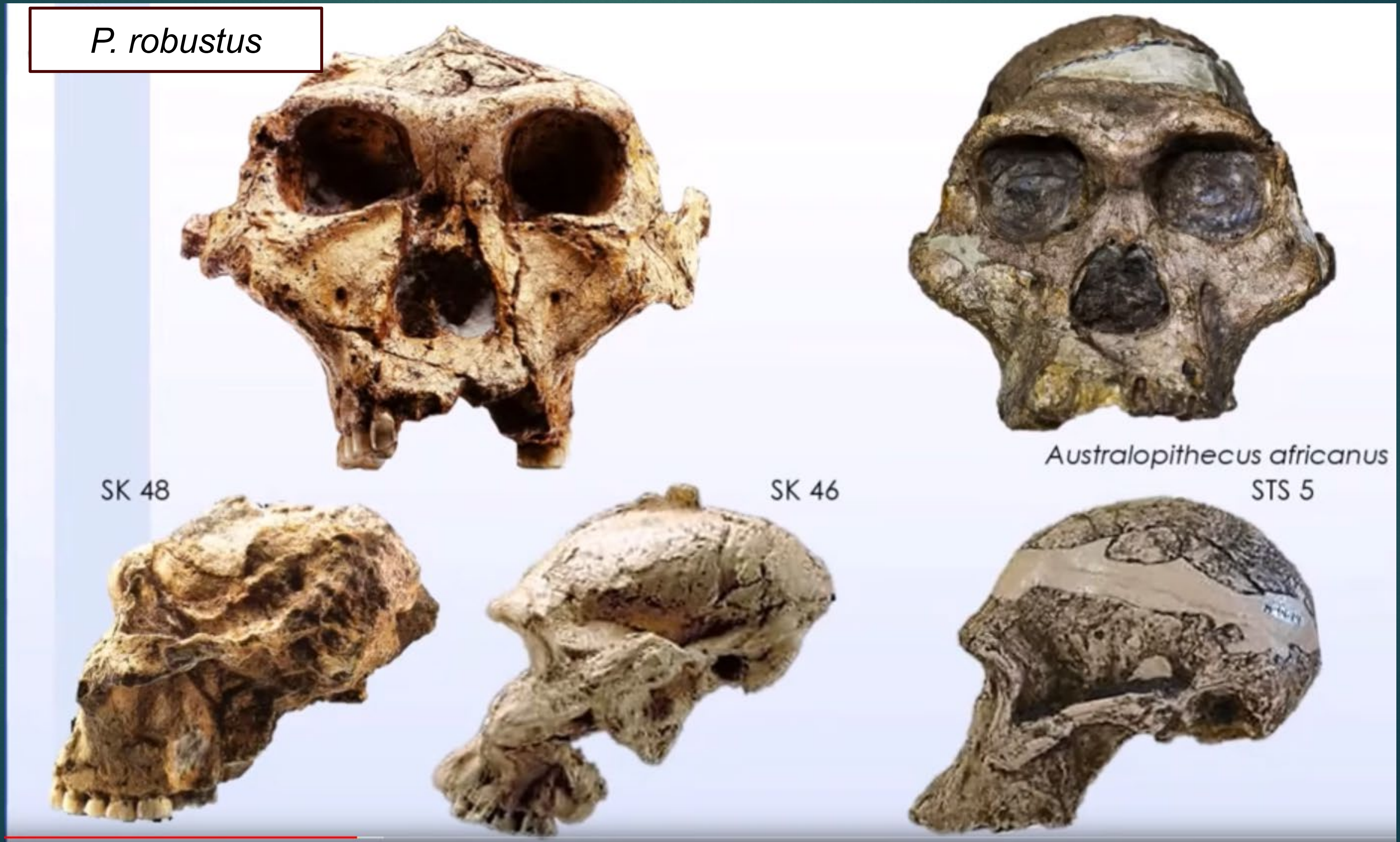
Ancient proteome

- The first ancient proteome, from mammoth bone, was published in 2012. Consisting of more than 100 proteins, it was a singular achievement and marked the field’s transition from the study of ancient proteins to true paleoproteomics.
- Although the majority of ancient microbiome research has focused on dental calculus, paleofeces are also now being explored.
- Databases are currently a major limiting factor in ancient protein identification.
- Although the proteomes of humans and some model organisms are now well curated and annotated, the proteomes of many taxa of archaeological interest, from molluscs to microbiomes, remain insufficiently or poorly characterized. Most databases suffer from inclusion bias, with model organisms and economically important taxa being vastly overrepresented compared to other species.

Human evolution examples of paleoproteomics

- *Lufengosaurus dinosaur* collagen – 195 Ma
- *Brachylophosaurus canadensis* – 80 Ma
- Ostrich eggshell at Laetoli – 3.8 Ma
- *H. erectus* tooth: 1.77 Ma
- Wooly rhino at Dmanisi*: 1.77 Ma*
- *Gigantopithecus* – 1.9 Ma*:* related to orangutans
- 3 Mammoths – 1.6 Ma
- *Homo antecessor*: 800 Ka
- Xiahe Denisovan jaw – 160 Ka
- Denisova 11: 90 Ka – Denny – N father, D mother
- Châtelperronian at the Grotte du Renne (France) Neandertal – 42 Ka

New proteomic study of *Paranthropus robustus*



Paranthropus

- The genus Paranthropus evolved ca. 2.8 million years ago (Ma) and persisted until 1 Ma, coexisting with Australopithecus species and members of the genus Homo.

- Resolving the relationships among these taxa is key to understanding the origins of our lineage.

- Even within Paranthropus, the phylogenetic relationships among the three currently identified species have been the subject of considerable discussion.

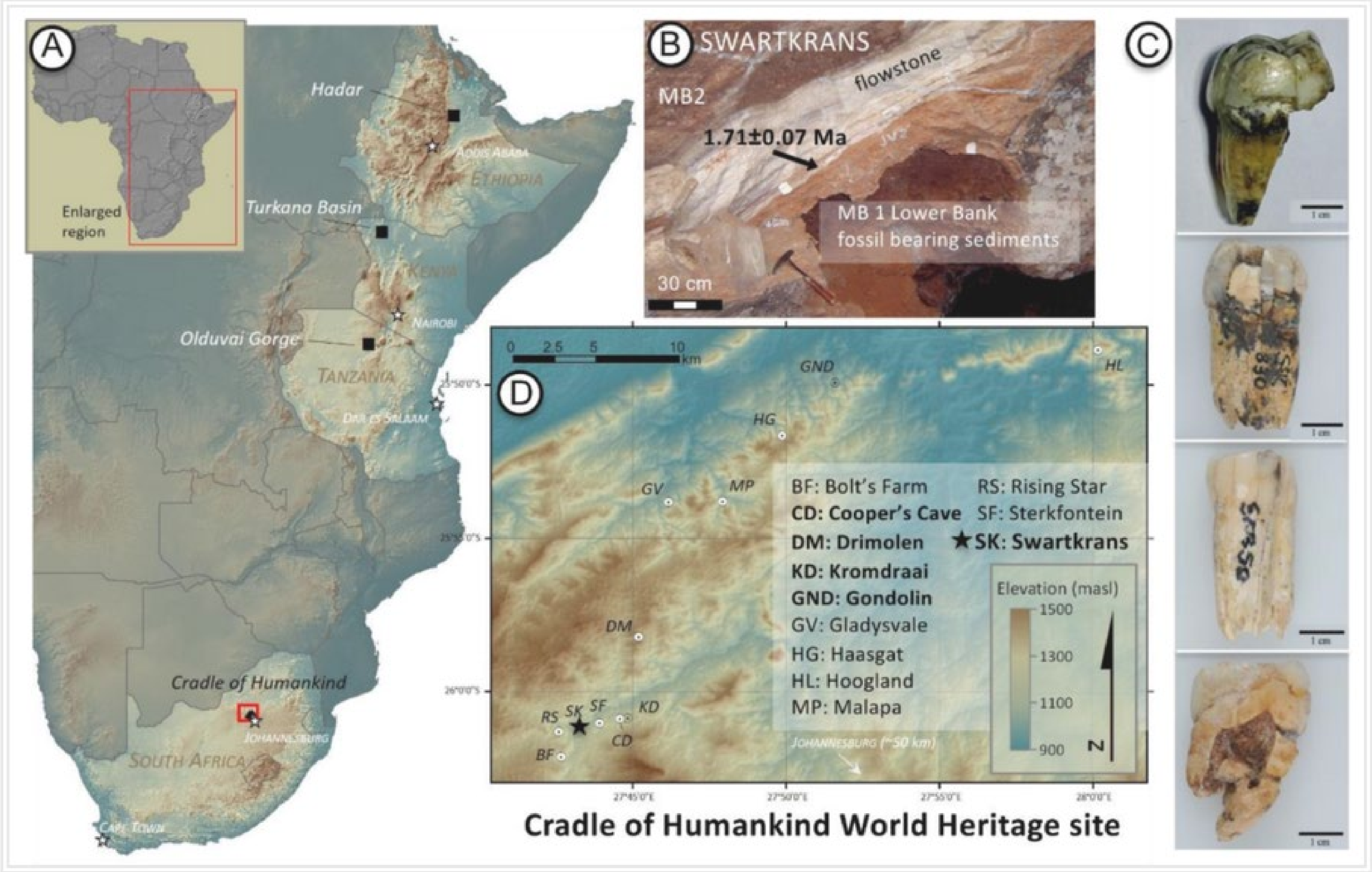
Clarification of Species diversification

- Most researchers consider Paranthropus taxa to be monophyletic (descent from common ancestor), however, morphological similarities between P. robustus and Au. africanus in a South African context, and between P. aethiopicus and Au. afarensis in an eastern African context, have raised the possibility of paraphyly or even admixture between species.

- Furthermore, analyses of the enamel-dental junction of southern African Paranthropus indicate significant variation, suggesting the possibility of substructuring within P. robustus or even the presence of more than a single species of this genus in paleoanthropological record of this region.

- Determining to what extent the variation within and between Plio-Pleistocene hominins is due to evolutionary diversification versus sexual dimorphism is therefore fundamental to resolving these relationships

4 Paranthropus teeth: First Proteomic study of African hominin



Swartkrans cave and context in the other sites called "Cradle of Humanity" in South Africa. Paranthropus teeth analyzed, from top to bottom: SK 835 (left M3), SK 830 (left P4), SK 850 (right P3), SK 14132 (right M3). Credit: PP Madupe et al., 2023

Enamel proteins reveal biological sex and genetic variability within southern African Paranthropus

- In Africa, the conditions for the conservation of genetic material are more challenging and mean that it has only been possible to study human DNA up to 18,000 years old.

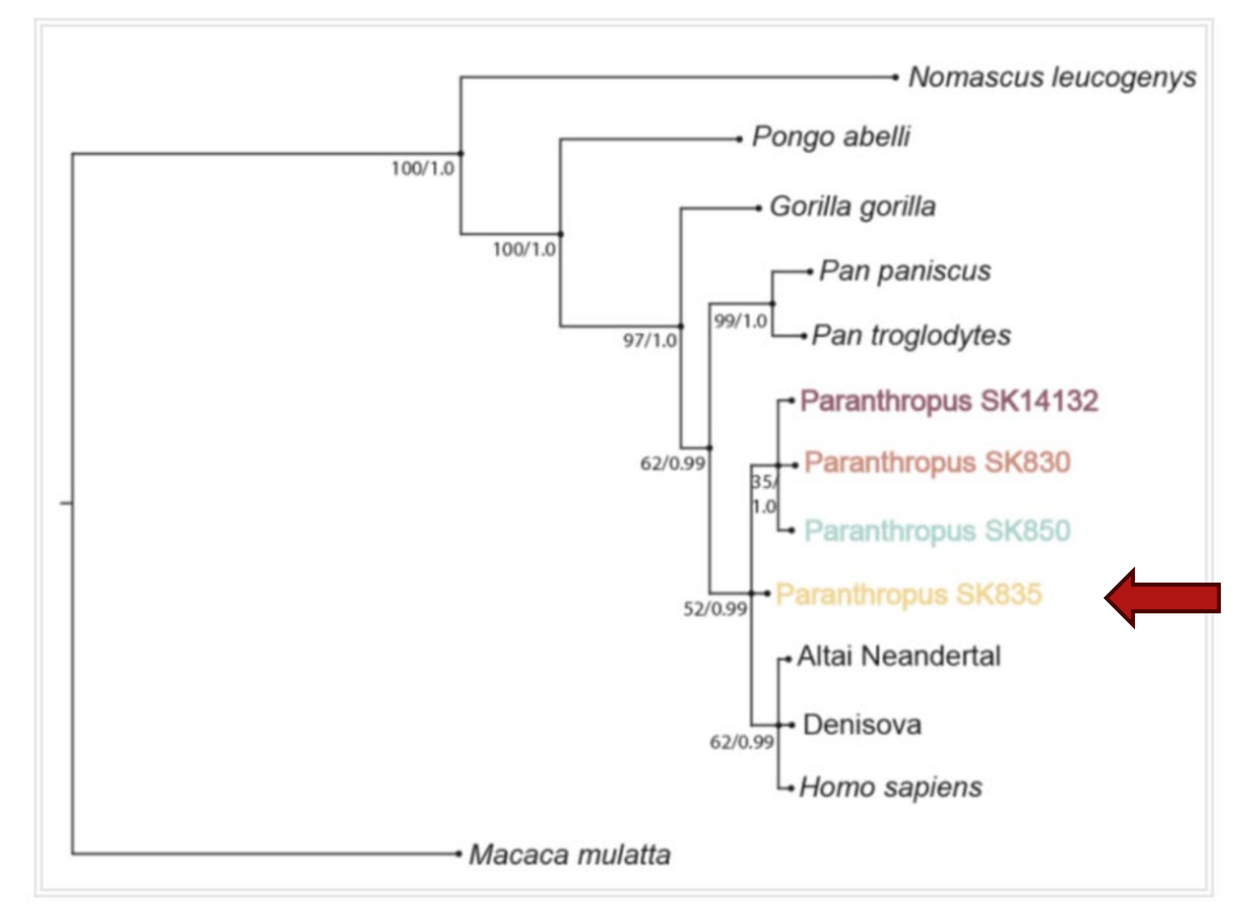
- A new work (PP Madupe et al., 2023, *preprint, pending peer review*) has managed to double the age of the sequenced hominin proteome, up to two million years, which is the age of the four *Paranthropus robustus specimens* studied: 4 molars SK 850, SK 835, SK 830 and SK 14132, from Member 1 of the Swartkrans cave, in South Africa (1.8-2.2 Ma); and to identify sex molecularly, rather than attribution to sexual dimorphism.

A transformative breakthrough in PaleoAnthropology

- *** The recovery of ca. 2 Ma phylogenetically-informative genetic material in African hominins can be considered a potentially transformative breakthrough for paleoanthropology. This is the first report of the recovery of Early Pleistocene hominin proteins from Africa.

- Possibility now of classifying *P. boisei, Au. Afarensis, Au. africanus, Au. sediba, H. naledi, H. floresiensis, and H. erectus*, to further refine the molecular-based reconstruction of hominin phylogeny.

- Molecular data also confirm the positioning of *Paranthropus* within the hominin clade. The sequences of the four paranthropes are closer to the *Homo* clade than any other primate. The group of paranthropes is distinguished from the clade consisting of Neanderthals, Denisovans, and modern humans.



Results provide an initial insight into the genetic relationships between *Paranthropus* and other hominins. The sequences recovered place *Paranthropus* within hominins and as an outgroup to the clade including *Homo sapiens*, Neanderthals and Denisovans.

The trees presented here, however, only provide a tentative phylogenetic placement of *Paranthropus*, as they are based on a small set of proteins

Paleoproteomic analysis

- Study reports the mass spectrometric (MS) sequencing of enamel proteomes from four ca. 2 Ma old dental specimens attributed morphologically to P. robustus, from the site of Swartkrans. The identification of AMELY-specific peptides enabled the determination of the biological sex of all the specimens.
- Provides compelling evidence of a significant degree of variation within southern African Paranthropus
- Combining the paleoproteomic analysis with the study of the enamel-dentin junction of the molars where it is best preserved (SK 835 and SK 830), it is observed that the specimens undoubtedly belong to Paranthropus and are distinguished from both Australopithecus and Homo . In fact, SK 835 is closer to the Paranthropus specimens from Drimolen than to those from Swartkrans and Kromdraai (the holotype of P. robustus , TM 1517 , comes from the latter site).

Paranthropus is a hominin

- Study confirms the taxonomic placement of Paranthropus within the hominin clade.

- This study demonstrates the feasibility of recovering informative Early Pleistocene hominin enamel proteins from Africa.

- Crucially, it also shows how the analysis of these proteins can contribute to understanding whether hominin morphological variation is due to sexual dimorphism or to taxonomic differences.

Significant Implications for the analysis of hominin diversity

- This methodology has clear implications for our understanding and interpretation of morphological variation in the deep-time human fossil record, as it enables us to control for sexual dimorphism and by implication the range of anatomical variation, in our identification of hominin species.

Last page of Berger's new book: Proteomics of H. naledi???

- Enrico Cappellini, Alberto Taurozzi, and Palesa Madupe, collaborators at the University of Copenhagen who are experts in paleoproteomics
- Lee Berger sent these scientists two sediba teeth and four naledi teeth representing different individuals, and he is eager to hear what their analysis finds.
- Dentin is in good shape: possible DNA and proteins

Climate shifts orchestrated hominin interbreeding events across Eurasia

- J. Ruan et al. study, in *Science*, of the potential for Neanderthal-Denisovan admixture using species distribution models that integrate extensive fossil, archaeological, and genetic data with transient coupled general circulation model simulations of global climate and biomes.
- Their Pleistocene analysis of past hominins' habitat suitability reveals pronounced climate-driven zonal shifts in the main overlap region of Denisovans and Neanderthals in central Eurasia. These shifts, which influenced the timing and intensity of potential interbreeding events, can be attributed to the response of climate and vegetation to past variations in atmospheric carbon dioxide and Northern Hemisphere ice-sheet volume.

Jiaoyang Ruan et al., 2023

Climate effects

- Therefore, glacial-interglacial climate swings likely played an important role in favoring gene flow between archaic humans

- Both Neanderthals and Denisovans are simulated to have lived primarily in environments characterized
  - by annual temperature, precipitation, and NPP of ~−10° to 20°C (50 to 68 °F), ~500 to 1300 mm/year (19 to 51 in),
  - and ~200 to 800 g of carbon per square meter per year, respectively.

- There are only ~20 archaeological sites attributable to Denisovans compared with more than 700 sites attributed to Neanderthals, which makes it difficult to draw conclusions from location alone.

Preferred environments of Ns and Ds

- Yet, compared to Neanderthals, Denisovans were present in hot and humid climates, which points to a comparatively wider niche space.

- Both species likely lived in a variety of environments, but Neanderthals were more abundant in temperate forests, Denisovans lived in a much wider range of habitats, being present in both boreal forest and tundra.

- Past changes in atmospheric CO_2 and corresponding shifts in climate and vegetation played a key role in determining when and where early human species interbred.

Climate shifts orchestrated hominin interbreeding events across Eurasia

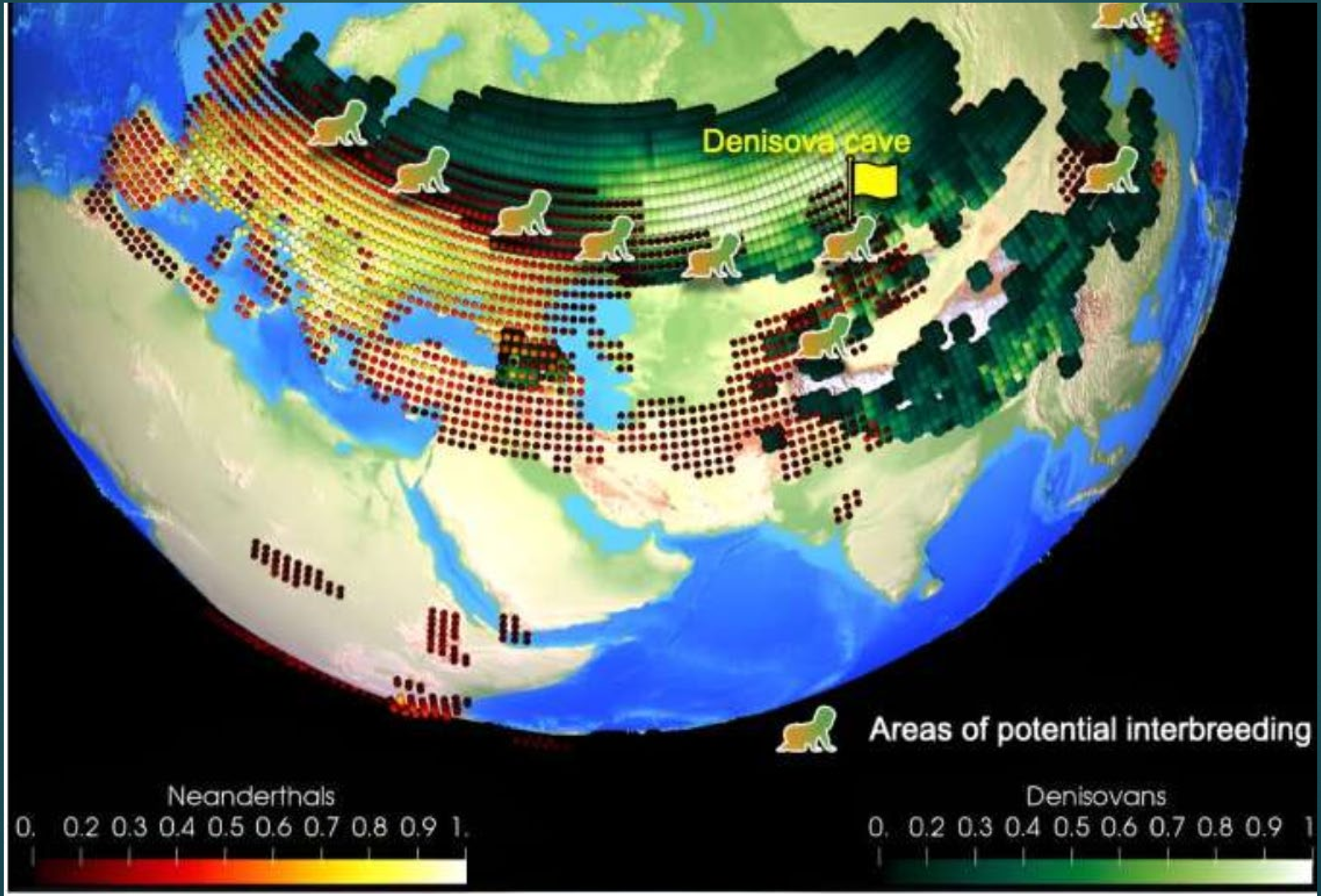
- In the new *Science* paper, the team of climate experts and paleo-biologists from South Korea and Italy pursued a different approach. Using existing paleo-anthropological evidence, genetic data and supercomputer simulations of past climate, the team found that Neanderthals and Denisovans had different environmental preferences.

- More specifically, Denisovans were much more adapted to cold environments, characterized by boreal forests and even tundra, compared to their Neanderthal cousins who preferred temperate forests and grassland.

Habitat preferences

- "This means that their habitats of choice were separated geographically, with Neanderthals typically preferring southwestern Eurasia and Denisovans the northeast.
- However, according to their realistic computer simulations the scientists found that in warm interglacial periods, when Earth's orbit around the sun was more elliptic and northern hemisphere summer occurred closer to the sun, the hominin habitats began to overlap geographically.
- Orbitally driven climate shifts in habitat caused the preferred habitats of Denisovans and Neanderthals to overlap. This occurred primarily during interglacial periods when an east-west zone of mutually preferred habitats formed, but interbreeding would have also been possible in Europe during glacial periods.
- When Neanderthals and Denisovans shared a common habitat, there were more encounters and interactions among the groups, which would have increased the chance of interbreeding,

Possible habitats of Neandertals and Denisovans



Testable computer simulations

- The simulation of past habitat overlaps puts known info into model: the first generation Neanderthal/Denisovan hybrid Denny, and other known episodes of interbreeding ~78, 120 thousand years ago. <u>Future paleo-genetic reconstructions can be used to test the robustness of the new supercomputer model-based predictions of potential interbreeding intervals around 210 and 320 thousand years ago.</u>
- Scientists also looked more closely at how vegetation patterns changed over Eurasia during the past 400 thousand years.
- They discovered that elevated atmospheric CO_2 concentrations and mild interglacial conditions caused an eastward expansion of temperate forest into central Eurasia which created dispersal corridors for Neanderthals into Denisovan lands.

What climate did Denisovans prefer?

- One of the key challenges the researchers faced in their study was to estimate the preferred climatic conditions for Denisovans.
- To our surprise, we found that, apart from areas in Russia and China, also northern Europe would have been a suitable environment for them.
- Whether Denisovans ever lived west of the Altai mountains is unknown; but it can be tested using large-sample genetic analyses of Denisovan ancestry in European populations.
- Despite the paper's strengths, any analysis of how hominins related to ancient climates suffer from the weakness of the fossil and archaeological data. We just don't know enough about where Denisova-like populations lived.

N and D Interactions

- Neandertal cold sites are a small fraction of their known sites, while the 3 Denisovan cold sites make up two-thirds of the record. Based on these data, the paper concludes that Denisovans may have been successful across a large swath of northern Eurasia, giving rise to possible contact and mixture with Neandertals across most of that area.
- J. Hawks doubts this conclusion.
- Still he thinks the main conclusion of the paper is probably accurate: These populations could have interacted across a large geographic space. Nothing stood in the way of these hominin groups traversing long distances across similar habitats. Connections of populations should have been possible across a wide span of time and space.

Extreme glacial cooling likely led to hominin depopulation of Europe in the Early Pleistocene

- Fossils and stone tools show that *Homo erectus* arrived in Europe from Asia between 1.8 million and 1.4 million years ago, previous research has found, but they seem to have died out throughout Europe about 1.1 million years ago.

- Show the presence of pronounced millennial-scale climate variability during a glacial period ~1.2 to ~1.1 Ma, culminating in a terminal stadial cooling comparable to the most extreme events of the last 400,000 years.

- Climate envelope–model simulations reveal a drastic decrease in early hominin habitat suitability around the Mediterranean during the terminal stadial.

- We suggest that these extreme climate conditions led to the depopulation of hominins in southern Europe, perhaps lasting for several successive glacial-interglacial cycles.

V. Margari, et al., 2023

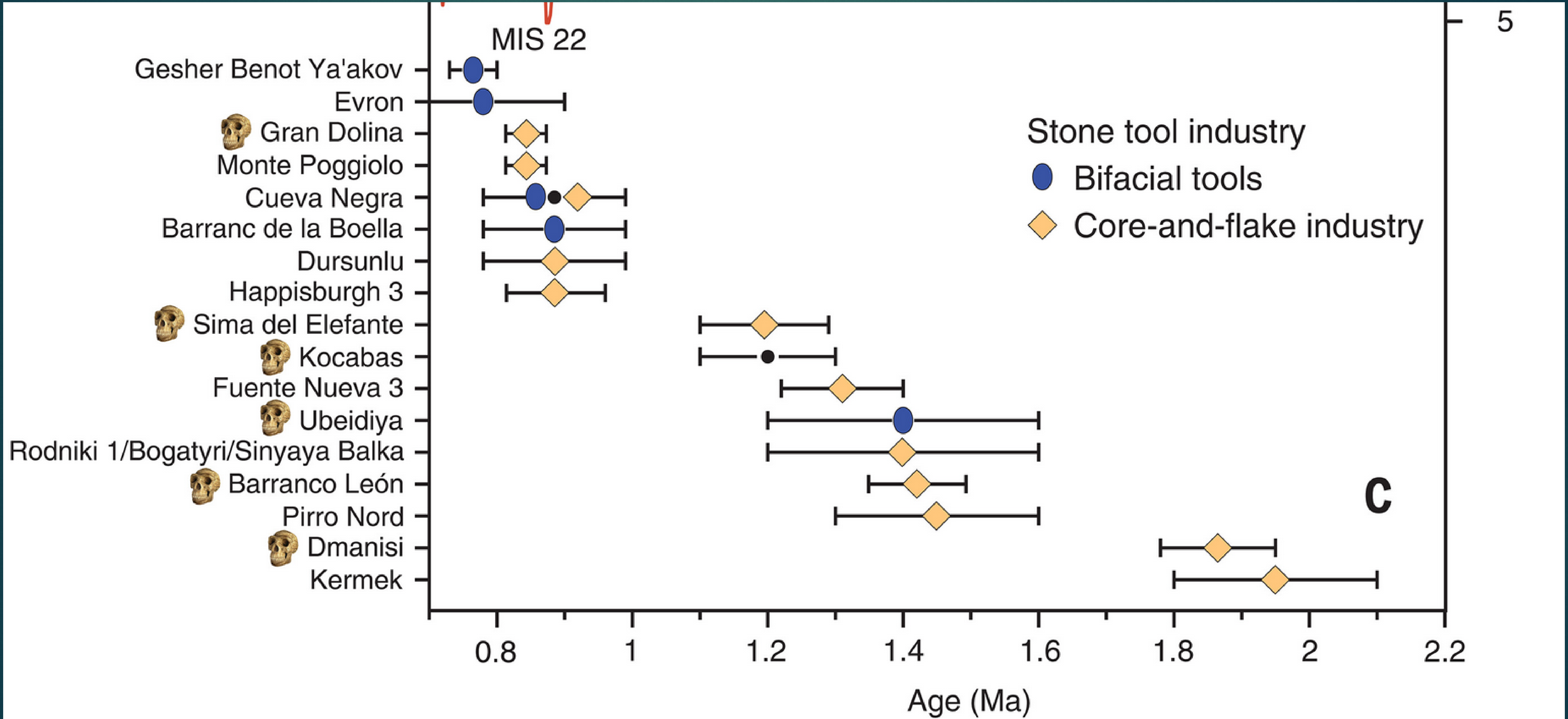
Earliest European hominins

- The earliest published fossil hominin (*Homo* sp.) evidence in Europe is
  - a mandible and a hand phalanx found with stone tools at the site of Sima del Elefante, dated to 1.2 Ma, Sierra de Atapuerca, northern Spain, as well as
  - a deciduous molar and stone tools from the sites of Barranco León and Fuente Nueva 3, Guadix-Baza Basin, southeastern Spain, at 1.4 Ma.

- Analysis of traits of the Sima del Elefante hominin suggests a possible Eurasian (rather than African) evolutionary origin for the population that it represents.

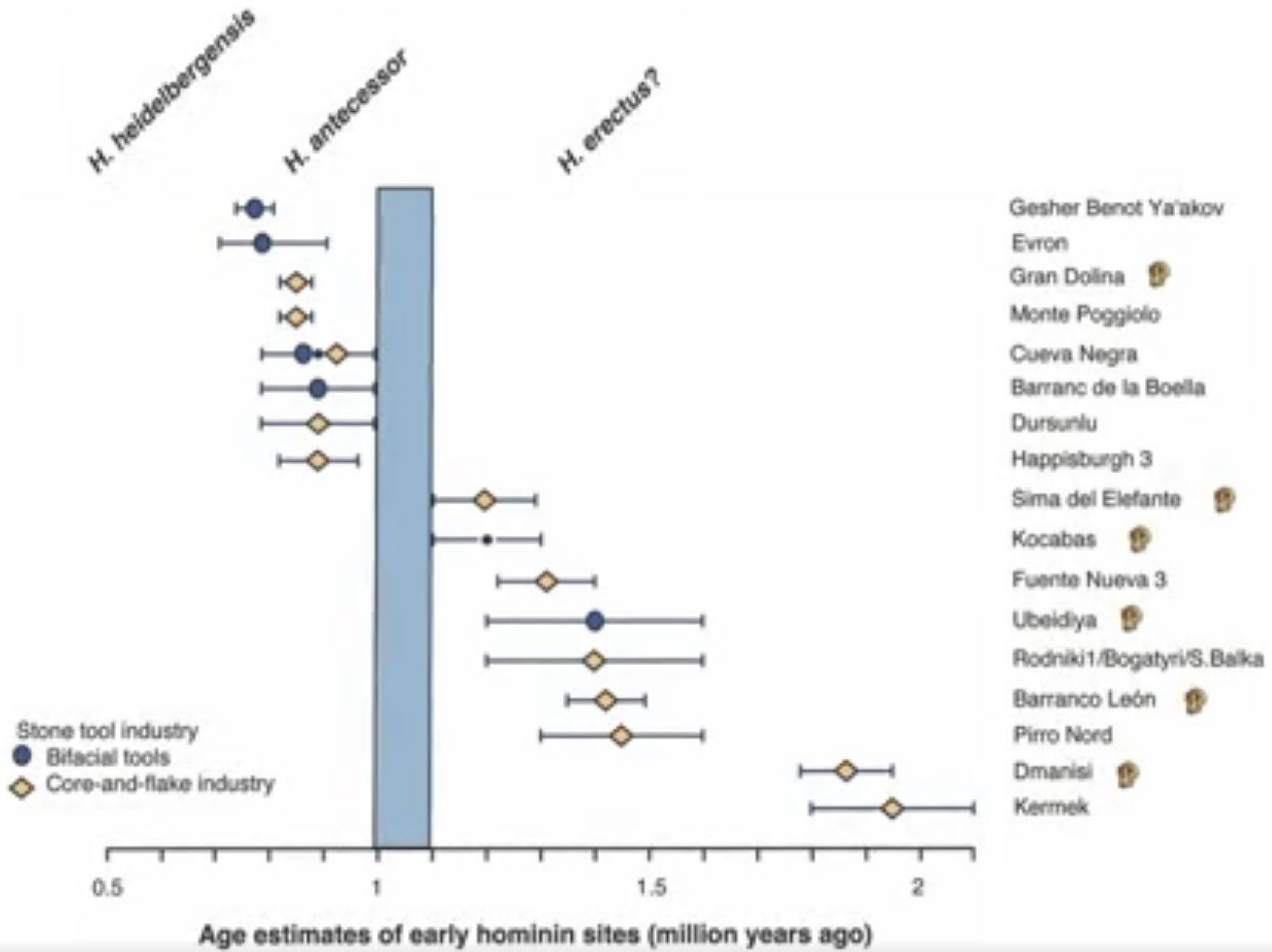
- Given that hominins were present at Dmanisi, Georgia, ~1.8 Ma ago, dispersal into Europe could have taken place at any time after that, but sites in Italy and Spain yielding stone tools and human remains over a broad time window of ~1.6 to ~1.1 Ma indicate a delay of ~200 thousand years.

Age estimates of European and SW Asian early hominin sites



Climate

- North Atlantic records point to the occurrence of iceberg discharges from marine-terminating ice sheets and disruptions of the Atlantic meridional overturning circulation (system of ocean currents that circulates water within the Atlantic Ocean) during the interval ~1.43 to ~1.25 Ma.
- Paleoenvironmental reconstructions based on animal and plant remains from the Atapuerca and Guadix-Baza occupation levels indicate a diverse mosaic of Mediterranean and temperate woodlands, open shrublands, and extensive wetlands, with mean annual temperatures similar to those of the present, but higher mean annual precipitation


H. heidelbergensis
H. antecessor
H. erectus?
Gesher Benot Ya'akov
Evron
Gran Dolina
Monte Poggiolo
Cueva Negra
Barranc de la Boella
Dursunlu
Happisburgh 3
Sima del Elefante
Kocabas
Fuente Nueva 3
Ubeidiya
Rodniki1/Bogatyri/S.Balka
Barranco León
Pirro Nord
Dmanisi
Kermek
Stone tool industry
Bifacial tools
Core-and-flake industry
0.5
1
1.5
2
Age estimates of early hominin sites (million years ago)

A devastating stadial

- The picture that emerges for the interval of hominin presence before 1.15 Ma is one of long, stable interglacial conditions and short glacials that would have allowed hominin establishment and occupation.
- However, the character of glacial periods changed at MIS 34. Its pervasive climatic instability would have placed hominin populations under considerable stress. Early hominins lacked sufficient fat insulation and the means to make fire, effective clothing, or shelters, leading to much-lower population resilience.
- The terminal stadial event represents a drastic climate disruption, which likely affected climate and vegetation patterns across southern Europe with potential implications for early hominin occupation.

Massive Climate drop at 1.1 MA

- The results show a massive drop in habitat suitability around the Mediterranean by more than 50% around 1.117 Ma.

- Climate conditions move far away from the preferred climate niche of early European hominins.

- Lasting for about 4000 years, this event triggered large-scale shifts in vegetation and ecosystems, as documented by the 45% increase of steppe pollen and the simulated reduction of 50% in net primary production over the Iberian Peninsula.

European depopulation

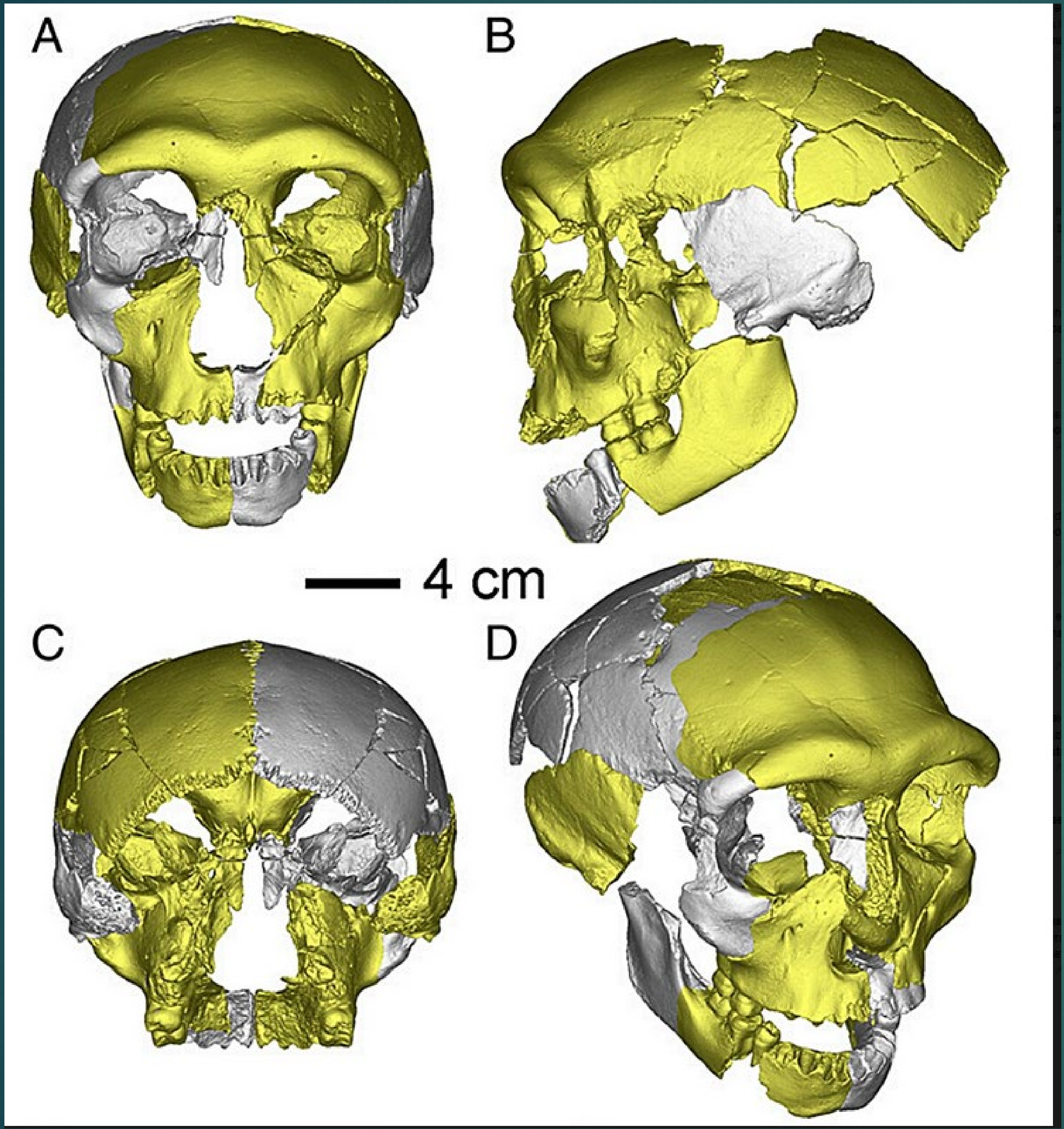
- The climatic instability of MIS 34 (1.122 Ma) and the severity of its terminal stadial emerging from this study imply that Iberia, and more generally southern Europe, was depopulated at least once in the Early Pleistocene.
- Dennell *et al.* suggested that the question "When was Europe first colonized?" might be rephrased, "How often was Europe uninhabited after hominins first entered it?"
- We propose that the question may be further qualified by adding, "and for how long [was Europe uninhabited]?" If Southwest Asia was depopulated during MIS 34, reoccupation of Europe may have been delayed until as late as MIS 25, or after the marked glaciation of MIS 22, during MIS 21.

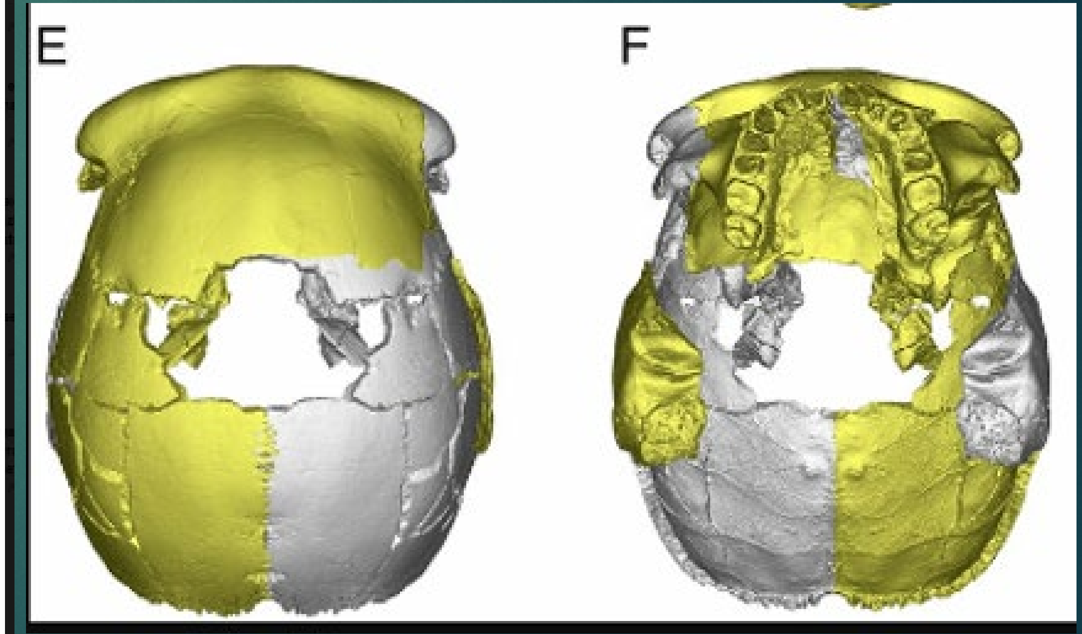
H. erectus replaced by *H. antecessor*?

- This hypothesis can be tested through newly discovered archaeological or hominin sites with robust chronological constraints.

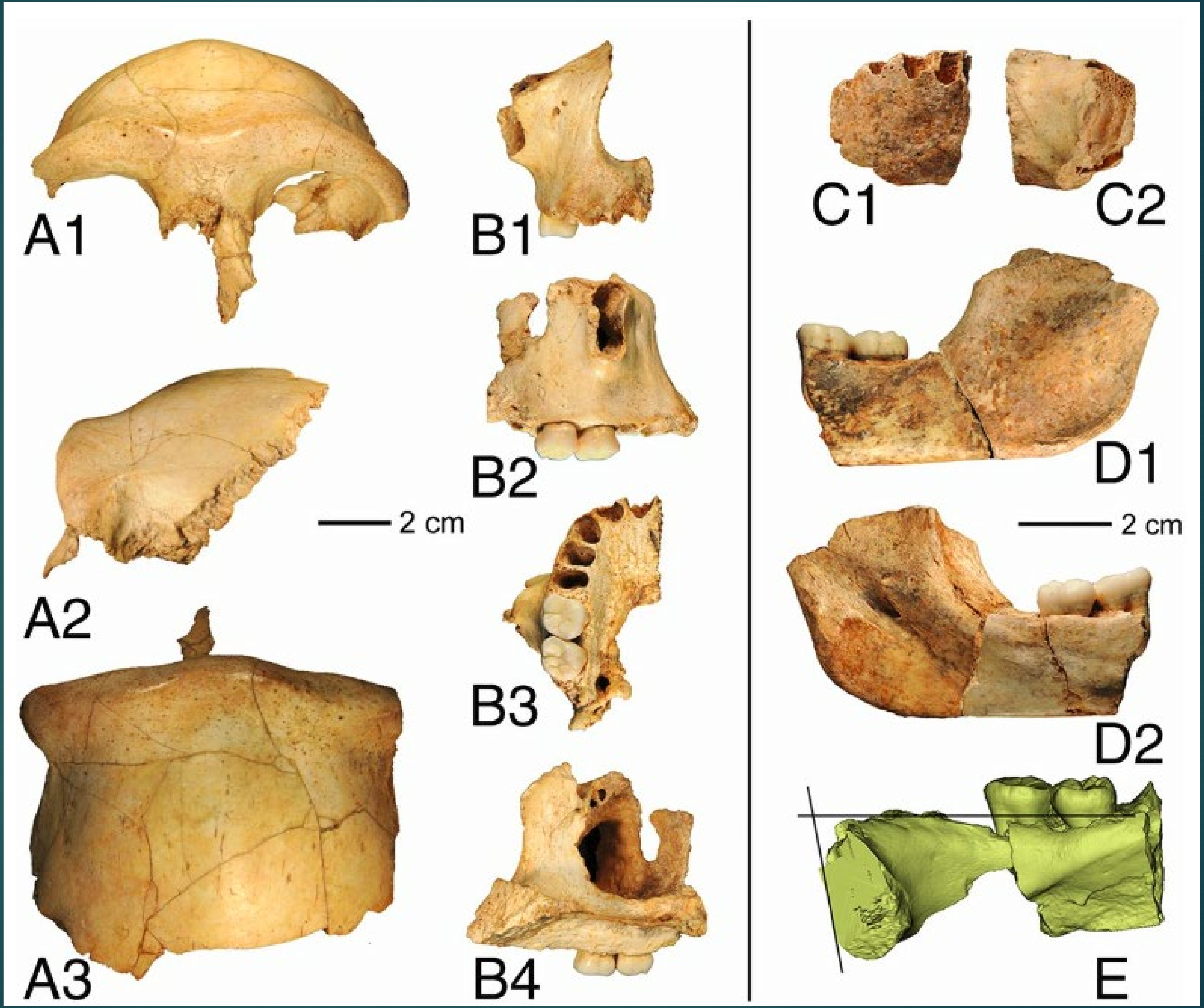
- If there was the disappearance of hominins in Europe for such an extended period, it implies that repopulation was by *Homo antecessor*, which may have been a more resilient species with evolutionary or behavioral changes that allowed survival under the increasing intensity of glacial conditions.

2021 study: HLD 6





HLD6



Morphological description and evolutionary significance of 300 ka hominin facial bones from Hualongdong, China

- 2021: The facial morphology of HLD 6 resembles that of Early and Middle Pleistocene hominins from Zhoukoudian, Nanjing, Dali, and Jinniushan in China, as well as others from Java, Africa, and Europe in some of these features (e.g., supraorbital and malar regions), and Late Pleistocene hominins and modern humans from East Asia, Africa, and Europe in other features (e.g., weak prognathism, flat face and features in nasal and hard plate regions). A 12–13 year old.
- Supports a close affinities of HLD 6 to Late Pleistocene hominins and modern humans. Expression of a mosaic morphological pattern in the HLD 6 facial skeleton further complicates evolutionary interpretations of regional morphological diversity in East Asia.

X. Wu, et al., 2021

HLD 6: regional continuity??

- The prevalence of modern features in HLD 6 suggests that the hominin population to which HLD 6 belonged may represent the earliest pre-modern humans in East Asia.

- Thus, the transition from archaic to modern morphology in East Asian hominins may have occurred at least by 300 ka

- At about 300,000 years old, HLD 6 may be evidence of regional continuity, a transitional human that represents the evolution of archaic East Asian H. erectus populations into East Asian AMHs. Or, quite frankly, HLD 6 may simply be an anomaly, an archaic hominin with some quirky variation

- ** CJV: Chinese researches have maintained the multiregional theory of regional continuity

Morphological and morphometric analyses of a late Middle Pleistocene hominin mandible from Hualongdong, China

- 2023: Excavations in Hualongdong (HLD), East China, have yielded abundant hominin fossils dated to 300 ka. There is a nearly complete mandible that fits well with a partial cranium, and together they compose the skull labeled as HLD 6.
- New comprehensive assessment of this mandible and compare it with both adult and immature specimens of Pleistocene hominins and recent modern humans.
- Results indicate that the HLD 6 mandible exhibits a mosaic morphological pattern characterized by a robust corpus and relatively gracile symphysis and ramus.
- However, the weak expression of all these features indicates that this mandible does not possess a true chin.

X. Wu, et al., 2023

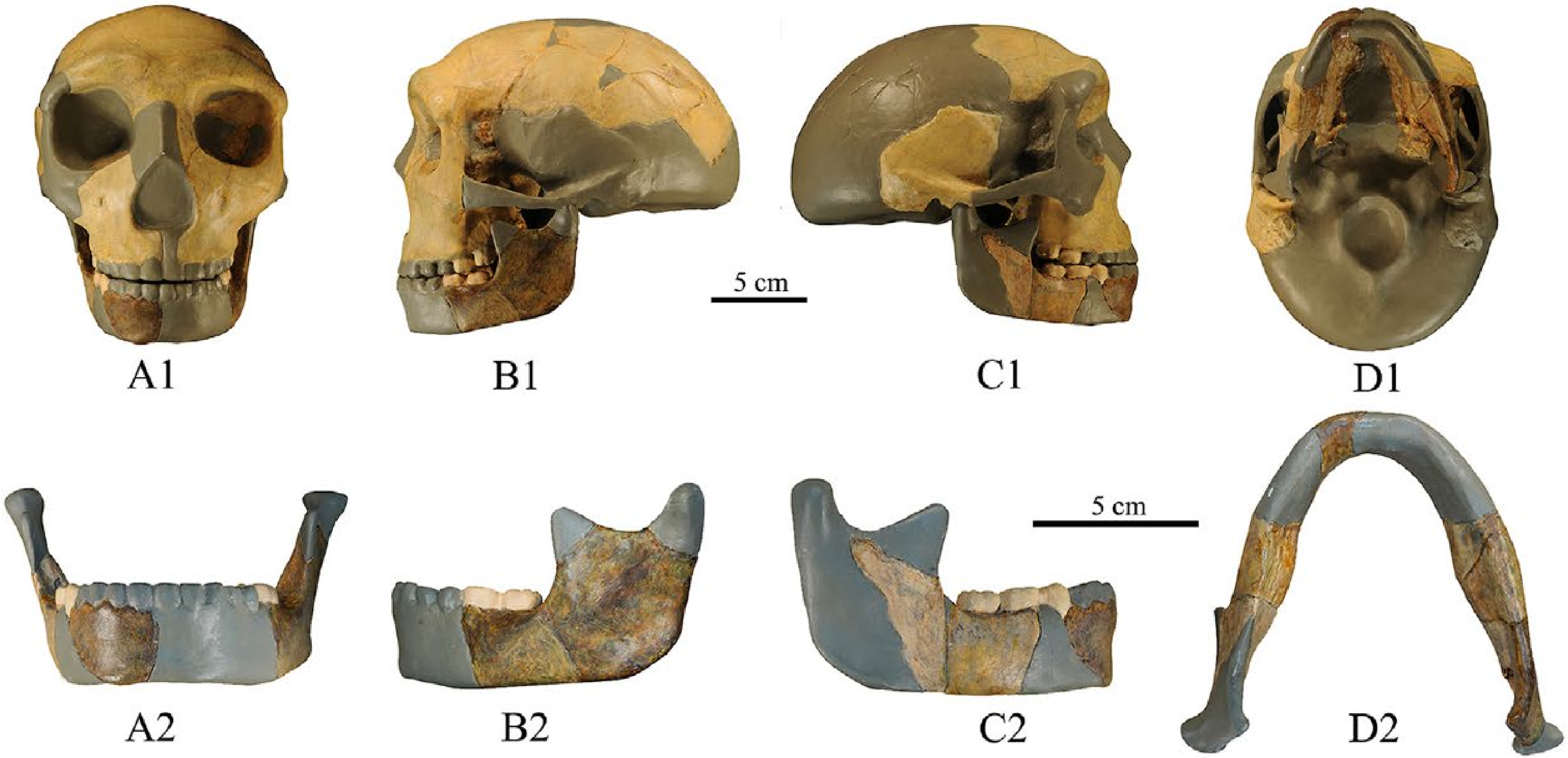


Figure 2. Views of the new reconstruction of the Hualongdong 6 mandible and its fit with the reconstructed cranium in anterior (A1 and A2), left lateral (B1 and B2), right lateral (C1 and C2), and basal (D1 and D2) views.

Hualongdong mandible

- The geometric morphometric analysis further confirms the mosaic pattern of the HLD 6 mandible. The combination of both archaic and modern human features identified in the HLD 6 mandible is unexpected, given its late Middle Pleistocene age and differs from approximately contemporaneous *Homo* members such as Xujiayao, Penghu, and Xiahe.
- This mosaic pattern has never been recorded in late Middle Pleistocene hominin fossil assemblages in East Asia. The HLD 6 mandible provides further support for the high morphological diversity during late Middle Pleistocene hominin evolution. With these findings, it is possible that modern human morphologies are present as early as 300 ka and earlier than the emergence of modern humans in East Asia.

Controversies

- These late Middle Pleistocene hominins have been named as early *Homo sapiens* or archaic *H. sapiens*. They were thought to be intermediate between *Homo erectus* and early modern humans, and the ancestors of modern humans in East Asia.
- The hominin fossil discovery and related studies in the last decade have changed this traditional view on the evolution pattern of the late Middle Pleistocene hominins in China radically. The hominin fossils from this time period, such as Dali, Jinniushan, Maba, Tongzi, Xujiayao, Xuchang, and Xiahe, exhibit high morphological variability and are not easily allocated to the existing taxonomic groups .
- Have been given variety of taxonomic names, incl. early MHs, an Eastern variant of Neanderthals, and Denisovans.

Mosaic features

- The HLD hominin sample comprises approximately 16 individuals dated to about 300 ka. Among them, there is a nearly complete skull with a partial cranium and a nearly complete mandible (HLD 6).

- The initial morphological studies show that HLD 6 displays a mixture of typically East Asian Middle Pleistocene hominins traits mostly in the cranial vault, together with a modern human-like face.

- The research team suggests that the unique features of the jawbone resemble those of both modern humans and Late Pleistocene hominids. But they also found that it did not have a chin, which suggests that it was more closely related to older species.

Claim not Denisovans

- They found other features that resemble hominins of the Middle Pleistocene, which, when taken together, suggested the individual most resembled a Homo erectus species. And that, they conclude, suggests a hybrid of modern human and ancient hominid. The new team found that the bones in its face were more similar to those in modern humans than was the case for the jawbone.

- In an effort to determine a species for the remains, the team ruled out Denisovan. That left them with the likelihood that the fossils represent a third lineage—one that is not Denisovan or Homo erectus, and is closer to Homo sapiens. ??

Database with 2,400 prehistoric sites, a tool for human evolutionary studies

Andrew W. Kandel, et al., 2023

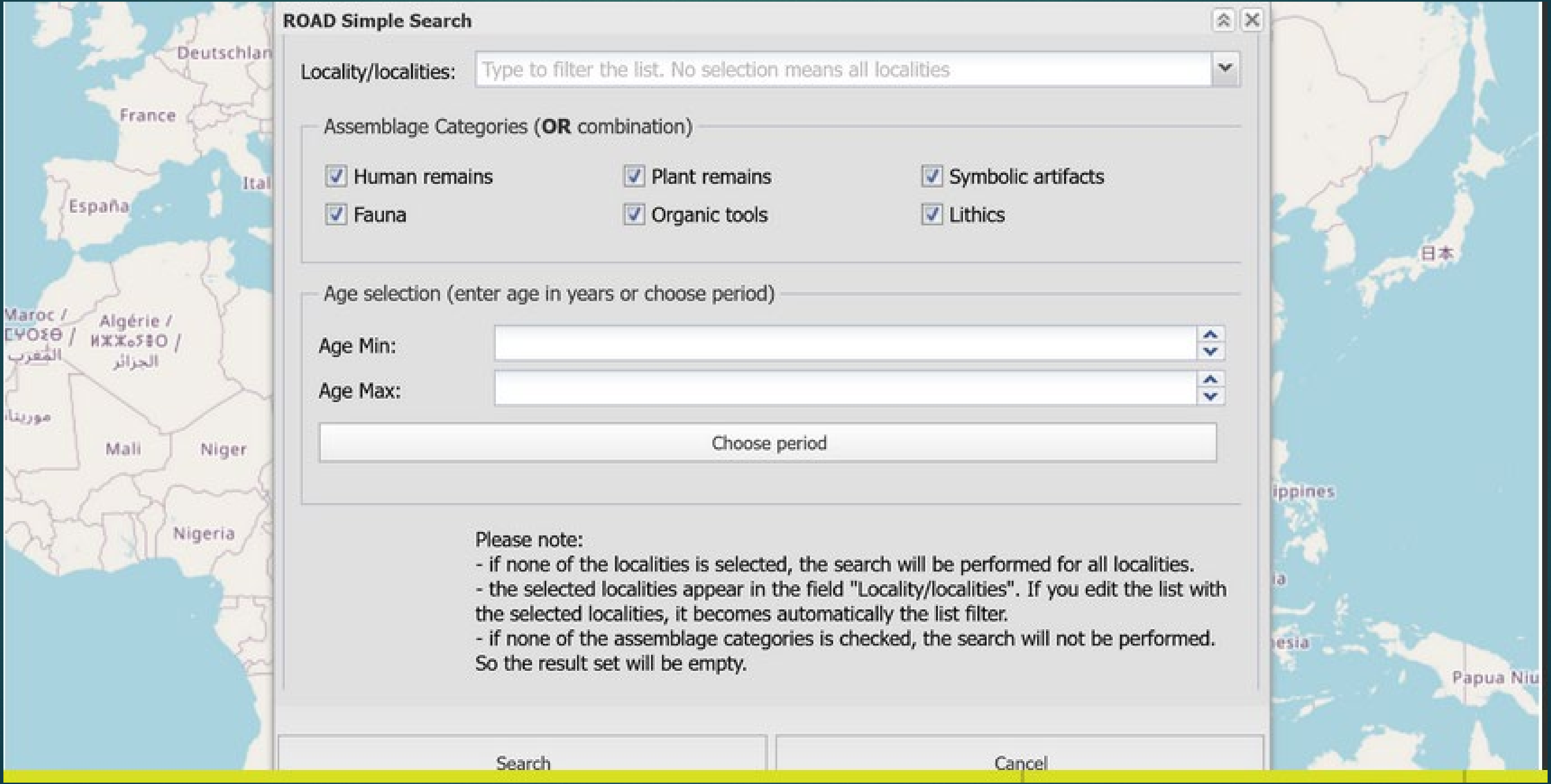
ROAD (ROCEEH Out of Africa Database)

- ROAD (ROCEEH Out of Africa Database) represents one of the largest digital collections of information about archaeology, anthropology, paleontology and botany based on 150 years of research history

- Numerous sites relating to the early history of mankind from 3 million to 20,000 years ago can be accessed in a large-scale database. Scientists from the research center ROCEEH (The Role of Culture in Early Expansions of Humans) have compiled information on 2,400 prehistoric sites and 24,000 assemblages from more than 100 ancient cultures. The digital data collection is available for free and was published in the journal PLoS ONE.

- More than 5,000 publications in multiple languages were analyzed, including Chinese, Russian, English, German, French, Italian, Spanish and Portuguese.

ROAD Website: https://www.roceeh.uni-tuebingen.de/roadweb/smarty_road_simple_search.php



ROAD Simple Search

Locality/localities: Type to filter the list. No selection means all localities

Assemblage Categories (**OR** combination)

☑ Human remains ☑ Plant remains ☑ Symbolic artifacts
☑ Fauna ☑ Organic tools ☑ Lithics

Age selection (enter age in years or choose period)

Age Min:

Age Max:

Please note:
- if none of the localities is selected, the search will be performed for all localities.
- the selected localities appear in the field "Locality/localities". If you edit the list with the selected localities, it becomes automatically the list filter.
- if none of the assemblage categories is checked, the search will not be performed. So the result set will be empty.

Preliminary study of two deciduous human molars from the Late Pleistocene layers of Song Terus (East Java): A window into the last *Homo erectus* and the first *Homo sapiens* in Java

- Java is one of the oldest places outside Africa which was occupied by early humans, from the first 'archaic' *Homo erectus* after 1.8 ma to the progressive form around 70-40 ka.
- Question of date of colonization of this island. Some previous scholars proposed scenarios presumed this to be as early as 125 ka, or just after the big eruption of young Toba after 74 ka, or at last to the late glacial maximum about 21 ka.
- Two unpublished deciduous teeth of Song Terus site are considered: ST06 is dated back from older than 80 ka and another tooth ST04 is younger than 60 ka.

S. Noerwidi, et al. 2023,

Two teeth

- ST04 is closer to *Homo sapiens* while ST06 belongs to the *Homo erectus s.l.* group.
- This result confirms that *Homo erectus* still survived at least until the beginning of the Late Pleistocene, during the last interglacial maximum period (125 ka).
- Moreover, it argues that *Homo sapiens* was present in Java Island just after the young Toba eruption 74 ka.
- The implication of this result could be the succession of chronological occupations between the last *Homo erectus* and early *Homo sapiens* in Southeast Asia.

Ghost admixture in eastern gorillas

- As in the case of Neandertal ancestry in living people, African eastern gorillas, but not western gorillas, have a 2.5% genetic contribution from a ghost lineage dating from ~40 Ka. Across individuals, a putative 16.4% of the autosomal genome of an extinct lineage was recovered.

- Up to 3% of the genome of these individuals is introgressed from an archaic lineage that diverged more than 3 million years ago from the common ancestor of all extant gorillas.

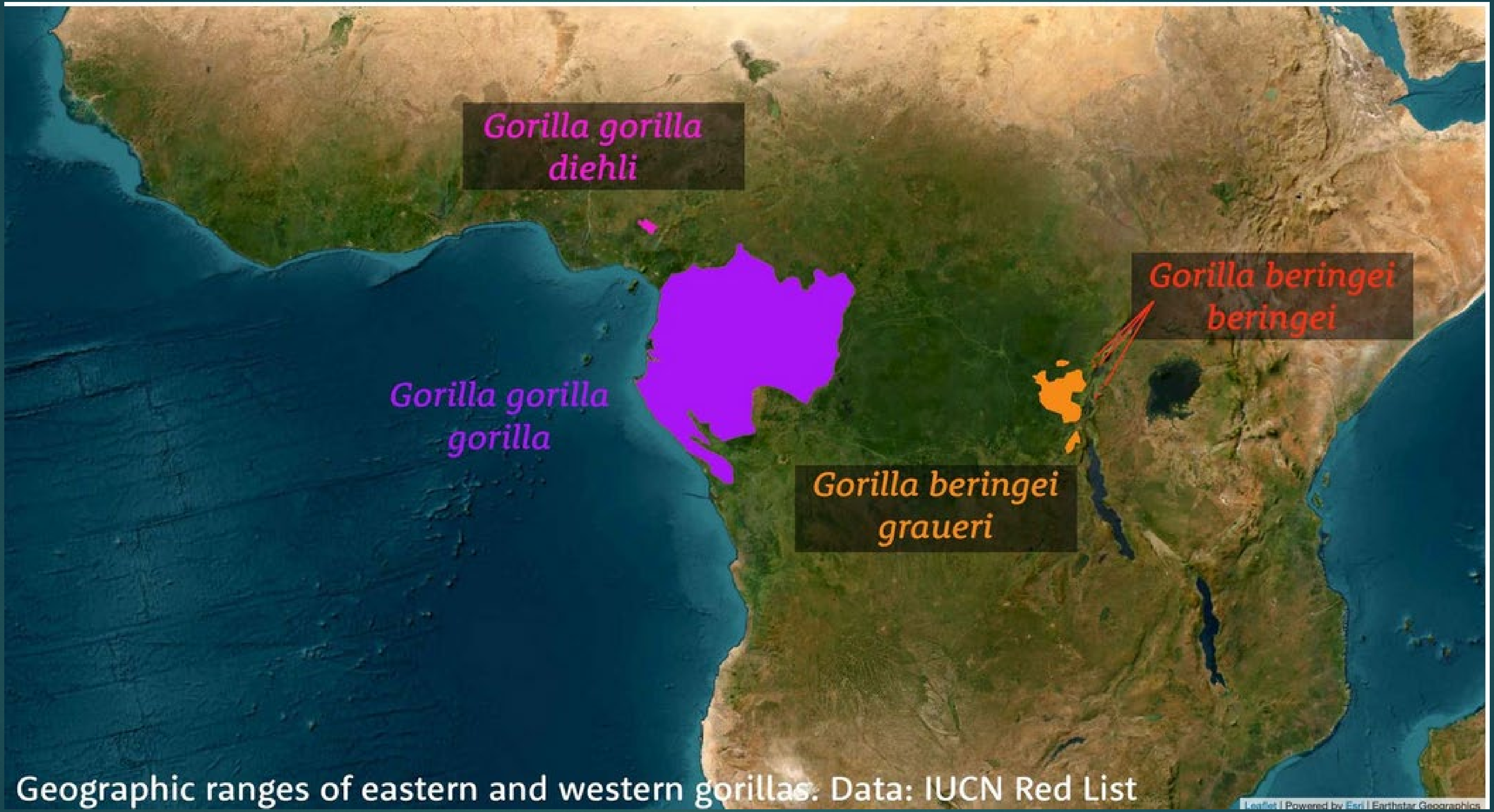
Harvinder Pawar, et al., 2023

Eastern gorillas

- This introgression event took place before the split of mountain and eastern lowland gorillas, probably more than 40 thousand years ago and may have influenced perception of bitter taste in eastern gorillas.

- When comparing the introgression landscapes of gorillas, humans and bonobos, we find a consistent depletion of introgressed fragments on the X chromosome across these species. However, depletion in protein-coding content is not detectable in eastern gorillas, possibly as a consequence of stronger genetic drift in this species.

Gorilla ranges

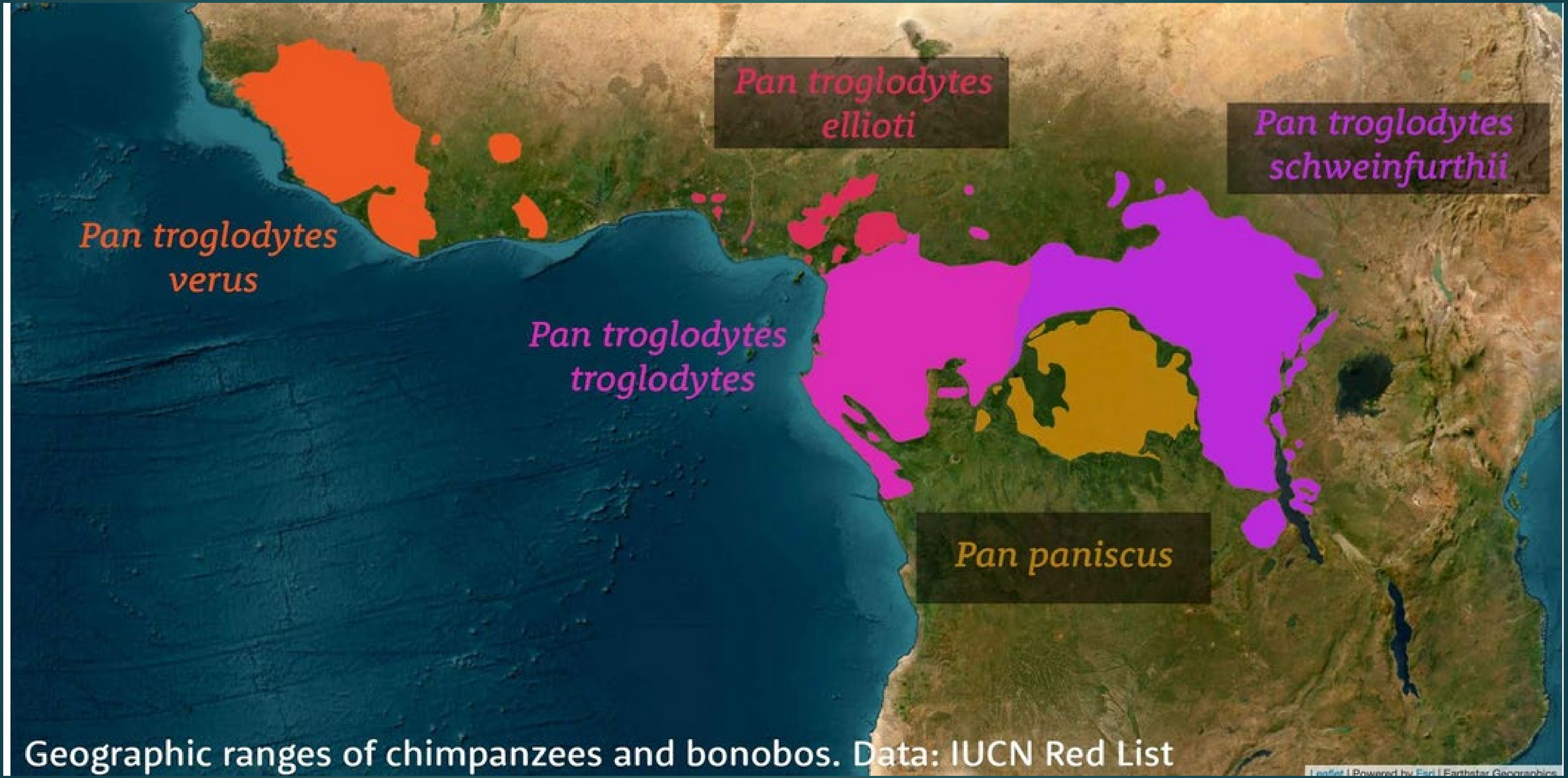


Geographic ranges of eastern and western gorillas. Data: IUCN Red List

Two living species of gorillas: *Gorilla gorilla* in the west and *Gorilla beringei* in the east.

- Each of these species can be divided into two subspecies. Western lowland gorillas, *Gorilla gorilla gorilla*, live across most of Gabon, Equatorial Guinea and parts of the Republic of Congo and Cameroon. The western lowland gorillas are by far the most numerous of today's populations and their genomes show that they maintained a large and diverse population throughout the last million years.
- The Cross River gorillas, *Gorilla gorilla diehli*, were an offshoot of the western population around a half million years ago and today live in small areas of western Cameroon and eastern Nigeria.
- The eastern gorillas include both mountain gorillas, *Gorilla beringei beringed*, in the highlands of Rwanda, Uganda, and Democratic Republic of Congo, and eastern lowland gorillas, *Gorilla beringei graueri*, in the eastern DRC. These two populations diverged only within the last 20,000 years, and both of them and their common ancestral lineage have been relatively small since their origin.

Bonobos and chimpanzees



Geographic ranges of chimpanzees and bonobos. Data: IUCN Red List

Bonobos and chimpanzees

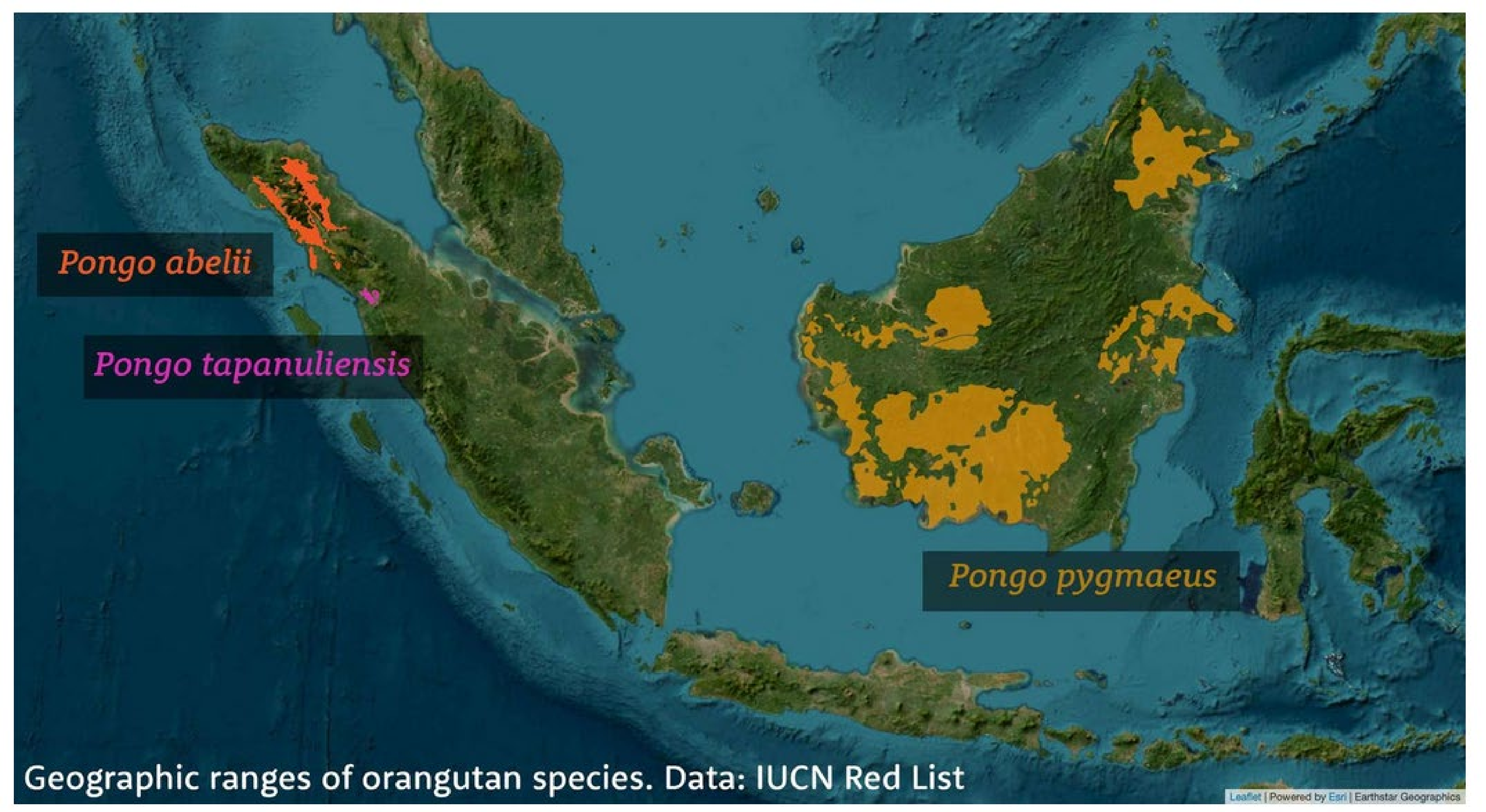
- Bonobos, *Pan paniscus*, live in the forested region south of the Congo River within the Democratic Republic of Congo. Their closest living relatives are chimpanzees, *Pan troglodytes*, which have diverse populations arrayed from Senegal in western Africa to Tanzania in the east.

- <u>Bonobos and chimpanzees diverged sometime between 2 million and 1.5 million years ago</u>, and subsequently the two species occasionally exchanged genes, with these exchanges amounting to less than one percent of the ancestry of either bonobos or central African chimpanzees.

Ghost populations

- Earlier work in 2019 by much of the same research group, led by Martin Kuhlwilm, found that bonobos descend in part from an ancient, highly-divergent population. That ghost population had an estimated origination around 3.5 million years ago.
- In the analysis by Kuhlwilm and collaborators, genetic ancestry from the ghost population makes up between 0.9 and 4.2% of bonobo genomes. Unlike the case of eastern gorillas, the mixture from the ghost population in bonobos happened a long time in the past, between 377,000 and 637,000 years ago.
- A separation of ancestral populations with the Congo River formation ~3.5 Ma or during later dry periods may provide the context for an early population split from the *Pan* clade,

Orangutans



Geographic ranges of orangutan species. Data: IUCN Red List

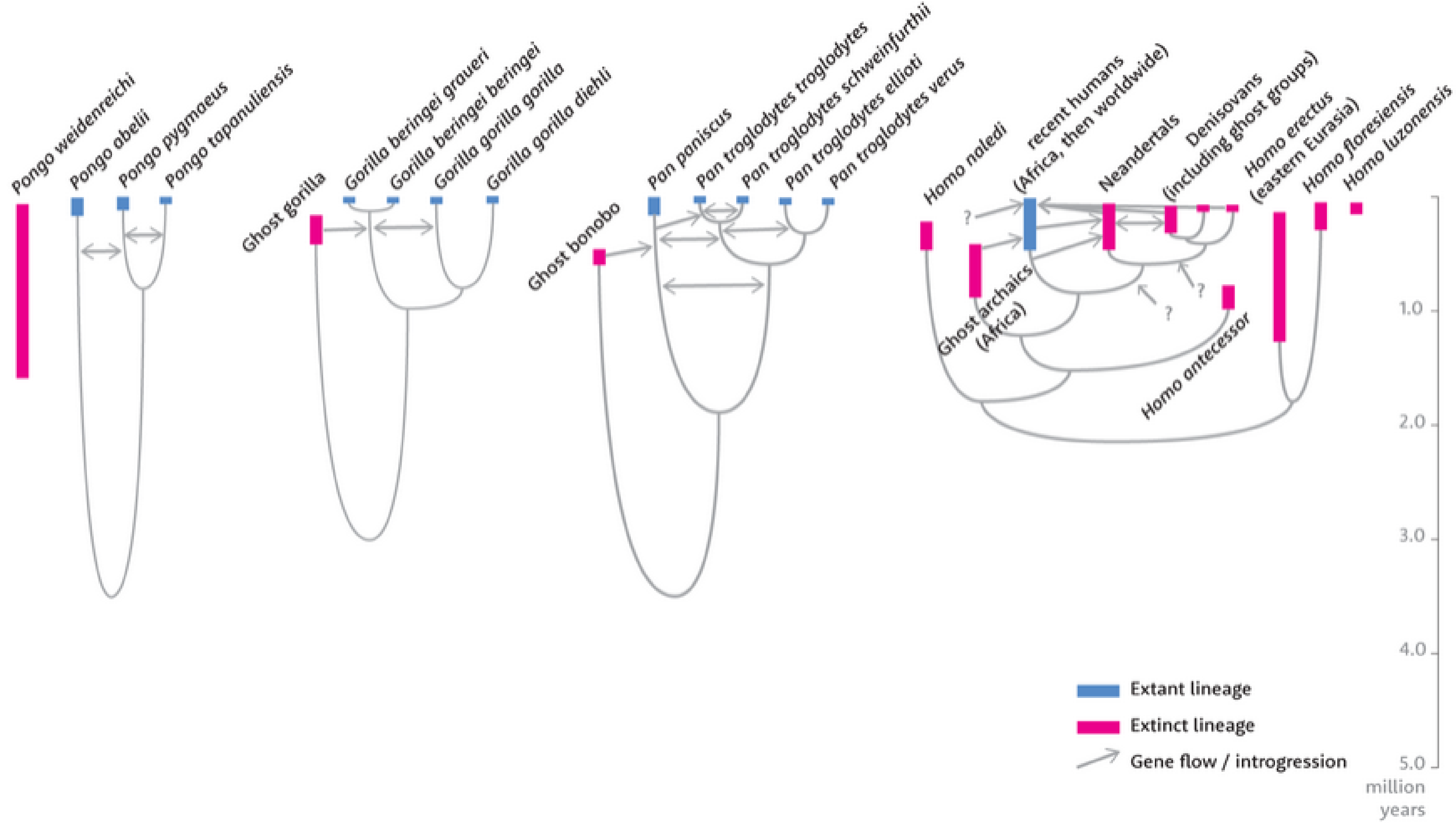
Leaflet | Powered by Esri | Earthstar Geographics

Orangutans

- In 2017 scientists recognized that a small population living today south of Lake Toba, Sumatra, is genetically and morphologically different from other Sumatran orangutans.
- Researchers recognize these orangutans as a third species, *Pongo tapanuliensis*, beside the other Sumatran orangutans, *Pongo abelii*, and the Bornean orangutans, *Pongo pygmaeus*.
- The deepest population divergence among the three species of orangutans dates back as early as 3.4 million years.
- The Tapanuli orangutans are closer to Bornean orangutans, with the two diverging an estimated 675,000 years ago. The other Sumatran orangutans themselves have deep lineage diversity, going back to a million years. All of these populations shared a small fraction of gene flow with each other after they first began to separate.

Finally a real effect of Mt. Toba eruption

- Borneo, Sumatra, and Java were all connected to each other and the Asian mainland during much of the Pleistocene. The Tapanuli and other Sumatran orangutans are separated today by Lake Toba, which resulted from a volcanic supereruption around 74,000 years ago.
- Bornean orangutans today have the largest numbers and extensive regional variation, but current genetic data suggests that their populations differentiated only very recently, within the last 20,000 years.



Hominins may look more complicated than the living great apes, but that may be an illusion based on our greater fossil and ancient DNA record.

More than half of life on Earth is found in soil

- A recent study has found that soil is home to 59% of all life on Earth, from an insect feeding on the soil surface to a tiny microbe nestled in a soil pore. This discovery crowns soil as the most biodiverse habitat on the planet.

- The paper estimates that around 2 million species of arthropod (think insects and spiders) inhabit the soil—some 30% of all known arthropod species. There are far fewer species of soil specialists such as enchytraeidae (resembling mini earthworms) and oligochaeta (worms), with only 770 and 6,000 species respectively. That might not seem like a lot, but it still represents around 98% and 63% of these animal groups.

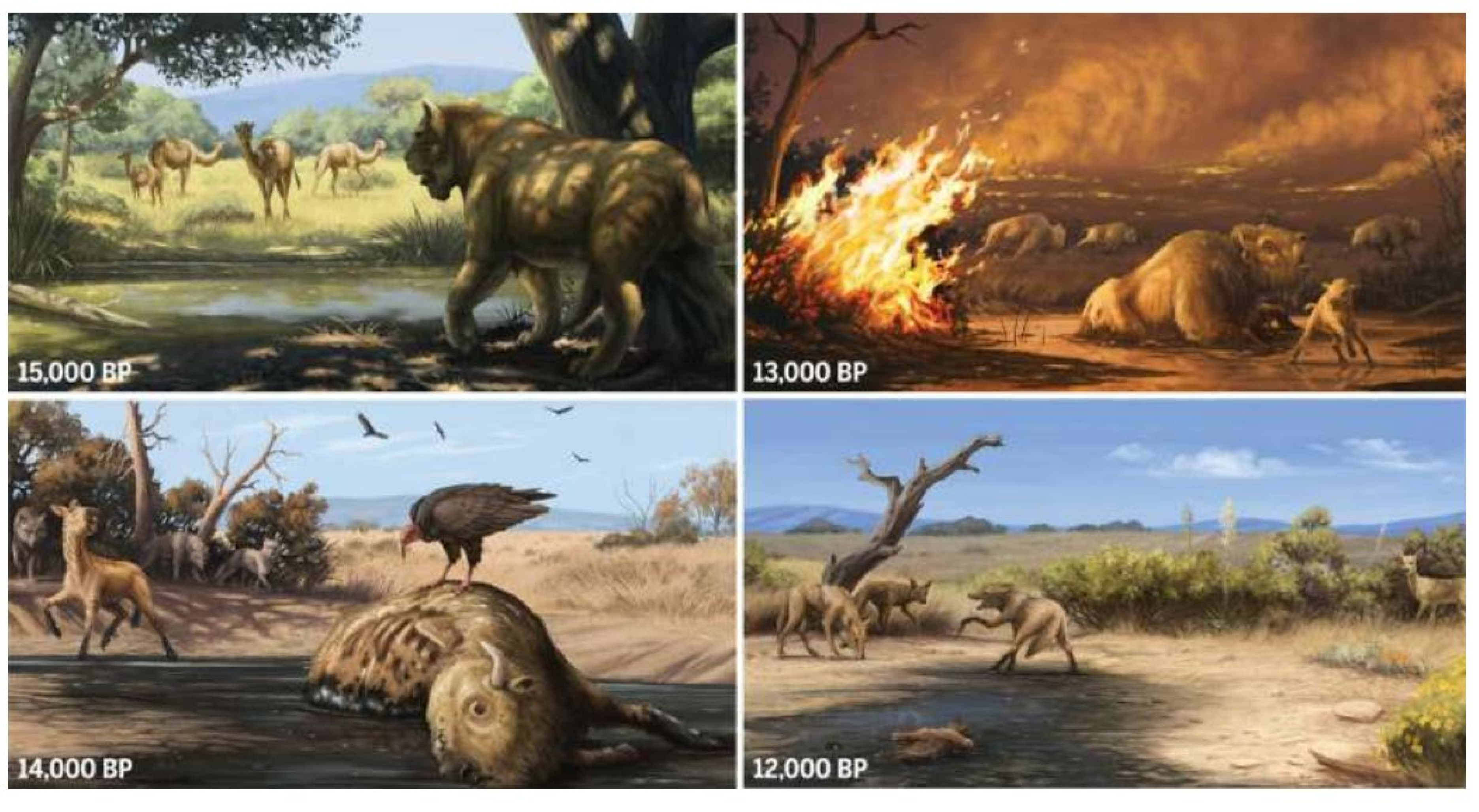
F. Robin O'Keefe, et al., 2023

Soil

- Only 3.8% of mammal species are associated with this habitat. On the other hand, 85% of plants have their roots buried in the soil and around 43% of nematode (tiny worms) species call soil their home, or reside within the plants and animals that inhabit it.
- However, the number of animal and plant species that live in soil are dwarfed by microscopic organisms. The researchers estimate that a mind-blowing 430 million species (or more than 50%) of bacteria and 5.6 million species (or 90%) of fungi have made soil their home.
- Enchytraeidae (segmented relatives of earthworms) have the greatest percentage of species in soil (98.6%), followed by fungi (90%), Plantae (85.5%), and Isoptera (termites) (84.2%).
- Results demonstrate that soil is the most biodiverse singular habitat

Pre–Younger Dryas megafaunal extirpation at Rancho La Brea linked to fire-driven state shift

- New study documents a transition from a postglacial megafaunal woodland to a human-mediated chaparral ecosystem in Southern California before the onset of the Younger Dryas. This transition began with gradual opening and drying of the landscape over two millennia, and terminated in an abrupt (300-year) regime shift characterized by the complete extirpation of megafauna and unprecedented fire activity. This state shift appears to have been triggered by human-ignited fires in an ecosystem stressed by rapid warming, a megadrought, and a millennial-scale trend toward the loss of large herbivores from the landscape. This event parallels processes occurring in Mediterranean ecosystems today.



Sequence of ecological events as recorded at Rancho La Brea, California. Top left: conditions at 15 Ka around the tar pits were moist and cool, with abundant trees and megafaunal mammals. Bottom left: at 14 Ka the onset of postglacial warming and drying begins as human pressure on herbivores increases. Top right: at 13 Ka the synergy between climatic and human impacts enables a sudden ecological state transition characterized by unprecedented fire activity. Bottom right: at 12 Ka, a chapparal ecosystem is established; megafauna are extinct, and only coyote entrapment continues at the tar pits.

Wildfires once fueled extinctions in Southern California; will it happen again?

- Tens of thousands of years ago, before the last ice age ended, vast herds of saber-toothed cats, giant sloths, American camels and other fantastic beasts roamed Southern California. Then they were gone. The cause has been unknown.
- Researchers used bones from the La Brea Tar Pits, ancient mud from the bottom of Lake Elsinore and an array of other evidence to piece together the region's archaeological record. The results paint an astonishingly detailed picture of the events that led to the animals' disappearance.
- Concluded that the magnificent mammals of the Ice Age vanished with shocking speed when a period of warm, dry climate conditions coincided with the arrival of humans and a tool they struggled to contain: fire.

California's first human-driven ecological catastrophe

- It took the area's earliest human inhabitants less than 300 years to utterly transform Southern California's landscape. Fires they started but could not control led to the swift demise of species that had ruled the land for millennia, and fundamentally reshaped the ecosystem from a prehistoric woodland to the chaparral of today.
- Humans were responsible for these fires, and the fires coincide exactly with the complete disappearance of megafauna from the environment
- The study began with an effort to use radiocarbon dating to determine the ages of a few hundred of the approximately 3.5 million bones unearthed over the years from the La Brea Tar Pits. Tar preserves a bone's collagen, which is more conducive to getting a precise radiocarbon date.

13 to 14 Ka at La Brea

- As the researchers started working through fossils extracted from Pit 61/67, they made a surprising discovery: The pit had been active during the years of the mass extinction.
- Specimens older than 13,000 years came from a variety of animals once common in Southern California: saber-toothed cats, dire wolves, western horses, bison, coyotes.
- But after the 13,000-year mark, that diversity disappeared. The only big mammal bones found in the pit from that point on were from coyotes. All taxa except coyotes were gone by 12.9 ka.
- Time-series modeling strongly implicates humans as the primary cause of the state shift and resulting extinctions.

Evidence from Lake Elsinore's mud

- Prior to 13,200 years ago, the mud cores from Lake Elsinore show minimal fire activity. But then there is unprecedented fire activity. The charcoal abundance increases by an order of magnitude, and then it remains high for the next few hundred years; a picture of ecological collapse that happened gradually, and then all at once.
- Worldwide, the period from 14,000 years ago to 13,000 years ago was unusually warm and dry. Air temperatures in Southern California rose an average of 5.6 degrees Celsius (10 degrees Fahrenheit). Vegetation grew incrementally drier. And then humans arrived at 13 Ka.
- The oldest human remains yet discovered in North America were found on the Channel Islands off the coast of Santa Barbara, and date back 13,000 years.

Humans and fire at La Brea

- As soon as humans arrive on the scene, suddenly, there's tons of fire in the record.
- Our Pleistocene ancestors had few tools at their disposal to extinguish a blaze once it spread out of control.
- Once-abundant junipers and oaks could tolerate drought, but had no defenses against fire. They disappeared, and fire-adapted pines and chaparral took their place. In a landscape stripped of shade, shelter and hiding places, food chains were upended. Intense fire may have altered water flows or cut off migration routes.
- According to the fossil record, all of this devastation took barely 300 years.

Similar to today

- The study's authors noted the unsettling similarities between the late Pleistocene extinction and present-day climate conditions in the American West: higher temperatures, drier vegetation and a growing human population that can't stop itself from setting things ablaze.
- The climate is heating up at an exponentially higher rate. In the late Pleistocene, it took 1,000 years for temperatures to rise 5.6 degrees C. In the Anthropocene, temperatures in California have risen nearly 2 degrees C in the last 100 years alone.
- It's not hard to imagine many species today shortly going the way of the saber-toothed cat.

Late Neanderthal "menu" from northern to southern Italy: freshwater and terrestrial animal resources

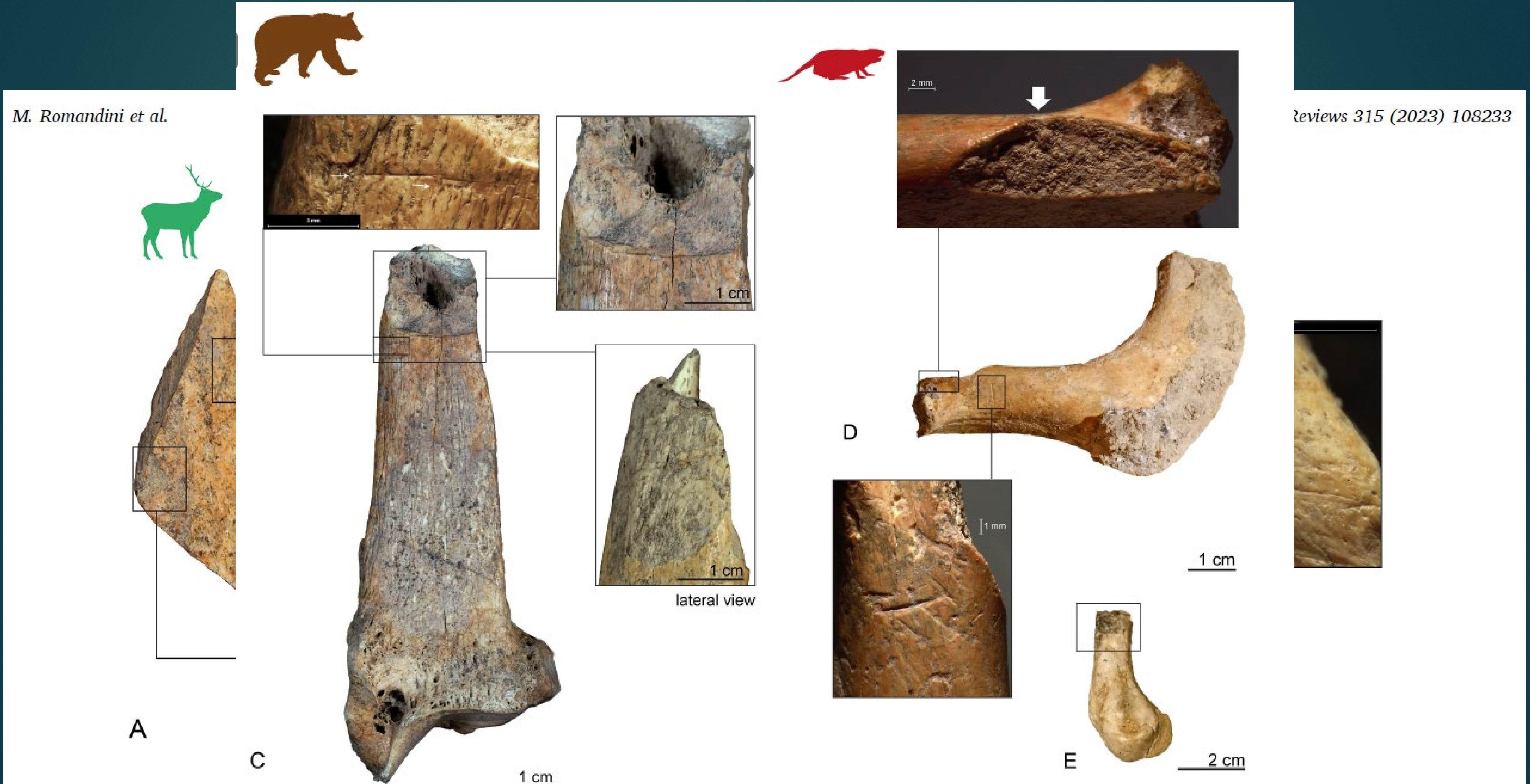
- The present paper aims to provide a thorough assessment of the unpublished faunal assemblages from two Late Mousterian Italian sites: Riparo del Broion (northern Italy) and Roccia San Sebastiano cave (southern Italy). These two sites occupy two distant and different areas of Italy, however providing late Neanderthals coeval occupations dated between 50,000–44,000 cal BP. In this study we analyzed more than 27,000 remains.
- Strontium isotope analysis of cervid (deer) remains, the most exploited prey in both sites. In general, the characteristics of the territory of the two sites highlight the exploitation of different resources that could vary from almost specialized small game (Riparo del Broion) to selective ungulates (Roccia San Sebastiano) hunting strategies.
- At Riparo del Broion, the main exploitation of red deer was accompanied by beaver hunting, fishing, and shellfish gathering from freshwater lake environments.

M. Romandini, et al. 2023

Italian food for Ns

- On the contrary, at Roccia San Sebastiano cave: red deer was hunted almost exclusively, despite the sea was not far from the cave. The absence of shellfish and fish remains is remarkable.
- In addition, the transformation and use of diaphyseal bone flakes as retouchers at both sites and the presence of a probable "bone awl" at Roccia San Sebastiano, further confirm an extended capacity in the use of a large range of materials for different subsistence activities.
- Present results consist of the first zooarchaeological comparison of the Late Mousterian levels of Roccia San Sebastiano cave and Riparo del Broion.

Examples of anthropogenic modifications from Riparo del Broion



M. Romandini et al.

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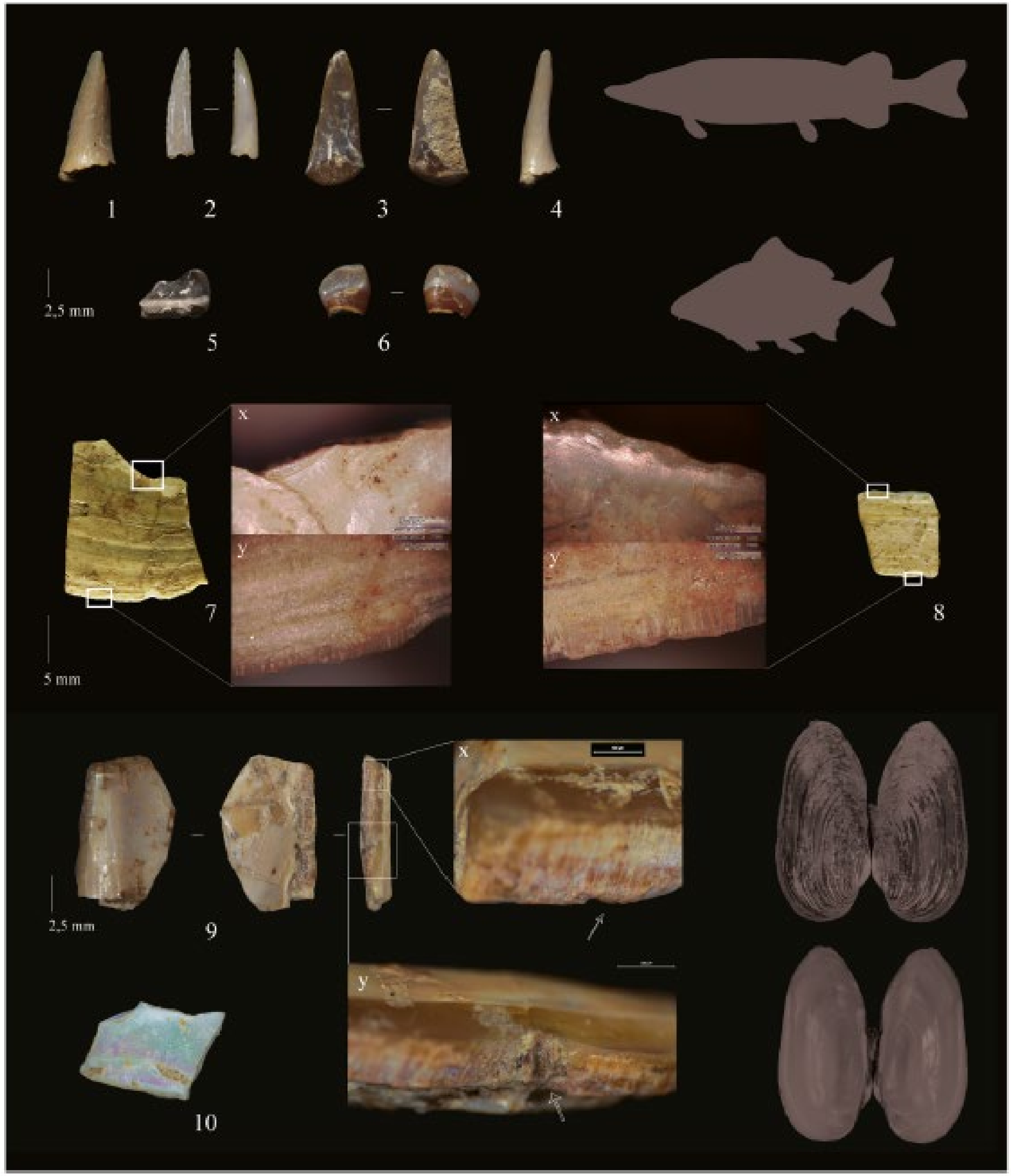
Ns going fishing: Fish and shells remains from Riparo del Broion



Ns fishing

- In recent years, archaeological research has provided solid evidence of the consumption of freshwater fish by Neanderthals. In some cases, fish bones from Middle Palaeolithic were found in inland caves near rivers, often alongside stone tools and animal remains.
- Their results suggest that for several sites, such as Vaufrey, Baume-Vallee, Barasses II, Baume Moula- Guercy, Walou, and Cueva Millan, Neanderthals possibly captured and consumed relatively large fish (over 1 kg). Several freshwater fish remains were found at Abri du Maras (France), dated to ~ 90 ka ago. These remains were associated with stone tools on the surface of which preserved flakes of what may be fish scales. Overall, however, the studies suggest opportunistic and intermittent fishing activities.
- The evidence recognized at Riparo del Broion, along with other studies, support the importance of freshwater resources in the Neanderthal diet and broaden our understanding of their eating habits and adaptability to different ecosystems.

Late Neanderthal adaptation to different environments

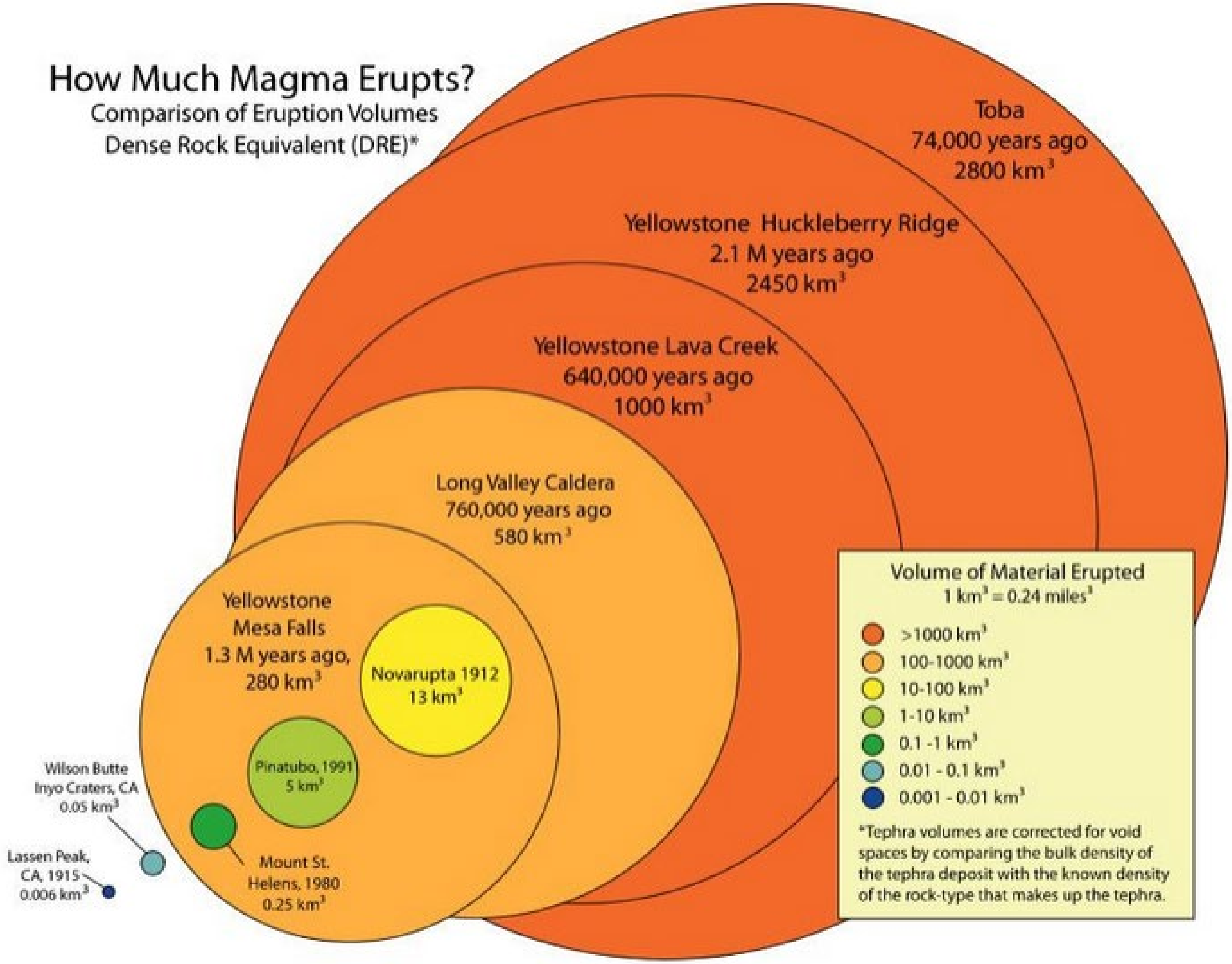
- The zooarchaeological data acquired through our analysis allow the reconstruction of Neanderthal subsistence economy and ecological exploitation during the first half of MIS 3 at Roccia San Sebastiano cave in south Italy and Riparo del Broion in north Italy. These two separate areas from Italy offer different possibilities of resource exploitation for the latest Neanderthal groups.
- In both areas, cervids are the most abundant ungulate prey, accessible in forests and meadows with temperate climate. The elk at Riparo del Broion marks the presence of low flow bodies of water.
- On the other hand, the presence of equids at Riparo del Broion, which is extremely rare regarding the coeval sites in northern Italy, documents the presence of open areas near the site, where hyenas and lions could also be found. The high variability of taxa among carnivores at this site is well suited to all the described types of environments.

2 different strategies

- Nevertheless, the most striking issue is the documentation of aquatic resources in Riparo del Broion. The presence of numerous beaver bones, fish remains, even of medium to large dimensions, freshwater shells and bird species such as Cygnus Walo and Gallinago media (the first fossils occurrence in north-Eastern Italy for both species) are related to the existence of water biotopes.
- On the contrary, Roccia San Sebastiano cave, the seacoast was 10–13 km (current at 5 km) away, but there is no evidence of exploitation of sea resources.
- Finally, both in the north and in the south, Neanderthals took advantage of their ungulate prey not only for food but also as non-food products. They used the diaphysis of long bones of medium and large animals as retouchers and points. This is a well-known practice seen in Italy and other areas of Europe.

Two N subsistence patterns in Italy

- This first archeozoological study carried out on two newly uncovered Late Mousterian contexts indicates that geographical regional setting played an important role in defining the exploitation of different resources: from almost specialized small game (Broion) to selective ungulates (San Sebastiano) hunting strategies. At Riparo del Broion, Neanderthals have probably practiced fishing and shellfish gathering from freshwater lake environment, as an additional source of food to be alternated with the exploitation of semi-aquatic resources like beavers and terrestrial ones like cervids.
- On the contrary, human groups at Roccia San Sebastiano cave almost exclusively practiced red deer hunting. Nevertheless, the complete absence of shellfish and fish remains, even though the sea was visible a few kilometers to the west of the cave, is remarkable.



Size of some supervolcanic eruptions of the Pleistocene, compared to a few smaller historic eruptions. Source: United States Geological Survey (public domain)

John Hawks: Ancient apocalypses are so disappointing

- Earth has suffered some pretty major catastrophes during the seven million years since the hominin lineage got its start
- The Messinian Salinity Crisis. Starting just under six million years ago, the Mediterranean Sea was cut off from the Atlantic Ocean, causing a 640,000-year-long evaporative period
- The Eltanin impact. Around 2.5 million years ago, a large meteorite struck somewhere in the southern ocean
- The Yellowstone caldera. A series of massive eruptions of the Yellowstone geological hotspot include events 2.1 million, 1.3 million, and 640,000 years ago. All of these would have had immediate atmospheric effects and longer-term climate effects as ashfalls increased the reflectivity of Earth's surface.

Apocalypses

- But despite their apocalyptic appearance, it has been extremely hard to trace their effects.
- We have a lot more evidence about climates and hominin populations of the Late Pleistocene and Holocene, within the last 130,000 years. The biggest catastrophic event during that time was the eruption of Mount Toba, Indonesia, around 74,000 years ago. Toba ejected some 2800 cubic kilometers of magma, or even more by some estimates. During the 1990s, geologists and some archaeologists speculated that this massive eruption may have caused a decades-long volcanic winter. They suggested that human populations in Africa and Eurasia had suffered a bottleneck, taking them down to a few thousand individuals, and proposed that survivors had dispersed rapidly from Africa sometime after the event.

Bottleneck did not happen

- Over the last 25 years, geologists, geneticists, and archaeologists have shown that the Toba event did not have such massive impacts on human populations. The Toba bottleneck simply didn't happen. Multiple lines of evidence, including high-resolution cores from ice sheets and lake bottoms, show that the climate impacts were much less than 1990s-era geologists imagined. Better archaeological and genetic records now show that populations of humans and other hominins survived without observable cultural or demographic changes.
- What archaeologists can look for is signs of abrupt change in cultural evidence—layers flanking the time of eruption with different archaeological material. This they have not found; to the contrary, in the few places where evidence occurs both before and after the Toba eruption, there is no evidence of change.
- It's sobering to realize that the largest catastrophic event of the last 100,000 years left no clear trace of any effects on humans, other hominins, or other terrestrial animals. Toba may have seemed apocalyptic, but we haven't seen anything that it ended.

Magnetic weakening?

- In early 2021 a team led by the geneticist Alan Cooper proposed that a weakening of the Earth's magnetic field around 42,000 years ago may have had atmospheric effects resulting in megafaunal extinctions and the final extinction of the Neanderthals. The authors even suggested that the atmospheric effects caused human populations to take refuge in caves, leading to a florescence in cave painting traditions. No evidence.
- One significant true finding: The 1980 work of Luis and Walter Alvarez, who provided evidence for a large meteorite impact that coincided with the Cretaceous-Paleogene boundary 65 million years ago, revived the idea that other mass extinctions might have been shaped by singular events.

Younger Dryas Impact?

- Idea that some meteorite or comet had a major effect on the Earth's climate and human populations around 12,900 years ago. That idea is widely known as the "Younger Dryas Impact Hypothesis", with the name Younger Dryas referring to the 1200-year-long period of colder climate. Claimed it caused end of the Clovis technocomplex in North America and extinctions of some megafaunal species.
- Holliday et al., 2023 spend 293 manuscript pages reviewing evidence that shows that the meteorite idea doesn't hold water.
- The known catastrophic events of the last seven million years seem to have produced very little evidence of impacts on hominins or other species. For the most part, that's because paleoclimate, genetic, and archaeological evidence doesn't have the resolution to show change on the short timescales necessary. In other words, the evidence of an apocalypse should look apocalyptic.
- For Mt. Toba, see: Chad Yost, et al., 2018: Subdecadal phytolith and charcoal records from Lake Malawi, East Africa imply minimal effects on human evolution from the ~74 ka Toba supereruption: no evidence of a volcanic winter event

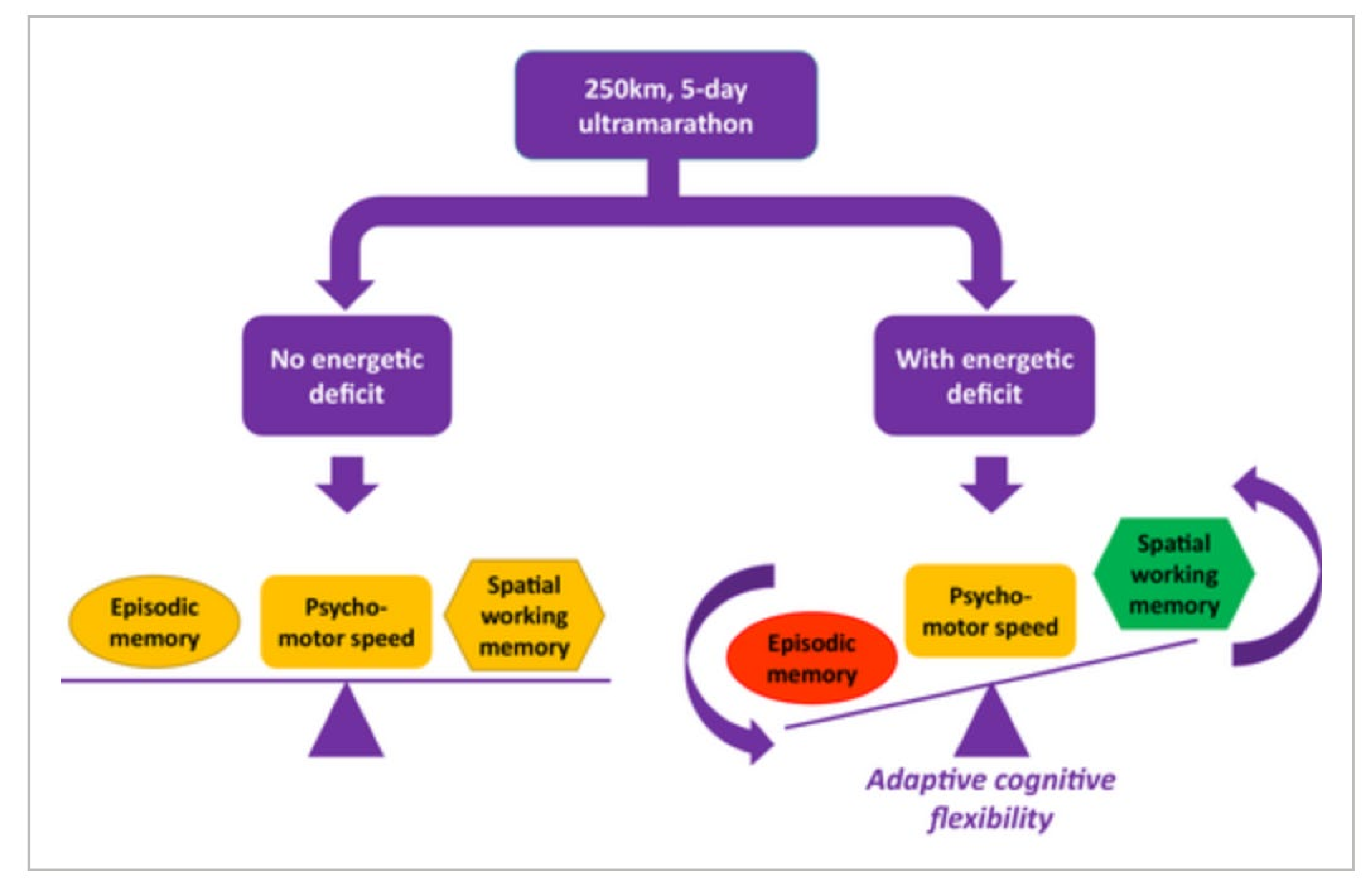
The root cause of the homelessness crisis

- Researchers at UC San Francisco have released the largest representative survey of homeless people in more than 25 years.
- Last month, researchers at UC San Francisco released the largest representative survey of homeless people in more than 25 years. It comprises survey data from 3,200 homeless people in California and in-depth interviews with more than 300 of them.
- Thirty percent of the American homeless population and 50 percent of its unsheltered population live in California, more than 170,000 people total.
- Homelessness is primarily a function of the broader housing-unaffordability crisis, which in turn is primarily a function of how difficult local governments have made building new housing in the places that need it the most.
- Pundits and politicians routinely claim that the California homelessness crisis is actually a result of people moving from other states for better weather or better public benefits. But new research casts doubt on this theory

Homeless

- Overwhelming majority of homeless surveyed were locals, not migrants from far away: 90 % lost their last housing in CA; 75 % lost it in same county where they were homeless. Of 10% who came from elsewhere, 30 % born in CA. Most of others had familial or employment ties, or had lived in CA
- CA is home for most of its homeless. Most frequent reported reason for loss of housing was income reduction due to unemployment or decrease in work hours

Ultramarathoners who lose weight have improved visual spatial working memory

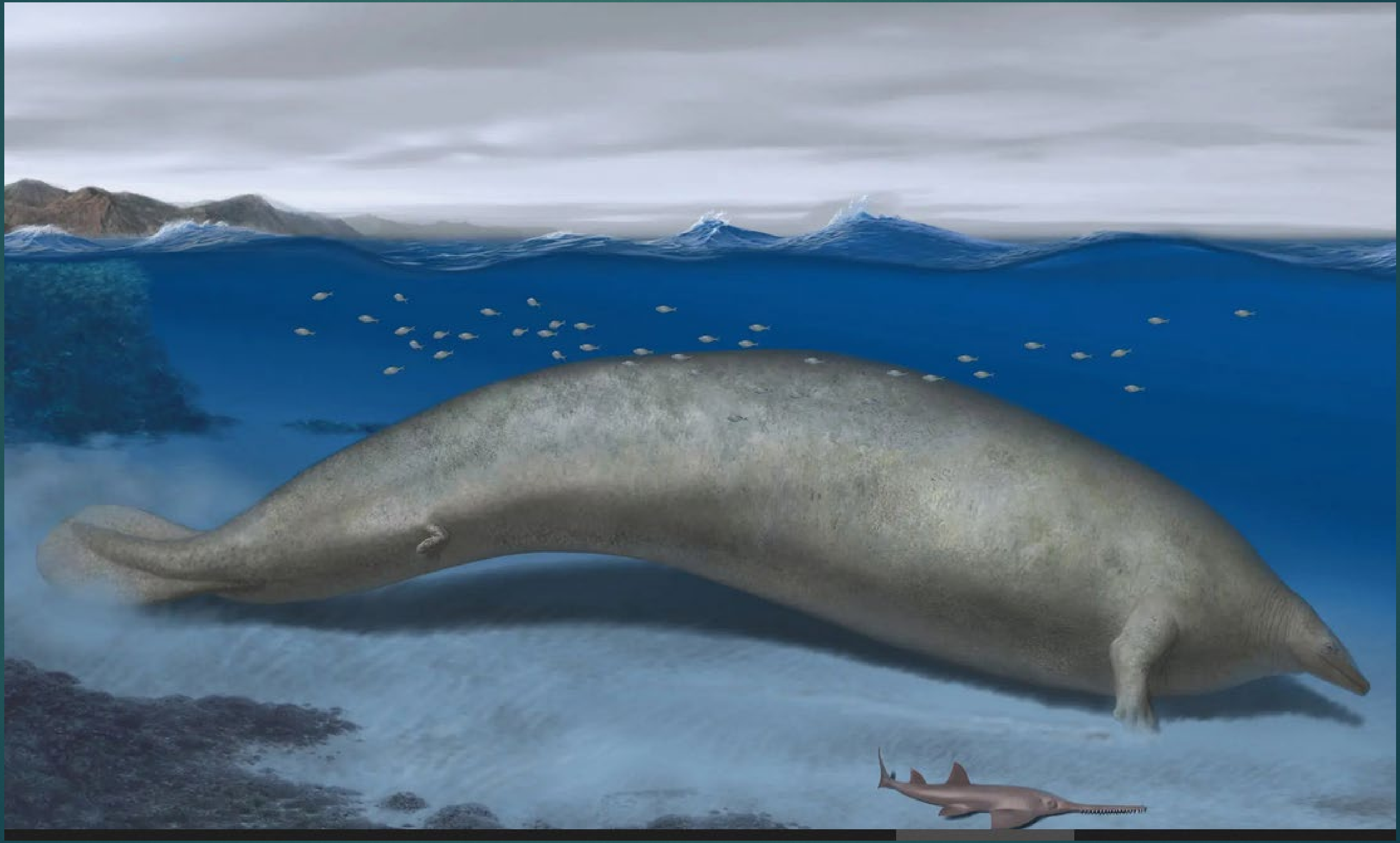


- Athletes who lose weight during these events, which often last days and cover hundreds of miles, show significant adaptation of cognitive function to promote foraging ability.
- This may increase ability to find food and increase survival chances during periods of energetic stress.
- It is believed that these changes appear as the athletes' brains remodeled to counteract a negative change in environment.

Spatial working memory

- We suggest that prioritization of SWM function during conditions of negative energy balance represents an adaptive response.
- SWM temporarily stores location information, enhancing an individual's ability to navigate a landscape. This could be beneficial during energetic deficit because it may improve (a) ability to find the way home following a foraging or long-distance hunting trip, and (b) ability to acquire food by facilitating recollection of the location and quality of previously visited feeding sites
- The ability to respond to changing environmental pressures through cognitive flexibility may be a consequence of our evolutionary history

Perucetus colossus: This colossal extinct whale was the heaviest animal to ever live. Paleontologists in Peru have described an ancient species of whale that was significantly heavier than a blue whale.



Heavyweight

- A colossal ancient species of whale that lived 39 million years ago was a true heavyweight, weighing more than double a blue whale and likely earning itself the title as the heaviest known animal to have ever lived.
- The newly described basilosaurid (a family of extinct cetaceans), called *Perucetus colossus*, eclipsed blue whales (*Balaenoptera musculus)* in sheer weight with an estimated body mass of between 187,000 to 750,000 pounds. It had an estimated body length of about 66 feet (20 meters).
- Paleontologists discovered the partial skeletal remains of the monstrous marine mammal 30 years ago in what is now Ica Province in southern Peru. Since then, they've unearthed 13 vertebrae, four ribs and a hip bone. Each vertebra alone weighs 330 pounds.

Like a manatee

- The team likened it to a modern manatee, but with a tiny head, an enormous body and little arms and legs.

- In terms of weight, *P. colossus* was definitely bulkier than a blue whale. But the overall body length was shorter than the blue whale [and measured] 20 meters (66 feet).

- This discovery means they reached their peak body mass 30 million years earlier than originally thought.

- Think it spent most of its time at the bottom of the ocean not burning a lot of energy to get its sources of food

Perucetus colossus: Very large vertebrae; each 330 lbs

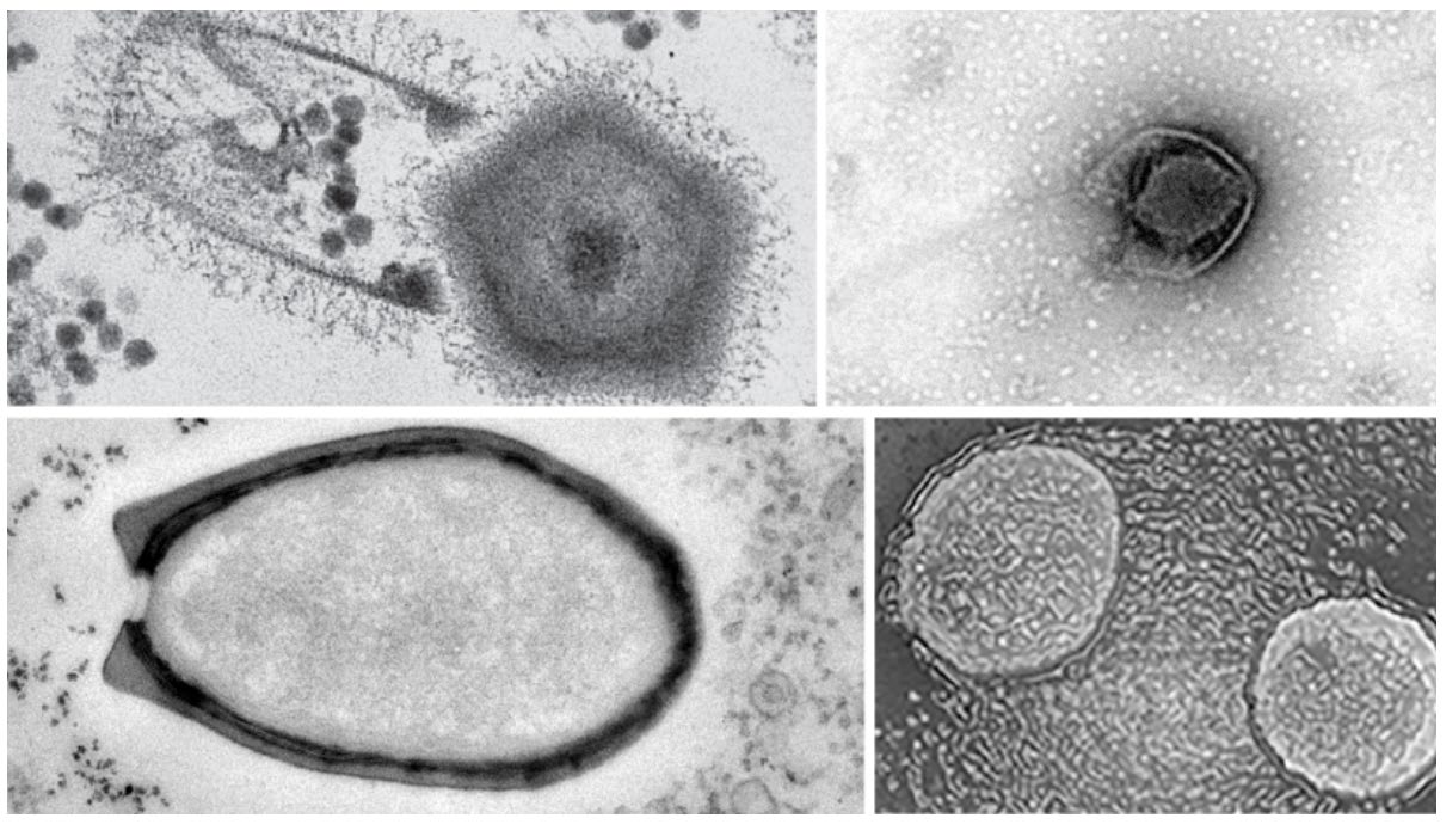
Might not: Science papers include less hedging now than two decades ago

- Scientists are often careful about how they state their findings—”experiments may mean this”, “findings probably indicate that”. But a broad analysis of Science papers from 1997 to 2021 finds that such hedging language has decreased significantly, a trend some experts find concerning.
- The team searched more than 2600 papers from multiple disciplines for about 50 terms that caveat or qualify findings—like “could,” “appear to,” and “seem.” Over the 24 years of studies, the prevalence of these terms decreased about 40%.
- The trend could reflect an increasingly competitive publishing environment where more confidence helps persuade editors to accept manuscripts. Science Executive Editor Valda Vinson wonders if it is indicative of a general shift in the language used in the journal’s papers—away from passive voice and towards a less formal tone - adding that Science does tone down overconfident language.
- Either way, the decrease in hedging could have consequences. “If academic writing becomes more about the rhetoric ... it will become more difficult for readers to decipher what is groundbreaking and truly novel. i.e. Lee Berger!

Gene-engineered flies clone themselves via ‘virgin birth’

- Flies, like most creatures, typically need a mate to reproduce. Researchers have found a way to eliminate this partner from the equation. The scientists identified an array of genes that seem to be responsible for the ability of a species of fruit fly known as Drosophila mercatorum to asexually reproduce, or effectively clone itself. Known formally as parthenogenesis,
- They then identified and altered the expression of corresponding genes in one of the most studied fruit fly species, D. melanogaster, which ordinarily relies on sexual reproduction. When those genes were altered in females of the species, before long, the flies began to lay viable eggs without the need for a male’s sperm. The offspring’s genome contains all their mother’s genes, including the introduced ones from the other fly species, ensuring that her ability to self-replicate is passed from generation to generation, Nature reports.

Giant viruses



Giant viruses

- Researchers have unearthed a trove of wonders in the soil of a Massachusetts forest, near Harvard Univ.: an assortment of giant viruses unlike anything scientists had ever seen.
- Giant viruses can exceed 2 micrometers in diameter, on par with some bacteria. They can also harbor immense genomes, which reach 2.5 megabases—larger than the genomes of far more complex organisms.
- Most of the research on the group has focused on viruses that inhabit freshwater environments. But DNA sequencing has long indicated that giant viruses are diverse and abundant elsewhere, too—especially in sediments and soils, which are estimated to host some 97% of all the viral particles on Earth.

Australian honey ants, ballooning with microbe-killing honey. Aboriginals have used them for antimicrobial (antibacterial and antifungal) properties for millennia

Honeypot ants

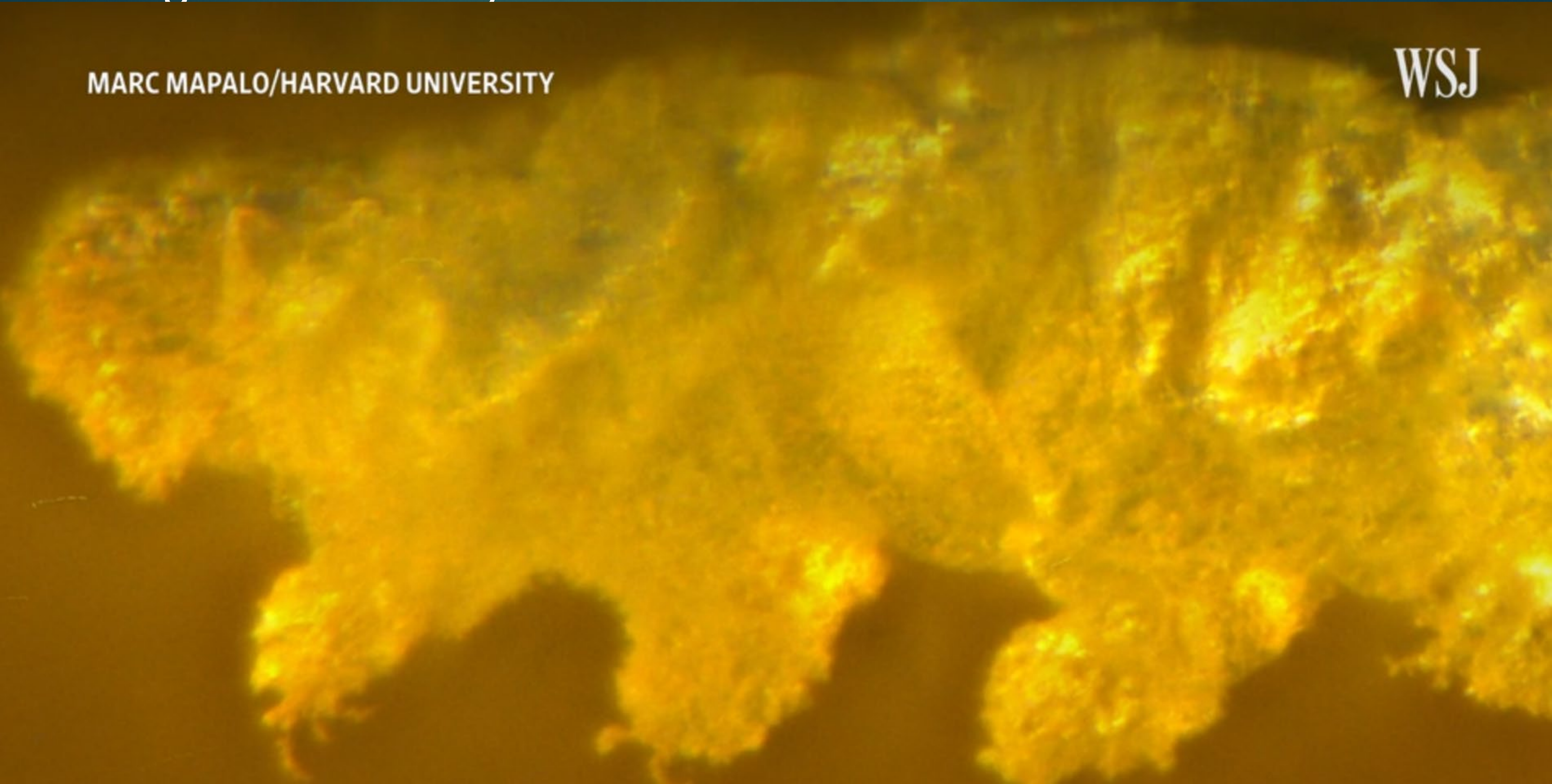
- The ingredients for the honeypot ant’s golden concoction come from rounded, shrublike mulga trees and the aphids that live on them. The ants stroke the aphids with their antennae. That movement causes the aphids “to excrete excess honeydew from their bums, which the honeypot ants then sip up.” Then, worker ants transfer the honey, mouth by mouth, drop by drop, to comrades that hang from the ceilings of their underground nests with the tips of their legs. There, the golden nectar balloons their abdomens to the size of a grape, making them look like glistening chandeliers.
- However, unlike honey bee honey, which displays a broad spectrum of activity against hundreds of different types of bacteria, honeypot ant honey exhibited little to no effectiveness against many other microbes the team tested, such as *Escherichia coli*.

It’s Alive! Worms Revived After 46,000 Years in Siberian Permafrost

- Talk about a long nap. Revived worms buried in Siberian permafrost for 46,000 years.
- The half-dozen creatures, a type of nematode or roundworm, were last awake when Neanderthals and woolly mammoths roamed the Earth. They survived for millennia in permafrost by entering a state of suspended animation.

Tardigrades

Tardigrade: 500 M years old



Tardigrades

- They have been found in diverse regions of Earth's biosphere – mountaintops, the deep sea, tropical rainforests, and the Antarctic. Tardigrades are among the most resilient animals known with individual species able to survive extreme conditions – such as exposure to extreme temperatures, extreme pressures (both high and low), air deprivation, radiation, dehydration, and starvation – that would quickly kill most other known forms of life. Tardigrades have survived exposure to outer space.
- There are about 1,300 known species in the phylum Tardigrada, a part of the superphylum Ecdysozoa consisting of animals that grow by ecdysis such as arthropods and nematodes. The earliest known true members of the group are known from Cretaceous (145 to 66 million years ago) amber, found in North America, but are essentially modern forms, and therefore likely have a significantly earlier origin, as they diverged from their closest relatives in the Cambrian, over 500 million years ago.

Tardigrades: revived after 30 years of cryptobiosis

- Scientists have reported tardigrades in hot springs, on top of the Himalayas (6,000 m; 20,000 ft, above sea level) to the deep sea (−4,000 m; −13,000 ft) and from the polar regions to the equator, under layers of solid ice, and in ocean sediments. Many species can be found in milder environments such as lakes, ponds, and meadows, while others can be found in stone walls and roofs. Like moisture.
- Tardigrades are thought to be able to survive even complete global mass extinction events caused by astrophysical events, such as gamma-ray bursts, or large meteorite impacts. Some of them can withstand extremely cold temperatures down to −460 °F (close to absolute zero), while others can withstand extremely hot temperatures up to 300 °F for several minutes, pressures about six times greater than those found in the deepest ocean trenches, ionizing radiation at doses hundreds of times higher than the lethal dose for a human, and the vacuum of outer space.
- Tardigrades are one of the few groups of species that are capable of suspending their metabolism (see cryptobiosis). While in this state, their metabolism lowers to less than 0.01% of normal and their water content can drop to 1% of normal, and they can go without food or water for more than 30 years, only to later rehydrate, forage, and reproduce.

Rotifer: Frozen in Siberian Permafrost and revived after 24,000 years

Rotifers

- Bdelloid rotifers may be the toughest, tiniest animal you've never heard of.

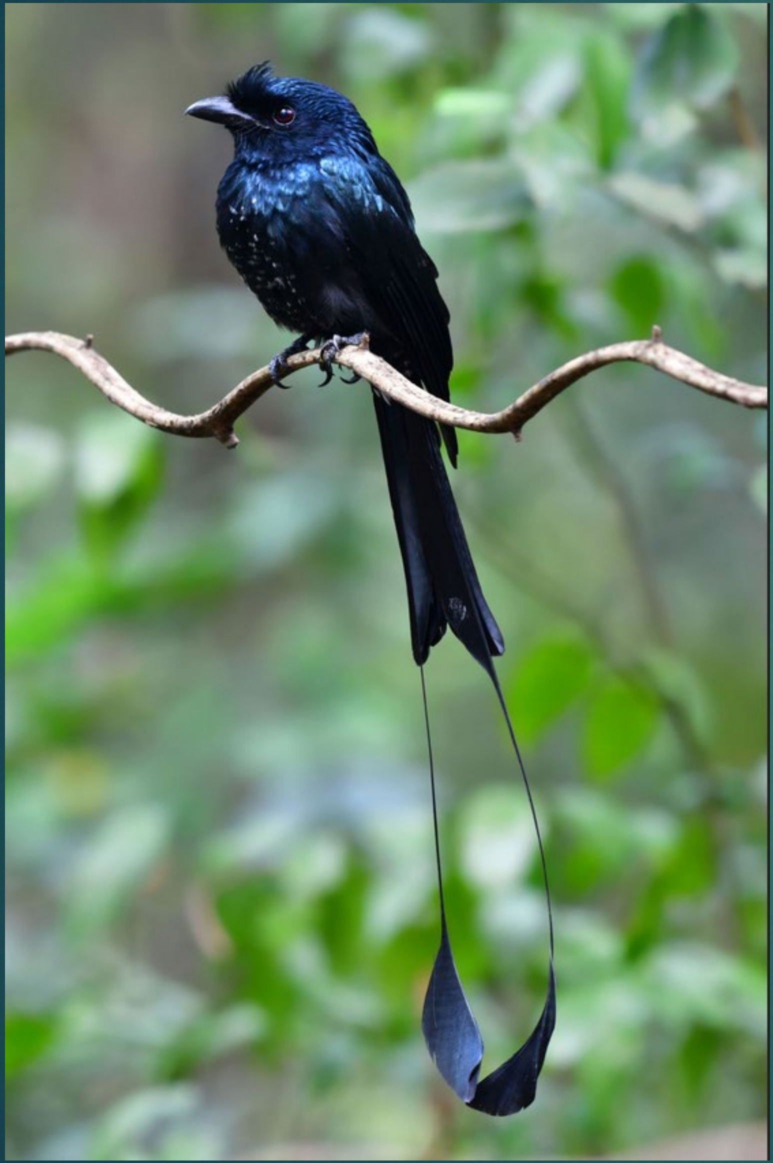
- The microscopic, multicellular creatures have complex anatomies and are one of the planet's most radiation-resistant animals.

- They can withstand extreme acidity, starvation, low oxygen and years of dehydration.

Time-traveling' pathogens in melting permafrost pose likely risk to environment

- Ancient pathogens that escape from melting permafrost have real potential to damage microbial communities and might potentially threaten human health
- The team found that in their simulations, the ancient invading pathogens could often survive and evolve in the modern community, and about 3% became dominant. While most of the dominant invaders had little effect on the composition of the larger community, about 1% of the invaders yielded unpredictable results. Some caused up to one third of the host species to die out, while others increased diversity by up to 12% compared to the control simulations.
- The risks posed by this 1% of released pathogens may seem small, but given the sheer number of ancient microbes regularly released into modern communities, outbreak events still represent a substantial hazard.

Drongo



African Cuckoo

Two drongo clutches parasitized by different African cuckoo females. Which one is the cuckoo egg in each clutch?

Egg 'signatures' allow drongos to identify cuckoo 'forgeries' almost every time

- Fork-tailed drongos, belligerent birds from sub-Saharan Africa, lay eggs with a staggering diversity of colors and patterns. All these colors and patterns are forged by the African cuckoo.
- African cuckoos lay their eggs in drongos' nests to avoid rearing their chick themselves (an example of so-called brood parasitism). By forging drongo egg colors and patterns, cuckoos trick drongos into thinking the cuckoo egg is one of their own.
- But drongos use knowledge of their own personal egg "signatures"—their eggs' color and pattern –to identify cuckoo egg "forgeries" and reject them from their nests.

Mimicry and defense via natural selection

- Through natural selection, the African cuckoo's eggs have evolved to look almost-identical to drongo eggs

- Despite near-perfect mimicry of fork-tailed drongo eggs, African cuckoo eggs still have a high probability of being rejected.

- On average, an African cuckoo would have its eggs rejected by a fork-tailed drongo host, 94% of the time.

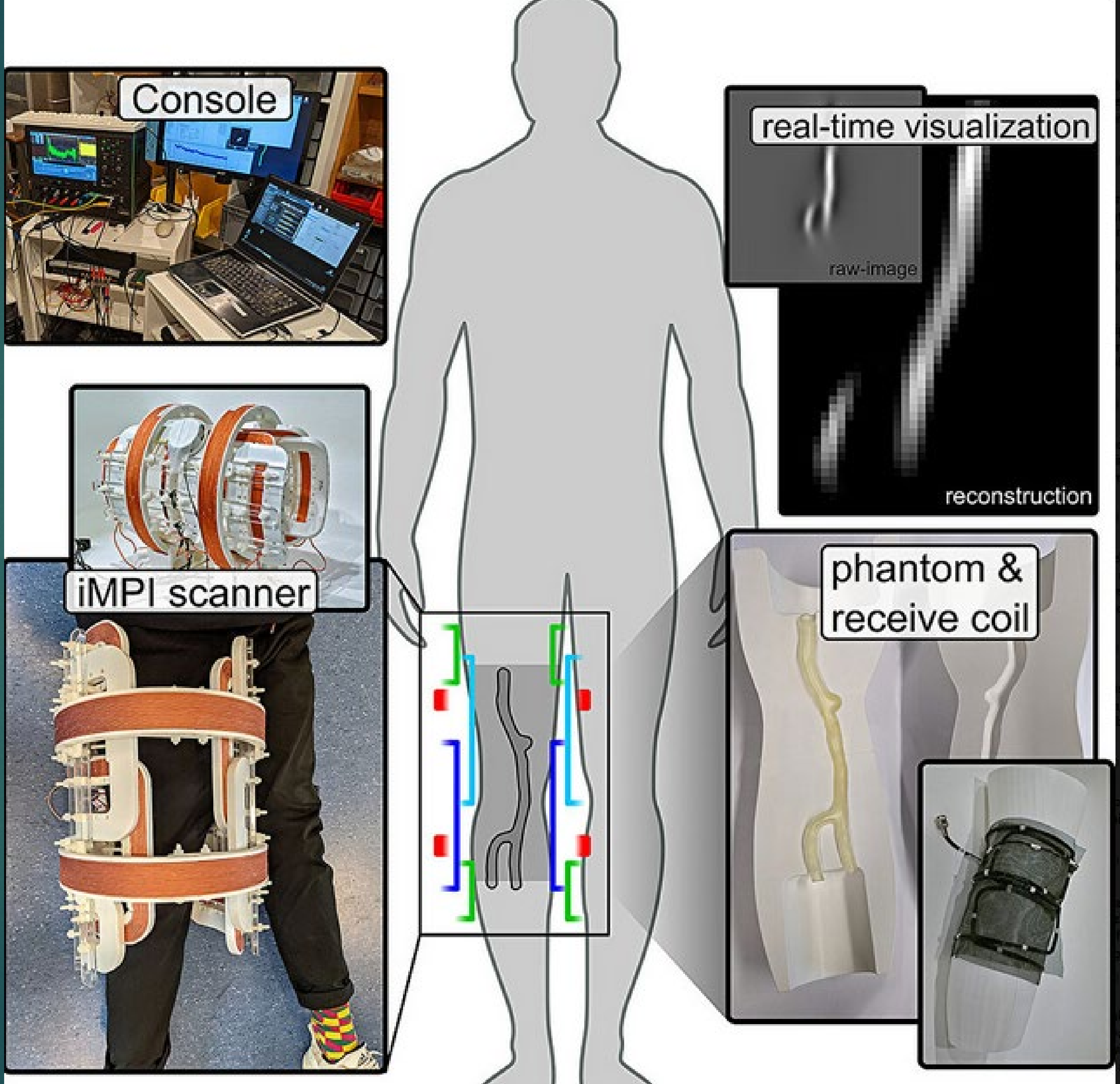
Physicists and doctors develop new radiation-free imaging technique

- A team of physicists and medical doctors from the Julius-Maximilians-Universität Würzburg (JMU) has now succeeded in making a radiation-free imaging technology ready for use on humans.

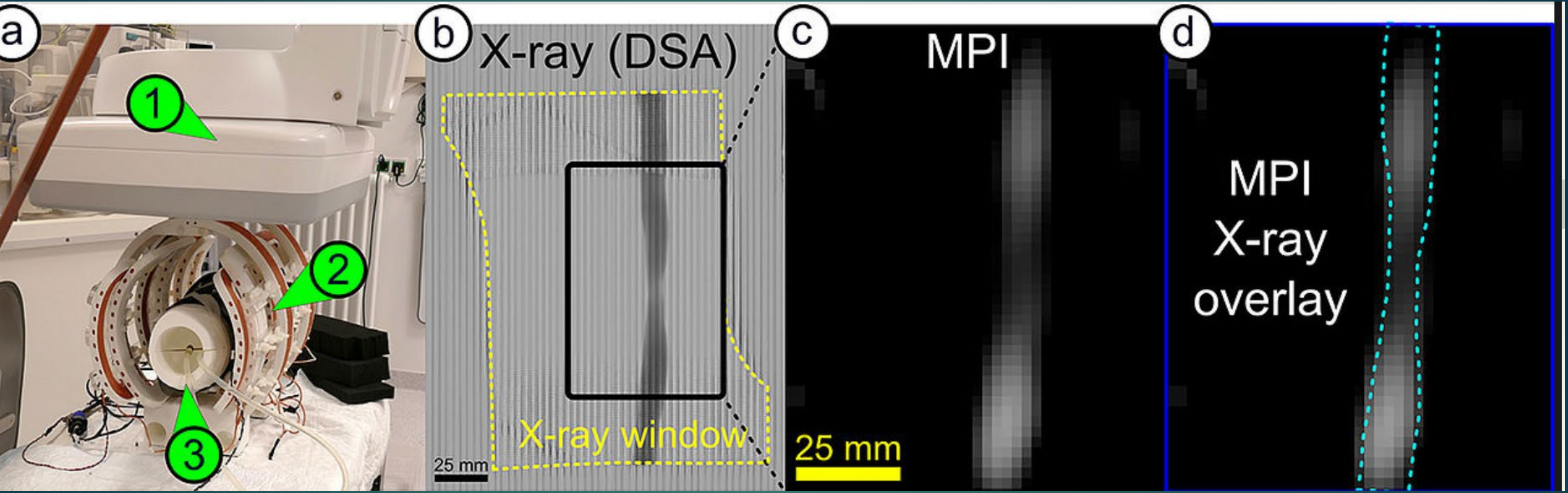
- It's called magnetic particle imaging (MPI). With the portable scanner they developed, it is possible, among other things, to visualize dynamic processes in the human body, such as blood flow.

- A technique based, as the name suggests, on the direct visualization of magnetic nanoparticles. Such nanoparticles do not occur naturally in the human body and must be administered as markers

The iMPI scanner is so small and light that you can take it with you and use it almost anywhere.



iMPI comparison



The iMPI scanner (left) provides new insights into the human body. Here you can see a constriction in a blood vessel—recorded with conventional X-rays (b), with the scanner (c) and in a combination of both techniques (d)

iMPI: portable human-sized magnetic particle imaging scanner for real-time endovascular interventions

- Uses the response signal of the magnetic nanoparticles to magnetic fields that change over time. "In this process, the magnetization of nanoparticles is specifically manipulated with the help of external magnetic fields, whereby not only their presence but also their spatial position in the human body can be detected
- MPI uses magnetic fields to detect the spatial distribution of tracer agents composed of magnetic nanoparticles (MNPs). The concept of MPI is based on the nonlinear magnetization response of those MNPs to time-varying magnetic fields.

P. Vogel, et al., 2023

Researchers created a facial approximation of a 45,000-year-old individual who is believed to be the oldest anatomically modern human ever to be genetically sequenced.

Stunning likeness of Zlatý kůň, the oldest modern human to be genetically sequenced

- In 1950, archaeologists discovered a severed skull buried deep inside a cave system in Czechia (the Czech Republic). Because the skull was split in half, researchers concluded that the skeletal remains were of two separate individuals. However, through genome sequencing done decades later, scientists concluded that the skull actually belonged to a single person: a woman who lived 45,000 years ago.

- Further analysis of her DNA revealed that her genome carried roughly 3% Neanderthal ancestry, that she was part of a population of early modern humans who likely mated with Neanderthals and that her genome was the oldest modern human genome ever to be sequenced.

Features based on skull data; mandible much more like Ns

Liang Bua, Flores, Indonesia

Claim that the Hobbit used fire

- Based on the initial excavations, researchers thought H. floresiensis used fire—a technology at the time only attributed to humans with much larger brains, such as Neanderthals and Homo sapiens. But by the mid-2010s, the thinking shifted as additional evidence weakened the case for hobbit fire use. A massive effort to better date the site revealed that later modern humans likely lit the blazes in Liang Bua, thousands of years after the hobbits disappeared.

- The resulting high-profile scientific articles and press releases tried to correct the record. But many people still imagine hobbits roasting meat over a campfire. As it turns out, it is *very* difficult to correct spectacular discoveries once they are solidified in the minds of scientists, educators, and the public.

- Lee Berger has now erroneously included *H. floresiensis* as supporting evidence, citing the earlier research that has been convincingly overturned.

Claim of fire usage

- In 2022, I was presenting results from my doctoral work, which showed how giant rats were captured and consumed by both *H. floresiensis* and modern humans at Liang Bua. (Yes, hobbits ate “Rodents of Unusual Size” a la *The Princess Bride*.) Among the conclusions from this research: Modern humans cooked their food with fire, while *H. floresiensis* did not.
- In 2004 and 2005, the hobbit flame claims appeared in scientific papers that described the most complete skeleton, known as LB1, and the associated artifacts. The evidence for fire, they claimed, included charred bones of small animals, clusters of reddened and fire-cracked rocks, and two charcoal fragments dated to 18,000 years ago, which were found just to the north of LB1. Thus, *H. floresiensis* made fire *and* survived astonishingly late, according to the early interpretations.
- Then the story changed.

Revised stratigraphy and chronology for *Homo floresiensis* at Liang Bua in Indonesia

- New stratigraphic and chronological evidence from Liang Bua does not support the ages inferred previously for the *H. floresiensis* holotype (LB1), ~18,000 before present
- Instead, the skeletal remains of *H. floresiensis* and the deposits containing them are dated to between about 100 and 60 kyr ago, whereas stone artefacts attributable to this species range from about 190 to 50 kyr in age. MHs arrived after 46 Ka.

Redating = no fire use by the hobbit

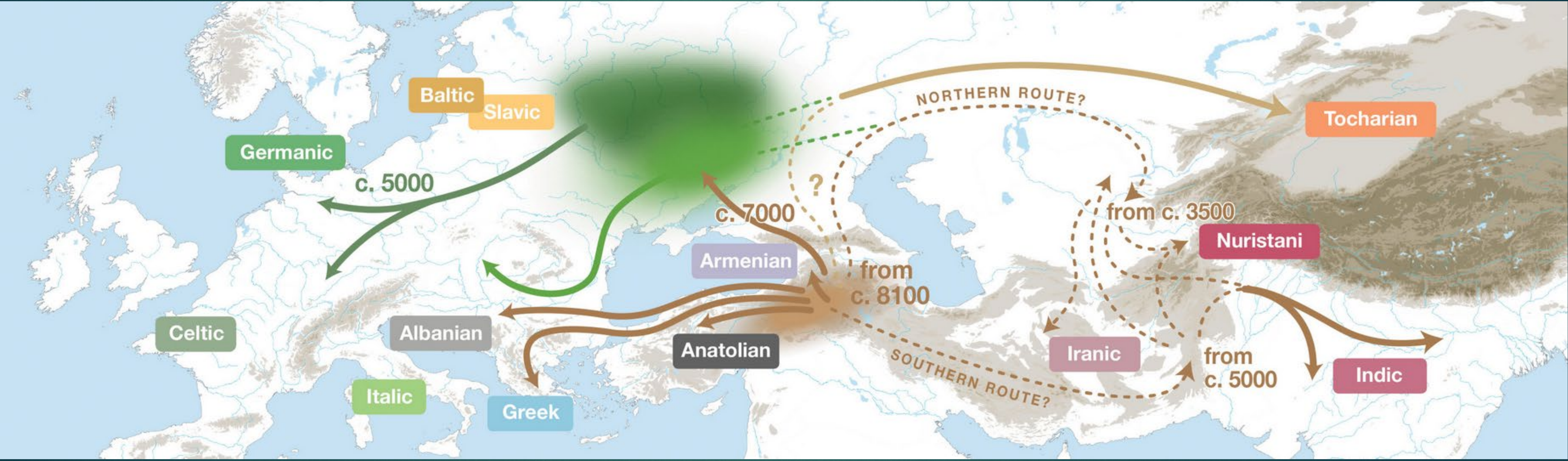
- Misunderstanding of stratigraphy: Unconformity deposits cut into layers that held fossils from *H. floresiensis* individuals (LB1, LB4, LB6, LB8). Younger materials, including charcoals radiocarbon dated to around 18,000 years ago, accumulated and then appeared adjacent to layers that held older *H. floresiensis* remains during excavations.

- So, when archaeologists excavated, in some places they found *younger* burnt bones and charcoal at lower depths adjacent to the *older* “hobbit” deposits. It also became apparent that the charcoal and burnt bone previously associated with *H. floresiensis* were, instead, due to modern human activity from the past 40,000 years or so.

New language database and tree

- So in 2015, P. Heggarty and colleagues began building a new collection of common words consisting of basic, universal concepts such as numbers, “water,” and “black,” which sound similar across Indo-European languages and presumably descend from the same ancient word.
- They assembled a team of more than 80 experts who analyzed 170 basic concepts such as “water” from 161 Indo-European languages, including 52 no longer spoken, such as ancient Greek.
- With their pooled expertise, the specialists weeded out loan words and identified 25,918 of these basic words across the 161 languages for tree building.

The language family began to diverge from around 8,100 years ago, out of a homeland immediately south of the Caucasus. One migration reached the Pontic-Caspian and Forest Steppe around 7,000 years ago, and from there subsequent migrations spread into parts of Europe around 5,000 years ago. Credit: P. Heggarty et al., *Science* (2023)



Origin of PIE

- According to the resulting tree, Indo-European emerged sometime before 8100 years ago and 1000 years later had already split into seven major branches. The analysis suggests something of a hybrid origin for PIE: The mother tongue originated and expanded with early farmers native to lands south of the Caucasus. One branch spread northward through these mountains between 7000 and 6500 years ago; it then expanded east and west over the Eurasian steppe as the herders rode out across the plains.
- There was this big migration from the steppe, but it wasn't the ultimate origin. It was just a secondary migration.
- Not everyone is convinced. University of Helsinki archaeologist Volker Heyd, says the archaeological and genetic evidence, such as the appearance of herder-style burial mounds and steppe ancestry in skeletal DNA in eastern Europe, still favor steppe people as the super-spreaders of Indo-European. Even if PIE first appeared earlier, somewhere to the south, the steppe region gave Indo-European languages “the momentum” to expand far and wide, Heyd says.

AI helps geneticists uncover the roots of upright walking in humans

Science

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AAAS

THESE BONES WERE MADE FOR WALKING

Fleshing out the genetic basis of the human skeletal form p. 283

New study maps the parts of the genome that create a bipedal skeleton

- A new study, published this week in Science, maps the genetic regions that might let us walk.
- Researchers used artificial intelligence to sift through photographs of 500,000 people in the health and genetic data repository UK Biobank, and then used these photos to estimate the skeletal proportions of 31,000 of the photographed people. Matching these measurements against the biobank's genetic data revealed 145 places in the human genome that may control the skeletal proportions key to walking, such as our long legs, narrow hips, and short arms.
- They also found genomic sites associated with osteoarthritis. The results may help begin to illuminate how we got up on our own two feet, even while our closest relatives stayed on all fours, Nature reports.

Unraveling 300,000 Year Old Ancient Footprints

Footprints at Schöningen

- Three footprints of *Homo heidelbergensis*, a direct ancestor of Neanderthals, as well as a myriad of footprints belonging to elephants and other herbivorous species. This discovery sheds light on what life might have been like in Lower Saxony approximately 300,000 years ago, offering valuable insights into the ancient environment and the diverse mammalian inhabitants of the area.
- The current study focuses on fossil footprints found at two key locations: Schöningen 13 I-Fs2 and Schöningen 13 II-2 Untere Berme.
- Site of famous nine throwing spears, one thrusting lance and two throwing sticks
- Assume that the hominin was a late form of *Homo heidelbergensis* at the threshold of the transition to the early *Homo neanderthalensis*. The hominin presence is accordingly assigned to MIS 9.

A late Neanderthal reveals genetic isolation in their populations before extinction

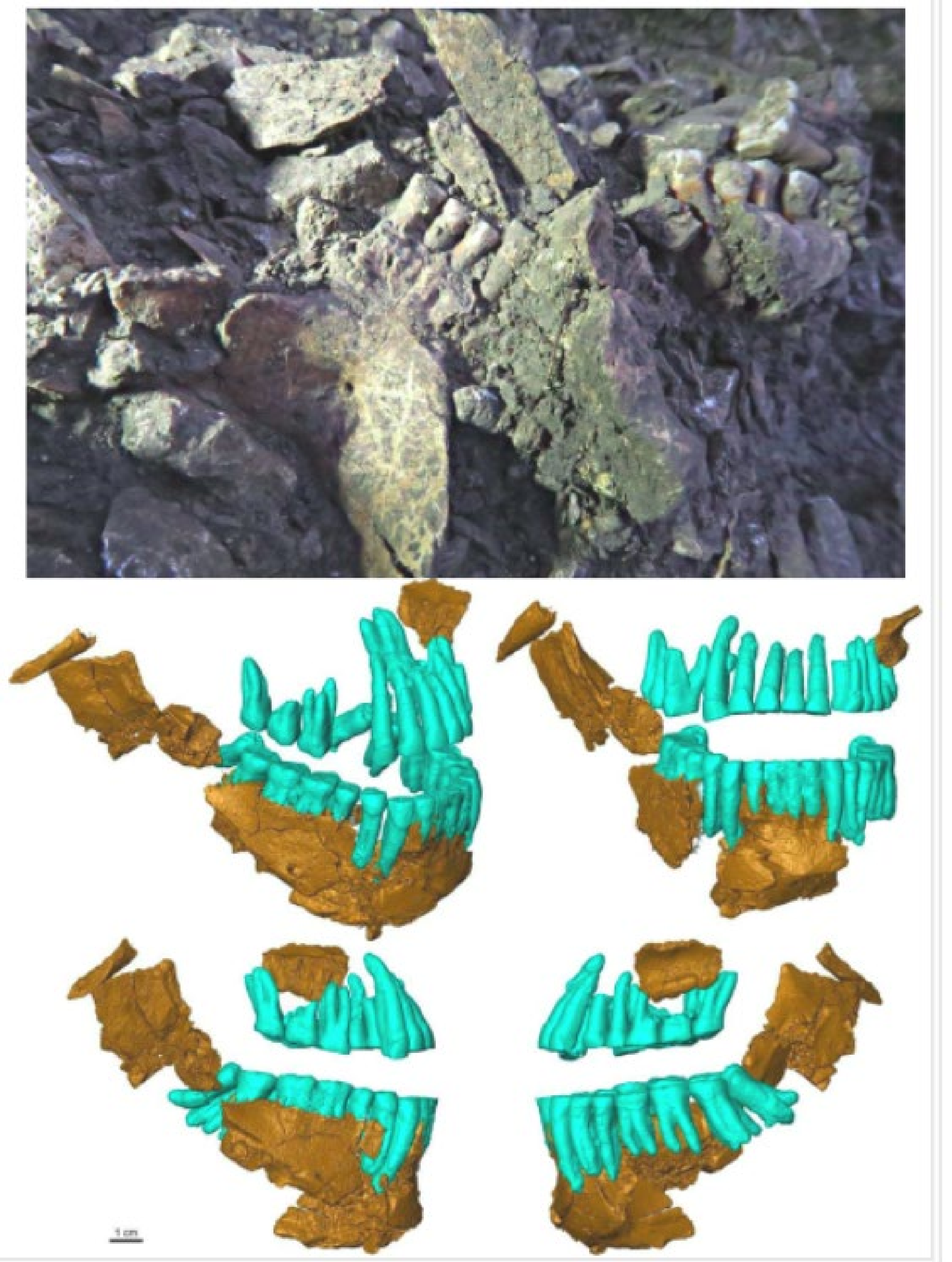
- Late European Neanderthals belonged to a single metapopulation with no significant evidence of deep population structure (= presence of a systematic difference in allele frequencies between subpopulations). In a randomly mating population, allele frequencies are expected to be roughly similar between groups.

- Report the discovery of a late Neanderthal individual, nicknamed "Thorin", from Grotte Mandrin in Mediterranean France, and his genome. Mandrin = 1 MH tooth, "arrowheads" with N layers above and below it, at 54 Ka

L Slimak, et al, 2023

Thorin = from isolated N group

- These dentognathic fossils, including a rare example of distomolars, are associated with a rich archeological record of their final technological traditions in this region ~50-42 thousand years ago.
- Thorin's genome reveals a deep divergence with other late Neanderthals. Thorin belonged to a population with small group size that showed no genetic introgression with other known late European Neanderthals, revealing genetic isolation of his lineage despite them living in neighboring regions.



- Remains of the Neanderthal individual nicknamed Thorin, from the Mandrin cave (France).
- Dentognathic fossils

Population types

- Low effective population sizes and signatures of inbreeding in Siberian and late European Neanderthals, suggesting social structure characterized by small group sizes and low intergroup mobility.
- This contrasts with recent results from early Eurasian modern humans, which showed low levels of inbreeding and higher intergroup mobility despite small group sizes.
- Whether these results are representative of wider Neanderthal social organization remains inconclusive.

Population diversity: Altai vs Vindija

- Since 2010, Neanderthal genomes have been recovered from sites across Eurasia, painting an increasingly complex picture of Neanderthal genetic structure.
- The deepest divergence among Neanderthal genomes sequenced to date is found between eastern and western Eurasian Neanderthal populations represented by the ~120 ka eastern Altai Neanderthal from Denisova Cave and the >44 ka western Vindija 33 individual from Croatia.

Neandertal lineages

- Genomic data of all other available Neanderthal remains, the earliest is in western Europe being ~120 ka (Scladina and Hohlenstein-Stadel (HST)), while the latest being ~40 ka, suggest genetic continuity in western Eurasia for ~80 ka.
- Recent results obtained from sedimentary DNA suggest that the genetic landscape was significantly altered by expansions of Neanderthal populations ~105 ka.
- This gave rise to lineages in western Europe represented by samples from Central Europe (Vindija), the Caucasus (Mezmaiskaya Cave), and Siberia (Chagyrskaya cave 8), the latter likely replacing the earlier Altai-like population.

Neandertal late lineages

- The genomes of late (<50 ka) European Neanderthals, including an individual from the Caucasus (Mezmaiskaya 2), were all found to be more similar to Vindija than to other known lineages, indicating further population turnover towards the last stages of Neanderthal history in the Caucasus or western Europe.

- The close correlation between genetic similarities and geographic location suggested an absence of major population structure among the sampled late Neanderthal populations

- The basic cause of population structure in sexually reproducing species is non-random mating between groups: if all individuals within a population mate randomly, then the allele frequencies should be similar between groups. Population structure commonly arises from physical separation by distance or barriers, like mountains and rivers, followed by genetic drift.

- It remains unknown whether these patterns result from long-term in situ evolution of late European Neanderthal populations, or as a consequence of a recent expansion of Vindijalike lineages into Europe

Thorin is a late European Neandertal, 53-48 Ka

- Study reports the discovery of a late Neanderthal individual, nicknamed "Thorin", in 2015 and progressively excavated since then at Grotte Mandrin in Mediterranean France, a site which also was temporarily occupied by early modern humans at 54 ka.
- Thorin belonged to a late Neanderthal population which had stayed genetically isolated for some 50 k years. We further find evidence of gene flow from a deeply divergent lineage distinct from the Thorin lineage in the Neanderthal individual from Les Cottés.
- Our results suggest the presence of multiple isolated late Neanderthal communities in Europe close to their time of extinction, and shed light on their social organization with limited, if any, level of interactions in between different Neanderthal populations in their last millennia.

Excavation issues

- Recent analyses of Paleolithic sites in Western Europe suggest that Mousterian lithic industries, traditionally attributed exclusively to Neanderthals, ended 39-41 ka.
- Throughout Eurasia, ten sites have yielded Neanderthal remains directly dated between 50 and 40 ka.
- Neanderthal remains safely attributed to the final stage of their long existence are particularly rare and come essentially from sites excavated decades ago, often with little or disputable stratigraphic and archeological context

Lineages

- Thorin’s mtDNA was most closely related to that of the Forbes Quarry N woman from Gibraltar.
- Analyses of the Y chromosome showed a similar result, with the Thorin sequence diverging prior to the other two male late Neanderthals (Spy94a, Mezmaiskaya2)
- Under this model we estimate a divergence time of the Thorin clade of 123 ka, while we estimate the divergence between Hohlenstein-Stadel and the rest of the Neanderthals to 215 ka

Thorin was different: no interbreeding with MH

- D-statistics confirmed that Neanderthals from Europe, the Caucasus, and Siberia younger than 80 ka shared significantly more alleles with Vindija 33 than with Thorin, and that the Thorin lineage forms an outgroup to those lineages.

- Furthermore, Thorin does not show excess allele sharing with modern humans in comparison to all other west Eurasian Neanderthals, indicating that the lineage interbreeding with modern humans diverged prior to the Thorin lineage, and ruling out the possibility of recent interbreeding with early modern humans at Mandrin cave

- The best-fit model indicates a divergence of the Thorin lineage from Vindija 33 at 103 Ka ago, considerably earlier than those of Mezmaiskaya 1 (83 Ka) or Chagyrskaya 8 (79 Ka)

Thorin population was isolated

- Our results suggest small group sizes and long-term genetic isolation of the Thorin population from other late Neanderthal populations

- Suggest the presence of at least two deeply divergent and isolated lineages in close geographic proximity during the late Neanderthal period, subsequently partially replaced by an expansion of Vindija-like lineages into western Europe within the last 10,000 years of their existence.

- Interestingly, the eastern European late Neanderthal from Mezmaiskaya cave also shows high levels of homozygosity, suggesting small group sizes were likely also common among late Neanderthals outside the expanding Vindija-like population.

Late Ns belonged to single metapopulation

- Thorin is the most complete Neanderthal individual found in France since 1979 and falls amongst a group of other Neanderthals dating to the last millennia of their existence in western Europe.
- So far population genetic analysis of other late Neanderthals has indicated they belonged to a single metapopulation with no significant evidence of deep population structure among them.
- But Thorin belongs to a deeply diverging European Neanderthal lineage, representing a remnant of earlier European Neanderthals.

Isolated group of late Ns

- Interestingly, the divergence of this lineage began at ~100-105 ka, during the MIS 5 interglacial, a period that saw fast climatic and environmental changes across Eurasia and repopulation by warm adapted fauna through the continent.
- The timing of this divergence also coincides with a period of population replacement detected in northern Spain among Neanderthal populations.
- Suggests the existence of an isolated group of late Neanderthals in western Europe 50 ka.

Thorin & Gibraltar Ns = SW Europe N population

- This population is associated with a distinctive lithic tradition, which is continuously attested in the last four Mousterian levels of Mandrin, from 53-43 ka, overlapping with the final disappearance of Neanderthal populations in Eurasia.
- Thorin therefore likely belonged to one of the last representative Neanderthal populations in this area of Mediterranean France, and poses the first direct genomic evidence of deep population structure among late European Neanderthals.
- The genetic relationship observed between Thorin and Gibraltar indicates that the Gibraltar Neanderthals might have been members of an extended southwest European metapopulation.

N population replacement

- The genetic differences between Thorin and the other Western European Neanderthals may signify a major process of population replacement following, or related to, the expansion of anatomically modern humans through Europe.

- Interestingly, Thorin corresponds to the phase of Neanderthal reoccupation of Grotte Mandrin after the earliest modern human incursions in Europe.

N ghost lineage

- The unexpected identification of an hitherto unrecognized late Neanderthal population reveals a much more complex population structure among late Neanderthals and raises new lines of questions to further explore their social or ethological organization, which potentially could have played an important role in their later extinction.
- Besides the lineage that is represented by Thorin, our demographic modeling provides indirect evidence of another deeply diverged “ghost” lineage present through the French Neanderthal Les Cottés.

2 N lineages in late N period

- Whether this ghost lineage forms part of an as yet unknown further radiation of lineages after 100 ka, but before the classical late Neanderthals, remains unknown without a denser sampling of genomic data from around that time period.
- Our results nevertheless suggest a minimum of two distinct Neanderthal lineages present in Europe during the late Neanderthal period. In the absence of any detectable gene flow between Thorin and other Neanderthal lineages after its divergence, we conclude that Thorin represents a lineage that has stayed isolated for ~50 ka.

Third Time's the Charm | Sapiens From the Levant Made Three Attempts to Settle in Europe

- Humans from the Levant migrated to Europe in three waves starting 54,000 years ago, but it took more than 10,000 years to conquer the continent

- Thrice Homo sapiens from the Levant migrated to Europe. Twice they were forced back – either due to lack of numbers, inability to adapt to the region's Ice Age climate or resistance from the indigenous Neanderthals. Only on their third attempt, some 42,000 years ago, did sapiens succeed in establishing a permanent presence in Europe, finally wresting the continent from the Neanderthals.

- That's the conclusion of a new study that compared flint tools found in a cave in Lebanon with artifacts unearthed across Europe to identify three distinct waves of sapiens migrations starting more than 54,000 years ago.

A. David, 2023

Related to prior study of Mandrin, France, humans at 54 Ka

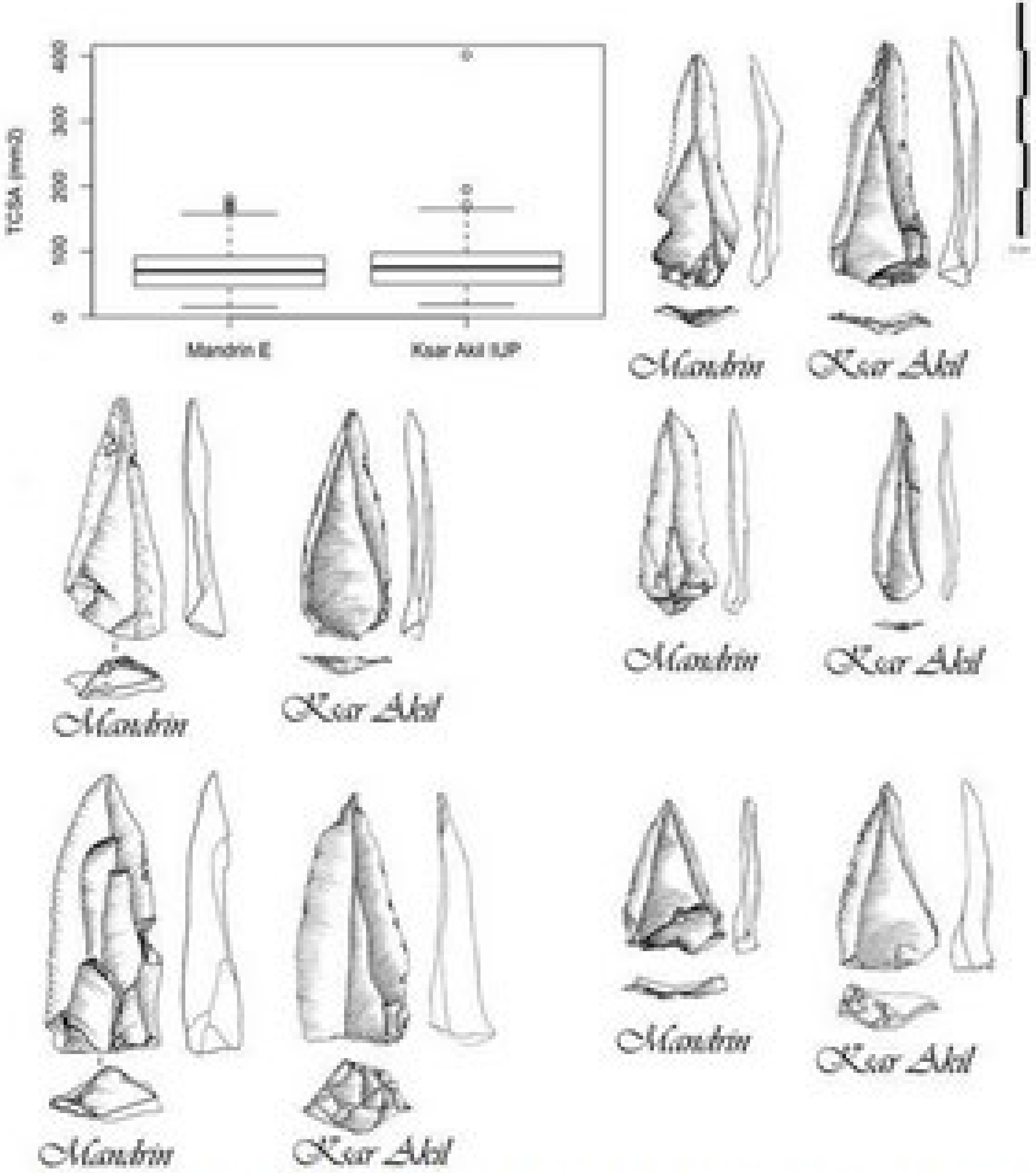
- Analysis based on lithic similarities: There are striking parallels between the tools belonging to three distinct Upper Paleolithic phases found at Ksar Akil, a prehistoric rock shelter just north of Beirut, and their contemporary equivalents in Europe
- The earliest anatomically modern human remains outside the continent have been found in Israel's Manot Cave and date to 55,000 years ago.
- Most scholars believed the earliest appearance of modern humans in Europe happened at least 10,000 years later, as evidenced by sapiens sites in Bulgaria and southern Italy that date to around 45,000 years ago.
- And then there is the headscratcher of how and why humans, having just expanded into the Near East, suddenly appeared in the Rhone Valley of southern France 54,000 years ago without leaving any traces between the two regions (more about this later).

Ksar Akil, Lebanon, lithics

- The puzzle is compounded by two problems: 50,000 years is roughly the upper limit for using radiocarbon dating, so employing this method to date early Upper Paleolithic sites doesn’t always produce precise results. Also, sapiens and Neanderthals often made the same tools and since human remains are relatively rare it can be difficult to assign a site to one species or the other based only on artifacts.
- The choice of Ksar Akil in Lebanon as a comparison point was made because the site tells the story of human habitation of the Levant through dozens of archaeological layers starting with the Middle Paleolithic occupation associated with Neanderthals and on into the arrival and subsequent development of sapiens stone tool cultures in the Upper Paleolithic (accompanied by a few human remains).
- “What we see at Ksar Akil and throughout the eastern Mediterranean in the Upper Paleolithic is something that is very continuous, very likely the same society and the same population gradually evolving throughout the millennia,” L. Slimak explains.

Same lithic types at both Ksar Akil and Mandrin Cave

- His analysis starts with artifacts belonging to the Initial Upper Paleolithic, a technological complex that is believed to mark the arrival of sapiens from Africa in the Levant and is characterized by the use of light, very standardized points that could be mounted on javelins or arrows.
- These artifacts are found at Ksar Akil, although they are dated to only around 46,000 years ago, and even earlier at sites like Boker Tachtit, in Israel's Negev desert, at around 50,000 years ago. These weapons are thought to have given sapiens a competitive edge over the heavier spearpoints of the Neanderthals, allowing our ancestors to hunt prey at a greater range.
- And lo and behold, those same projectiles are associated with the brief occupation by sapiens of Mandrin Cave 54,000 years ago, and are also found in a few sites in eastern Europe.



Comparison of flint points found at Grotte Mandrin (Mediterranean France) and Ksar Akil (Lebanon), separated by 3000km. Credit: Drawings and measurements of points: Laure Metz

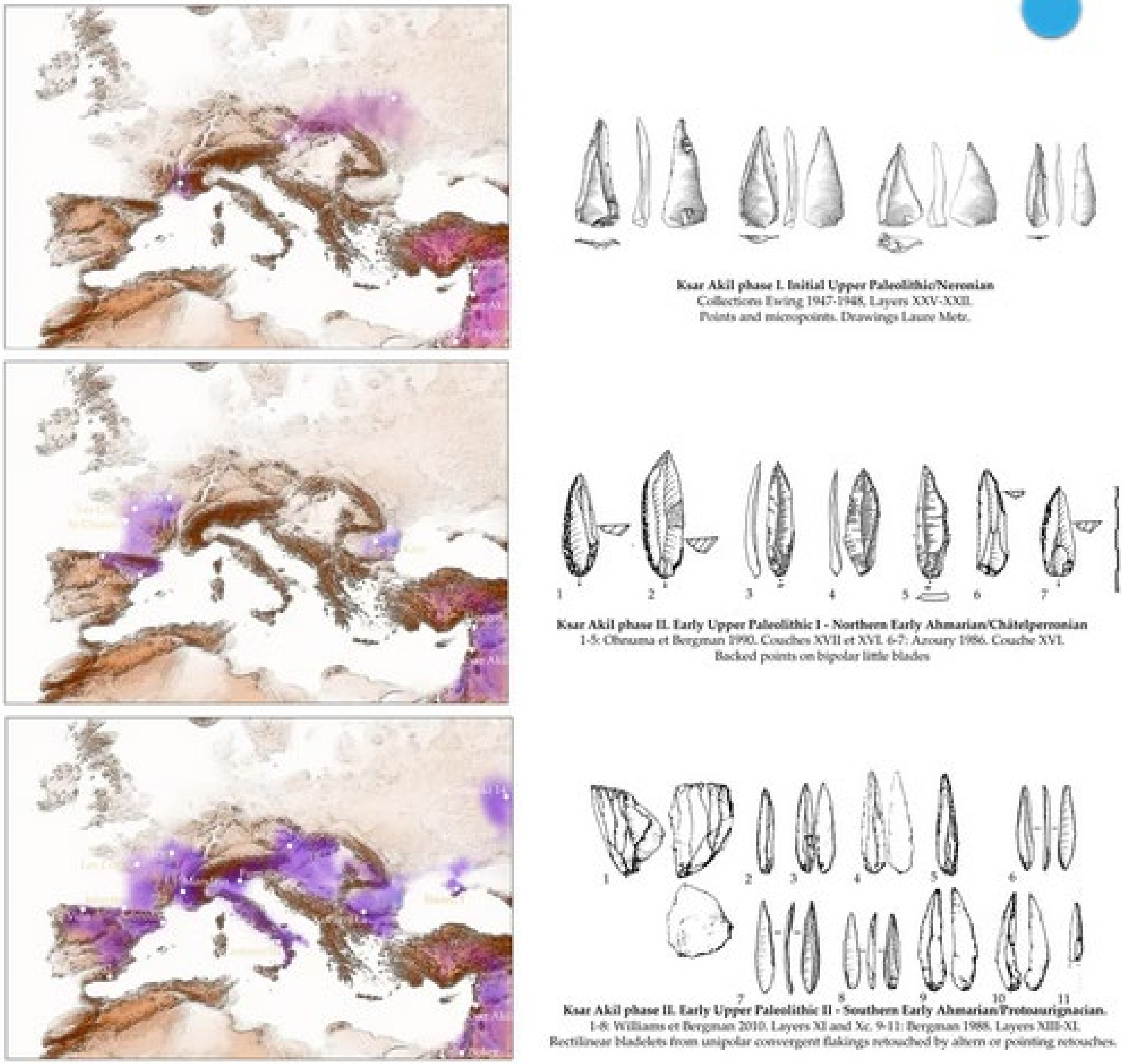
Time discrepancy

- Because they haven’t been compared carefully and are located in such distant regions, researchers call these stone tool cultures by different names: Initial Upper Paleolithic in the Levant, Neronian in France, Bohunician in eastern Europe – but they are all the same thing, and represent the first wave of sapiens colonization in Europe.
- ???: By the way, the fact that the human occupation of Mandrin (54,000 years ago) is dated a bit earlier than the first IUP tools in Israel (50,000 years ago) doesn’t detract from the narrative that the first sapiens came to Europe from the Levant. He puts the discrepancy down to the difficulties of using radiocarbon dating for this period.

By boat?

- One possibility is that we simply haven’t discovered intermediate sites, which were likely located along the coast and may have been covered by the rise of sea levels since the end of the Ice Age.
- Another hypothesis, which Slimak favors to explain the colony in the Rhone Valley, is that sapiens had already mastered the ability to navigate the seas and reached the coast of France by boat.
- This is not as far-fetched as it may sound, as there is little doubt that humans, tens of thousands of years ago, must have reached Australia by some form of vessel since that landmass was never connected to Eurasia by any land bridge. In the Mediterranean, there is evidence that even pre-sapiens hominins, like Homo erectus, may have reached the Aegean Islands presumably by raft already half a million years ago.

3 attempts to reach Europe



Ksar Akil phase I. Initial Upper Paleolithic/Neronian
Collections Ewing 1947-1948, Layers XXV-XXII.
Points and micropoints. Drawings Laure Metz.

Ksar Akil phase II. Early Upper Paleolithic I - Northern Early Ahmarian/Châtelperronian
1-5: Ohnuma et Bergman 1990. Couches XVII et XVI. 6-7: Azoury 1986. Couche XVI.
Backed points on bipolar little blades

Ksar Akil phase II. Early Upper Paleolithic II - Southern Early Ahmarian/Protoaurignacian.
1-8: Williams et Bergman 2010. Layers XI and Xc. 9-11: Bergman 1988. Layers XIII-XI.
Rectilinear bladelets from unipolar convergent flakings retouched by altern or pointing retouches.

Slimak reports on evidence of strikingly similar tools in France and the Mediterranean in three distinct periods, attesting to three distinct waves of early sapiens migrations from the Levant to Europe: The image shows the technical traditions of each of the three migrations. 1) 54,000 years ago 2) 45,000 years ago 3) around 42,000 years ago. Credit: Ludovic Slimak

Seeking N brides

- However it happened, the first wave of sapiens colonization in Europe was short-lived – in Mandrin it lasted just around 40 years. They likely reproduced there (one tooth of a sapiens child was found in the cave) but may have had insufficient numbers to hold on in the long term.
- “My guess would be the two populations were so divergent that the fertility was very partial, and in the first two waves the attempt to build social networks with the locals didn’t work out,” Slimak says.

2nd wave

- The second wave of migration that the archaeologist identifies occurred around 45,000 years ago.
- This wave is marked by an evolution of the IUP which produced two-sided knapped points found at Ksar Akil, at the sapiens site of Bacho Kiro Cave in Bulgaria as well as at sites in southwestern France and northern Spain.
- This part of his narrative may be the most controversial among researchers. The sites in Spain and France he refers to contain few human remains and the Chatelperronian lithic industry

2nd wave failed

- Most researchers believe that the Chatelperronian was a Neanderthal industry, possibly influenced by sapiens technology.

- This of course clashes with Slimak's analysis that sees parallels between this western European stone tool culture and the artifacts at Ksar Akil.

- Be that as it may, this second wave of sapiens colonization also failed to establish a permanent presence in Europe.

The final wave

- It was only around 42,000 years ago that a third wave of sapiens from the Levant managed to colonize the entire continent, roughly at the same time when the final decline and extinction of the Neanderthals occurred. This wave would birth Europe's earliest human culture, the Aurignacian.

- Again Slimak identifies parallels between stone tools at Ksar Akil and sapiens artifacts found in Europe: long, thin blades that are the hallmark of the Aurignacians.

- The third wave was much larger than the previous ones and sapiens ultimately overwhelmed the Neanderthals.

Critiques: no intermediate lithic sites

- Other researchers are even more cautious about the existence of the two early migration waves identified by Slimak: "Although the similarities between stone tools are clear, it is always difficult to draw direct parallels and suggest migrations on the basis of lithic data alone – especially given the absence of similar sites between the Levant and western Europe," says Yossi Zaidner.

- Ultimately, it seems everyone agrees that the narrative of humanity's dispersal through Europe is much more complicated than just that of a single arrival and a rapid expansion 42,000 years ago.

- "The early arrival in Mandrin is probably just the tip of the iceberg," Slimak concludes

New Hip Bone Discovery Suggests Previously Unknown Homo sapiens Lineage

- Individuals exhibiting anatomically modern human characteristics within the assemblage of Châtelperronian hominins found at Grotte du Renne (Arcy-sur-Cure, Northeast France)
- Around 42,000 years ago, aMH appear in Europe. New techno-cultural complexes appear, such as the Châtelperronian that extends from northern Spain to the Paris Basin. The Grotte du Renne (Arcy-sur-Cure) is a key site for discussing the biological identity of its makers. This deposit has yielded several Neanderthal human remains in its Châtelperronian levels.
- However, the last inventory of the paleoanthropological collection attributed to this techno-complex allowed the identification of an ilium belonging to a neonate (AR-63) whose morphology required a thorough analysis to assess its taxonomic attribution. Using geometric morphometrics, we quantified its morphology and compared it to that of 2 Neanderthals and 32 recent individuals deceased during the perinatal period to explore their morphological variation.

•Arthur Gicqueau, et al., 2023,

New neonate hip: not fully MH

- Our results indicate a morphological distinction between the ilia of Neanderthals and anatomically modern neonates.
- Although AR-63 is slightly outside recent variability, it clearly differs from the Neanderthals. Propose that this is due to its belonging to an early modern human lineage whose morphology differs slightly from present-day humans.
- We also explore different hypotheses about the presence of this anatomically modern neonate ilium among Neanderthal remains.
- Among new techno-cultural complexes, the Châtelperronian, present in the north of Spain, the south-west, the center of France and in the Paris Basin between around 43,760 and 39,220 BP, is the subject of a passionate scientific debate about the identity of its makers, Neanderthals or *Homo sapiens* (only 24 papers!!).

Châtelperronian material: MH or N?

- Recently, Gravina et al. conducted a taphonomic, spatial, and typo-technological reassessment of Châtelperronian lithic material from the *EJOP sup* level of La Roche-à-Pierrot (Saint-Césaire, Southwest France) in which a well-preserved Neanderthal skeleton was uncovered.

- The study showed that it is no longer possible to associate the Neanderthal human remains with Châtelperronian material given that the level in question contains "*an extremely limited quantity of Châtelperronian cultural material clearly mixed with an overwhelmingly Middle Palaeolithic component*".

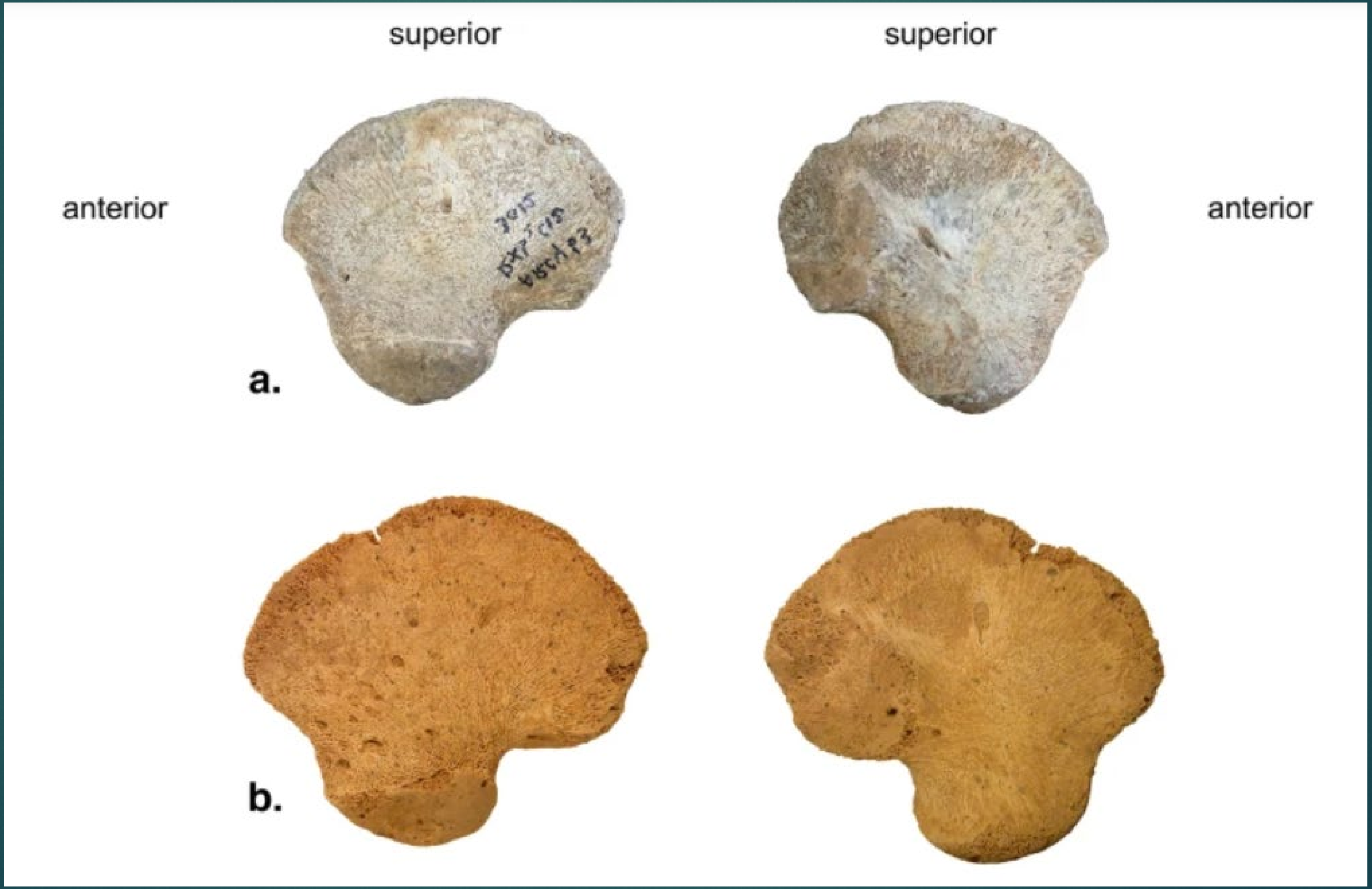
- In the context of this debate, the Grotte du Renne (GDR) of Arcy-sur-Cure (Yonne, France), 35 km south of Auxerre (France) is now the only site where several Châtelperronian layers have yielded human remains, until now all assigned to Neanderthals

Due to stratigraphic disturbances?

- According to some authors, the discovery of these Neanderthal fossils in layers containing a lot of material with features considered as "typical" of the UP (production of blades, bone industries, ornaments and coloring materials) is a result of inter-stratigraphic disturbances that mixed Mousterian human remains with remains from overlying levels reported to the UP.

- To date, studies of the human fossils of the GDR identified 64 remains attributed to layers X, IX and VIII. 38 of them exhibit morphological and genetic traits assigning them to the Neanderthal lineage:

New Neonate ilium



MH or Ns?

- To date, research conducted on the transition between the MP and the UP in southwestern Europe considers that the Châtelperronian is a techno-complex of the beginning of the UP.
- According to some, it shows a Mousterian component only when overlying Mousterian layers, suggesting that these component primarily results from post-depositional admixture.
- Moreover, this techno-complex shares many techno-typological traits with the Protoaurignacian industries due to the predominance of laminar production.
- For others, however, the Châtelperronian is rooted in the Mousterian of Acheulean tradition. This view is based on some other techno-typological similarities between the two techno-complexes, such as the presence of backed and elongated pieces or the use of direct percussion with a soft hammer and a similar geographical distribution of the two assemblages.

Ilium found in Chatelperronian layer

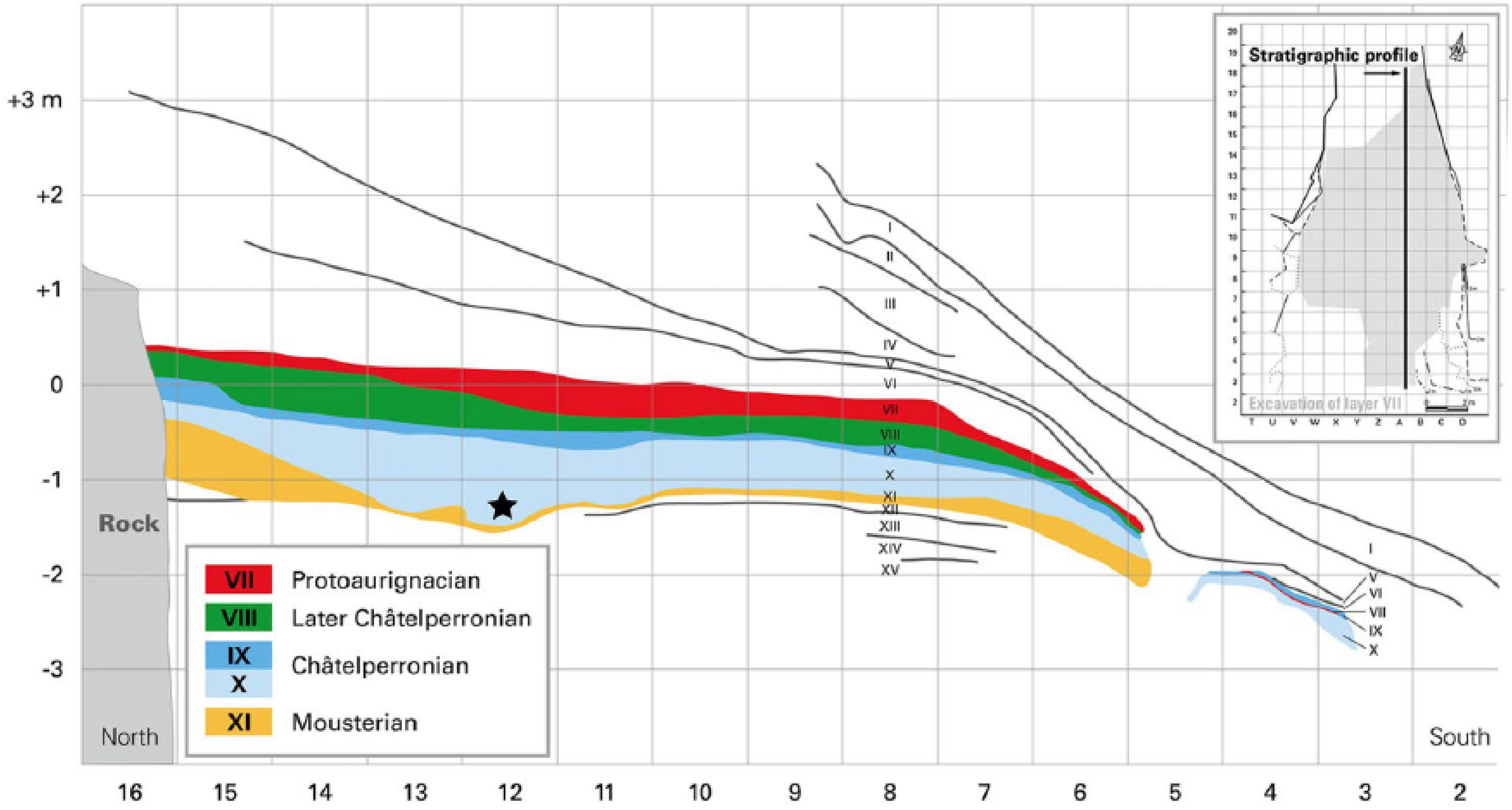


Figure 2. North–south stratigraphic section between the A and B raws of the excavation grid. Each square represents 1 m. The black star represents the projection of the localization of the perinatal ilium AR-63 discovered in the Xb2 sublayers. Modified from Hublin et al. (2012); original field drawing R. Humbert, archives A. Leroi-Gourhan (Connet, 2002).

Hypothesis 1: Ns made the Châtelperronian

- In this view, the Châtelperronian would therefore result from the evolution of local Neanderthal production either independently from any external influence or under the cultural influence of contemporaneous AMH.
- The first option implies an independent development of symbolic artifacts such as Châtelperronian body ornaments within Neanderthal populations.
- The second implies direct or indirect contacts of late Neandertals with AMH bearing the early Aurignacian or other early UP assemblages resulting in acculturation and possible population admixture.

Hypothesis 1: Ns made the Châtelperronian

- Hypothesis H1: If we assume that Neanderthals (acculturated or not) are the only makers of the Châtelperronian then the AR-63 ilium could be considered intrusive within the Xb2 level.

- This hypothesis would be consistent with the suggestion by some that layer admixture occurred at the GDR. The bone could have come from overlying layer of the Aurignacian, as a result of human or large carnivore activities.

Hypothesis 2: MHs made the Châtelperronian

- If one assumes that AMH are the makers of the Châtelperronian, then the AR-63 ilium could be *in situ* but all the Neanderthal remains of the layer should be intrusive and derived from the underlying Mousterian (hypothesis H2). We consider H2 unlikely.
- Although a large number (n=38) of Neanderthal human remains were unearthed at the GDR in association with Châtelperronian material, much less were discovered in the underlying Mousterian layer (n=6).
- This situation contrasts with that observed in the nearby Grotte du Bison where many Neanderthal remains were found in the late Mousterian levels (n = 50) and none in the Châtelperronian.
- Furthermore, the surface distribution of Neanderthal remains in the Châtelperronian layers at the GDR seems hardly compatible with H2.
- Finally, and even more critically, H2 is at odds with the direct dating of one genetically identified Neanderthal from the Châtelperronian layer of the GDR matching the radiocarbon dates obtained in this layer and postdating the Mousterian layers at the site.

Hypothesis 3: Ns made the Châtelperronian

- A third hypothesis (H3) could be that all human remains, both AR-63 and the Neanderthal fossils, are intrusive.
- Vertical movements, from top to bottom, in the case of AR-63, and from bottom to top, in the case of the Neanderthal pieces, would explain the presence of these remains within the Châtelperronian sequence. If such disturbances had occurred, they would have necessarily mobilized all the archaeological material, including the most characteristic Châtelperronian lithic pieces.
- Unlikely since, none of the previous published studies that question the integrity of the archaeological levels of the GDR have documented such significant disturbances.

Hypothesis 4 & 5

- If we assume that the integrity of the Châtelperronian levels is as good as that of the underlying Mousterian and those of the overlying UP, and that the perinatal ilium is indeed contemporary with the Neanderthal human remains of layer Xb2, then AR-63 would attest the presence of AMH in this area of western Europe during the Châtelperronian period.
- Hypothesis H4: The makers of the Châtelperronian could then be human groups where Neanderthals and AMH coexisted
- Hypothesis H5: Or the GDR could have been occupied alternately by distinct human groups, makers of the same techno-complex.

Hypothesis 4: coexistence & diffusion of knowledge

- If validated, H4 would bring strong support to the notion that the development of an UP like assemblage such as the Châtelperronian associated to Neanderthal makers at the time of the transition resulted from cultural diffusion or acculturation processes with possible population admixture between the two groups.

- H4: is the most parsimonious hypothesis, in the absence of any direct absolute dating, that this ilium originates from the chronological period corresponding to the transition between the MP and UP in this region of western Europe, between 45 and 41 kya cal BP. Only a direct dating of AR-63 would give reliable information on its antiquity.

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