Human Evolution Update

September 2023

by

Charles J Vella, PhD

This Human Evolution Interest Group reduces your dementia risk

- People who take adult education classes have a lower risk of developing dementia five years later. Adult education is likewise associated with better preservation of nonverbal reasoning with increasing age.
- 282,421 participants from UK Biobank: participants were given an individual predictive "polygenic risk score" for dementia. Participants self-reported whether they took any adult education classes, without specifying the frequency, subject, or academic level.
- Participants who were taking part in adult education at enrollment had 19% lower risk of developing dementia than participants who did not.
- Participants who took part in adult education classes kept up their fluid intelligence and nonverbal reasoning performance better than peers who did not. However, adult education didn't affect the preservation of visuospatial memory or reaction time.

Hikaru Takeuchi & Ryuta Kawashima, 2023

People with long COVID have distinct hormonal and immune differences to those without the condition

- Long COVID patients have clear differences in immune and hormone function to patients without the condition.
- Known sxs = These symptoms included cognitive impairment or "brain fog," extreme fatigue, shortness of breath, and chronic pain.
- Clear, measurable differences in blood biomarkers of people with long COVID compared with people who recovered fully from an acute infection and a group of people who have never been infected with Covid.
- This is a decisive step forward in the development of valid and reliable blood testing protocols for long COVID.

COVID blood test

- Algorithm was able to differentiate between people with and without long COVID with 96% accuracy

- Biomarkers indicating:
  - abnormal T cell activity,
  - reactivation of multiple latent viruses (including the Epstein-Barr virus and other herpes viruses) and
  - significant reductions in cortisol levels.

World's oldest aquarium fish 'Methuselah' could be decades older than we originally thought, DNA clock reveals

The Australian lungfish "Methuselah" swims in her tank at Steinhart Aquarium in California. She was believed to be 84 years old but a new study suggests she could be over 100. She is hand fed.

Methuselah

- A new study has found that the famous Australian lungfish Methuselah could be up to 101 years old.
- Methuselah is a female Australian lungfish (*Neoceratodus forsteri*) that resides at Steinhart Aquarium in San Francisco, California. She first arrived at the aquarium in 1938 after being sent to the U.S. along with more than 200 other fish from Fiji and Australia.
- Aquarium staff have never been sure how old Methuselah is, but until now the best guess was that she is 84 years old, which makes her the oldest known fish in captivity. (In the Bible, Methuselah was a man who reputedly lived to be 969 years old.)
- The elderly fish, who loves belly rubs and is hand-fed figs by her doting keepers, shows no signs of slowing down. DNA results suggest that she is most likely age 92, but the level of uncertainty with this type of experiment means she could be up to 101 years old. The study will be published later this year.

Methuselah

- The researchers compared the DNA of 30 Australian lungfish from captivity and the wild, including two other lungfish at the Steinhart Aquarium. The team analyzed the amount of methylation in the fishes' genetic material.
- Native to Australian Queensland rivers. During dry periods, the rivers can stagnate, which reduces the level of available oxygen in the water. When breathing underwater becomes too difficult, the fish are capable of swimming to the surface and breathing air through a single lung
- The oldest fossil of a lungfish from the genus *Neoceratodus* dates back to around 380 million years during the Devonian period. They are an endangered species.

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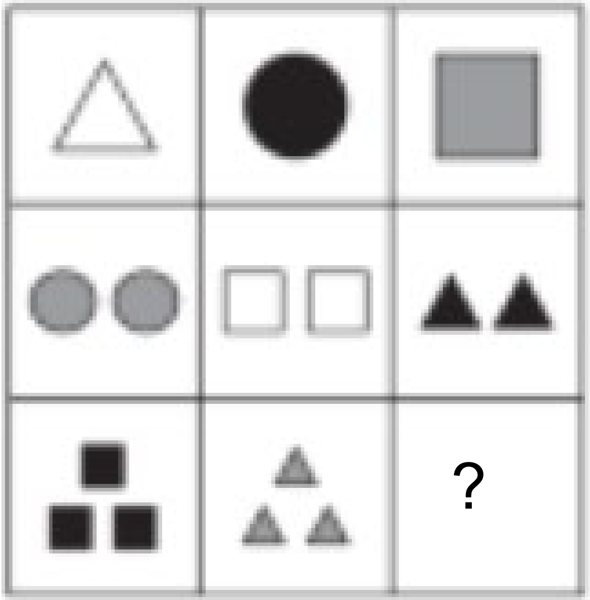

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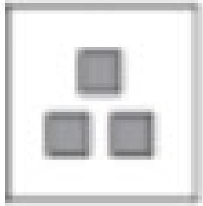

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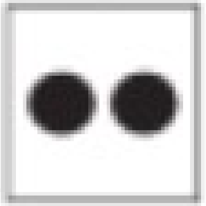

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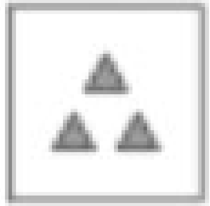

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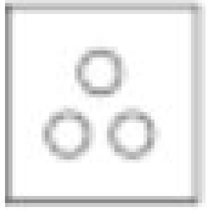

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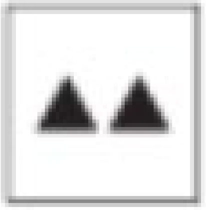

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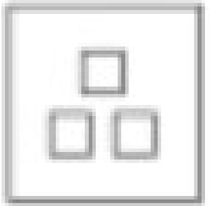

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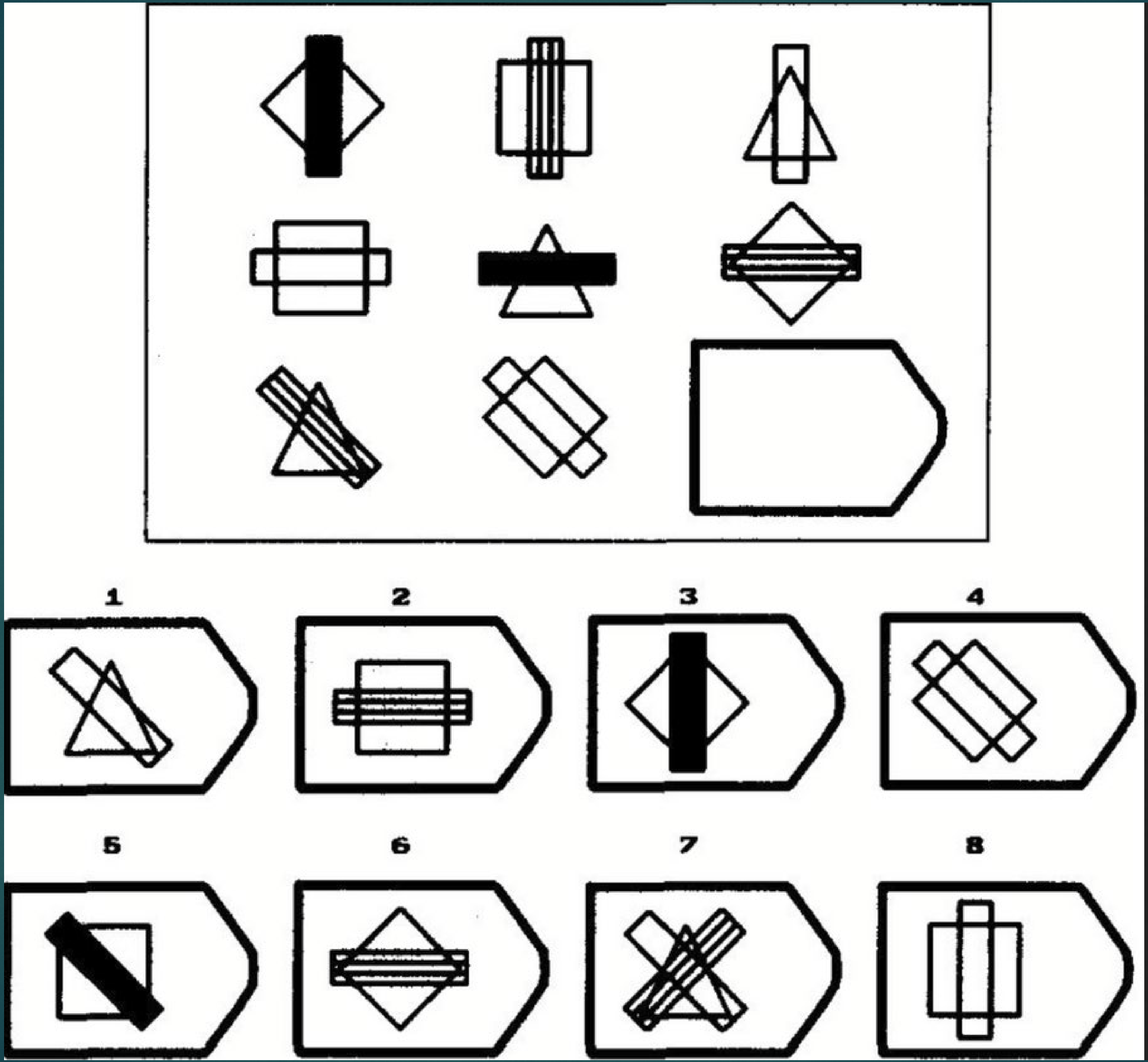


- GPT-3.5, without prior contact or training, solved this in less than 1 second
- ChatGPT had an IQ of 147 on a Verbal-Linguistic IQ Test. This would place it in the 99.9th percentile.

Large-scale AI language systems display an emergent ability to reason by analogy

- Analogical reasoning is a hallmark of human intelligence, as it enables us to flexibly solve new problems without extensive practice.

- New Study: By using a wide range of tests, demonstrates that GPT-3, a large-scale artificial intelligence language model, is capable of solving difficult analogy problems at a level comparable to human performance.

- The recent advent of large language models has reinvigorated debate over whether human cognitive capacities might emerge in such generic models given sufficient training data.

GPT-3 can reason by analogy

- Of particular interest is the ability of these models to reason about novel problems zero-shot (no prior exposure), without any direct training. In human cognition, this capacity is closely tied to an ability to reason by analogy.
- Here we performed a direct comparison between human reasoners and a large language model (GPT-3) on a range of analogical tasks, including a non-visual matrix reasoning task based on the rule structure of Raven's Standard Progressive Matrices.
- We found that GPT-3 displayed a surprisingly strong capacity for abstract pattern induction, matching or even surpassing human capabilities in most settings; preliminary tests of GPT-4 indicated even better performance.
- Results indicate that large language models such as GPT-3 have acquired an emergent ability to find zero-shot solutions to a broad range of analogy problems.

GPT-3

- Has now passed US Medical Licensing Exam, the Legal bar exam, but not the neonatal-perinatal pediatric board exam

- It scores 99.9% on Stanford-Binet IQ test

- Gemini is a large language model (LLM) developed by Google AI. It is still under development, but it is expected to be released in early 2024. Gemini is said to be 5 times more powerful than GPT-4.

Box of donated artifacts turns out to be treasure trove of Neanderthal bones

Remains of 3 Neanderthal found at the Simanya Gran gallery from Cova Simanya (Barcelona, Spain). Skeletal remains are distributed according to their attribution to specific individuals. **(A)** Left humerus; **(B)** shaft, caudal view; **(C)** bones of the foot; **(D)** bones of the right hand; **(E)** upper P^3 and M^3; **(F)** fragment of the atlas and first phalanx of the hand; and **(G)** fragment of the ascending branch

J. Morales, et al. 2023

Spanish Museum box

- A box of artifacts donated to a museum in Spain back in 1986 contained 53 Neanderthal bones.
- Study of the bones has revealed that they all belonged to just three N individuals; an adult, probably a woman, a child, probably aged 11 or 12 years old at the time of death and another young child, which the team estimates to have been 7 to 8 years old at their time of death.
- Back in the late 1970s, amateur paleontologist Miguel Aznar uncovered a vast assortment of artifacts and bones outside of a cave called Cova Simanya, which is located in a park just outside of Barcelona. Aznar cleaned the materials and gave them a cursory inspection and then dumped them all together in a box. He then put them in a storage bin at his home, where they stayed until 1986; the year he donated the box to the Archaeology Museum of Catalonia, where it sat unexplored until 2020.

A N family?

- The bones have been dated back to approximately 50 Ka ago.
- A tooth was later found at the cave.
- Attempts to extract aDNA have been unsuccessful.
- Simanya Neanderthals’ apomorphic traits align with other late Neanderthals; part of the final evolutionary phase of the evolution of western Neanderthals

Broken Hill/Kabwe Skull

Broken Hill/Kabwe Skull: Repatriation from England to Zambia

- Nearly all of Kabwe, Zambia's children have blood lead levels so high that their health is in serious danger. Environmentalists consider Kabwe to be one of the most polluted cities on Earth.

- 1921 discovery of skull & bones in lead mine- Rhodesian Man/*H. heidelbergensis* = first early human fossil discovered in Africa; 1,300 cc;

- Refocused research from Asia to Africa; recently redated to 300 Ka (therefore not ancestral to *H. sapiens*); represents an increase in size of the *Homo erectus* morphology

- Mining officials sent the fossils to the British Museum for study; now resides in London's Natural History Museum. The Zambians have been trying to get it back for decades, to no avail. But now repatriation negotiations are happening.

H. sapiens origins: Multiregionalism in Africa

- Comment by Thackeray (1995), in the context of *H. erectus (sensu lato*) and Heisenberg's "Uncertainty Principle":
- "All modern humans can trace their origin to descendants of *H. erectus*, but both the ancestral populations of *H. erectus* and descendant populations of *H. sapiens* have expanded and contracted in response to many climatic and habitat changes, with the result that the very concept of "origin" in the context of gene pools can never be precisely determined; continuity occurred in some areas, replacement occurred in other regions, but the net effect was a very high degree of morphological variability within the single species which we today refer to as *H. sapiens*".

Earliest structural use of wood?

Might have been a raised platform, a shelter or something else entirely. Whatever it was, it pre-dates the evolution of Homo sapiens by more than 100,000 years, hinting that hominins that lived long before our own species were already working wood.

Evidence for the earliest structural use of wood at least 476,000 years ago.

- Wood artefacts rarely survive from the Early Stone Age since they require exceptional conditions for preservation; consequently, we have limited information about when and how hominins used this basic raw material[1].
- Study: earliest evidence for structural use of wood in the archaeological record. Waterlogged deposits at the archaeological site of Kalambo Falls, Zambia, dated by luminescence to at least 476 ± 23 ka, preserved two interlocking logs joined transversely by an intentionally cut notch.
- This construction has no known parallels in the African or Eurasian Palaeolithic. The earliest known wood artefact is a fragment of polished plank from the Acheulean site of Gesher Benot Ya’aqov, Israel, more than 780 ka.

Barham, L.,, et al., 2023

Earliest use of trees

- Wooden tools for foraging and hunting appear 400 ka in Europe, China and possibly Africa.

- At Kalambo we also recovered four wood tools from 390 ka to 324 ka, including a wedge, digging stick, cut log and notched branch.

- The finds show an unexpected early diversity of forms and the capacity to shape tree trunks into large combined structures. These new data not only extend the age range of woodworking in Africa but expand our understanding of the technical cognition of early hominins, forcing re-examination of the use of trees in the history of technology

Kalambo Falls

- Kalambo Falls was first excavated in the 1950s and 1960s, British archaeologist J. Desmond Clark and his team found stone tools and wooden objects that might have been tools, as well as a large wooden object interpreted as being part of a structure. But no dating.
- Barham and his team started visiting Kalambo Falls in the early 2000s to date the site using modern techniques
- But on the first day of a 2019 excavation, the researchers slid down a slope to the shores of the Kalambo River and noticed a piece of wood jutting out of a cliff face.
- Excavations of the waterlogged site turned up several pieces of wood that seemed to have been modified, as well as one big surprise: a 1.4-metre-long log that had tapered ends and a deeply carved notch where it rested on another large piece of wood (like Lincoln Logs). Many of the wooden objects harbored signs of intentional modification, such as scrape marks

Like Lincoln Logs

- In BLB5, one modified object was recovered from basal sands containing flake tools, cleavers and handaxes. Object 1033 is a wooden log 141.3 cm long × 25.6 cm, with tapering ends in three parts, which overlies a larger tree trunk at a 75° angle. The area of overlap is a U-shaped notch 13.2 cm long by 11.4 cm wide, transverse to the long axis. The underlying trunk, also modified, and left in situ, passes through the notch.

- Evidence of chopping and scraping occurs on the upper surface of the notch and on the lower surface. Surface modification occurs on the underlying trunk at its midpoint and along the narrowed end that passes through and beyond the notch

Woodworking

- The notch is interpreted as intentional, made by scraping and adzing to create a joint between the log and trunk, forming a construction of two connected parts.

- Clark described a similar find, from the Acheulean in Site B, of comparable length (165 cm long) with a "wide and deepish groove" transverse to the long axis, with tapered ends. He interpreted the groove as anthropogenic and suggested it was part of a structure.

- The excavation of two interlocking logs in BLB5, with shaped ends on both objects supports this interpretation. We know of no comparable construction in the early archaeological record

- The recovery of modified wood with an exceptional level of preservation at Kalambo Falls places woodworking firmly in the Mid-Pleistocene of Africa.

New appreciation of MP technological abilities

- Hominin use of the Kalambo River basin coincides with an extended period of forest cover (470–274 kyr). Availability of forest resources and a permanent elevated water table created a habitat conducive to sustained occupation. Life in a periodically wet floodplain would be enhanced by constructing a raised platform, walkway or foundation for dwellings.

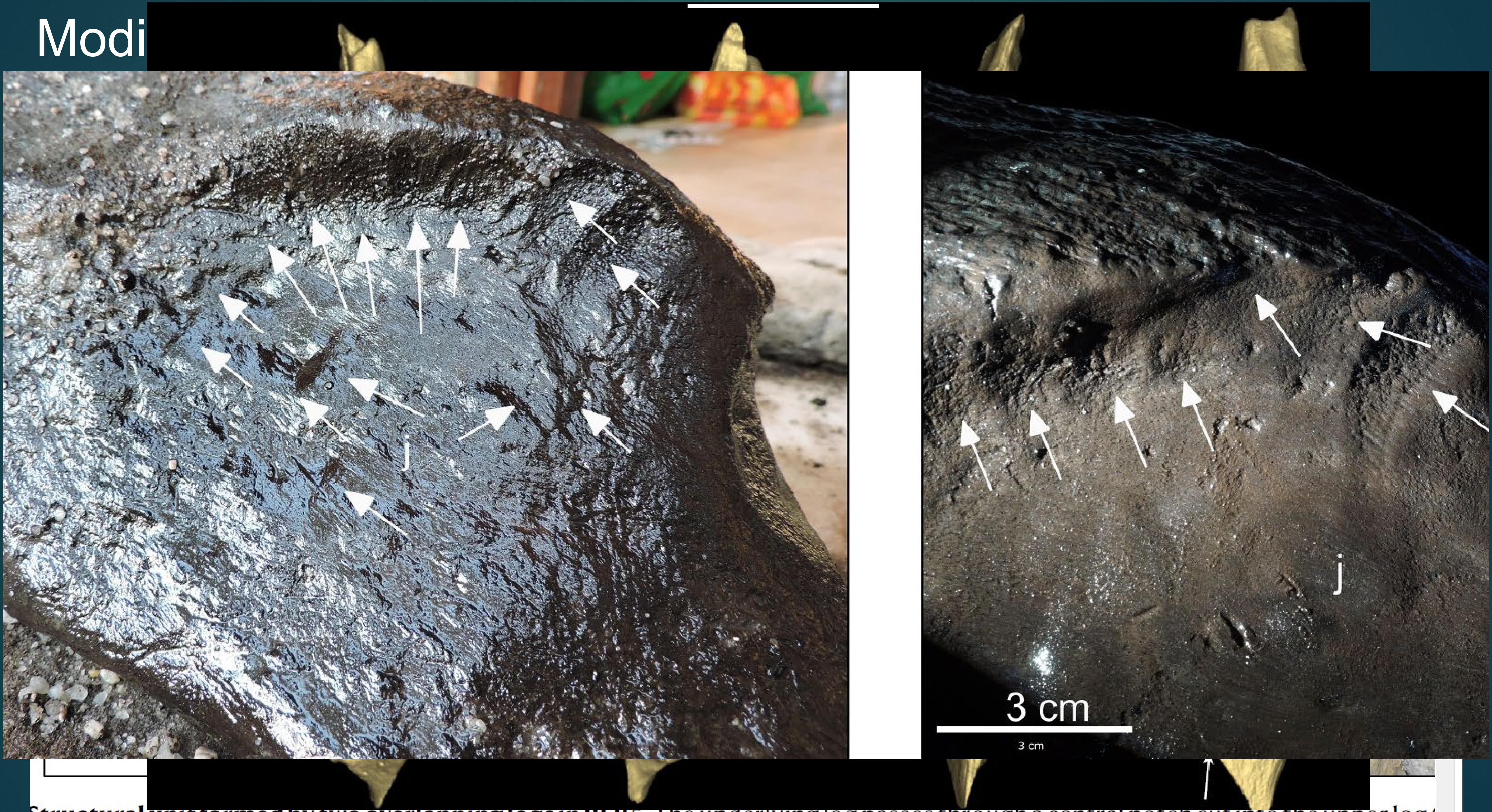
- The interlocking logs from BLB5 anticipate hafting's core concept: the combination of two or more parts to make a construction, enhancing our understanding of the technical cognition of these toolmakers.

- Exceptional conditions of preservation give us this glimpse of a capacity to create a built environment by hominins hitherto perceived as mobile foragers with limited technological diversity.

Raised wooden structure?

- Barham wonders whether the wood was used to make a platform for fishing or to keep things off the muddy forest floor, some kind of raised track or even a simple shelter.
- A technique called luminescence dating suggests that the large wooden objects are at least 476,000 years old, and some of the smaller tools are slightly younger.
- No hominin remains have been found at Kalambo Falls, but a 300,000-year-old skull from another Zambian site has been identified as *Homo heidelbergensis*,

Modi



Structural unit formed by two overlapping logs in BLB5. The underlying log passes through a central notch cut into the upper log (

Does a brain in a dish have moral rights?

- No longer limited to the realm of science fiction, bio-computing is here, so now is the time to start considering how to research and apply this technology responsibly,
- Combining biological neural systems with silicon substrates to produce intelligence-like behavior has significant promise, but it raises potential ethical questions.
- Biotech start-up Cortical Lab was made famous by their development of DishBrain—a collection of 800,000 living brain cells in a dish that learnt to play Pong.
- At what point does a neuron brain organoid become conscious, or experience pain? English philosopher Jeremy Bentham argued that, with respect to the moral status of animals, "the question is not, 'can they reason?' nor, 'can they talk?' but, 'can they suffer?'".
- If new biologically based computers show human-like intelligence, does it necessarily follow that they have moral status?

Morality of biocomputers

- Silicon-based computing is massively energy-hungry with a supercomputer consuming millions of watts of energy. By contrast, the human brain uses as little as 20 watts of energy—biological intelligences will show similar energy efficiency.

- "As it stands, the IT industry is a massive contributor to carbon emissions. If even a relatively small number of processing tasks could be done with bio-computers, there is a compelling environmental reason to explore these alternatives.

RNA has been recovered from an extinct species for the first time

- A new study shows the isolation and sequencing of more than a century-old RNA molecules from a Tasmanian tiger specimen preserved at room temperature in a museum collection. This resulted in the reconstruction of skin and skeletal muscle transcriptomes from an extinct species for the first time.
- Has implications for international efforts to resurrect extinct species, including both the Tasmanian tiger and the wooly mammoth, as well as for studying pandemic RNA viruses.

Emilio Mármol-Sánchez, et al., 2023

Historical RNA expression profiles from the extinct Tasmanian tiger

- DNA sequencing cannot reveal tissue-specific gene expression, cellular identity, or gene regulation, which are only attainable at the transcriptional level. Pioneering studies have shown that useful RNA can be extracted from ancient specimens preserved in permafrost and historical skins from extant canids, but no attempts have been made so far on extinct species.
- Extraction, sequence, and analyze historical RNA from muscle and skin tissue of a ~130-year-old Tasmanian tiger (Thylacinus cynocephalus) preserved in desiccation at room temperature in a museum collection.
- The transcriptional profiles closely resemble those of extant species, revealing specific anatomical features such as slow muscle fibers or blood infiltration. RNA sequences are used to improve protein coding and noncoding annotations, evidencing missing exonic loci and the location of ribosomal RNA genes while increasing the number of annotated thylacine microRNAs from 62 to 325.

Tasmanian Tiger

- Discovery of a thylacine-specific microRNA isoform that could not have been confirmed without RNA evidence.

- Detection of traces of RNA viruses, suggesting the possibility of profiling viral evolution.

- These results represent the first successful attempt to obtain transcriptional profiles from an extinct animal species, providing thought-to-be-lost information on gene expression dynamics.

- These findings hold promising implications for the study of RNA molecules across the vast collections of natural history museums and from well-preserved permafrost remains.

New field of paleotranscriptomics

- Sequencing, for the first time, the transcriptome of the skin and skeletal muscle tissues from a 130-year-old desiccated Tasmanian tiger specimen preserved at room temperature in the Swedish Museum of Natural History in Stockholm. This led to the identification of tissue-specific gene expression signatures that resemble those from living extant marsupial and placental mammals.
- The last known living Tasmanian tiger died in captivity in 1936 at the Beaumaris Zoo in Hobart, Tasmania.
- This pioneering study opens up new exciting opportunities and implications for exploring the vast collections of specimens and tissues stored at museums across the globe, where RNA molecules might await to be uncovered and sequenced.

The other type of Intelligence on planet Earth

Read: The Mountain in the Sea by Nayler;
Watch on Netflix: The Octopus, my Teacher

Octopuses used in research could receive same protections as monkeys

- Cephalopods such as octopuses and squid could soon receive the same legal protection as mice and monkeys do when they are used in research

- The US National Institutes of Health has proposed new guidelines for work with cephalopods (such as octopuses and squid) because of growing evidence that the animals perceive pain and have advanced cognitive abilities. Cephalopod researchers have welcomed the move.

- Little is known about how to effectively anaesthetize the animals.

Virgin Galactic's VSS Unity Soars Into Space with fossils

[redacted]

Virgin Galactic launched fossilized human remains to space

- Virgin Galactic completed its third commercial suborbital spaceflight on September 8. Aside from the three private astronauts aboard the company's spaceplane, Virgin Galactic also launched fossilized remains of ancient humans to suborbital space (15 Kms).

- Fossils from Homo naledi and Australopithecus sediba become the oldest astronauts to travel to space, flying on Virgin Galactic's spaceship VSS Unit

- One of the fossils is a two-million-year-old South African fossil hominin species *Australopithecus sediba* and the other is a 250,000-year-old hominin species *Homo naledi*. The first is a fossilized clavicle and the second is a fossilized thumb bone.

- Both fossils were placed in a carbon fiber container prior to the spaceflight and were carried by astronaut Timothy Nash, who is a South African-born, South African and British citizen. Virgin Galactic charges between $250,000 and $450,000 per sea

- Berger hand delivered them to NM. Also now claims H. naledi and sapiens may have interbred.

Ancient-human fossils sent to space: scientists slam ‘publicity stunt’

- The fossils’ journey has drawn extraordinary rebuke from archaeologists, paleoanthropologists and other researchers. They say that it was an unethical publicity stunt that put priceless hominin fossils at risk, raising questions about the protection of cultural heritage in South Africa, as a government agency signed off on the mission.
- “To treat ancestral remains in such a callous, unethical way — to blast them into space just because you can — there’s no scientific merit in this,” says Robyn Pickering, a geologist at the University of Cape Town in South Africa.
- The shoulder bone is especially valuable because it was the first *A. sediba* fossil to be discovered and is the type specimen that defines the species.
- A representative of the University of the Witwatersrand referred *Nature* to Lee Berger, but he did not respond to *Nature*’s request for comment.

Researchers are labeling the Virgin Galactic mission as a significant violation of ethical standards.

- Alessio Veneziano, a biological anthropologist and co-organizer of the AHEAD conference (Advances in Human Evolution, Adaptation and Diversity), succinctly identified four main issues that have been discussed: 1) the lack of scientific justification for the flight; 2) ethical issues surrounding respect for human ancestral remains; 3) Berger's access to the fossils, which few other researchers share; and 4) the misrepresentation of the practice of paleoanthropology.

- This event commercializes anthropology and archaeology and exploits human history for profit; trivializes the discipline and turns it into a form of entertainment; the absence of ethical oversight in allowing a private company to conduct such a flight with human remains.

Critiques

- The fossils' space journey has been roundly criticized for lacking a scientific purpose, especially since a malfunction on the mission could have destroyed the priceless specimens
- We should ask: can the University of the Witwatersrand and Lee Berger be trusted to care for these fossils going forward, if this is what they think is an appropriate thing to do with them?
- Claim that its granting of the permit was part of neocolonial practices
- ** Nash has also been friends with Lee Berger for over a decade and owns most of the so-called Cradle of Humankind — including the land where the Bergers discovered *A. sediba*, which he hopes to develop into a "paleotourism" industry.

NASA’s Asteroid Hunter Lucy Soars into the Sky - with Diamonds

- While the idea to take fossilized remains of a different *Australopithecus* species into space this summer may have seemed innovative to Berger and Nash, the Australopithecus “Lucy” has already been honored in space exploration in 2021, not by taking any of her *priceless* bones into space, but by giving her name to a NASA spacecraft. The space probe known as “Lucy” is currently enroute, on a 12-year exploration, to our solar system’s asteroid belt on a mission to better understand both main belt asteroids and Jupiter trojan asteroids. It was named both for the spacecraft’s Thermal Emission Spectrometer, which contains diamonds, and for a flight path that will take it past an asteroid named for *Australopithecus afarensis* discoverer, Donald Johanson

A NASA mission shows a different way to honor an ancestor of humanity. (credit: NASA)

Lucy's Nasa mission patch includes a graphic representation of its namesake hominin's skeletal remains, bringing the name and image of this ancient being into outer space, while leaving her remains safely on Earth.

2023 Balzan Prize

- One of 3 winners this year's Balzan Prize ($840K): Frenchman Jean-Jacques Hublin of the Max-Planck-Institute for evolutionary anthropology in Leipzig was cited for his discoveries of the oldest Homo sapiens in Jebel Irhoud, Africa, contributing to the study of human evolution.
- The citation also praised his ability to synthesize data, organize scientific teams and his qualities as a teacher "

2023 Balzan Prize: Eske Willerslev

- Eske Willerslev of the University of Copenhagen in Denmark was cited for studies of human DNA, focusing on population migrations to "transform our understanding of human history." The citation said he used ancient DNA from teeth to identify human pathogens and retrieved DNA from environmental samples "opening a new scientific field."

First shoe prints? Gukamma, S Africa

Footprints circa 100 Ka

- 3 possible footprint sites in S Africa
- Found a slab of rock 55 centimeters across. It has at least two well-preserved footprints, plus two other impressions that might be prints. The two best footprints have extremely clean edges and no sign of details like toes, which is suggestive of shod feet. One of them also has three small divots, which could be where straps were attached to the sole of the footwear.
- In addition, the team found a slab of rock in Addo Elephant National Park. It has four tracks, one of which is partial, with no toe marks. They also redescribed a slab of rock from Goukamma Nature Reserve, which has four tracks. Three have crisp edges and no signs of toes.
- Did experimental imitation cowhide sandals which matched the above.
- The oldest known items of footwear are sandals found in Fort Rock cave in Oregon, dated to just 9200 to 10,500 years ago

Despite their reputation as nature's buzziest pollinators, the vast majority of bee species spend most of their lives underground.

Bees are miners: live underground

- Despite their reputation as nature’s buzziest pollinators, the vast majority (85%) of bee species spend most of their lives underground.
- Some nests extend meters down
- One, the spring mining bee (*Colletes cunicularius*), is solitary; each female builds a nest over a few days, collecting pollen by herself and laying eggs before abandoning it.
- The other species, the sweat bee (*Lasioglossum malachurum*), reproduces communally with multiple generations, so the colony expands its nest through the year.
- Most bee species line the larval chambers to make them waterproof, using leaves or flower petals or secretions. One burrow lasted 16 months.

Early Humans Deliberately Made Mysterious Stone 'Spheroids'

Three limestone "spheroids" from the 'Ubeidiya site in Israel, which researchers believe were deliberately made into spheres 1.4 million years ago

A collection of 150 limestone spheroids from the 'Ubeidiya archaeological site, dating back to approximately 1.4 million years ago; earliest Acheulean site

The limestone spheroids of ‘Ubeidiya: intentional imposition of symmetric geometry by early hominins?

- The early ancestors of humans deliberately made stones into spheres 1.4 million years ago, though what prehistoric people used the balls for remains a mystery.

- Archaeologists have long debated exactly how the tennis ball-sized "spheroids" were created.

- Did early hominins intentionally chip away at them with the aim of crafting a perfect sphere, or were they merely the accidental by-product of repeatedly smashing the stones like ancient hammers?

A. Muller, et al., 2023

Spheroids

- Using 3D analysis to reconstruct the geometry of the stones, the researchers determined that their sphericalness was "likely to have been produced intentionally".

- Had a "mentally preconceived" idea of what they were doing. That in turn indicates that our ancient relatives had the cognitive capacity to plan and carry out such work.

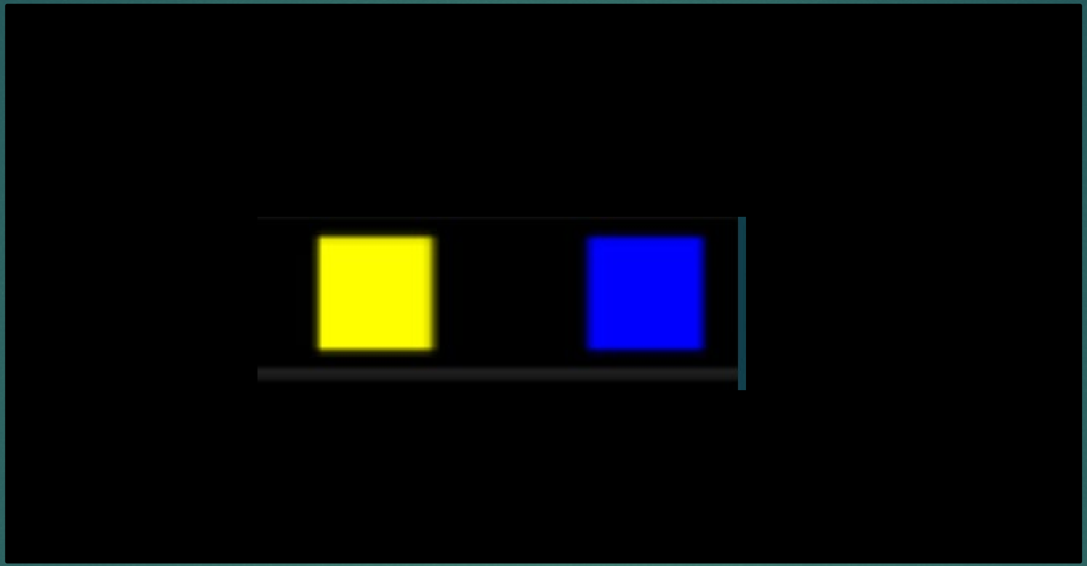
- Cabanas said the same technique could be used on other spheroids. For example, it could shed light on the oldest known spheroids, which date back two million years and were found in the Olduvai Gorge of modern-day Tanzania.

Spheroids

- But exactly why our ancestors went to the effort of crafting spheres remains a mystery.
- Possible theories include that the hominins were trying to make a tool that could extract marrow from bones or grind up plants.
- Some scientists have suggested that the spheroids could have been used as projectiles, or that they may have had a symbolic or artistic purpose.

Working memory of Stimuli presented simultaneously

Memory for material presented in temporal sequence



Delay durations were 0, 2, 5, and 10 seconds.

Delayed matching-to-sample

- Ability to faithfully recognize and represent arbitrary sequential information, that is, how an organism represent multiple arbitrary stimuli that are separated in time

- Hundreds of delayed matching-to-sample studies have been performed on birds and non-human mammals showing that animals will learn this task to near perfection with zero-second delays, given sufficient training.

- However, performance of all non-human species degrade rather quickly, even after short delays.

Delayed matching-to-sample

- Humans can, on the other hand, easily reach error-free performance with delays of 48 hours.
- These differences in a general-purpose memory system, that birds and non-human mammals quickly forget arbitrary stimuli, whereas humans can retain such information for days and weeks, have been put forward as a tentative cause for the observed cognitive and cultural divide between humans and other animals

A test of memory for stimulus sequences in great apes

- There are key differences between humans and other animals in how information is recognized and remembered
- Results show that bonobos' general working memory decays rapidly and that they fail to learn the difference between the order of two stimuli even after more than 2,000 trials.
- Humans solve the same sequence discrimination almost immediately.
- Non-human animals, including the closest relatives to humans, lack a memory for stimulus sequences.

Lind J,, et al., 2023

Naked Mole Rat: University of Rochester researchers successfully transferred a longevity gene from naked mole rats to mice, resulting in improved health and an extension of the mouse's lifespan.

Zhihui Zhang, et al., 2023

Naked Mole Rat

- Naked mole rats are mouse-sized rodents that have exceptional longevity for rodents of their size; they can live up to 41 years, nearly ten times as long as similar-sized rodents.

- Unlike many other species, naked mole rats do not often contract diseases—including neurodegeneration, cardiovascular disease, arthritis, and cancer—as they age.

- The researchers previously discovered that HMW-HA is one mechanism responsible for naked mole rats' unusual resistance to cancer. Compared to mice and humans, naked mole rats have about ten times more HMW-HA in their bodies.

Successful Transfer the Longevity Gene

- Naked mole rats, noted for their resistance to age-related diseases, have a gene that produces high molecular weight hyaluronic acid (HMW-HA), which when introduced to mice, demonstrated potential anti-aging benefits. This led to improved health and an approximate 4.4 percent increase in the median lifespan for the mice.

- Mice that had the naked mole rat version of the gene had better protection against both spontaneous tumors and chemically induced skin cancer. The mice also had improved overall health and lived longer compared to regular mice

Discovery of a 300,000-Year-Old Giant Handaxe Sheds Light on Ice Age Technology

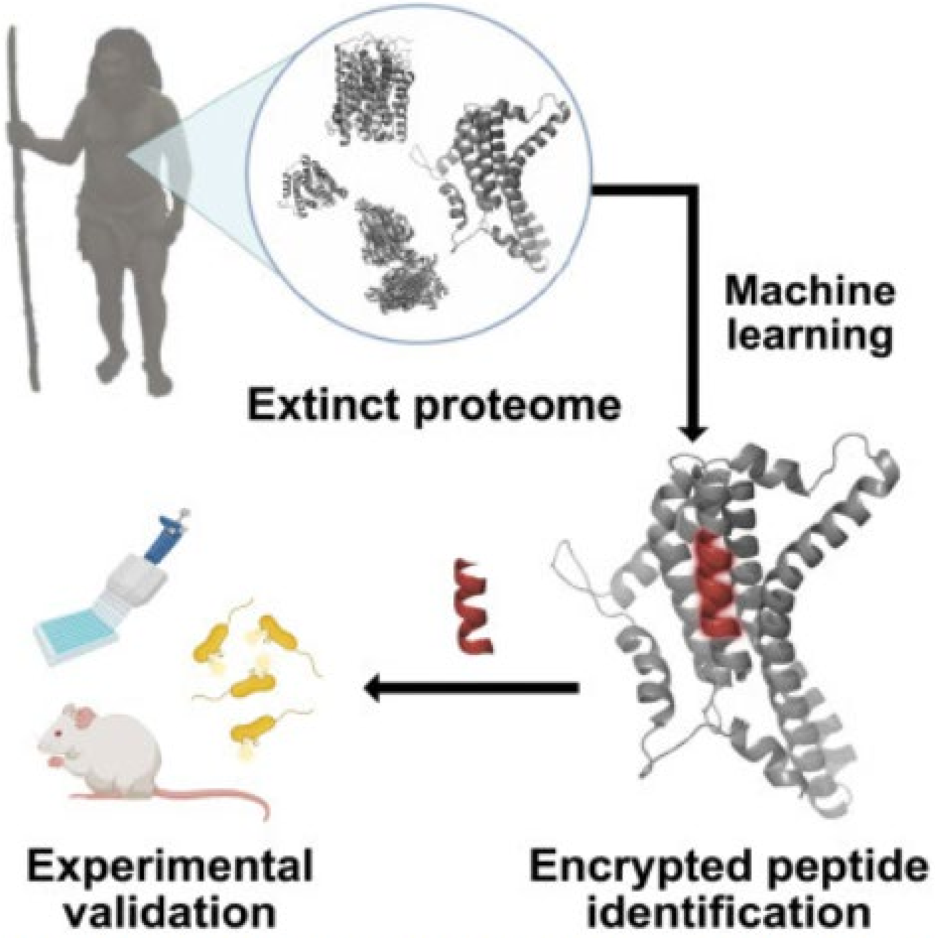
Giant handaxes in England in a rare Ice Age site

- The remarkable size of these handaxes were likely impractical in daily use, perhaps they served a purpose beyond mere practicality, possibly carrying a more symbolic or abstract significance

- What sets this discovery apart is not just its age, but its sheer size—a whopping 10 inches long and expertly crafted.

- Where there huge H. erecti/H. heidelbergensis? Where they symbolic. Currently unknown function.

Hunt for extinct proteins with potential antibiotic properties



Machine learning tools helped to identify archaic peptides that could have beneficial medicinal properties

Molecular De-Extinction of N peptides with antiobiotic effects

- Some resurrected peptides from Neanderthals and Denisovans exhibit antibiotic effects
- Researchers, driven by the concept of 'molecular de-extinction,' have explored these peptides in Neanderthal proteins, revealing a promising source of medicinal molecules, including peptides with antibiotic properties.
- The idea of resurrecting molecules from the past to address contemporary challenges has evoked comparisons to "Jurassic Park," albeit with a focus on small molecules. Unlike attempts to revive entire extinct organisms, this method carries fewer ethical concerns while offering significant technological potential.

N peptides

- In the face of the growing crisis of antibiotic resistance, the discovery of peptides with potential antibiotic properties from Neanderthal proteins offers a hopeful avenue for novel drug development.

- As de-extinct peptides present a compelling strategy for uncovering new antibiotics, this study marks a pivotal starting point for further exploration and innovation in the realm of ancient biomolecules and their contribution to modern medicine.

The Flowers of Shanidar, Iraq

Shanidar et ses fleurs (Shanidar and its flowers)? Reflections on the palynology of the Neanderthal ‘Flower Burial’ hypothesis

- The Shanidar Cave ‘Flower Burial’ hypothesis proposed by Arlette Leroi-Gourhan and developed by Ralph Solecki, along with other findings from his 1951–1960 excavations of Shanidar Cave, in Iraqi Kurdistan, had a transformative impact on ensuing debates about the abilities and humanness of Neanderthals

- The ‘Flower Burial’ hypothesis arose from palynological research. Six ‘soil’ samples were taken by Solecki in the sediment layers immediately below and adjacent to the Shanidar 4 Neanderthal and sent to Arlette Leroi-Gourhan, the leading cave palynologist of the day.

- Along with the clumps of pollen were fragments of woody tissue as Juniper pine

Reevaluating Neanderthal Flower Burial Theory: New Study Raises Questions

- The idea of Neanderthals practicing flower burials gained prominence with the discovery of Shanidar Cave in Iraq, where clusters of pollen were interpreted as evidence of intentional floral deposits. These findings sparked debates about whether Neanderthals engaged in ritualistic behaviors and had a level of symbolic understanding previously unattributed to them.
- Through his excavations in Shanidar Cave in the 1950s and 1960s, Ralph Solecki put forward the "Flower Burial" hypothesis. According to this hypothesis, the Neanderthal known as Shanidar 4 was placed on a bed of flowers, possibly for medical reasons, as a mark of affection, or as a sign of respect.

Debates

- Later study suggested emplacement of the pollen by jirds – small rodents known to bring flowers into their burrows – whose skeletal remains are known from the Shanidar Cave sediments in small numbers

- The new study discounts the possibility that Solecki and his colleagues introduced the pollen. Instead, they conclude that the pollen is likely to be approximately contemporary with the Neanderthal with which it is associated.

- However, the current study has cast doubt on the flower burial theory

Chris O. Hunt, et al., 2023

Ritual burials?

- The team questioned the assumption that the pollen clusters were purposefully placed and instead suggested alternative explanations.
-
- It seems likely that at least some of the pollen clumps were emplaced by nesting solitary bees, though other mechanisms may also have been involved.
- Team lays out the case for the pollen found in the grave sites being of non-human placement, likely by bees.

Pollen did not blossom at same time

- While Hunt and his team largely agree with the earlier identification of the plant species, they discovered that the plants actually grow at slightly different times of the year, calling into question the previous interpretation that Neanderthals gathered flowers to bestow on the dead.

- During excavations by Hunt and his team in 2016, they noticed a potential alternative explanation for the pollen: ancient mud-lined bee burrows close to Shanidar 4. These ground-nesting bees could have drilled into the dirt and deposited collected pollen as they moved through the burrows.

Bees

- Pollen was collected and deposited in clumps by bees.

- Hunt and his team think the pollen is likely ancient, perhaps even closely contemporaneous with the Neanderthal burial. But neither the pollen nor the bees can be directly dated.

- Presence of taxonomically mixed clumps is inconsistent with the clumps of pollen from the deposition of whole flowers. Instead, the researchers suggest it is far more likely that the taxonomically mixed pollen was collected and deposited by bees.

Bees

- Under modern conditions, the flowers represented in the Shanidar 4 pollen cannot all be collected simultaneously in any season, ruling out the excavation team and flowers being gathered immediately at the time of death.
- Bees could easily have deposited the pollen throughout a growing season.
- The possibility of other mechanisms, such as small mammals or Neanderthal activities, according to the researchers, cannot be completely ruled out.

Wood fragments

- Wood fragments and pollen were also found within the body cavity of the nearby Shanidar Z (latest N skeletal discovery). It seems likely that these had filtered into the rib-cage from above.
- While microscopic wood fragments can be fairly common in sediments of caves frequented by early people, the coincidence of wood fragments and pollen of immature plants might point to branches and other vegetation being placed over the bodies

Wood branches over the bodies?

- Unexplained wood fragments (juniper tree wood) found within the grave dirt of Shanidar Z, a more recently discovered Neanderthal skeleton that significantly overlaps with the Shanidar 4 site, suggests there is still more funerary mystery left in the cave.

- The tight cluster of burials at Shanidar remains incredibly significant to our understanding of Neanderthals and noted that "woody tissue" samples collected from the site may hold the key to learning more about their burial rituals.
- "I favor the idea that the Neanderthals put branches and other vegetation over the bodies," Hunt said

A Painful Legacy frin grandparents

- Mice hint at how people's emotional trauma may affect the biology of their children—and their children's children
- Emotional trauma of separation from their parents in children in orphanages also triggers subtle biological alterations
- That idea would have been laughed at 20 years ago.
- But today the hypothesis that an individual's experience might alter the cells and behavior of their children and grandchildren has become widely accepted.
- In animals, exposure to stress, cold, or high fat diets has been shown to trigger metabolic changes in later generations.

Andrew Curry, 2023

But what is the mechanism: Epigenetics?

- The implications are profound. If our experiences can have consequences that reverberate to our children or our children’s children, that’s a powerful argument against everything from smoking to immigration policies that split families.
- Current data indicates changes to the epigenome, a swirl of biological factors that affect how genes are expressed, can be passed down through multiple generations.

Epigenetics

- Tantalizing early results came from maize, in which plants with identical DNA had variations in traits such as kernel color that persisted for hundreds of generations.
- The work was initially controversial, as geneticists saw it as a revival of the non-Darwinian ideas of 19th century scientist Jean-Baptiste Lamarck. But experiments in many organisms suggested epigenetic inheritance was real.

Epigenetics

- In simple creatures like C. elegans worms, researchers found that genes turned off once by altering the RNA they produced remained silenced for 80 generations or more.

- Some examples were even more dramatic: Water fleas exposed to the scent of a predator have offspring with spiky, armored heads. And in mice, researchers found that parents exposed to altered diets, low temperatures, or toxins had descendants with behavioral changes and weight gain.

- Epidemiological studies of people have revealed similar patterns. One of the best known cases is the Dutch hunger winter, a famine that gripped the Netherlands in the closing months of World War II. The children of women pregnant during the food shortages died earlier than peers born just before, and had higher rates of obesity, diabetes, and schizophrenia. Studies of other groups suggested the children of parents who had starved early in life—even in the womb—had more heart disease.

Epigenetics vs parenting

- And a look last year at historical records showed the sons of Civil War soldiers who had spent time as prisoners of war (POWs) were more likely to die early than the sons of their fellow veterans.

- But the human studies faced an obvious objection: The trauma could have been transmitted through parenting rather than epigenetics. Something about the POW experience, for example, might have made those veterans poor fathers, to the detriment of their sons' lives.

- Answering that objection is where mouse models come in.

Mice studies of epigenetics

- Mansuy began in 2001 by designing a mouse intervention that re-creates some aspects of childhood trauma. She separates mouse mothers from their pups at unpredictable intervals and further disrupts parenting. When the mothers return to the cage and their pups, they're frantic and distracted.

- Unsurprisingly, the pups of stressed mothers displayed altered behavior as adults. The behavioral changes persisted in the offspring's offspring. Mice traumatized as pups could have been bad parents, replicating the neglect they experienced in childhood. Thus they might simply be passing on a behavioral legacy.

Mice studies

- To rule out the parenting possibility, Mansuy studied only the male line, breeding untraumatized, “naïve” female mice with traumatized males, and then removing males from the mother’s cage so that their behavior did not impact their offspring. After weaning, she raised the mice in mixed groups to prevent litter mates from reinforcing each other’s behaviors.
- Her lab repeated the procedure, sometimes going out six generations. Descendants of stressed fathers displayed more risk-taking behavior, and showed indicators of depressive like behavior in mice.

RNA as culprit?

- The experience of the parent can be passed on. The question is how.
- Three massive freezers - mouse blood, liver, milk, microbiome, and other tissues. These serve as a –80°C archive of more than 10 years of data.
- Many of the early mammalian epigenetics studies focused on DNA methylation, which “tags” DNA with methyl groups that switch genes off. But In mammals, methylation is mostly erased when egg and sperm come together to form an embryo.
- Newer research on tiny information-rich molecules called small noncoding RNAs (sncRNAs). Most RNA is copied from DNA, and and produce specific proteins.

Stressed sperm?

- But cells also contain short strands of RNA that don’t produce proteins. Instead, these noncoding RNAs piggyback on the messenger RNAs, interfering with or amplifying their function, thus causing more or less of certain proteins to be produced.
- Mansuy and others think stress may influence sncRNAs from higher levels of hormones like cortisol to inflammation.

Stressed sperm

- They have focused on the sncRNAs in sperm, which may be especially vulnerable to stress during the weeks that newly formed sperm spend maturing in a twisting tube on top of the testes.
- Later, when sperm and egg come together, altered sncRNAs could modify the production of proteins at the very beginning of development in a way that ripples through the millions and millions of cell divisions that follow.

sncRNAs

- Bale found evidence that trauma can affect sncRNAs in sperm—and that the effects might be transmitted to offspring. She stressed mice during adolescence
- Then, she examined the sncRNAs in their sperm and offspring. She found differences in nine types of sncRNAs, including one that regulates SIRT1, a gene that affects metabolism and cell growth.
- If you do the same RNA changes, you produce offspring with the same phenotype.
- Mansuy found similar RNA changes in her male mice traumatized as pups. Sheis convinced those molecular changes account for some of the inherited behavioral traits she documented.

Healing experience

- Another study of sperm donors: The higher the men’s ACE score, the more likely they were to have sperm sncRNA profiles matching what is seen in stressed mice.

- In 2016, Mansuy published evidence that traumatized mice raised in this enriched environment didn’t pass the symptoms of trauma to their offspring. Suggest life experience can be healing as well as hurtful at the molecular level.

- Environmental enrichment at the right time could eventually help correct some of the alterations which are induced by trauma. That means negative environmental effects are likely reversible.

Bottleneck at 900 Ka?

- Population size history is essential for studying human evolution.
- Developed a new computational model, fast infinitesimal time coalescent process (FitCoal) to circumvent this difficulty and calculated the composite likelihood for present day human genomic sequences of 3154 individuals.
- Results showed that human ancestors went through a severe population bottleneck with about 1280 breeding individuals between around 930,000 and 813,000 years ago.
- The bottleneck lasted for about 117,000 years and brought human ancestors close to extinction. This bottleneck is congruent with a substantial chronological gap in the available African and Eurasian fossil record. Suggests a coincident speciation event.

Wangjie Hu, et al., 2023

Bottleneck at 900 Ka

- Reveals a significant reduction in the population of our ancestors long before the emergence of our species, Homo sapiens.
- This technique spotlighted the period between 800,000 and one million years ago, a time of climatic turmoil and significant environmental change.
- During the Early-Middle Pleistocene transition, characterized by dramatic shifts in climate and lengthening glacial cycles, Africa faced prolonged periods of drought. These harsh conditions likely played a pivotal role in the near-extinction of our early human ancestors, driving new human species to emerge, adapting to these new challenges.

Bottleneck only in African groups?

- The severe bottleneck was not directly detected in all 19 non-African populations, but was directly detected in each of the 10 African populations

- This ancient severe bottleneck was directly found in all 10 African populations, but only a weak signal of the existence of such was detected in all 40 non-African populations.

- The bottleneck could also have increased the inbreeding level of our ancestors, thus contributing to the 65.85% loss in present-day human genetic diversity.

Consequence of climactic effects

- During this transition period known as the “0.9Ma event”, glaciations were changed from predominantly short-term to long-term events with more extreme thermic intensity, especially at the peak of glaciation.
- This event resulted in a decrease in marine surface temperature to the lowest that occurred during the entire transition period, with an inferred long period of drought and extensive wildlife turnover in Africa and Eurasia.
- The existence of the ancient severe bottleneck could explain the extreme scarcity of the available hominin fossil record in Africa and Eurasia between 950 and 650 kyr BP

Few fossils for this period

- In Africa, only a few fossil specimens dated in this time period have been found, including the cranial fragments from Gombore in Ethiopia and the fossil samples from Tighenif in Algeria. They have features resembling those of later fossils attributed to *Homo heidelbergensis*.
- In addition, coincident with this bottleneck, two ancestral chromosomes are believed to have fused to form chromosome 2 in humans around 900 to 740 kyr BP. Therefore, the ancient severe bottleneck possibly marks a speciation event leading to the emergence of the LCA shared by Denisovans, Neanderthals, and modern humans, whose divergence has been dated to about 765 to 550 kyr BP.
- A rapid population recovery was detected in all 10 African populations with a 20-fold increase in size around 813 kyr BP.

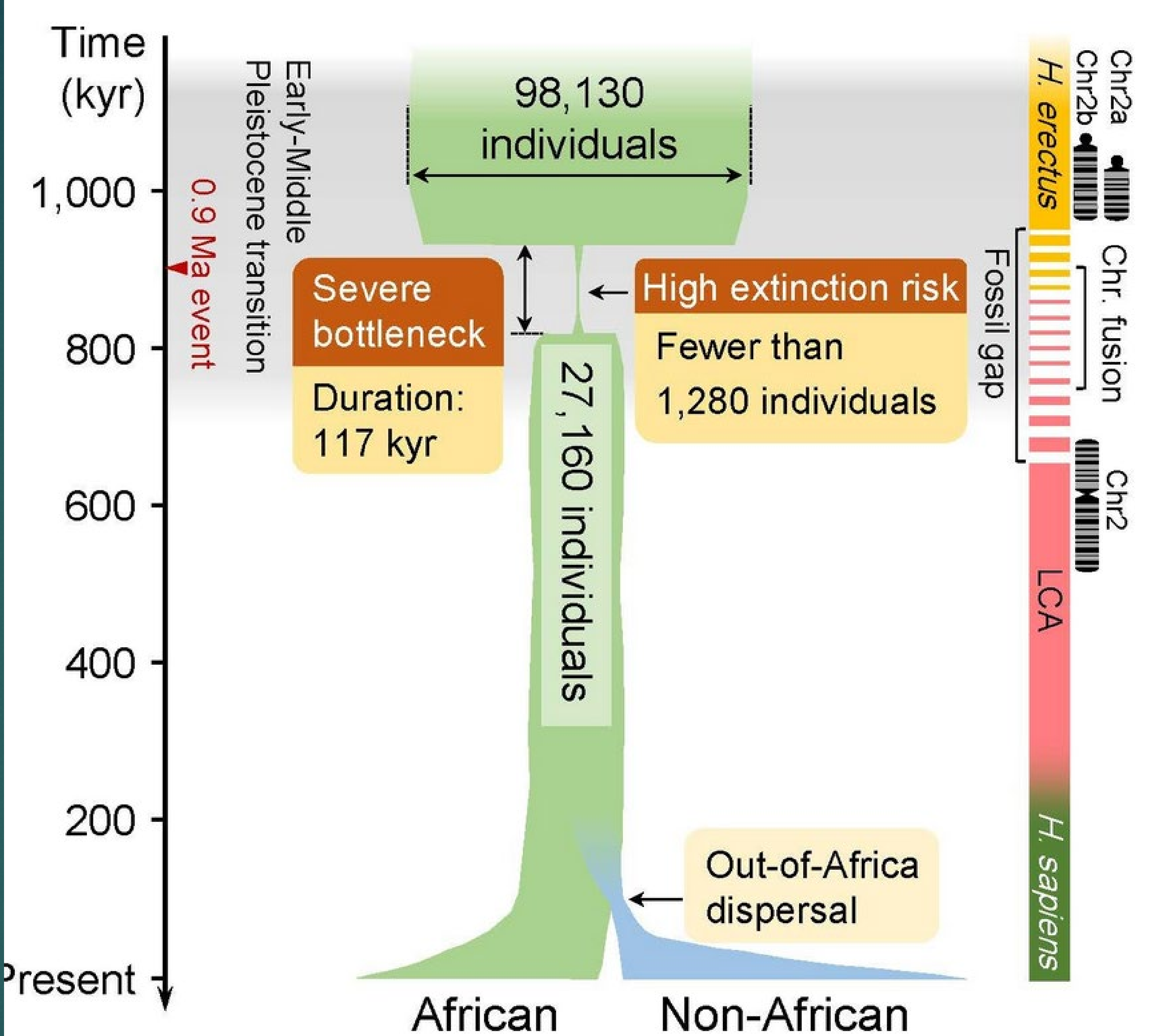
Reexpansion

- Control of fire could be part of the explanation for this population expansion, which is shown by the early archaeological evidence found in Israel dated about 790 kyr BP.
- Other factors, such as climatic changes, might also be a driving force for this rapid population recovery.
- Study revealed that an extremely small human population lasted for about 117 kyr around 930 to 813 kyr BP.
- Many questions remain unanswered, such as where these individuals lived, how they overcame the catastrophic climate changes, and how the ancient population remained so small for so long.

Bottleneck at 900 Ka: *H. heidelbergensis?*

- Hu *et al.* argue that the proposed bottleneck correlates with a chronological gap in the African and Eurasian fossil records and may have led to the evolution of a new human species, ancestral to *Homo sapiens*. They favor a widely defined *H. heidelbergensis* as this ancestral species, probably emerging in Africa by 800,000 years ago.

- However, this bottleneck also may have contributed to a speciation event, which happens when two or more species are created from a single lineage. During this speciation event, two ancestral chromosomes may have converged to form what is now chromosome 2 in modern humans.



The African hominin fossil gap and the estimated time period of chromosome fusion is shown on the right. The gap in the African and Eurasian fossil records can be explained by this bottleneck in the Early Stone Age chronologically, It coincides with this proposed time period of significant loss of fossil evidence.

John Hawks comment

- The authors, Wangjie Hu and coworkers, developed a new statistical approach to look for changes of population size in deeper time than previous methods. The approach relies on the site frequency spectrum of genetic variants across the genome, which is broadly similar to the method developed by Aaron Ragsdale and coworkers to examine ancient population structure (the 2 stem model).
- Where the new approach is different is that Hu and coworkers have not focused on structure or partial isolation among ancient groups; they have instead narrowed their approach to consider only ancient changes in population size.
- Does this hypothesis hold water?

Recent studies of demography of ancestral humans.

- Some recent demographic studies have concluded that ghost populations existed for hundreds of thousands of years, later merging with recent populations.
- Ragsdale and coworkers earlier this year found the ghost population idea didn't work as well as a structured ancestral population, in which groups were intermittently connected by gene flow. In their analysis, this ancestral structure was established around a million years ago.

Hawks

- That raises a problem with the new results from Hu and collaborators. Clearly if ancestral humans had divided into two or more ancestral stem populations by a million years ago, the present-day variation shouldn't look like it came from a bottlenecked population of 1280 individuals for a hundred thousand years of that time.

- Something doesn't add up. Population size is not the only factor that can restrict genetic variation; population structure matters also. The two are not independent of each other.

Both theories are right

- Since Hu and coworkers used some of the same genetic data as Ragsdale and coworkers, they ought to at least arrive at a similar timeline. A close look at the methods of both papers shows that they actually do.
- What seems like a discrepancy between the million years for population structure and the 800,000 years for the end of a species-wide bottleneck comes down to different assumptions about generation time: Ragsdale and coworkers assumed 29 years; Hu and coworkers 24 years. Their datasets actually show the same pattern, at roughly the same time. This may be 800,000 years ago, or it may be a million.
- The important question is whether the pattern of genetic variation reflects diversification from a single ancestral group, or instead an increase of population size from a bottleneck. I imagine that the real story is some of both. Finding the proportion of each is likely to take better genetic data from much earlier in time.

H. floresiensis: a revised history by Paige Madison

- Homo floresiensis was first uncovered by an Indonesian, Benyamin Tarus
- After *H. floresiensis* was announced to the world, a leading Indonesian archaeologist condemned the international reporting of the discovery as “unethical”. A few days later, he surprised his colleagues by helping another Indonesian researcher take possession of the bones. When they were returned several months later, some were damaged beyond repair.
- Obtaining an Indonesian perspective on *H. floresiensis* is challenging: in a country made up of over 17,000 islands, diversity rules. The islands are populated by people of distinct ethnicities, religions and languages. This variation is a source of pride, reflected in the national motto, *bhinneka tunggal ika* (“unity in diversity”).

Paige Madison, 2023

▲ **Benyamin Tarus, seen in Liang Bua cave**

Liang Bua Team

Indonesia

- Archaeological excavations have been a part of Indonesian life for more than 130 years. For instance, the first known fossils of Homo erectus were discovered on the Indonesian island of Java in the 1890s.
- For decades, Indonesians received little credit for such finds, being viewed as mere laborers. In a country that had been largely under Dutch control since the 17th century, it was the European colonialists who directed excavations and became famous for the discoveries made there.
- Understandably, many Indonesians resented this. After the country gained independence in a revolution during the 1940s, some Indonesian researchers were determined to free the country's archaeological heritage from foreign control. They included Raden Pandji Soejono, who worked at an institute in Jakarta that is now part of Indonesia's Organization for Archaeology, Language, and Letters, and Teuku Jacob, who worked at Gadjah Mada University in Yogyakarta.

Indonesian researchers

- For many years, they were successful. Their excavation teams began digging at Liang Bua in the 1970s and discovered a rich collection of artefacts for archaeologist Soejono to analyze. They unearthed several ancient H. sapiens skeletons in the cave. These were sent to the lab of Jacob, who was one of Indonesia’s leading paleoanthropologists.
- Few people are aware of this early research at Liang Bua, much of which was never published.
- Within those unpublished reports are important details, including Jacob’s thoughts on an idea he became increasingly convinced was true: that the ancient *H. sapiens* who lived on Flores were unusually short in height. Such conclusions never made major headlines. But that was hardly the point. More important to Soejono and Jacob was that the excavations were finally under Indonesian control.

Indonesian research

- That changed around 2000. Funding for excavations at Liang Bua had dried up and Soejono reluctantly admitted he would have to seek foreign help. He worried about the consequences. I found an account from the time in a local Indonesian publication in which Soejono expressed concern that scientists from abroad "will try to dominate the situation"
- By 2001, excavations were under way again. Soejono was now working with Michael Morwood, an archaeologist at the University of New England in Australia. Just a couple of years later, the team made the discovery that would shake up paleoanthropology – and apparently convince Soejono and Jacob that they had been right to worry about working with international researchers.
- It was an all-Indonesian team on site that day 20 years ago when Benyamin struck bone. The excavators soon realized they had discovered more than a skull: it was an almost complete skeleton. Indonesian Archaeologist Wahyu Saptomo was the supervisor of that excavation pit

H. floresiensis

- To learn more, the team needed to consult a paleoanthropologist. Soejono was keen to recruit Jacob, his long-time colleague and partner on research at Liang Bua, but Morwood insisted that was impossible. A contract he and Soejono had signed years earlier required any new finds from the cave to be analyzed by scientists from either Soejono's institution in Indonesia or Morwood's institution in Australia – not the university where Jacob worked. Tense discussions resulted in the arrival of Peter Brown, a paleoanthropologist from the University of New England.
- Brown spent 10 days examining the skeleton and eventually concluded that it belonged to a very unusual human with a small body and – more significantly – a small brain. It was inconceivable, he argued, that the skeleton belonged to our species. He suggested placing it in a new species: *H. floresiensis* was born.

H. floresiensis

- Originally dated to 18 Ka. That wasn't all. Stone tools and blackened bones at the cave indicated that *H. floresiensis* had a sophisticated set of behaviors and controlled fire to cook its food. Perhaps most surprising of all was that *H. floresiensis* had existed in south-east Asia rather than somewhere in Africa,
- In other words, *H. floresiensis* suggested that Indonesia had international significance for understanding human evolution. The discovery should have been a moment of triumph for Indonesian researchers like Soejono. But he didn't see things that way.
- In October 2004, the Liang Bua team published its findings in two research papers. Neither had an Indonesian researcher as the lead author – rather, Morwood had this role for one and Brown for the other. The papers were unveiled in two press conferences, in London and Sydney. There was no press conference in Indonesia.

Theft?

- Soejono was incensed. P. Madison came across an article published in an Indonesian newspaper after news of the discovery broke – overlooked by many interested in the *H. floresiensis* story because it was written in Indonesian. It quoted Soejono blaming the Indonesian government for failing to provide “sufficient funds”. Morwood later said there had been a plan to hold a press conference in Indonesia, but it fell through.

- Jacob was no less annoyed. In particular, suggest news reports from the time, he was unimpressed that Brown had studied the *H. floresiensis* bones without examining the other ancient human remains unearthed in Liang Bua and elsewhere on Flores during the 20th century. As researchers around the world began excitedly debating the significance of *H. floresiensis*, Soejono and Jacob reverted to their decades-old practice of working together. They packed the *H. floresiensis* bones into a suitcase, which Jacob then carried 425 kilometers east across Java to his own laboratory in Yogyakarta – without Morwood and much of the *H. floresiensis* team’s knowledge. When news of this act broke, the international media accused Jacob of theft.

Jacob concludes small H. sapiens

- A few months later, Jacob announced he had finished analyzing the bones and was ready to return them to Jakarta. Holding his own press conference – in Indonesia – he declared that the remains belonged to an unusually small member of our species, albeit one with some unusual bone pathologies that gave it the deceptive appearance of otherness.

- “This is not a *new species,” said Jacob. His viewpoint seemed bizarre to many researchers – but Jacob presumably saw the logic, given that he was merely continuing his* earlier work that claimed Flores had once been home to a population of unusually small *H. sapiens*.

Wreckage

- An intellectual disagreement was one thing. But when the bones arrived back in Jakarta, some of the fragile remains were now broken. The hip bone had been shattered “into a thousand crumbs”, said Brown, and others were damaged. Jacob denied direct responsibility, saying the damage must have occurred while the remains were being transported from his lab in Yogyakarta back to Jakarta.
- But the conservator who came from the UK to work on the bones the following year, Lorraine Cornish at London’s Natural History Museum, later told me there was evidence that Jacob’s team had caused some of the damage by trying to mold and cast the delicate specimen.
- Left with the wreckage, the Liang Bua team tried to put the bones back together and mend relationships. Morwood regretted the lack of an Indonesian press conference and I was told by members of the research team that he privately vowed to do better. Excavations were paused in an attempt to ease tensions, only resuming in 2007.

New discoveries

- Twenty years on from the moment *H. floresiensis* emerged from Liang Bua, it is possible to view the discovery with more clarity.

- It remains a startlingly unexpected find, but curiously enough, the species no longer stands alone as a bizarre outlier in the human family tree. In the years since *H. floresiensis* came to light, we have learned of two more species of small-brained human that were present on our planet at the same time as our species. *Homo naledi*, discovered in South Africa, was revealed to the public in 2015, while *Homo luzonensis*, unearthed in the Philippines, made headlines in 2019.

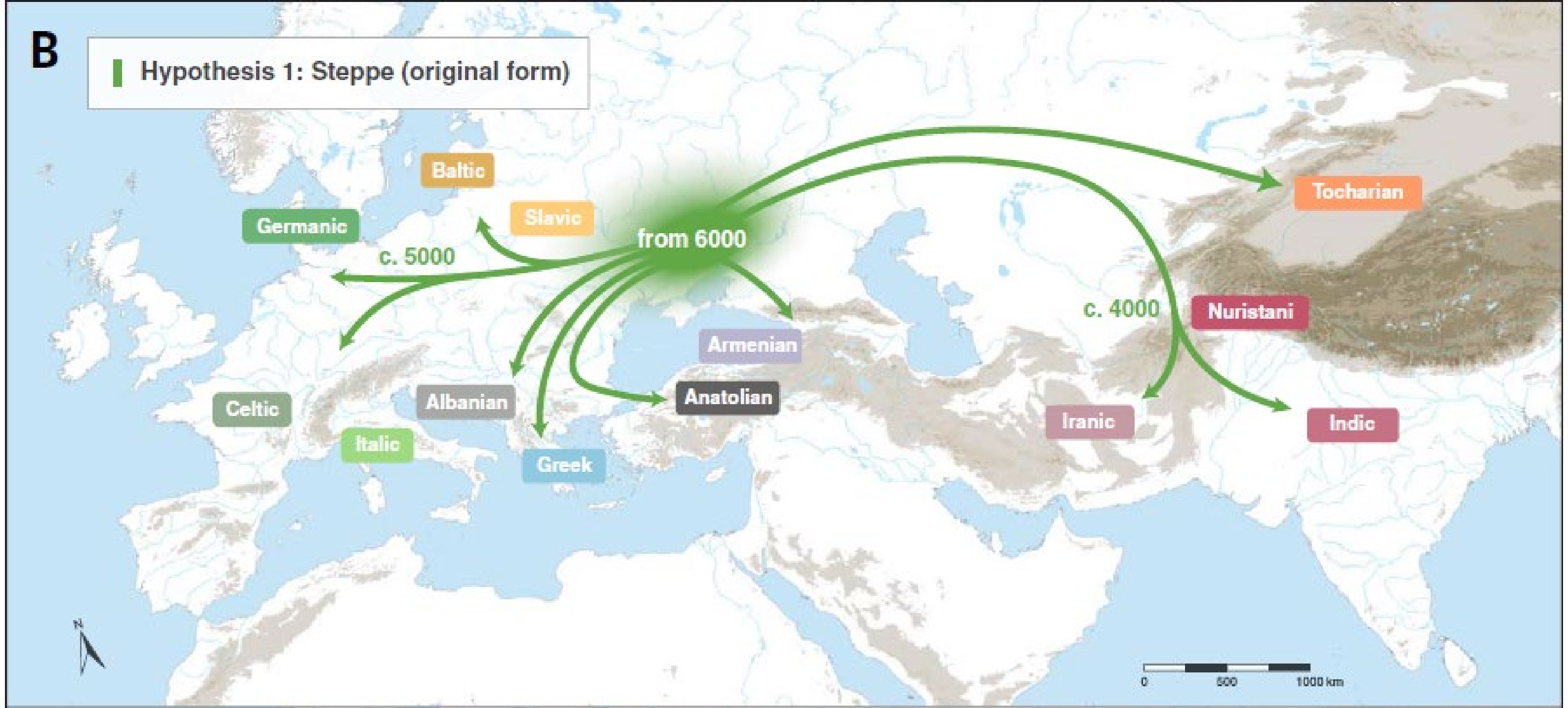
Revisions of data

- Researchers working at Liang Bua have walked back some of the claims made about the species at the time of its discovery.
- In 2016, they pushed *H. floresiensis*'s extinction back to around 50,000 years ago, which is more in line with the accepted date for the disappearance of other ancient human species, as well as the arrival of modern humans in what is now Indonesia. The researchers also abandoned the idea that *H. floresiensis* controlled fire: "charred" bones that Morwood had identified were blackened naturally by soil minerals.
- The group now is focused on exploring Liang Bua's past in all its complexity. The cave sediments preserve a near-continuous record spanning 200,000 years, offering a rare opportunity to understand how *H. floresiensis* differed from *H. sapiens* in its interactions with the environment. In other words, the Liang Bua researchers today are less interested in rewriting the global story of human evolution. Rather, they are motivated by a desire to understand the nuances of Indonesia's ancient prehistory. In a sense, their work is now more aligned with the research conducted at Liang Bua shortly after Indonesia gained its independence almost 80 years ago. Jacob and Soejono would perhaps have approved.

Language trees with sampled ancestors support a hybrid model for the origin of Indo-European languages

- The Indo-European language family encompasses more than 400 languages. These languages are spoken by almost half of the world’s population, and all derive from the same source language: Proto-Indo-European (PIE). For more than 200 years, the origins of Indo- European have been disputed
- It remains unclear where this family’s common ancestral language (Proto-Indo-European) was initially spoken and when and why it spread through Eurasia. The “Steppe” hypothesis posits an expansion out of the Pontic-Caspian Steppe, no earlier than 6500 years before present (yr B.P.), and mostly with horse-based pastoralism from ~5000 yr B.P. An alternative “Anatolian” or “farming” hypothesis posits that Indo-European dispersed with agriculture out of parts of the Fertile Crescent, beginning as early as ~9500 to 8500 yr B.P.
- In this study, we tested between the time-depth predictions of the Anatolian and Steppe hypotheses, directly from language data. Present a new dataset of cognacy (shared word origins) across Indo-European.

Paul Heggarty, et al., 2023



B Hypothesis 1: Steppe (original form)

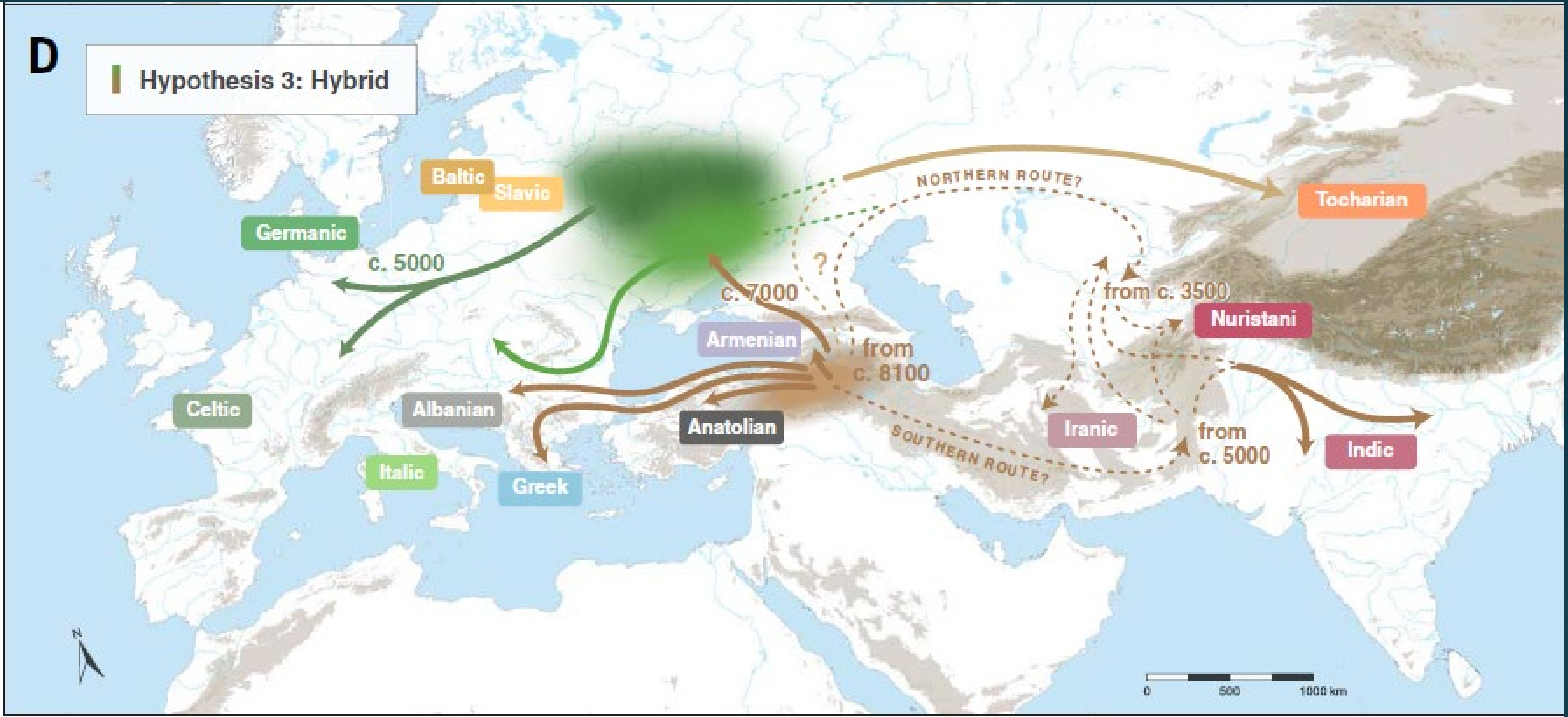
C Hypothesis 2: Farming

Not spread via the steppe

- Study: a median root age for Indo-European of ~8120 yr B.P. (6740 to 9610 yr B.P.). Ancestry-enabled phylogenetic analysis of this dataset indicates that few ancient languages are direct ancestors of modern clades and produces a root age of ~8120 yr B.P. for the family.
- Although this date is not consistent with the Steppe hypothesis, it does not rule out an initial homeland south of the Caucasus, with a subsequent branch northward onto the steppe and then across Europe.
- We reconcile this hybrid hypothesis with recently published ancient DNA evidence from the steppe and the northern Fertile Crescent.
- Indo-European had already diverged rapidly into multiple major branches by ~7000 yr B.P., without a coherent non-Anatolian core. Indo-Iranic has no close relationship with Balto-Slavic, weakening the case for it having spread via the steppe.

PIE origins: hybrid model

- Results are not entirely consistent with either the Steppe hypothesis or the farming hypothesis.
- Recent aDNA evidence suggests that the Anatolian branch cannot be sourced to the steppe but rather to south of the Caucasus. For other branches, potential candidate expansion(s) out of the Yamnaya culture are detectable in aDNA, but some had only limited genetic impact.
- Our results reveal that these expansions from ~5000 yr B.P. onward also came too late for the language chronology of Indo-European divergence. They are consistent, however, with an ultimate homeland south of the Caucasus and a subsequent branch northward onto the steppe, as a secondary homeland for some branches of Indo-European entering Europe with the later Corded Ware–associated expansions.
- Language phylogenetics and aDNA thus combine to suggest that the resolution to the 200-yearold Indo-European enigma lies in a hybrid of the farming and Steppe hypotheses.


D
Hypothesis 3: Hybrid
Baltic
Slavic
Germanic
c. 5000
c. 7000
?
NORTHERN ROUTE?
Tocharian
from c. 3500
Nuristani
Armenian
from
c. 8100
Celtic
Albanian
Anatolian
Iranic
from
c. 5000
Indic
SOUTHERN ROUTE?
Italic
Greek
N
0
500
1000 km

2012: Graecopithecus

- Graecopithecus is an extinct genus of hominid that lived in southeast Europe during the late Miocene around 7.2 million years ago. Originally identified by a single lower jawbone bearing a molar tooth found in Pyrgos Vasilissis, Athens, Greece, in 1944, other tooth specimens were discovered from Azmaka quarry in Bulgaria in 2012.
- In 2017, an international team of paleontologists led by Madelaine Böhme of the Eberhard-Karls-University Tübingen, Germany, published a detailed analysis of the teeth and age of the specimens, and came to the conclusion that it could be the oldest hominin, meaning that it could be the oldest direct ancestors of humans after splitting from that of the chimpanzees.

Graecopithecus, 2012: "North Side Story"

- Claimed that contrary to the generally accepted evidence of the African origin of the hominin lineage, the ancestors of humans originated from the main ape ancestry in the Mediterranean region (before migrating into Africa where they evolved into the ancestors of *Homo* species).
- They named the origin of human theory as the "North Side Story."
- Since 1994, Begun had adhered to a hypothesis that African hominids (including living apes) descended from Eurasian apes since the older ape fossils are found in Europa and Asia. This is a feasible explanation as it is possible that the African ape ancestors could move to Africa around 9 million years ago from Europe.

2017: Hominid Findings and Controversies

- A single *Graecopithecus* tooth from Bulgaria dating to around 7 Ma might be from the earliest known hominid, and if so, it could suggest that hominids originated in Europe, not Africa.

- 5.7 Ma footprints on Crete: Gierliński et al. (2017) describes fossil footprints from Trachilos in western Crete that are reliably dated to a Late Miocene age of about 5.7 million years. These footprints are from a large bipedal primate with human-like feet.

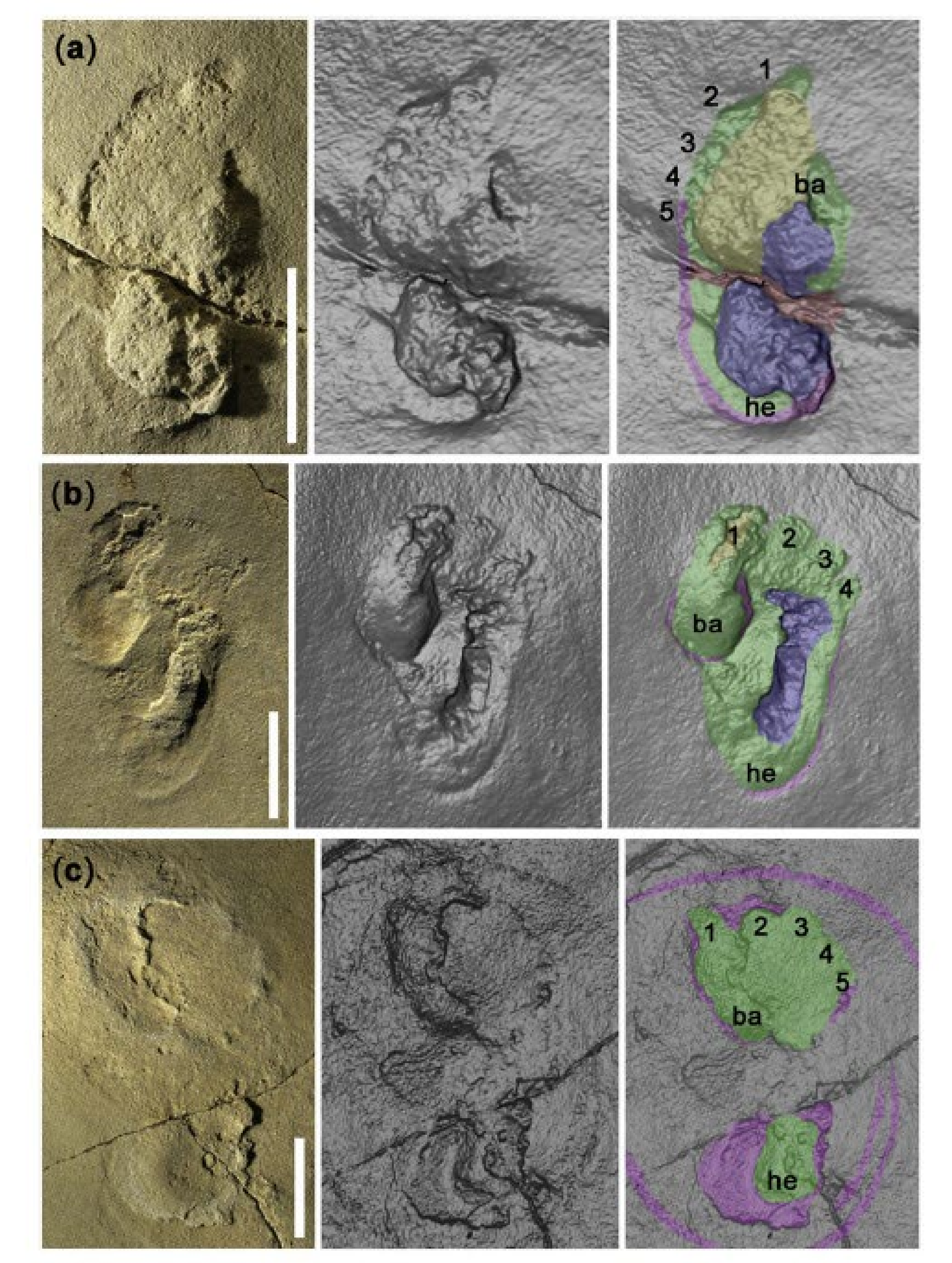
- The oldest hominin fossils, *Sahelanthropus, Orrorin, & Ar. Kadabba,* do not have fossil feet. All of the early hominins that are older than 1.8 million years have only been found in Africa

2017: 5.7 Mya footprints on Crete

5.7 Mya footprints

Similar to Ardi:
But may indicate how apelike Ardi's feet were.

Bernard Wood:
Miocene ape



2017: Findings and Controversies

- Does this refute the "Out of Africa" story? These footprints differ from those of all other land animals, including the more ape-like feet (without ball and with the big toe sticking out sideways) of the much younger *Ardipithecus ramidus* (prior earliest known feet).

- Or are they made by an European Miocene ape, which convergently evolved a bipedal locomotion. Remember similar claims had been made about two other fossil apes: *Ramapithecus* (14 Mya, member of *Sivapithecus,* an orangutan fossil) and *Oreopithecus* (9 Mya, parallel evolution of bipedalism).

- Tim White: "study tries to resurrect Begun's tired argument with a long-known crappy fossil, newly scanned".

Critique: Apes not hominins

- These claims have been disputed by other scientists. Rick Potts and Bernard Wood argued that the evidence is too flimsy to even say it is a hominin.
- Tim D. White commented that the claim was only to support a biased argument that Africa is not the birthplace of humans; while Sergio Almécija stated that single characters such as teeth cannot tell the claimed evolutionary details.
- Systematic re-analysis by paleontologists from the University of the Witwatersrand in 2017 did not find enough evidence to support the species as hominin or as the oldest ancestor of human lineage separating from the apes.

A new face and partial brain case of Anadoluvius turkae, a fossil hominine—the group that includes African apes and humans—from the Çorakyerler fossil site located in Central Anatolia, Türkiye

A new ape from Türkiye and the radiation of late Miocene hominines

- Abstract: Fossil apes from the eastern Mediterranean are central to the debate on African ape and human (hominine) origins. Current research places them either as hominines, as hominins (humans and our fossil relatives) or as stem hominids, no more closely related to hominines than to pongines (orangutans and their fossil relatives).

- Study: based on our analysis of a newly identified genus, Anadoluvius, from the 8.7 Ma site of Çorakyerler in central Anatolia, that Mediterranean fossil apes are diverse, and are part of the first known radiation of early members of the hominines.

- The members of this radiation are currently only identified in Europe and Anatolia; generally accepted hominins are only found in Africa from the late Miocene until the Pleistocene.

•Ayla Sevim-Erol, D. R. Begun, et al., 2023

Alternate theory

- Hominines may have originated in Eurasia during the late Miocene, or they may have dispersed into Eurasia from an unknown African ancestor. The diversity of hominines in Eurasia suggests an in situ origin but does not exclude a dispersal hypothesis.
- Hominines includes African apes (chimpanzees, bonobos and gorillas), humans and their fossil ancestors (including Homo neanderthalensis and Homo erectus).
- The origin of the hominines is among the most hotly debated topics in paleoanthropology. The traditional view, ever since Darwin, holds that hominines and hominins originate in Africa, where the earliest hominins are found and where all extant non-human hominines live.
- More recently a European origin has been proposed, based on the phylogenetic analysis of late Miocene apes from Europe and Central Anatolia.

Alternate theory

- The fossils described here attest to a lengthy history of hominines in Europe, with multiple taxa in the eastern Mediterranean known for at least 2.3 Ma. Our phylogenetic analysis, based on the new specimens described here and a large sample of other fossil and extant hominoids supports previous research confirming the hominine status of the eastern Mediterranean apes.
- Our most parsimonious phylogenetic results suggest that hominines in the eastern Mediterranean evolved from dryopithecins in central and western Europe, though there are alternative interpretations. Either way, the oldest known hominines are European. They may have dispersed into Europe from ancestors in Africa, only to become extinct.
- However, the more likely and more parsimonious interpretation is that hominines evolved over a lengthy period in Europe and dispersed into Africa before 7Ma.

David Begun again

- A new fossil ape from an 8.7-million-year-old site in Türkiye is challenging long-accepted ideas of human origins and adding weight to the theory that the ancestors of African apes and humans evolved in Europe before migrating to Africa between nine and seven million years ago.
- Analysis of a newly identified ape named Anadoluvius turkae recovered from the Çorakyerler fossil locality near Çankırı in Türkiye, shows Mediterranean fossil apes are diverse and are part of the first known radiation of early hominines—the group that includes African apes (chimpanzees, bonobos and gorillas), humans and their fossil ancestors.

Sevim-Erol, A., Begun, D.R., et al., 2023

Anadoluvius

- Anadoluvius is distinguished from other eastern Mediterranean apes in the palate, face, neurocranium, mandible, dental root and root canal configuration, and in dental crown proportions and morphology. Ouranopithecus, Anadoluvius and Graecopithecus may be members of an evolving lineage, with the new data from Çorakyerler further supporting the hominine affinities of these taxa.

- Hominines were more diverse in the late Miocene of the eastern Mediterranean than previously understood, with a known range from at least 9.6–7.2 million years ago

Late Miocene apes

- Ouranopithecus, Graecopithecus and Anadoluvius share a suite of derived characters of the jaws and dentition that support their status as a distinct clade.

- The core attributes of the Balkan/Anatolian late Miocene apes are large, thickly enameled transversely robust mandibles, small canines, and large size.

- The animals that lived alongside *Anadoluvius turkae* are those commonly associated with African grasslands and dry forests today, such as giraffes, wart hogs, rhinos, diverse antelopes, zebras, elephants, porcupines, hyenas and lion-like carnivores.

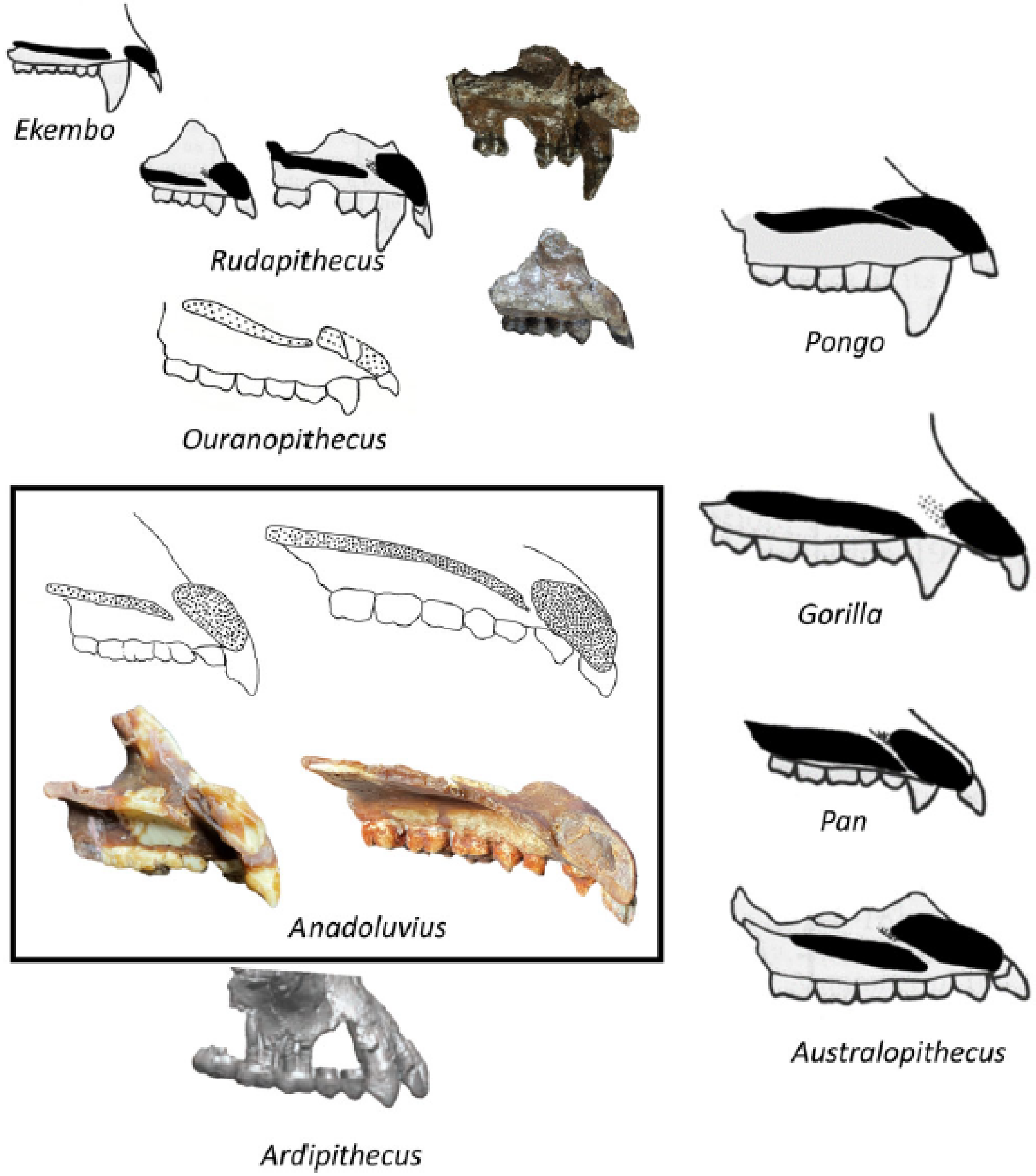
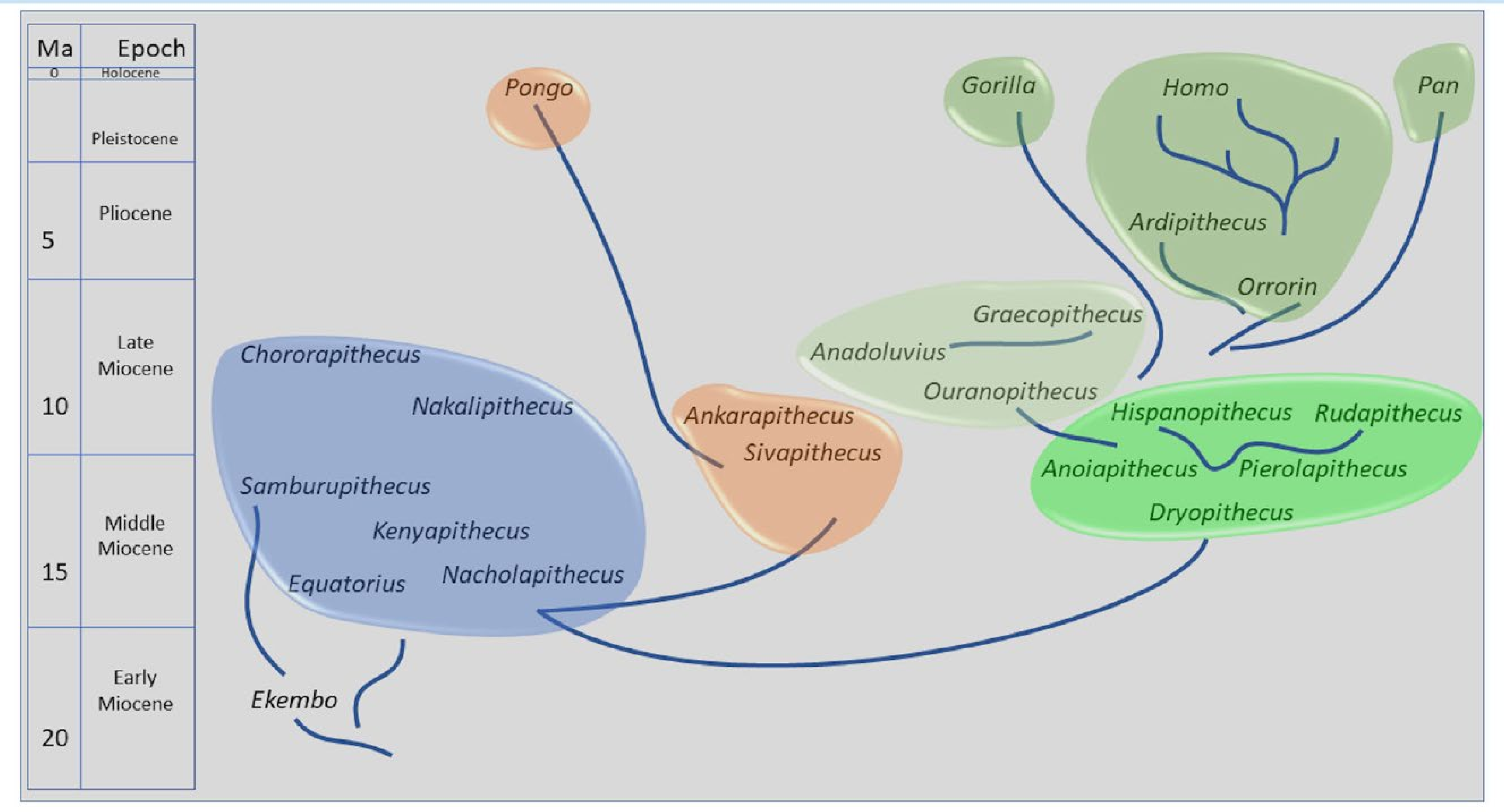


Fig. 2 Cross sectional anatomy of the palate in *Anadoluvius* and other hominids (not to scale). *Ekembo* and extant hominids redrawn from[31]

A new ape from Türkiye and the radiation of late Miocene hominines

- "Our findings further suggest that hominines not only evolved in western and central Europe but spent over five million years evolving there and spreading to the eastern Mediterranean before eventually dispersing into Africa, probably as a consequence of changing environments and diminishing forests," said David Begun, professor in the Department of Anthropology in the Faculty of Arts & Science at U of T. "The members of this radiation to which Anadoluvius belongs are currently only identified in Europe and Anatolia."
- The conclusion is based on analysis of a significantly well-preserved partial cranium uncovered at the site in 2015, which includes most of the facial structure and the front part of the brain case.



Blue puddle taxa are stem hominids and are all confined to Africa. The three green-shade puddles represent the hominine clades. The light green puddle includes the Balkan and Anatolian taxa. The darker green puddle represents the crown hominines. The various lineages diverge from unknown ancestors, but probably a member of either of the older green shade puddles. Gorillas diverge first, followed by chimpanzees and humans. Orrorin and Ardipithecus are depicted in a manner consistent with their sister clade status, without implying a direct ancestor-descendant relationship.

Anadoluvius

- The researchers say Anadoluvius was about the size of a large male chimpanzee (50-60 kg)—very large for a chimp and close to the average size of a female gorilla (75-80 kg)—lived in a dry forest setting, and probably spent a great deal of time on the ground.
- We have no limb bones but judging from its jaws and teeth, the animals found alongside it, and the geological indicators of the environment, Anadoluvius probably lived in relatively open conditions, unlike the forest settings of living great apes. More like what we think the environments of early humans in Africa were like. The powerful jaws and large, thickly enameled teeth suggest a diet including hard or tough food items from terrestrial sources such as roots and rhizomes.
- Research shows that the ecological community appears to have dispersed into Africa from the eastern Mediterranean sometime after about eight million years ago.

African Apes Originate from Europe theory

- Although African apes today are only known from Africa, as are the earliest known humans, the study's authors conclude that the ancestors of both came from Europe and the eastern Mediterranean.

- Anadoluvius and other fossil apes from nearby Greece (Ouranopithecus) and Bulgaria (Graecopithecus) form a group that come closest in many details of anatomy and ecology to the earliest known hominins, or humans. The new fossils are the best-preserved specimens of this group of early hominines and provide the strongest evidence to date that the group originated in Europe and later dispersed into Africa.

Begun theory

- The study's detailed analysis also reveals that the Balkan and Anatolian apes evolved from ancestors in western and central Europe. With its more comprehensive data, the research provides evidence that these other apes were also hominines and means that it is more likely that the whole group evolved and diversified in Europe, rather than the alternative scenario in which separate branches of apes earlier moved independently into Europe from Africa over the course of several million years, and then went extinct without issue.
- “There is no evidence of the latter, though it remains a favorite proposal among those who do not accept a European origin hypothesis," said Begun. "These findings contrast with the long-held view that African apes and humans evolved exclusively in Africa. While the remains of early hominines are abundant in Europe and Anatolia, they are completely absent from Africa until the first hominin appeared there about seven million years ago.

Need more fossils

- "This new evidence supports the hypothesis that hominines originated in Europe and dispersed into Africa along with many other mammals between nine and seven million years ago, though it does not definitively prove it. For that, we need to find more fossils from Europe and Africa between eight and seven million years old to establish a definitive connection between the two groups."
- Critique:
- The theory that humankind originated in Europe is an old one. It was abandoned after 1924 when the first *Australopithecus* was discovered in South Africa.

***African vs European origins of Hominins

- Extraordinary claims need extraordinary evidence to support them.
- The African origin of humankind (Hominini) is currently supported by two really important elements.
- Firstly, thousands of hominin fossils have been found on African soil since the first fossil African hominin, *Australopithecus africanus*, was discovered in South Africa in 1924. Nearly a century of fossil findings has followed, chronicling the complete evolution of hominin on African soil.
- Secondly, our closest ape relatives, the Chimpanzees and the Gorilla are also from Africa. Our last common ancestors lived somewhere between eight and 12 million years ago, which strongly suggests that the origin of humankind is deeply rooted in Africa. This leave little room for a putative European origin.
- Much more and far better preserved material would be necessary to totally disprove the African origin of humankind.

Who were the first American Cowboys? Black slaves in Hispaniola and Mexico!

Americas’ first cowboys were enslaved Africans, ancient cow DNA suggests

- Cattle may have been imported from Africa centuries earlier than historians thought
- Think “cowboy,” and you might picture John Wayne riding herd across the U.S. West. But the first cowboys lived in Mexico and the Caribbean, and most of them were Black.
- That’s the conclusion of a recent analysis of DNA from 400-year-old cow bones excavated on the island of Hispaniola and at sites in Mexico. The work, published in *Scientific Reports*, also provides evidence that African cattle made it to the Americas at least a century earlier than historians realized.
- The timing of these African imports—to the early 1600s—suggests the growth of cattle herds may have been connected to the slave trade,

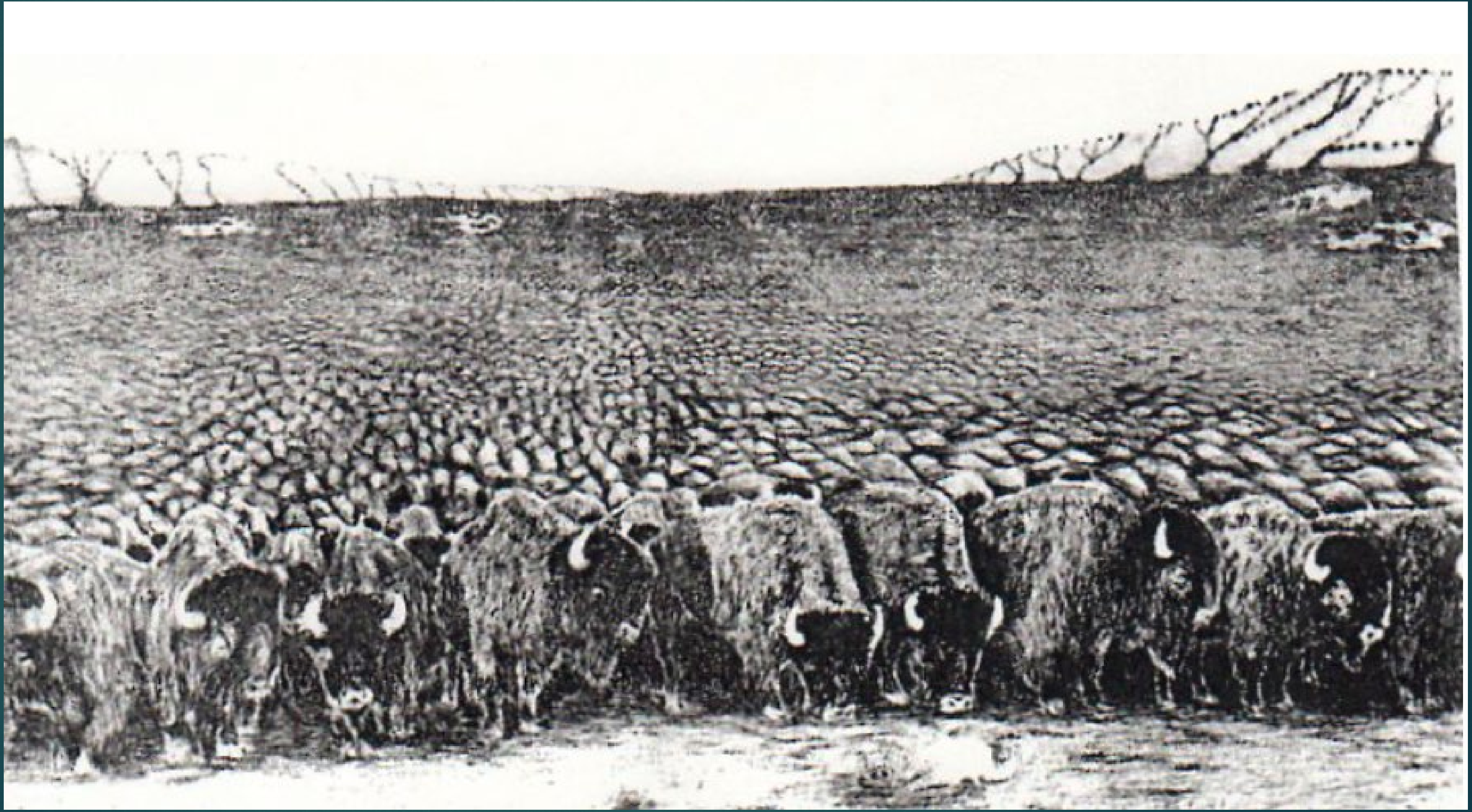
First cowboys

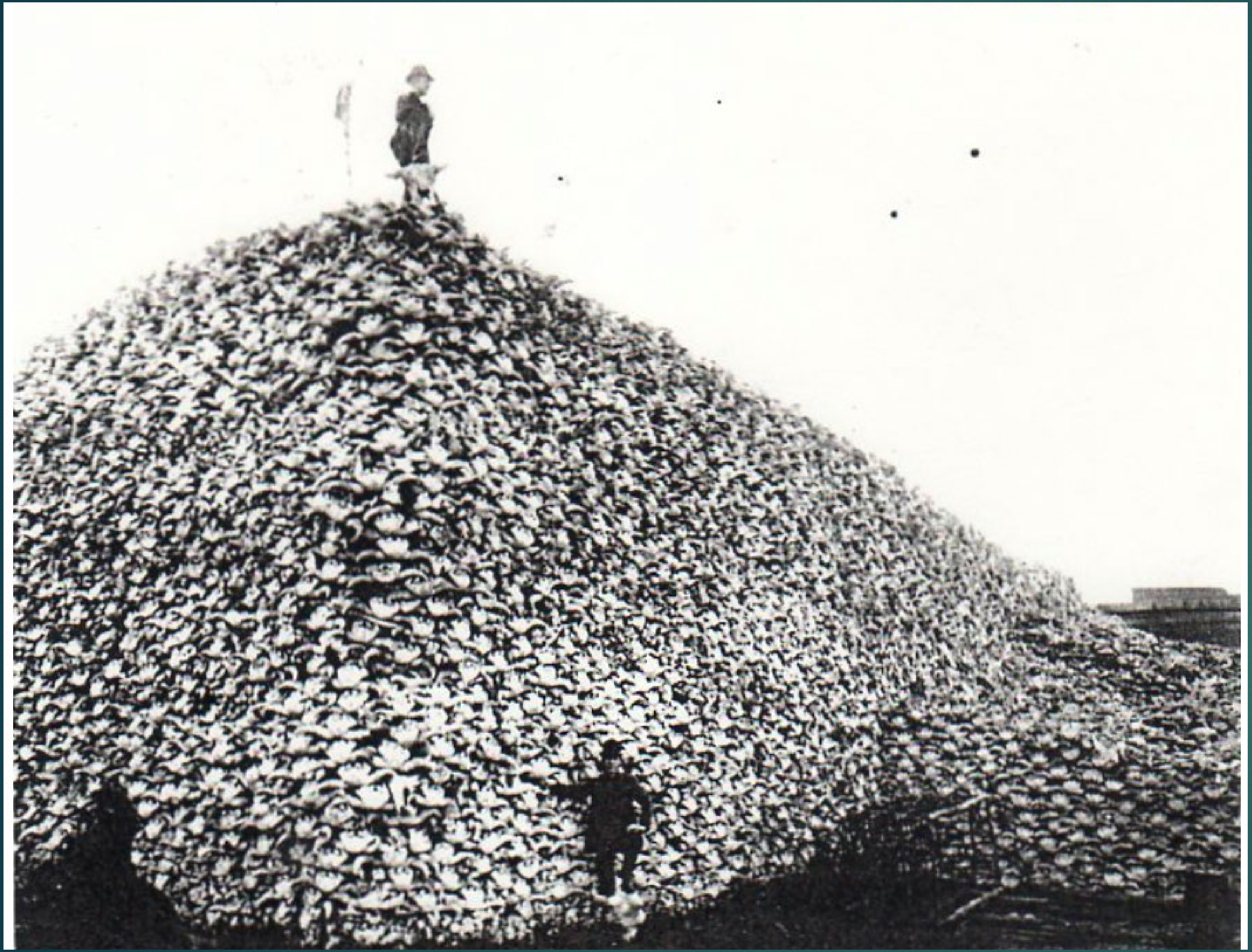
- The first cattle in the Americas came from Spain, brought by Christopher Columbus to the island of Hispaniola on his second voyage in 1493. More came in subsequent voyages in the early 1500s. The vast herds that later spread across the Americas, historians have assumed, descended from this small founding population of about 500 cows.
- Compared genetic signatures in the DNA from 21 cows found at early Spanish sites in Mexico and Haiti to known European and African breeds.
- One of the bones was African, not Spanish: The sample dates to the early 1600s, more than 100 years before the first historical records of imported African cattle.
- Bringing cattle that were more adapted to hot, wet environments could have been a deciding factor. African ranchers were more knowledgeable about raising cattle in tropical environments. Now, we have different lines of evidence that connect African ranchers and Spanish colonies.

African cowboys

- In the early 1600s, historical records show slave traders targeted African groups familiar with cattle herding, like the Fulani of modern-day Cameroon. The new study shows at least one cow was brought directly from the region at the same time, suggesting herders and their cattle might have come as a sort of package.
- The find should help shift a fundamental misconception around the origins of an iconic American figure—the cowboy. Innovations like herding cattle from horseback and the lasso appeared first in the Americas at a time when most cowboys were enslaved Africans, spreading to Europe only later.

When Native Americans first populated the Great Plains of the West and Midwest, there were an estimated 60-million buffalo roaming the prairies. Herds so large that they measured 20 miles wide and 50 miles long.





- Millions upon millions of the animals were slaughtered in the late 1700's and throughout the 1800's. Only hide & tongues taken.
- It is estimated that by 1889, there were only 541 of these animals left in North America
- Destroying Native American's source of food, clothing, lodging, and spiritual relevance
- 2 South Dakota ranchers (married to NA women) basically saved the remaining buffalo..

American buffalo

- For more than 10,000 years, bison served as the primary source of the livelihood for many Native Americans in regions of the Great Plains, the Northwest and the Rocky Mountains.

- Along with nutrition, the animals provided hides for clothing, lodging and blankets as well as bones for tools and implements. Nearly every part of the animal was used, including the brains to obtain grease for tanning hides and the stomach for creating bags and water containers.

- Evidence suggests that bison-reliant Indigenous societies enjoyed living standards comparable to, or in some cases better than, their European contemporaries.

Bison

- A gradual decline of the bison population started with the introduction of the horse and the arrival of Europeans. By 1870, however, mass slaughter of the animals began.
- Factors that drove the kill-off included the completion of the transcontinental railroad, improvements in European tanning technology that made bison hides more desirable and encouragement by the U.S. Army to eliminate the animals to help in their efforts to force Indigenous peoples onto reservations.
- In some regions, the bison was eliminated in a little more than a decade.
- Indigenous people were forced onto reservations, their movements were restricted and they were not allowed to become citizens of the United States until 1924

Buffalo slaughter left lasting impact on Indigenous peoples

- The mass slaughter of North American bison by settlers of European descent is a well-known ecological disaster. An estimated eight million bison roamed the United States in 1870, but just 20 years later fewer than 600 of the iconic animals remained.
- The mass slaughter provided a brief economic boon to some newly arriving settlers, hunters and traders of the Great Plains who sold the hides and bones for industrial uses.
- In contrast, Indigenous peoples whose lives depended on the bison suffered a devastating economic shock—one that still reverberates in these communities today

Donn L Feir et al., 2023

The Slaughter of the Bison and Reversal of Fortunes on the Great Plains

- New study quantified both the immediate and long-term economic impacts of the loss of the bison on Indigenous peoples whose lives depended on the animals.

- The economists defined nearly 24 Indigenous nations as "exposed to the slaughter," based on geographic location and whether bison served as their primary food source.

- By the early 1880s, there were no bison, little game, and inadequate or non-existent government food supplies. Mass starvation began to make reservations look more appealing.

Height reduction

- Changes in the average height of bison-related people is one striking example of the fallout. Adult height across a population is one proxy of wealth and health given that it can be impacted by nutrition and disease, particularly early in development.
- Bison-reliant Indigenous men stood around six feet tall on average, or about an inch taller than Indigenous men who were not bison-reliant.
- They were among the tallest people in the world in the mid-19th century, But after the rapid near-extinction of the bison, the height of the people born after the slaughter also rapidly declined.
- Within one generation, the average height of Indigenous peoples most impacted by the slaughter dropped by more than an inch.

Consequences of loss of the buffalo

- By the early twentieth century, child mortality was 16 percentage points higher and the probability of reporting an occupation 19 percentage points lower in bison nations compared with nations that were never reliant on the bison.
- Throughout the latter half of the twentieth century and into the present, income per capita has remained 25% lower, on average, for bison nations. This persistent gap cannot be explained by differences in agricultural productivity, self-governance, or application of the *Dawes Act*. Provide evidence that this historical shock altered the dynamic path of development for formerly bison-reliant nations. Demonstrate that limited access to credit constrained the ability of bison nations to adjust through re-specialization and migration.

Assembly of 43 human Y chromosomes reveals extensive complexity and variation

- The prevalence of highly repetitive sequences within the human Y chromosome has prevented its complete assembly to date and led to its systematic omission from genomic analyses.
- The Y chromosome associated with male development, which is the last mysterious piece of the human genome, has been fully sequenced by a team of more than 100 researchers around the world including Johns Hopkins University scientists.
- Original completer human genome was done with two X chromosomes. Now, using a donor with both an X and a Y chromosome, the consortium built a complete blueprint of the Y chromosome and every element of its DNA.

Pille Hallast, et al., 2023

Y chromosome

- The achievement completes the Y chromosome's genetic code and unveils key details that could provide a crisper picture of the role the chromosome plays in male-specific development, fertility, and genetically triggered diseases like cancer.
- The Y chromosome has been particularly challenging to decode because of its repetitive molecular patterns, but new sequencing technology and bioinformatics algorithms allowed the team to resolve these DNA sequences.
- The complex structure of the Y chromosome has lent itself to rapid evolution within its gene families. In fact, the Y chromosome is the most rapidly changing human chromosome, and even the most rapidly changing chromosome among great apes. This means two healthy people's Y chromosomes can look very different—for example, one person might have 40 copies of one gene, while another person has 19 copies.

Y chromosome

- The Y chromosome is very different from X and the 22 other chromosomes of the human genome. It is smaller and bears few genes (only 27 compared to about 1,000 on the X).
- The proto-Y degenerated fast, losing about 10 active genes per million years, reducing the number from its original 1,000 to just 27. It may disappear in a million years.
- These include SRY, a few genes required to make sperm, and several genes that seem to be critical for life—many of which have partners on the X. Many Y genes (including the sperm genes RBMY and DAZ) are present in multiple copies. Some occur in weird loops in which the sequence is inverted and genetic accidents that duplicate or delete genes are common. And a lot of non-gene DNA.

Y chromosome

- Study finally completes the set of end-to-end human chromosomes and adds 30 million new bases to the human genome reference, mostly from challenging-to-sequence satellite DNA.

- These bases reveal 41 additional protein-coding genes, and provide crucial insight for those studying important questions related to reproduction, evolution, and population change.

- The team revealed the structures of sperm-regulating gene families. They also unveiled the structures of genes thought to play significant roles in growth and functioning of the male reproductive system.

Y chromosome

- The structure of the Y chromosome has been challenging to decode because some of the DNA is organized in palindromes—long sequences that are the same forward and backward—spanning up to more than a million base pairs. Moreover, a very large part of the Y chromosome that was missing from the previous version of the Y reference is satellite DNA—large, highly repetitive regions of non-protein-coding DNA. On the Y chromosome, two satellites are interlinked with each other, further complicating the sequencing process.
- The researchers were able to achieve a gapless read of the Y chromosome due to advances in long-read sequencing technology and new, innovative computational assembly methods that could deal with the repetitive sequences and transform the raw data from sequencing into a usable resource.

First 100% complete sequence of the Y chromosome

- Here report on de novo assemblies of 43 Y chromosomes spanning 182,900 years of human evolution and report considerable diversity in size and structure. Half of the male-specific euchromatic region is subject to large inversions with a greater than twofold higher recurrence rate compared with all other chromosomes.

- Ampliconic regions typically harbor massively amplified gene families that exhibit testis-specific or testis-biased expression**.** Ampliconic sequences associated with these inversions show differing mutation rates that are sequence context dependent, and some ampliconic genes exhibit evidence for concerted evolution with the acquisition and purging of lineage-specific pseudogenes.
- The largest heterochromatic region in the human genome, Yq12, is composed of alternating repeat arrays that show extensive variation in the number, size and distribution, but retain a 1:1 copy-number ratio.

Y chromosome

- An unexpected finding from this paper was that Y chromosome DNA has been repeatedly mistaken to be bacterial DNA in past studies due to the incomplete removal of human contamination in bacterial DNA. This discovery promises to improve the study of bacterial species' genomes.

- The availability of fully sequence-resolved Y chromosomes from multiple individuals provides a unique opportunity for identifying new associations of traits with specific Y-chromosomal variants and garnering insights into the evolution and function of complex regions of the human genome.

Paleogenetics, Pt. 18
Africa

September 2023

by Charles J Vella, PhD

A required dictionary of most important definitions in aDNA genetics

- Allele -- one of two or more alternative/different forms of a gene that arise by mutation and are found at the same place on a chromosome.
- Allele frequency -- how common an allele is in a population
- Genotype –an individual's complete set of genes

Aaron Pfennig, et al., 2023

Genetic dictionary 2

- Linkage disequilibrium (LD)—The nonrandom association of two alleles at different loci/physical proximity. When alleles from different loci are found together in a population, at higher than expected frequencies.

- Genetic drift--variation in the relative frequency of different genotypes in a small population, owing to the chance disappearance of particular genes as individuals die or do not reproduce. Causes lower genetic variation in small populations

- Effective population size (Ne)—The number of breeding individuals in an idealized randomly mating population. Ne determines the strength of genetic drift acting on a population.

Genetic dictionary 3

- **Population structure**—Systematic differences in allele frequencies between subpopulations.
- **Admixture**—The interbreeding of individuals from two or more subpopulations that were isolated for a relatively short evolutionary time.
- **Serial founder effect**—The successive loss of genetic variation when populations are sequentially founded by a small number of individuals.
- **Haplotype**—A set of linked genetic variants that are coinherited.

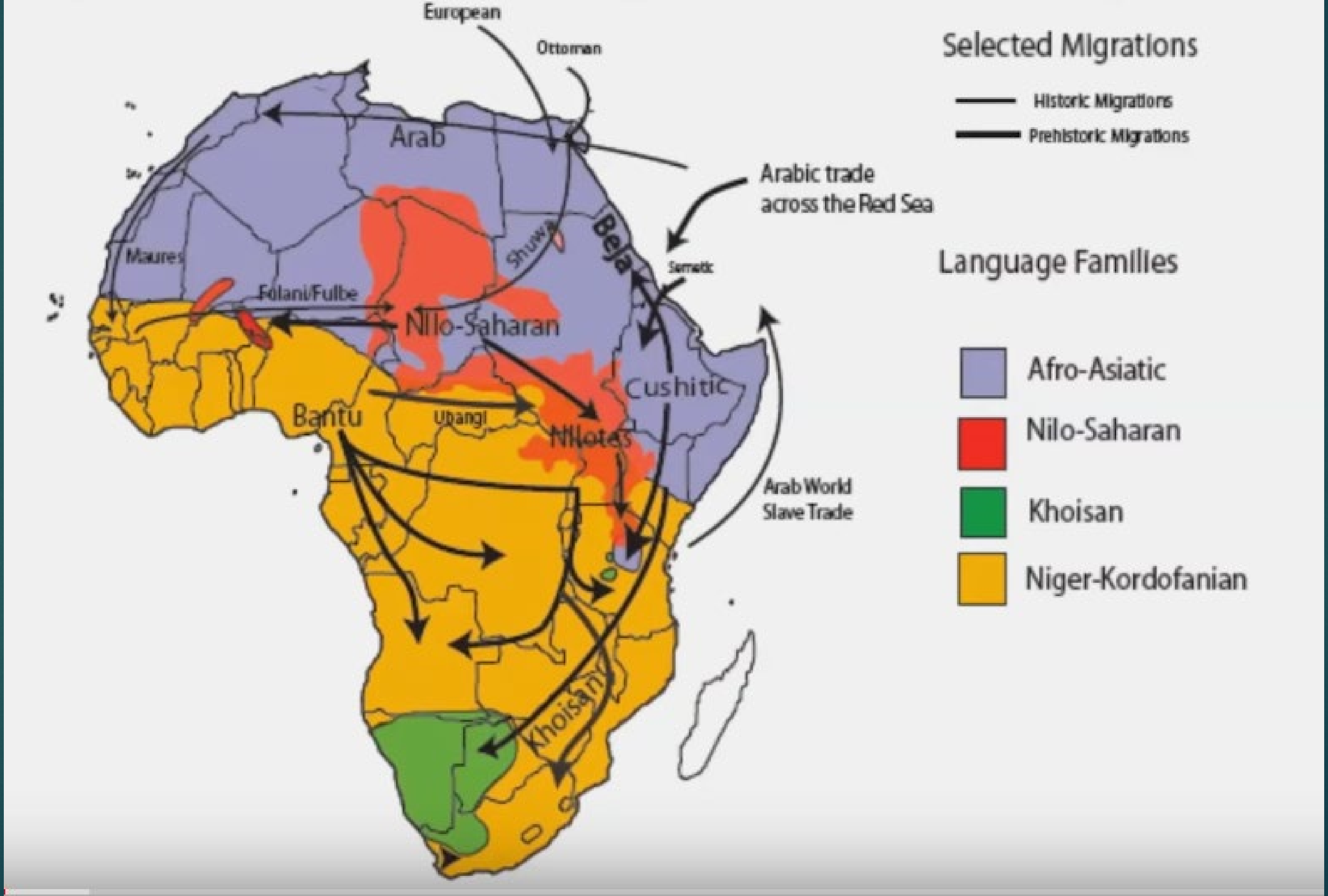
Genetic dictionary 3

- **Population bottleneck**—An event that drastically reduces the effective size of a population, leading to increased genetic drift/lower genetic variation.
- **Genetic cline**—A gradual change of allele frequencies over a specified geographic area.
- **Out-of-Africa (OOA) model** —Hypothesis that anatomically modern humans evolved in Africa and subsequently peopled the rest of the world.
- **Isolation-by-distance model**—A theoretical framework explaining how genetic differentiation between populations increases with geographic distance due to spatially limited gene flow, that is, decreasing migration rate with increasing distance.

Genetics dictionary 4

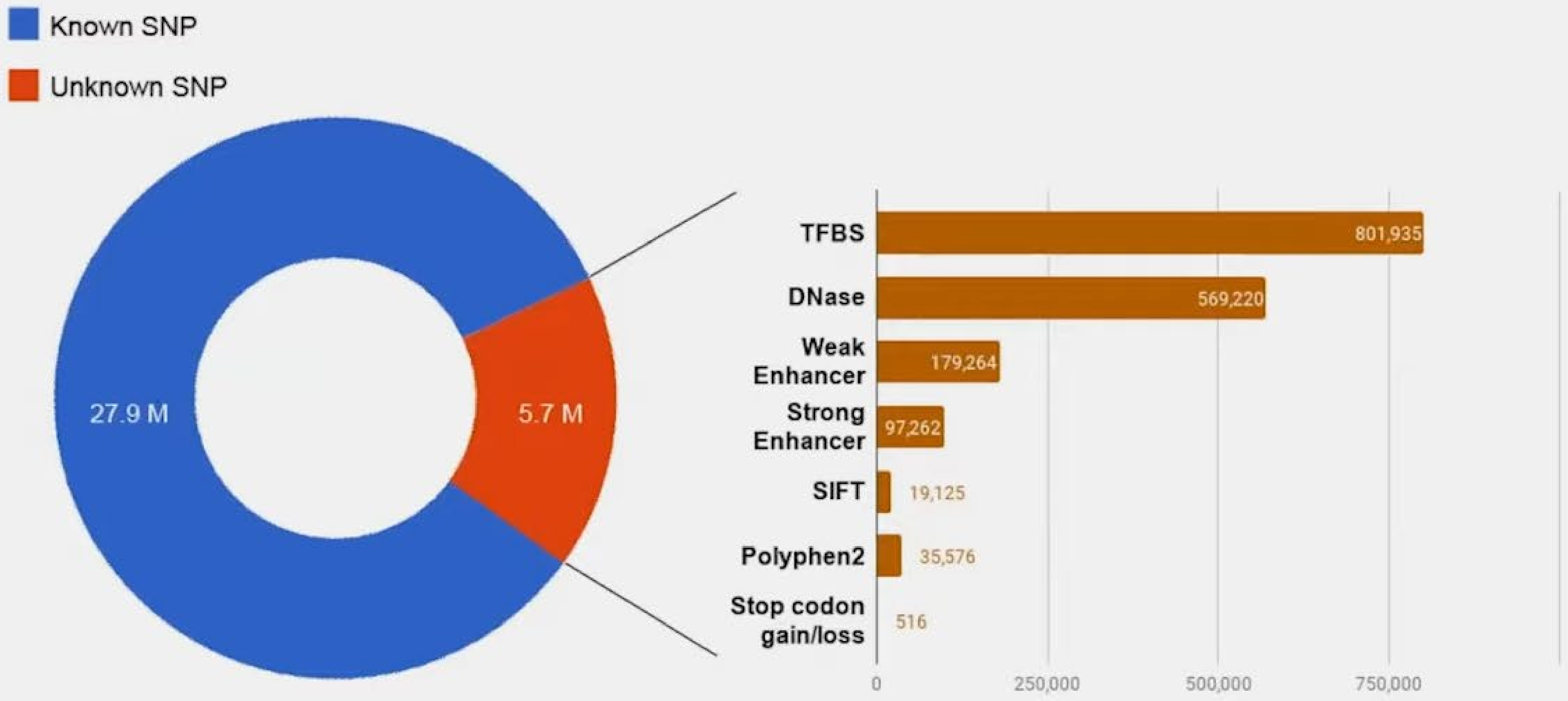
- **Genetic ancestry**—The genealogical paths through which an individual inherits DNA from specific ancestors in a reference population. Individuals with shared genetic ancestry tend to be more genetically similar.
- **Principal components**—A statistical set of uncorrelated variables derived from the original data set through linear transformations, which maximize the variance between samples and reduce the dimensionality of the data while preserving the most important information. i.e. skull variation, populations
- **Gene flow**—The movement of individuals and their genetic material from one population to another population (via sex).
- **Introgression**—The interbreeding of individuals from two or more populations that were isolated for a long evolutionary time but are not yet reproductively isolated.

African Cultural Variation: 2000 ethnic groups, 4 major language groups, 8000 dialects

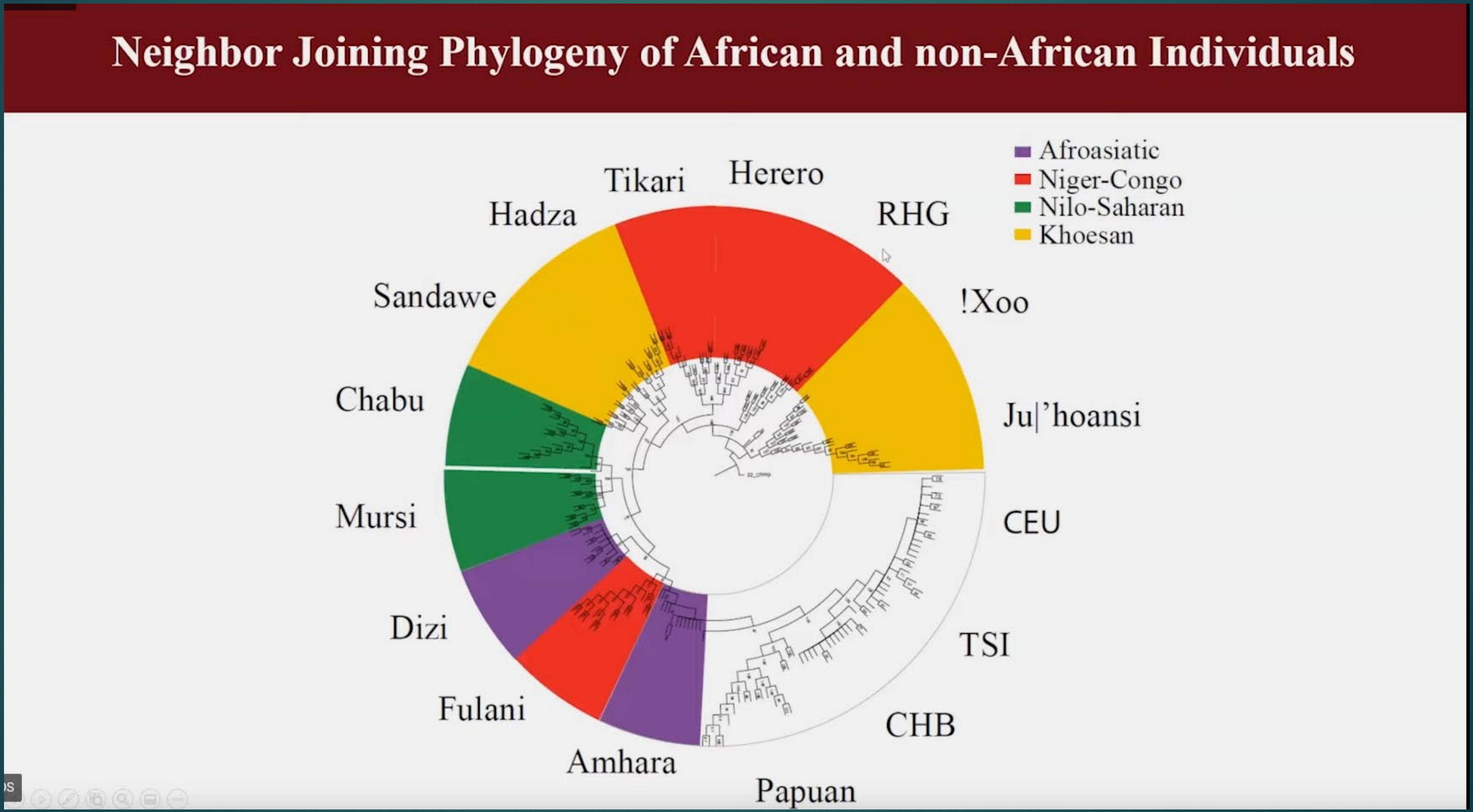


African Genetic Variation

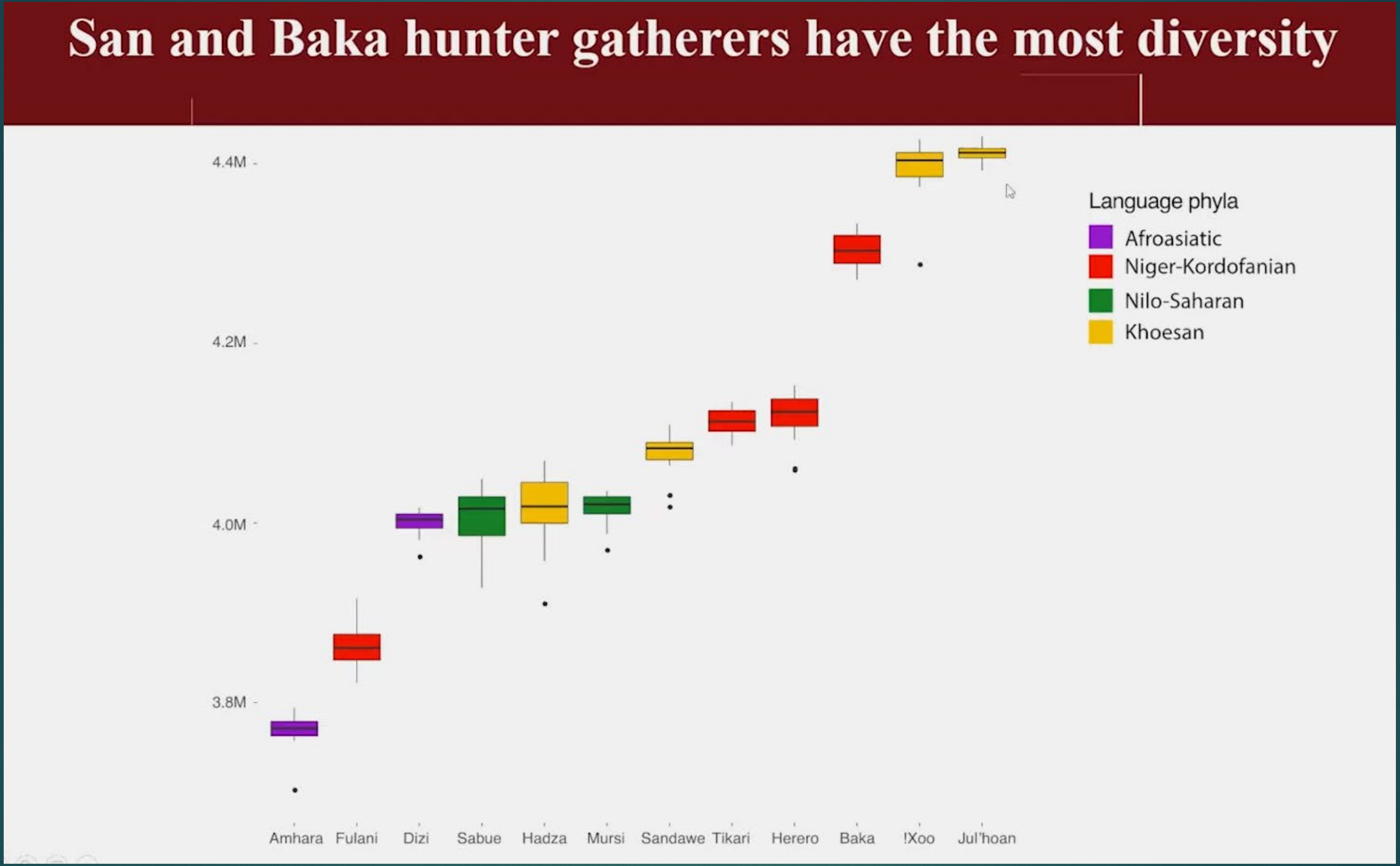
33.6 million SNPs identified, 17% are novel and many are predicted to be functional



Most basal lineage = Klick-speaking San population, followed by rainforest HGs, then Bantu speakers of central & western Africa



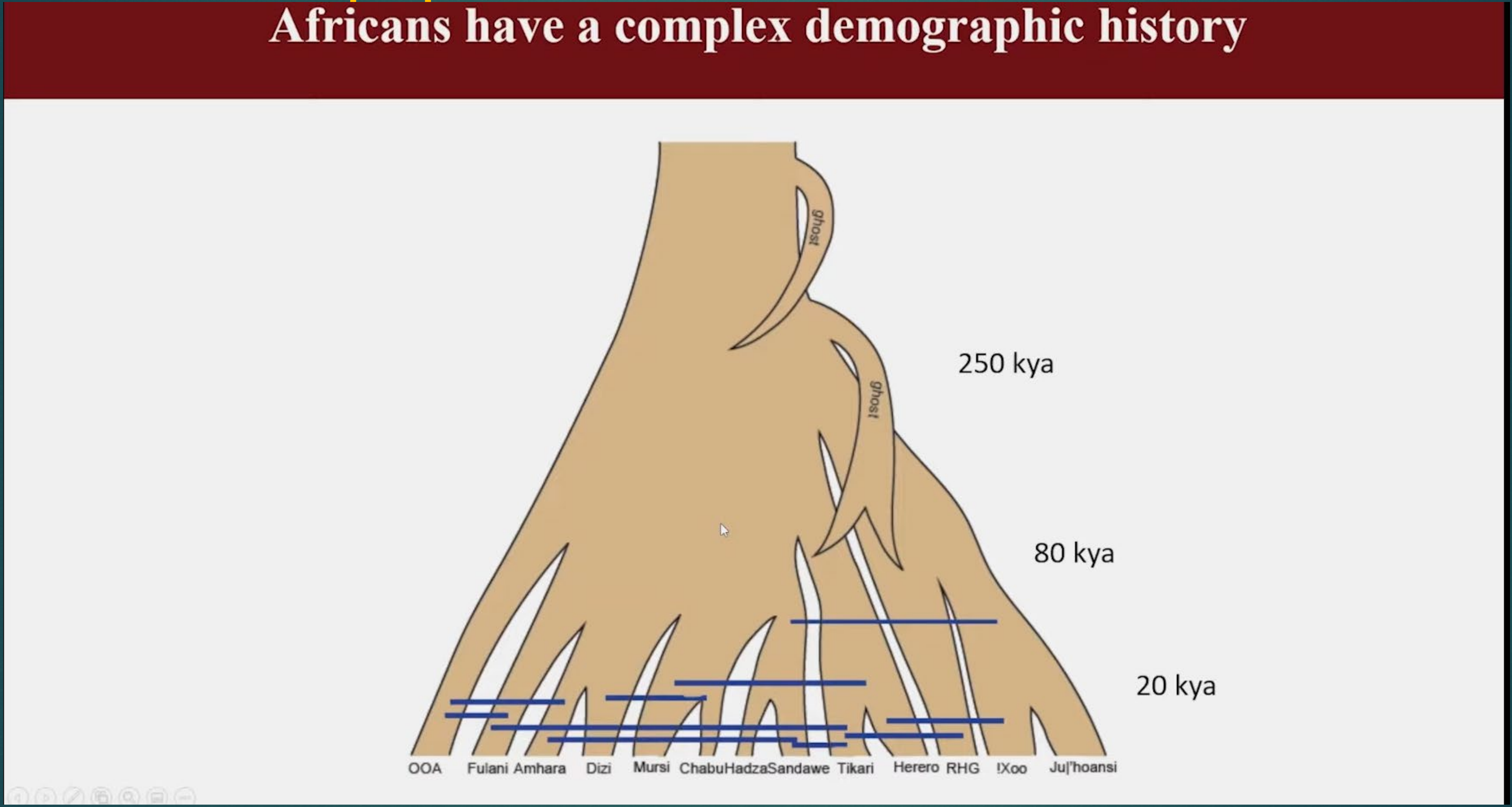
Neighbor Joining Phylogeny of African and non-African Individuals



San and Baka hunter gatherers have the most diversity

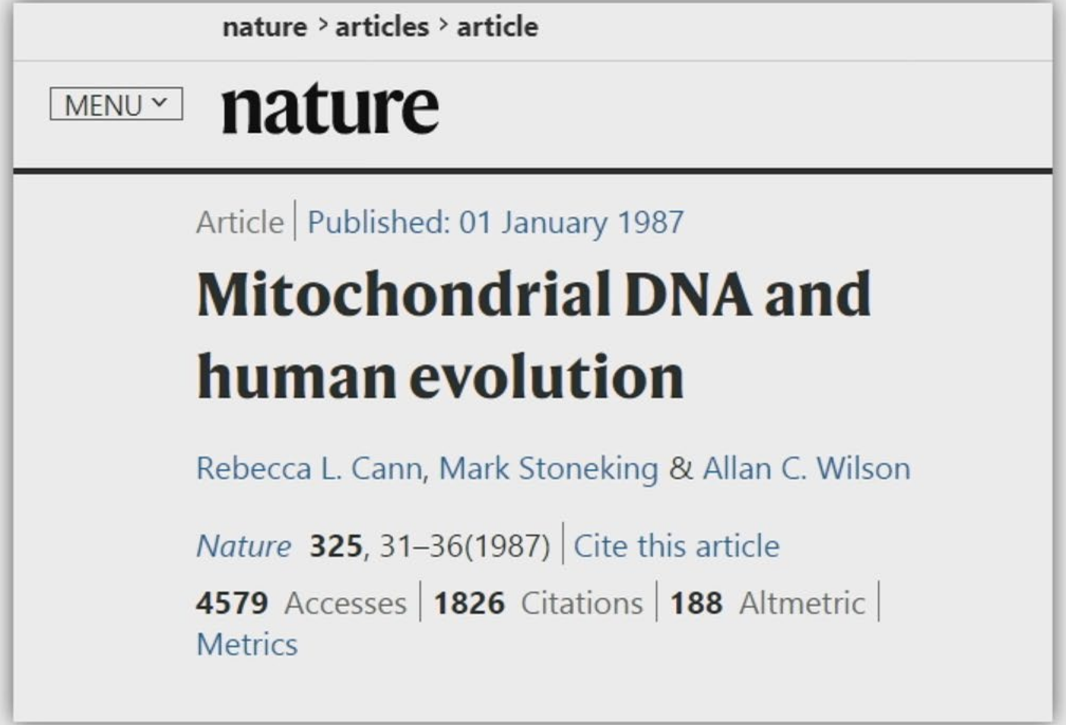
San & Baka Hunter-Gathers Have Largest Effective Population Size before 50 kya

San and RHG form a sister clade and are ancestral to all modern African populations



Africans have a complex demographic history

The genetic history of Africa based on modern and ancient DNA, *Carina Schlebusch,* 2022



Article | Published: 01 January 1987

Mitochondrial DNA and human evolution

Rebecca L. Cann, Mark Stoneking & Allan C. Wilson

Nature **325**, 31–36(1987) | Cite this article

4579 Accesses | **1826** Citations | **188** Altmetric | Metrics

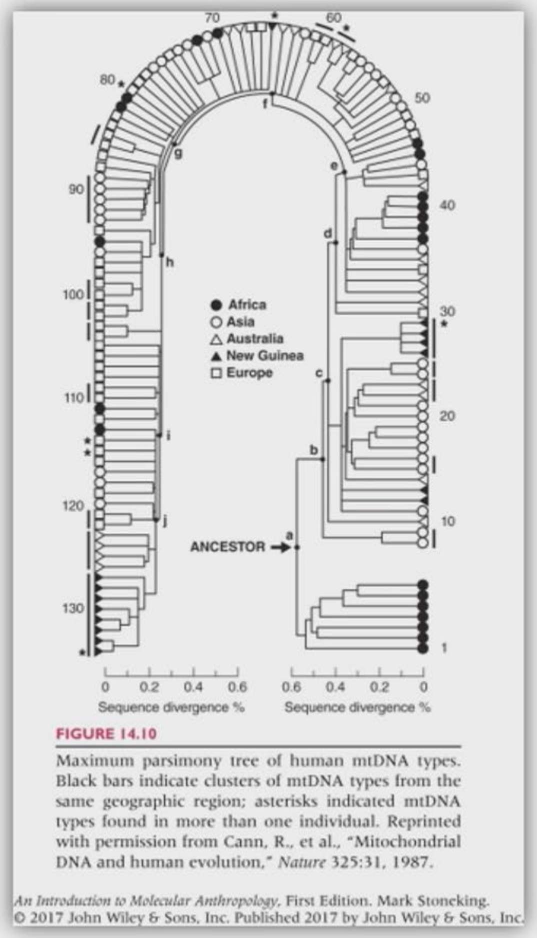


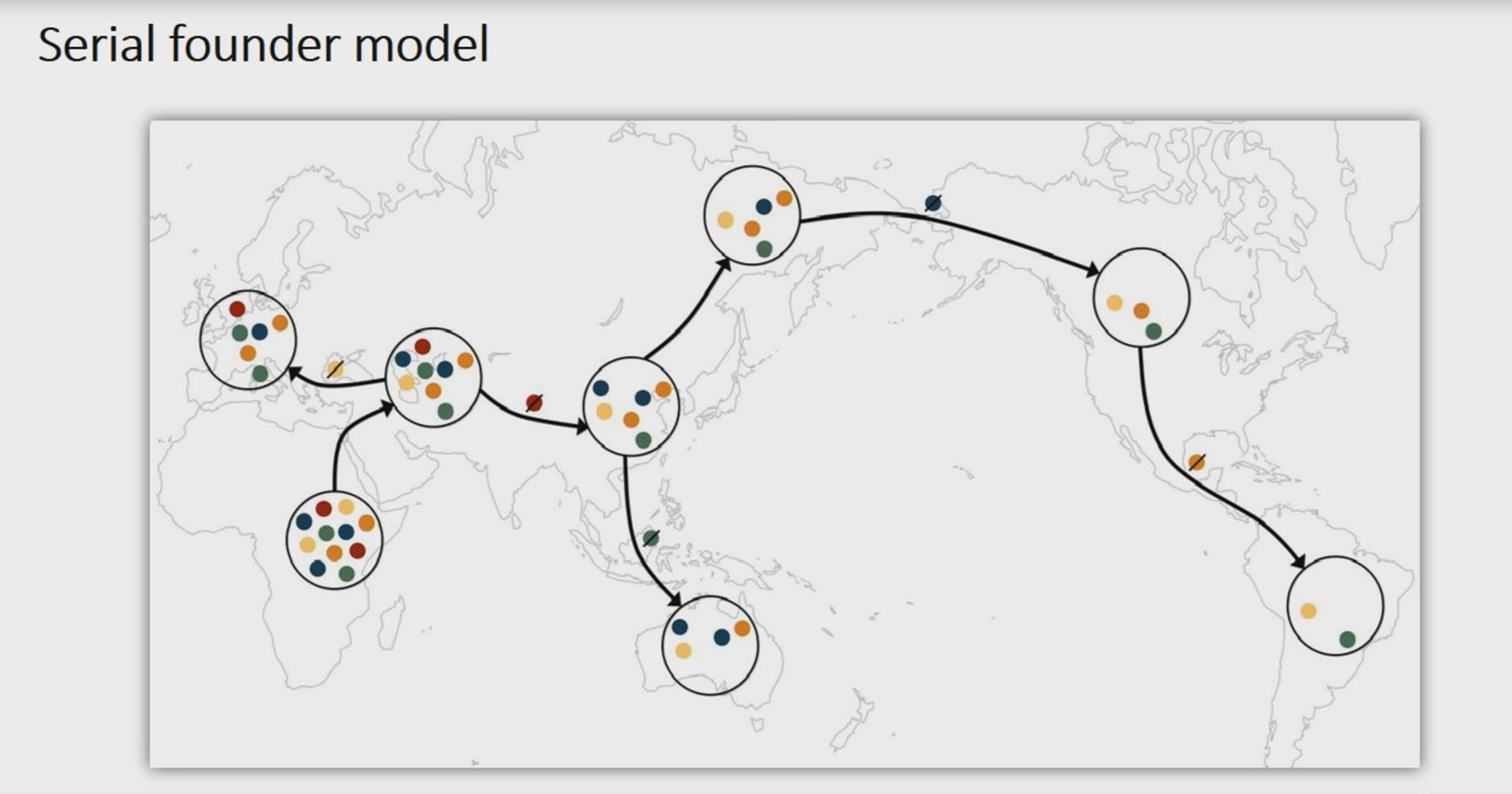
FIGURE 14.10

Maximum parsimony tree of human mtDNA types. Black bars indicate clusters of mtDNA types from the same geographic region; asterisks indicated mtDNA types found in more than one individual. Reprinted with permission from Cann, R., et al., "Mitochondrial DNA and human evolution," *Nature* 325:31, 1987.

An Introduction to Molecular Anthropology, First Edition. Mark Stoneking.
© 2017 John Wiley & Sons, Inc. Published 2017 by John Wiley & Sons, Inc.

1987, R. Cann: First mtDNA study: highest mtDNA variation in Africa;
the farther from Africa, the less genetic variation due to serial founder effect

Genetic effect of OoA migration: With each new migration, less genetic variation in new founding group

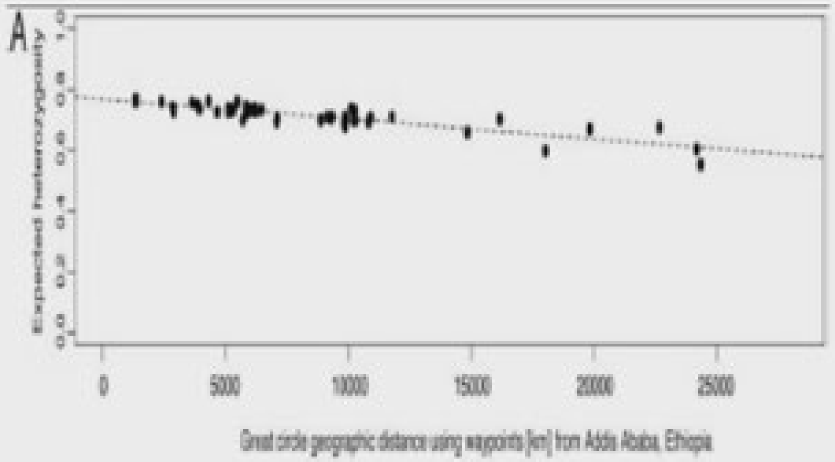


Serial founder model

Summary statistics used to confirm Out of Africa model

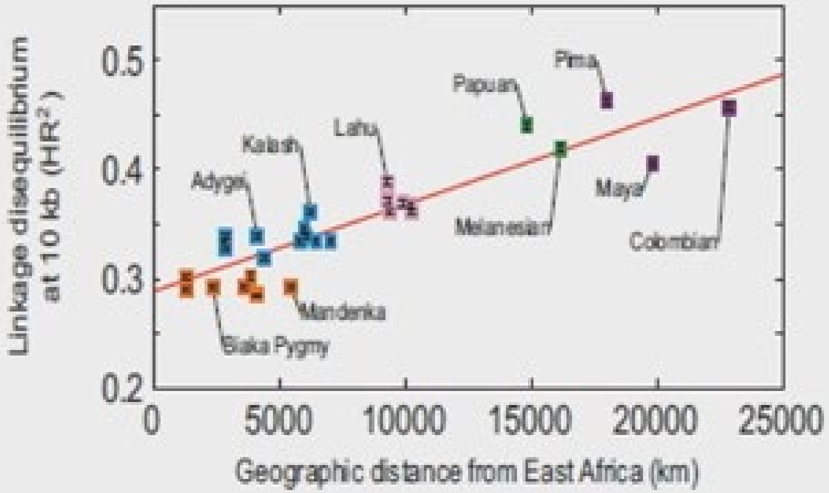
Genetic diversity/heterozygosity declines with distance from Africa, while linkage disequilibrium increases = serial founder model

Heterozygosity vs. Distance from Africa



Ramachandran *et al.*, *PNAS* (2005)

LD vs. Distance from Africa



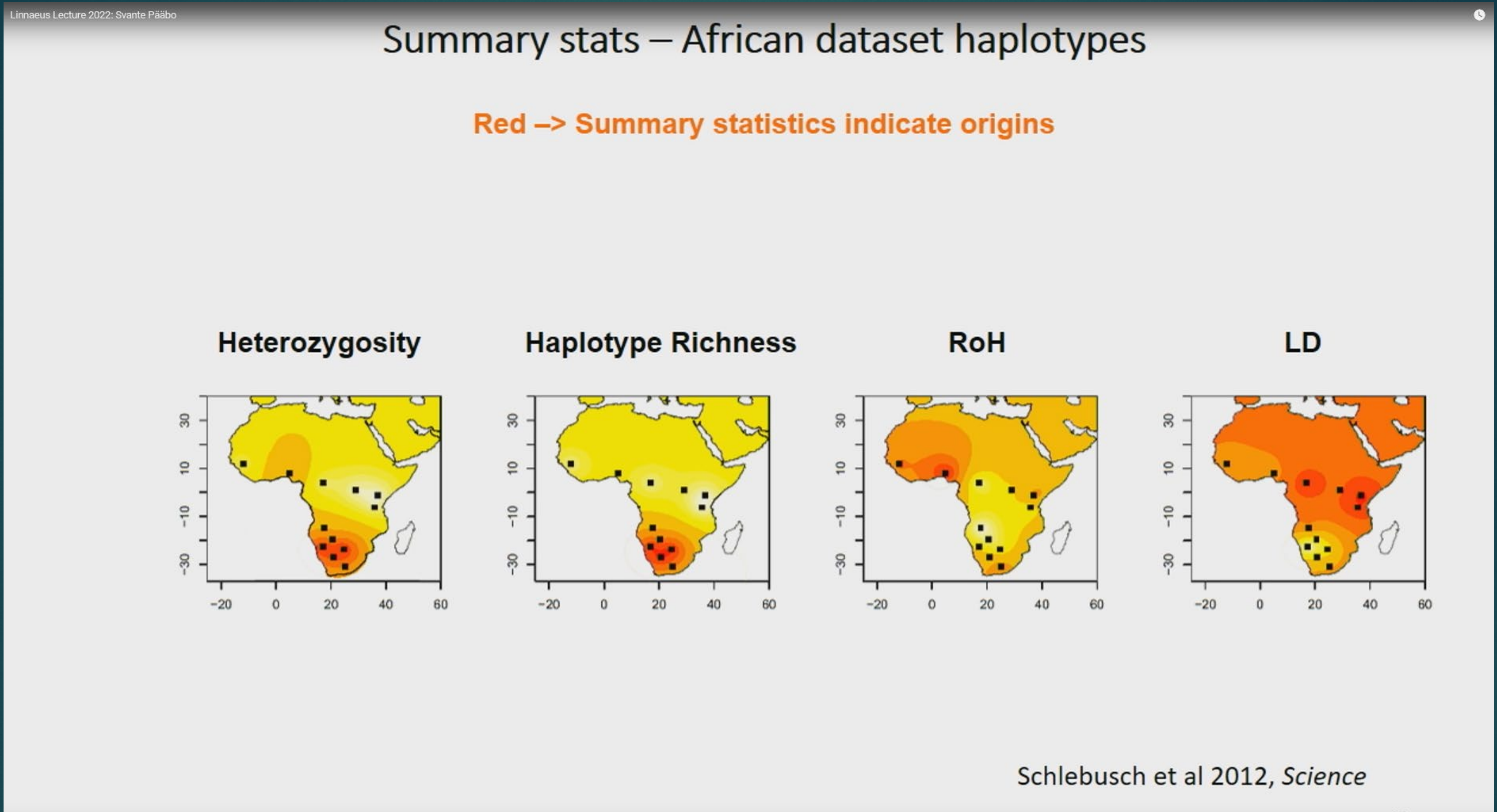
Jakobsson *et al.*, *Nature* (2008)

Linkage disequilibrium: genetic hitchhiking

- Particular alleles at neighboring loci tend to be co-inherited. For tightly linked loci, this might lead to associations between certain alleles in the population = linkage disequilibrium (LD).

- LD = degree to which an allele of one genetic variant is inherited or correlated with an allele of a nearby genetic variant within a given population; non-random association of alleles at different loci

- When alleles from different loci are found together in a population, at higher-than-expected frequencies, they are said to be in linkage disequilibrium. Levels of LD are highest for loci that are physically close in the genome and are reduced by recombination and recurrent mutations.



Linnaeus Lecture 2022: Svante Pääbo

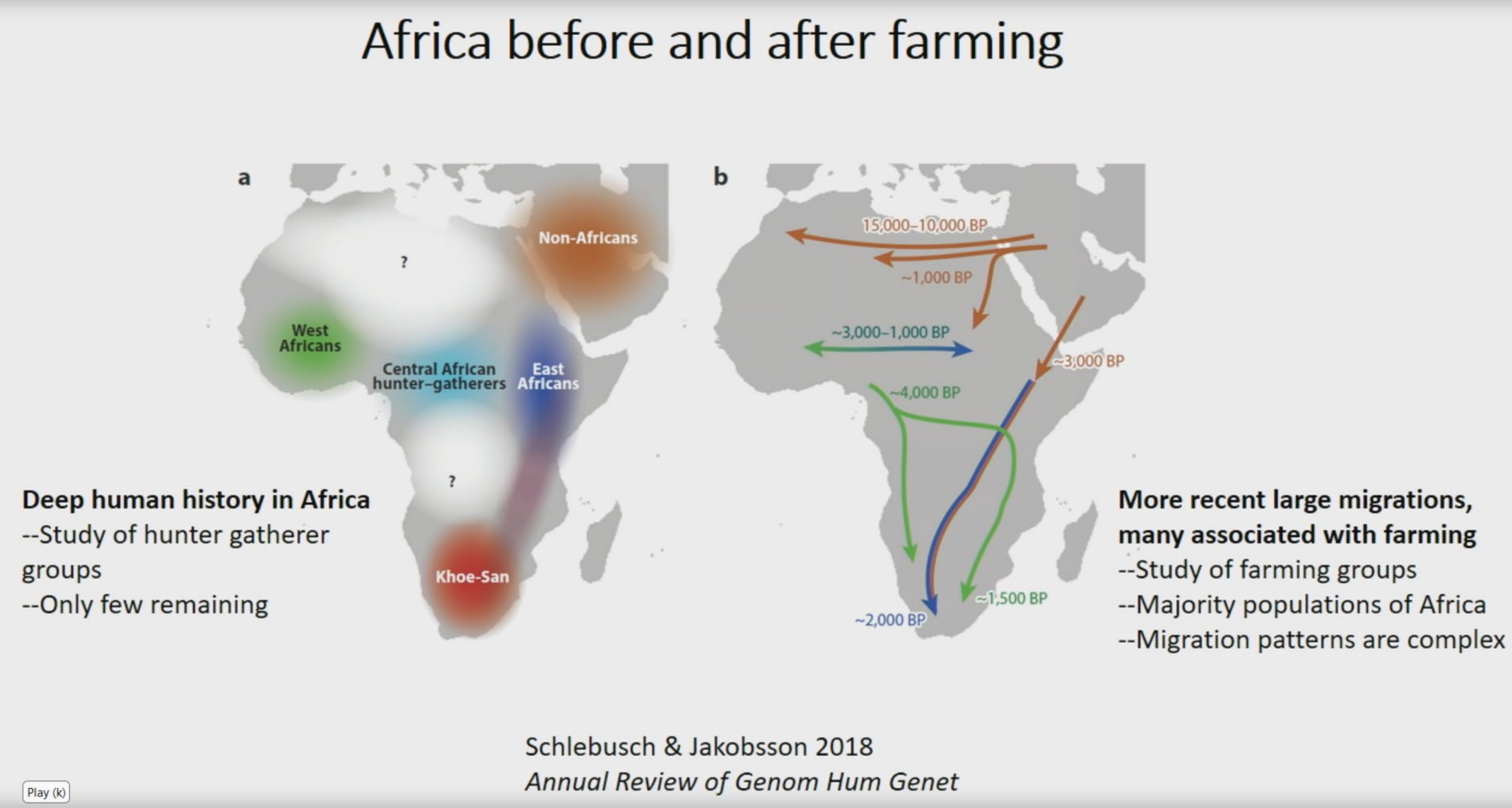
Summary stats – African dataset haplotypes

Red –> Summary statistics indicate origins

Schlebusch et al 2012, *Science*

Where in Africa did MHs originate? Summary statistics are not unanimous; serial founder model does not work well in Africa

African HGs came first, then farming immigrations

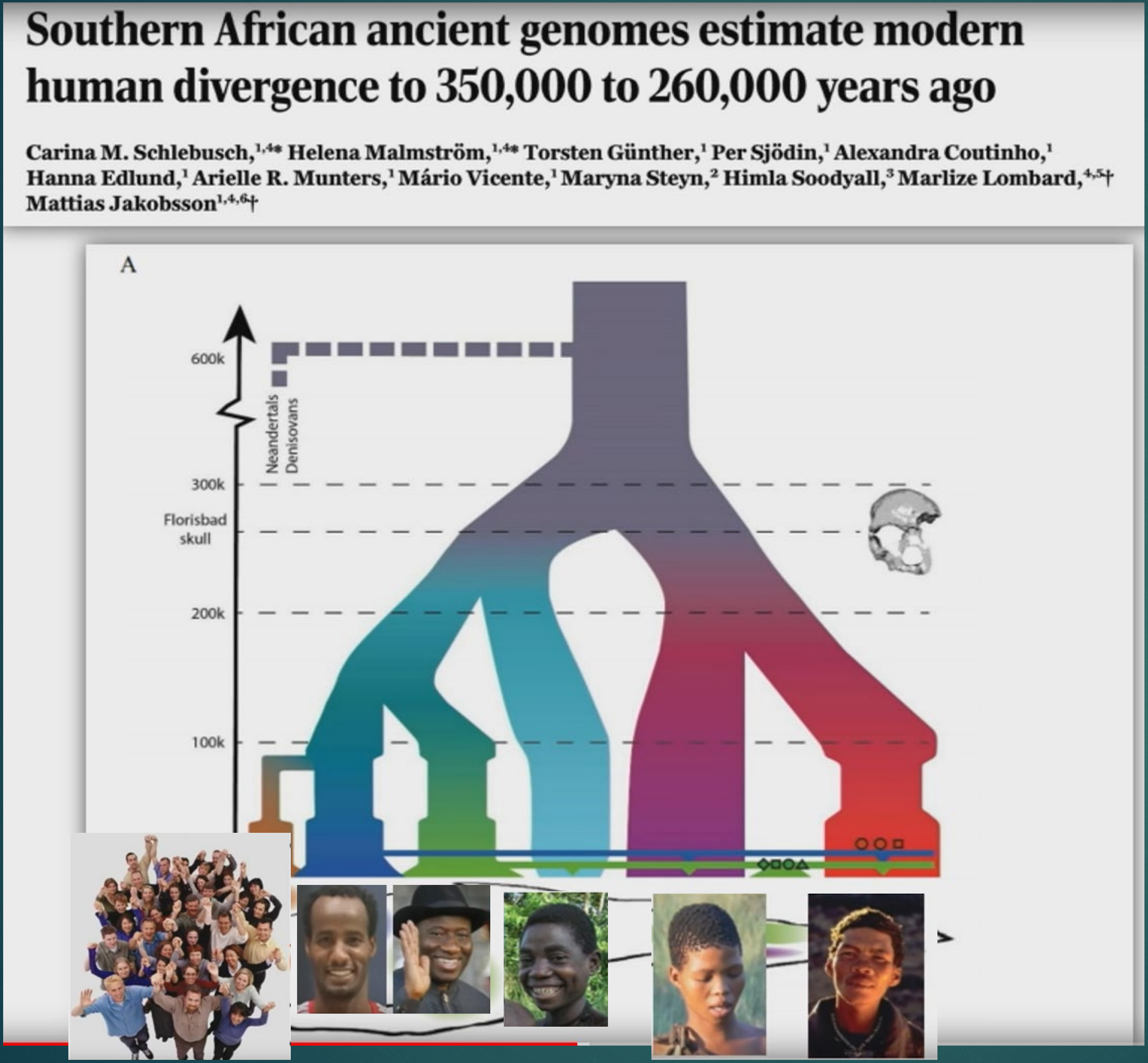


Africa before and after farming

Deep human history in Africa
--Study of hunter gatherer groups
--Only few remaining

More recent large migrations, many associated with farming
--Study of farming groups
--Majority populations of Africa
--Migration patterns are complex

Schlebusch & Jakobsson 2018
Annual Review of Genom Hum Genet

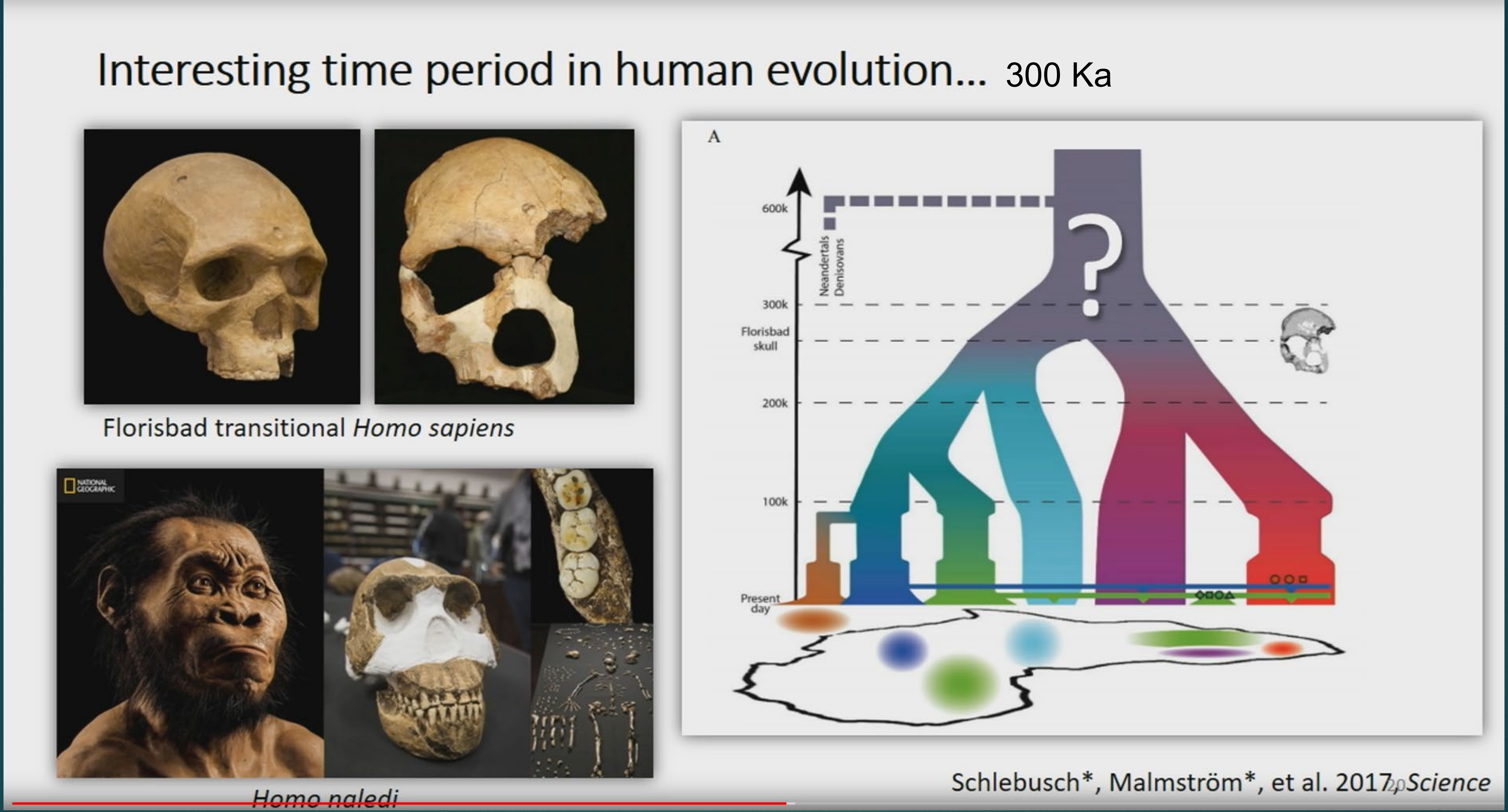


Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago

Carina M. Schlebusch,[1,4]* Helena Malmström,[1,4]* Torsten Günther,[1] Per Sjödin,[1] Alexandra Coutinho,[1] Hanna Edlund,[1] Arielle R. Munters,[1] Mário Vicente,[1] Maryna Steyn,[2] Himla Soodyall,[3] Marlize Lombard,[4,5]† Mattias Jakobsson[1,4,6]†

- First split was with Southern San at 300 Ka – into N and S San
- Second were rain forest HGs (the pygmies)
- Third: East & West Africans
- 4th: Out of Africa group
- Large genetic variation occurred long before OofA migration

Interesting time period in human evolution… 300 Ka



Florisbad transitional *Homo sapiens*

Homo naledi

Schlebusch*, Malmström*, et al. 2017, *Science*

Both archaic and derived features at 200-300 Ka: gradient toward modern human

300 Ka

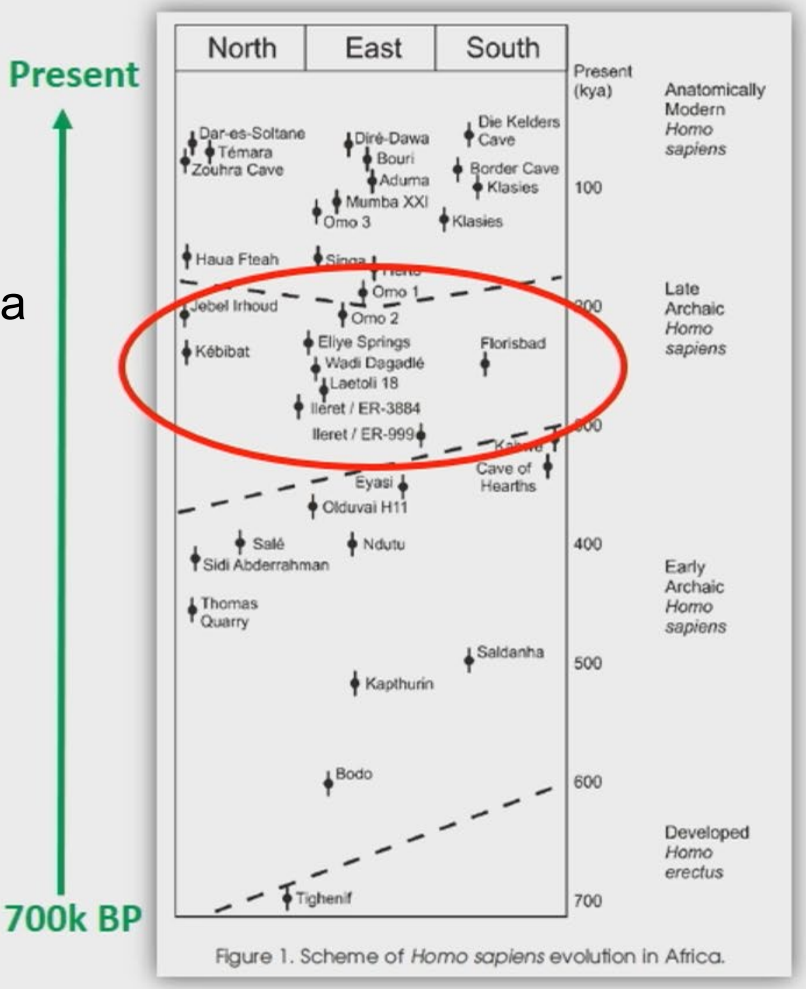
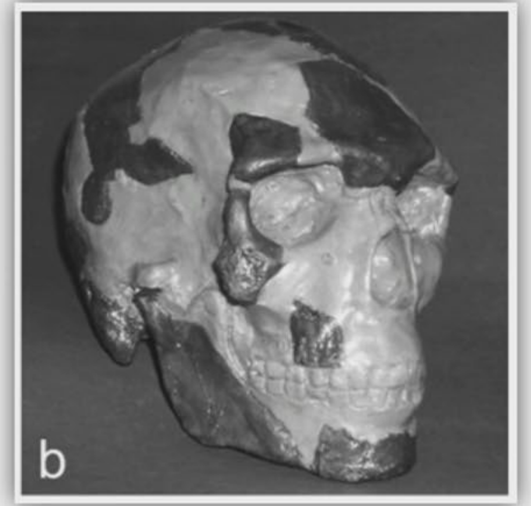


Figure 1. Scheme of *Homo sapiens* evolution in Africa.

Brauer 2008, *Evolutionary Anthropology*

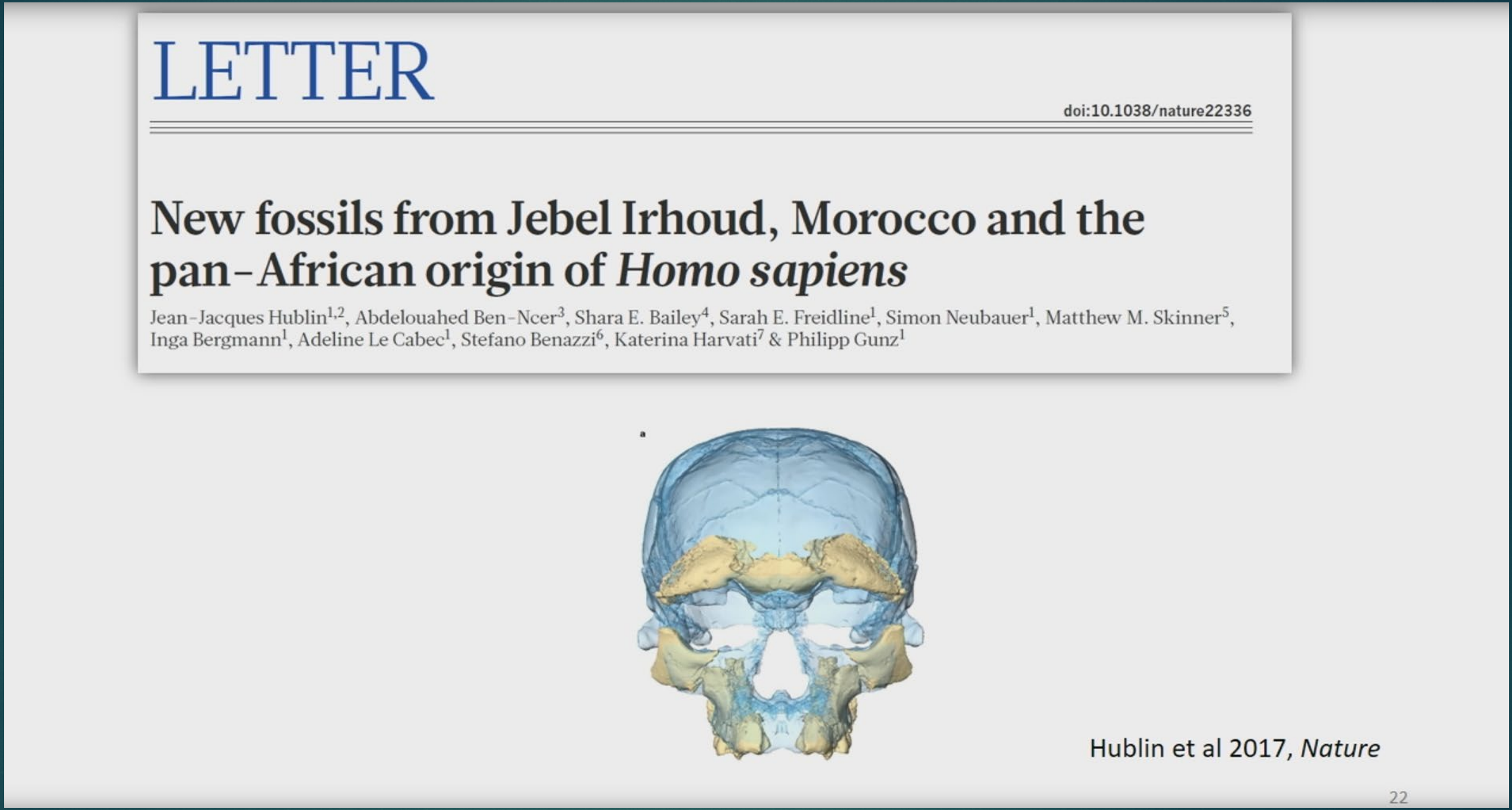
Omo 1, Ethiopia



Herto, Ethiopia

Jebel Irhoud, Morocco

Florisbad, South Africa



LETTER

doi:10.1038/nature22336

New fossils from Jebel Irhoud, Morocco and the pan-African origin of *Homo sapiens*

Jean-Jacques Hublin[1,2], Abdelouahed Ben-Ncer[3], Shara E. Bailey[4], Sarah E. Freidline[1], Simon Neubauer[1], Matthew M. Skinner[5], Inga Bergmann[1], Adeline Le Cabec[1], Stefano Benazzi[6], Katerina Harvati[7] & Philipp Gunz[1]

Hublin et al 2017, *Nature*

Pan-African theory

Ongoing issues about human origins in Africa

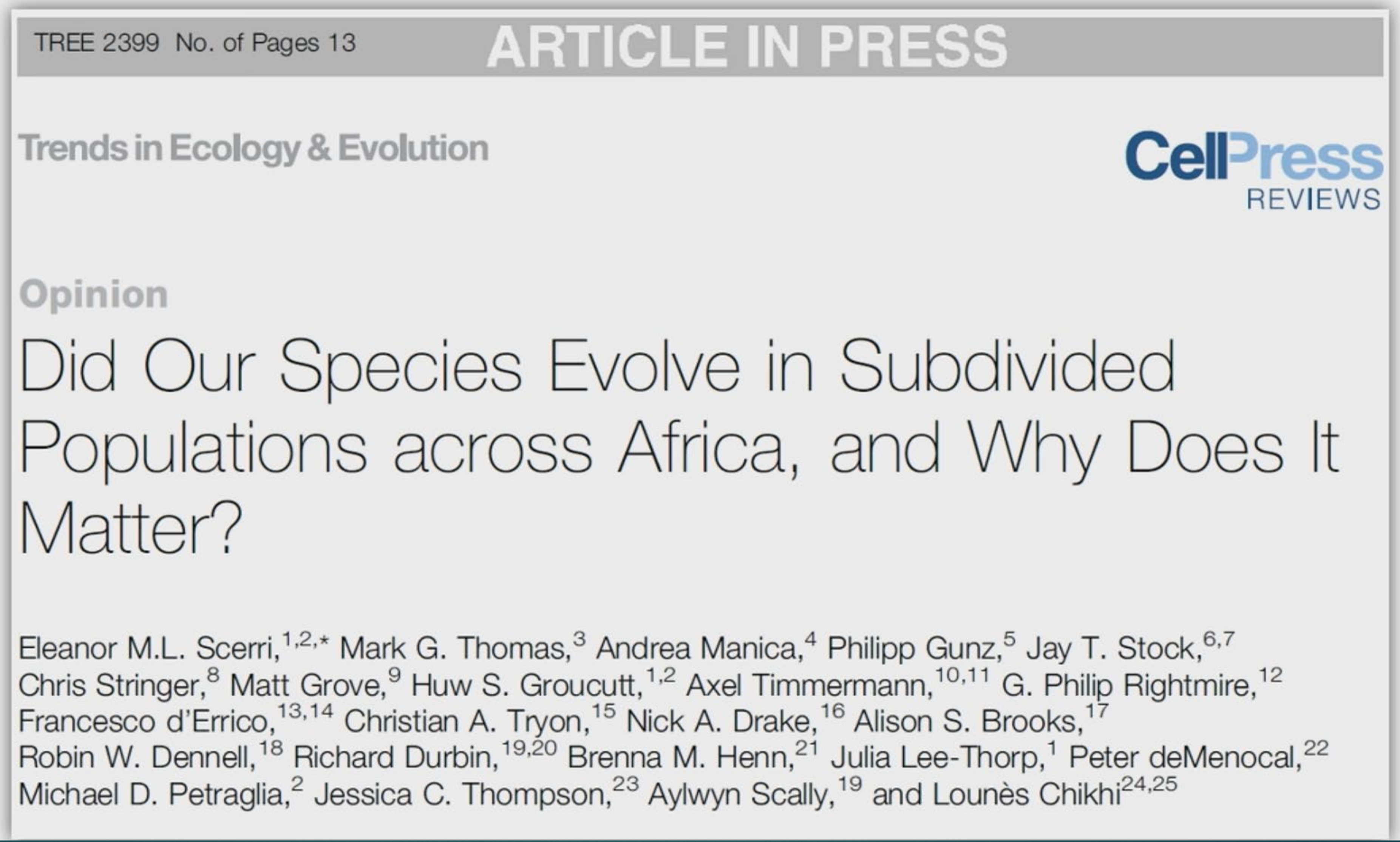
- Transitional Homo fossils present in various geographic locations in Africa
- Other locations might suffer from sampling hiatus (West Africa)
- Despite gaps in fossil record - Archeology potentially suggest continuous occupation at various geographic locations in Africa
- Is belief in single origin in Africa any longer warranted?
- Does genetics point to one PLACE?

Summary

- Africa has complex demography - Not simple tree-like structure nor single origin – rather akin to a complex river delta network that split and merge throughout space and time

- What we need is rigorous testing of models, simulation of representative models, various appropriate summary statistics, geographic and climatic modelling, more data from African aDNA studies, more sampling of all major African areas

2018: Multiregionalism theory in Africa



TREE 2399 No. of Pages 13 **ARTICLE IN PRESS**

Trends in Ecology & Evolution

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REVIEWS

Opinion

Did Our Species Evolve in Subdivided Populations across Africa, and Why Does It Matter?

Eleanor M.L. Scerri,[1,2,*] Mark G. Thomas,[3] Andrea Manica,[4] Philipp Gunz,[5] Jay T. Stock,[6,7]
Chris Stringer,[8] Matt Grove,[9] Huw S. Groucutt,[1,2] Axel Timmermann,[10,11] G. Philip Rightmire,[12]
Francesco d'Errico,[13,14] Christian A. Tryon,[15] Nick A. Drake,[16] Alison S. Brooks,[17]
Robin W. Dennell,[18] Richard Durbin,[19,20] Brenna M. Henn,[21] Julia Lee-Thorp,[1] Peter deMenocal,[22]
Michael D. Petraglia,[2] Jessica C. Thompson,[23] Aylwyn Scally,[19] and Lounès Chikhi[24,25]

ELSEVIER

Clarifying
Africa

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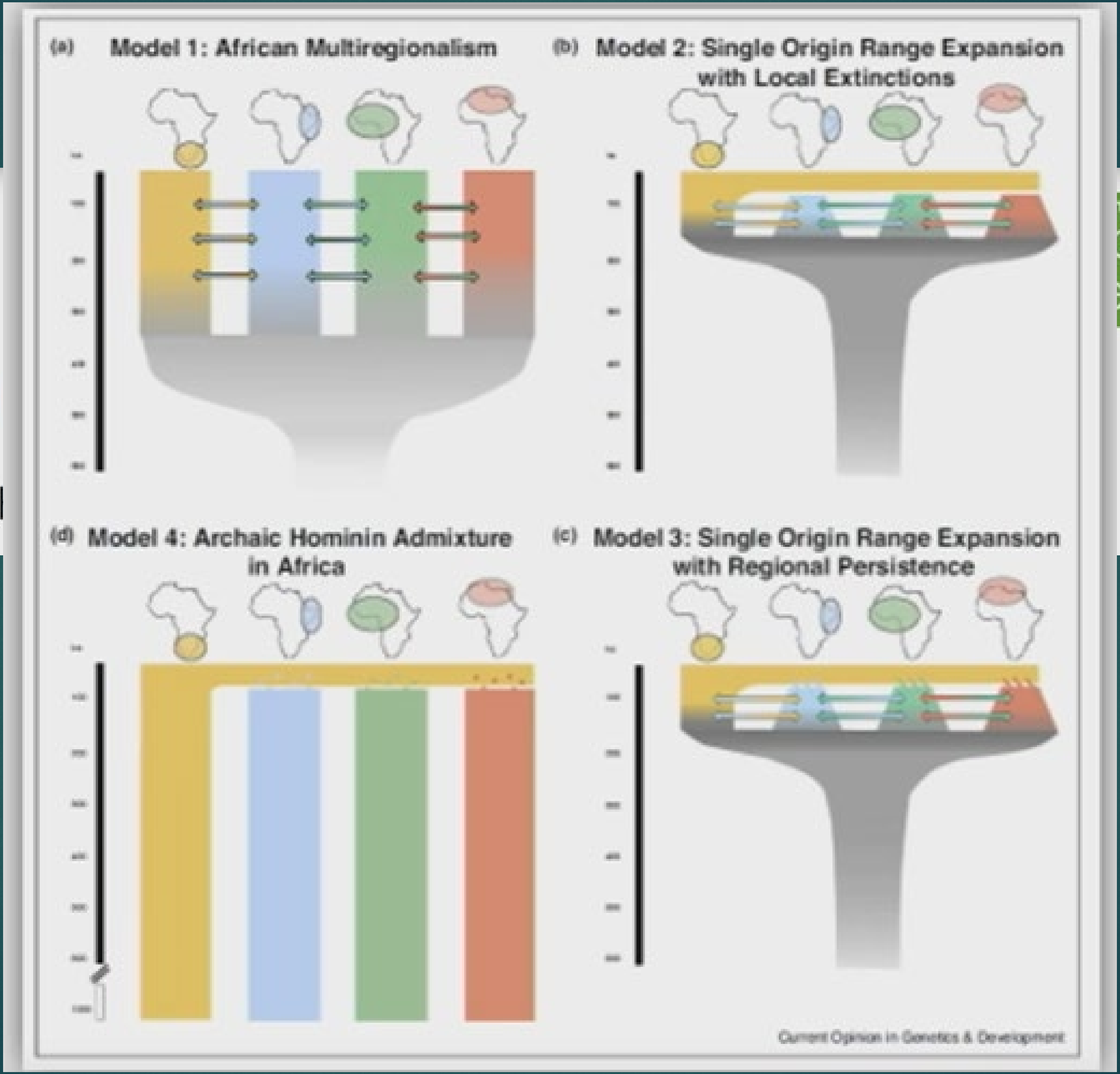


(a) Model 1: African Multiregionalism

(b) Model 2: Single Origin Range Expansion with Local Extinctions

(d) Model 4: Archaic Hominin Admixture in Africa

(c) Model 3: Single Origin Range Expansion with Regional Persistence

Current Opinion in Genetics & Development

nature

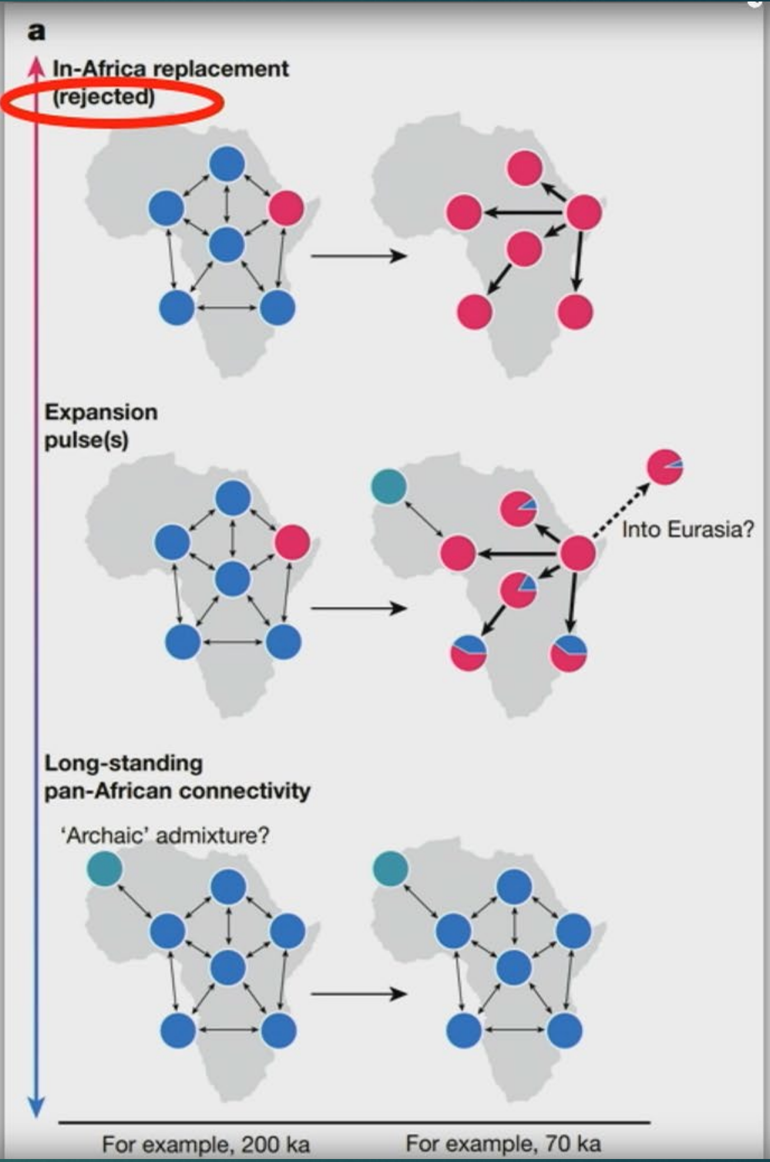
nature > review articles > article

Review | Published: 10 February 2021

Origins of modern human ancestry

Anders Bergström, Chris Stringer, Mateja Hajdinjak, Eleanor M. L. Scerri & Pontus Skoglund

Nature **590**, 229–237(2021) | Cite this article



Single origin within Africa with replacement model was rejected

Africa – The Bantu expansion

- Poor preservation conditions make it more challenging to recover ancient DNA from Africa than from colder parts of the world.

- The first ancient African genome sequence was from a late 4.5 Ka individual from Mota Cave in highland Ethiopia.

- There was a profound impact on Modern African ancestry from the agricultural expansion associated with western African–like ancestry and Bantu languages.

- This expansion followed the earliest evidence of agriculture in western Mali around 4.5 Ka and brought farming to eastern Africa by ~2 Ka as well as to southern Africa by ~1.5 Ka.

Africa: Bantu expansion

- The Bantu expansion disrupted a long-standing group of hunter–gatherers that stretched from Ethiopia to South Africa and had existed since at least ~8.1 Ka.

- In Malawi, a hunter–gatherer population that survived at least until 2.5 Ka contributed almost no ancestry to present-day Bantu-speaking groups in Malawi, suggesting a complete or near-complete replacement.

- In other parts of Africa, the Hadza of Tanzania, the Khoe-San of southern Africa, and the Aari in Ethiopia, carry more genetic ancestry from preagricultural populations

Africa: 2 to 3 Ka

- Genetic data confirms archaeological evidence of a pastoralist expansion through eastern Africa arriving in southern Africa by ~2 Ka.

- This pastoralist ancestry is also prevalent in present-day southern African Khoikhoi speakers.

- Notably, approximately 40% of the ancestry of the ~3.1 Ka Tanzanian individual was closely related to Early Neolithic individuals in the Levant .

Africa & Eurasia in Holocene

- There was extensive Holocene (post 11 Ka) gene flow between northern Africa, eastern Africa, and the Levant.

- Northeastern African populations also have additional ancestry related to Neolithic Levantine and Iranian populations, also seen in prehistoric Egypt.

- These connections emphasize the extent of Holocene interactions between Africa and Eurasia.

Ghostbusters of human origins

- Ghost populations are one of the biggest topics in human evolutionary research today. The term refers to ancient groups that no longer exist, but that left footprints of ancestry within the genomes of more recent people.
- Geneticists identify them by highlighting long, linked stretches of DNA that are unusually divergent and found only within a few populations.
- Sometimes ancient DNA turns out to match the genetic signature of a ghost population, confirming that it really existed.

John Hawks, 2023

Ghostbuster paper: don’t need to use ghost populations

- New paper by Aaron Ragsdale and collaborators. In it, they try an older—but challenging to model—way of looking at the population history of Africa during the last million years.

- Where recent work leaned on ghost populations to explain current African diversity, Ragsdale et al., 2023 (which we will review next) applied the common sense idea that past populations probably interacted a lot like recent ones have.

- They found this idea does a better job of explaining today's genetic variation, without ghost populations. Instead, ancestral Africans lived in a network of groups that have been interacting with each other for most of the last million years.

Ghosts in Africa

- For the last decade, most reconstructions of African population history have been seeing ghosts. This got started as early as 2007, when a study looked at West African and European population samples to consider how much of their genomes might have come from divergent ancestral groups. They estimated that 5% of European ancestry came from a very divergent group, which they speculated was Neandertals. This was later confirmed in the general sense by Neandertal ancient DNA evidence in 2010.

- Meanwhile, Plagnol and Wall also found that around 5% of West African ancestry likewise came from a divergent ancestral group, different from the first. They suggested that a parallel population of archaic humans had existed in Africa and mixed in with the other ancestors of modern people: a ghost population.

African genome research: only up to 20 Ka ago

- In 2012, Joseph Lachance et al. suggested that a ghost contribution could explain some aspects of the variation of whole genome sequences from African foraging groups.
- One of the strongest recent analyses, by Arun Durvasula and Sriram Sankararaman, modeled ghost introgression in West African ancestry populations, estimating between 2% and 19% of their ancestry came from unknown ancestral groups.
- No one has yet recovered DNA from hominin material in Africa older than 20,000 years. Still, geneticists have succeeded in DNA retrieval from many later sites in Africa. The oldest have given some hints about the location and relationships of human groups before early herding and farming cultures began to grow and spread.

S African aDNA

- Carina Schlebusch and coworkers made news in 2017 with some of the first ancient DNA from southern Africa. The skeletal remains they studied, only a few thousand years old, were ancestors or relatives of living people of Khoesan language-speaking groups.

- Compared to these ancient relatives, genomes of today's Khoesan peoples show a few more genealogical connections to other populations in Africa and Eurasia. The closeness of today's people partially resulted from gene flow connecting peoples during the Holocene, from the spread of Bantu-speaking peoples and trade routes connecting peoples across the continent.

Africa at 300 Ka

- Schlebusch and collaborators saw that the slightly greater genetic diversity of early Holocene people might imply a deeper evolutionary history. They suggested a model in which today's populations belong to a tree with its deepest branches starting around 300,000 years ago.

- At the same time, a group of paleoanthropologists led by Jean-Jacques Hublin provided new age estimates for early MH fossils and Middle Stone Age artifacts from Jebel Irhoud, Morocco, placing them between 250,000 and 350,000 years old.

Ghosts

- More ancient DNA work built from this timeline, showing a large role for ghost populations. Mark Lipson and collaborators in 2020 reported on ancient DNA from Shum Laka rockshelter, Cameroon. Again, these were skeletal remains of early Holocene people, their genomes showing connections to some of today's forest-living peoples of central Africa.

- As Lipson and coworkers built the tree connecting genomes from varied African populations, they found that they needed more deep branches to explain them. The resulting trees included “ghost archaics” and “ghost moderns”, unknown populations from two different nodes.

Population tree with ghost populations

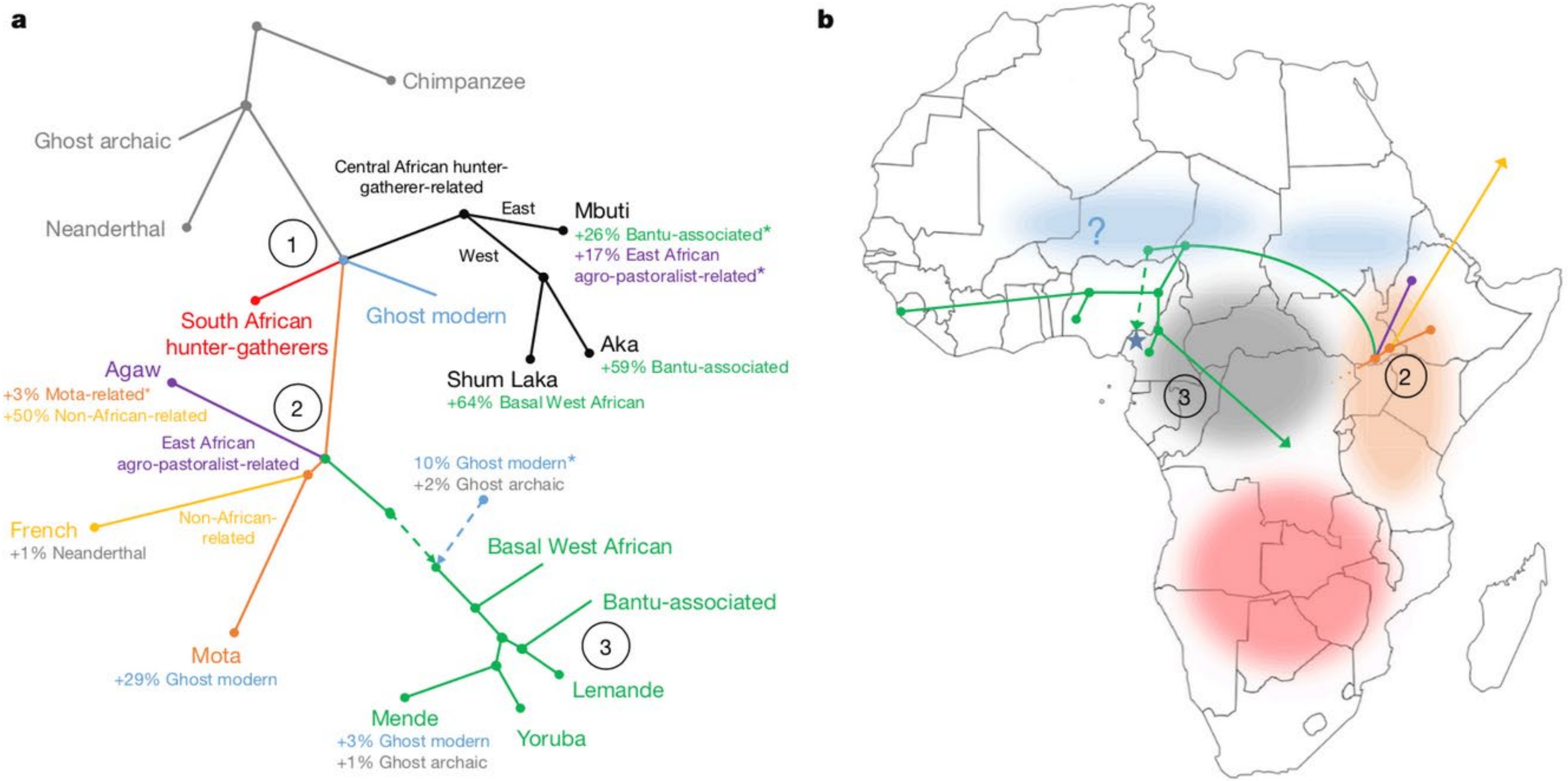


Figure showing a population tree with “ghost archaic” and “ghost modern” populations contributing to the ancestry of various African groups. From Lipson and coworkers 2020.

Gene flow and ghosts

- Genomes of individuals from the same population have a shared history of genetic drift, and also may have ancestry from other populations by gene flow.
- The lengths of haplotypes shared by different individuals and the alleles that differentiate those haplotypes are outcomes of that history, and geneticists can fit a model of population branching, ancestral population sizes, and gene flow to those data.
- Long haplotypes with many alleles separating them from other haplotypes in the population are more likely to have been introduced by gene flow. When geneticists can't find these or similar haplotypes in other population samples, they assume that they came from some population that they haven't sampled. This is a ghost population.

Weakly-structured stems

- A ghost population is one solution to a mathematical equation that relates genetic drift and gene flow when populations are strongly isolated and gene flow occurs in short bursts.

- There are other ways to look at genomes. If genetic exchanges were more continuous over time, the equation changes. What seems like a ghost may dissolve.

- Ragsdale et al. began their work with the idea that long periods of isolation between groups in Africa just weren't very realistic when you look at how recent people behave. From the outside, it may appear that many small-scale human societies have been culturally isolated. Most have been faced with exploitation by colonizing population for hundreds of years, requiring high social solidarity for cultures and languages to persist.

More gene glow between isolated groups

- But cultural persistence is not demographic isolation. Small-scale human societies have high rates of intermarriage across cultural and linguistic divides.

- Yet most geneticists have relied on models that assume early members of our species lived in small groups that remained in hermetic isolation for tens of thousands of generations.

- Ragsdale et al. wondered whether a model with more gene flow might yield different results.

Gene flow between two groups

- A model with long, continuous gene flow among the most ancient human groups matched the data better than models with isolation and ghost populations.

- Ragsdale et al. call their range of models *weakly-structured stem models*.

- In such models, today's populations all share a common ancestry from groups that mixed over time, somewhat separate but connected by gene flow. For these models to fit today's genomes, the separation with gene flow had to persist for a very long time—starting up to a million years ago.

Divergence of S Africans at later time, 100 Ka.

- Hawks: most interesting part of this study was the branching of recent groups across Africa.

- Since the 2017 work by Schlebusch and coworkers, most models have included an early differentiation of southern African from other African groups—placing the node that connects these living people as early as 300,000 years ago. The coupling with the age of the Jebel Irhoud fossils has led some anthropologists to think of this as the “origin” of our species.

- But Ragsdale et al. find a much more recent differentiation of today's groups, placing it a bit more than 100,000 years ago.

Model built on gene flow

- A model built on gene flow can have ancient high variation without isolation.
- In the weakly-structured stem models, the differentiation of today's groups can be a lot more recent, because some ancient variation between them can come from the ancestral stem that they share.

Two Stems

- As they tinkered with different kinds of models, Ragsdale et al. found a complicated nesting of ancestral groups that fit today's genomes better than any other.

- In this model, the ancestry of southern African groups like the Nama coalesced from two stem populations around 100,000 years ago.

- At around the same time, the ancestors of other populations coalesced from one of these stems. The branch leading to Neandertals itself emerged from this deep structure, one bottlenecked thread ultimately spilling across Africa into every living group.

Braided stream model vs models with isolation of groups

- When you look at the details of this model, recent events are not so different in their topology from models with ghost populations.
- For example, in this model the "stem 2" population contributes late to the ancestry of western African people, sometime before 10,000 years ago. This plays a similar role to the ghost archaics found in models with more isolation.
- But in the weakly-structured stem model, this stem population was never isolated from all others. It was one of several that interacted repeatedly during the earlier history of our species.

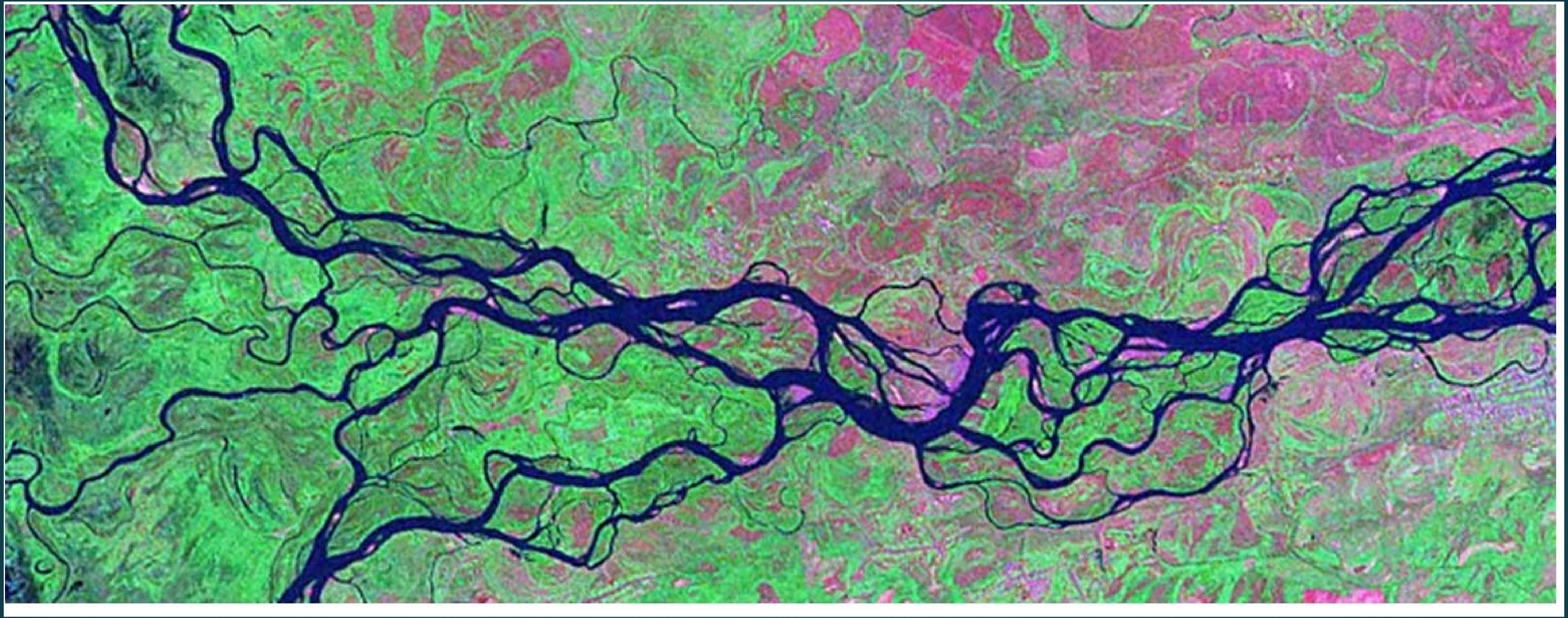
Braided stream

- In other words, this model is truly a braided stream. The groups that form early in our species' evolution continue to play new roles as time passes, remixing with each other in different combinations.

- These ancestral groups existed long before any fossils with anatomy that paleoanthropologists have recognized within the range of variation of recent people.

- Our transformation into the form that people around the world share today took place over a million years of interactions.

Image of brained streams



Structured stem population

- Many geneticists in the last years of the twentieth century thought that our species underwent a tight bottleneck at some time in the last 200,000 years.

- Much of the fuel for this idea came from analyses of the mitochondrial DNA and Y chromosome.

- But as geneticists increased the representation of African populations, they began to find that these populations did not show the same signs of a founder effect as populations of Eurasia.

Structured stem population

- Fifteen years later, researchers could examine data from across the nuclear genome, which reinforced that the diversity of African populations had endured for a very long time.

- More researchers began to think about the relationship of population structure and population growth, trying to find a combination of isolation and demographic growth that might fit the data better.

- One solution, proposed by Michael Blum and Mattias Jakobsson, was a structured stem population.

Need for matching archeological evidence

- Both models with ghost populations and structured stem models share the insight that recent populations emerged from the interaction of groups that lived long before 200,000 years ago. Some of them go back at least 700,000 years or longer.

- That makes it very important to evaluate these models with other kinds of evidence. Fossil and archaeological material are crucial to understand the succession of ancient populations, and a number of specialists in the Middle Stone Age archaeology of Africa have already begun to use structured metapopulation models in their work.

Shared material culture

- Leaders in this area of research include Eleanor Scerri, who has emphasized that shared material culture across large parts of Africa during the Middle Stone Age may reflect population contacts across the continent.
- Gene flow and cultural interactions were part of the landscape that made us human.

Lack of Fossil evidence

- But the fossil record of this crucial time and place presents some tough challenges. The implication of the weakly-structured stem idea is that the genetic structure of humans today began to form long before any fossil evidence of so-called modern humans existed.
- But the fossils give very little information about populations of Africa between a million and 200,000 years ago.
- Only a few have clear geological age estimates, and most regions of Africa have no evidence at all.

New theory of origins of *Homo sapiens* – *Ragsdale, et al. 2023*

- Newly published research appearing in the journal *Nature* (Ragsdale, A. P. et al., "A weakly structured stem for human origins in Africa," *Nature* [2023]) proposes a new interpretation regarding the origin of our species—*Homo sapiens*.

- The current dominant theory holds that *Homo sapiens* evolved from a single, local population of a previous species of the genus *Homo* somewhere in Africa, between roughly 300,000 and 100,000 years ago. According to this scenario, the new species then spread widely, eventually replacing the other existing species of genus *Homo*.

Ragsdale, et al. 2023

- However, the relatively small number of human fossils known from Africa and the lack of ancient DNA during that time period have made a more precise tracing of the evolution of modern humans problematic.

- The new study, based primarily on detailed genetic studies of recent populations, posits that *Homo sapiens* evolved from merging multiple, geographically distinct people that maintained close enough ties for gene flow to cause their evolution to occur roughly simultaneously despite superficial morphological differences.

Modern humans may descend from two or more genetically distinct streams that split but continued to occasionally mix over time in Africa.

- New modeling study of complex origin of *H. sapiens*: rejecting the long-held argument that modern humans arose from one place in Africa during one period in time.

- Ragsdale analyzed the genomes of 290 living people: four current groups were used: 44 new sequenced genomes from the Nama (Khoe-San from South Africa), 85 from the Mende (from Sierra Leone), 23 from the Gumuz (descendants of a group from hunter-gatherers from Ethiopia) and 46 from farmers from East Africa (Amhara and Oromo from Ethiopia, very similar genetically); also Europeans and a Neandertal

Carl Zimmer, 2023

2 populations

- Ragsdale concluded that modern humans descended from at least two populations that coexisted in Africa for a million years before merging in several independent events across the continent.
- Modern humans arose after a complex history of intermingling between ancestors on at least two different but closely related evolutionary branches
- Created many models of different populations existing in Africa over different periods of time and then observed which ones could produce the diversity of DNA found in people alive today. They tested hundreds of possible scenarios of gene flow between populations in different parts of Africa.

A new model of the origin of human evolution in Africa

- This final new model, just published in *Nature*, claims that at least two evolutionary branches of *Homo sapiens* split (but continued to mix) over hundreds of thousands of years.
- This so-called "weakly structured stem" (made up by a mixture of these two branches) is proposed to have contributed to the formation of an ancestral African human group, which then branched off into contemporary African populations, as well as populations living outside of Africa

H. naledi not a relative

- The authors predict that, according to this model, 1-4% of genetic variation in modern human populations can be attributed to variation in the two different, but closely related and anatomically-similar African *Sapiens* branches/ stem populations
- This model may have important consequences for the interpretation of the fossil record.
- Owing to migration between the branches, these multiple lineages were probably morphologically similar, which means morphologically divergent hominid fossils (such as *Homo naledi*) are unlikely to represent branches that contributed to the evolution of *Homo sapiens*.

Arose From Multiple Closely Related Populations

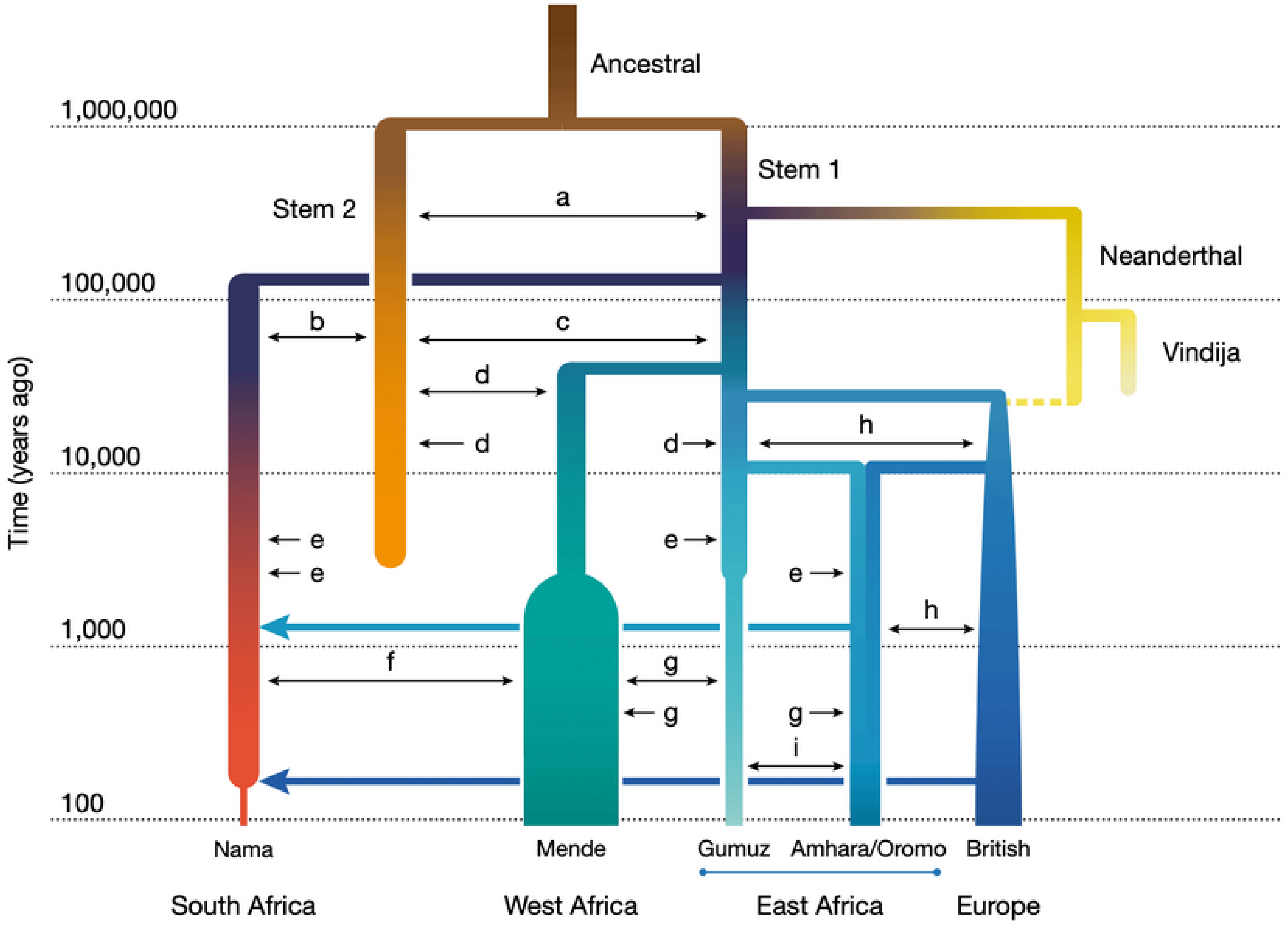
- The model suggests the earliest African population split among early humans that is detectable in contemporary populations occurred 120,000 to 135,000 years ago, after two or more weakly genetically differentiated *Homo* populations had been mixing for hundreds of thousands of years.

- After the population split, people still migrated between the stem populations, creating a weakly structured stem.

- This offers a better explanation of genetic variation among individual humans and human groups than do previous models,

Stem1 and Stem2 populations

- As far back as a million years ago, the ancestors of our species existed in two distinct populations. = Stem1 and Stem2.
- About 600,000 years ago, a small group of humans budded off from Stem1 and went on to become the Neanderthals.
- But Stem1 endured in Africa for hundreds of thousands of years after that, as did Stem2.



One of the population models from Ragsdale and coworkers, showing a long ancestry in two stem populations for up to a million years, with interbreeding between them during that time.

2 Stems

- If Stem1 and Stem2 had been entirely separate from each other, they would have accumulated a large number of distinct mutations in their DNA.
- Instead, they found that they had remained only moderately different — about as distinct as living Europeans and West Africans are today.
- The scientists concluded that people had moved between Stem1 and Stem2, pairing off to have children and mixing their DNA.

Khoe San at 120 Ka and 3 other fusions

- The model does not reveal where the Stem1 and Stem2 people lived in Africa. And it’s possible that bands of these two groups moved around a lot over the vast stretches of time during which they existed on the continent. About 120,000 years ago, the model indicates, African history changed dramatically.

- In southern Africa, people from Stem1 and Stem2 merged, giving rise to a new lineage that would lead to the Nama (Khoe San) and other living humans in that region.

- Elsewhere in Africa, a separate fusion of Stem1 and Stem2 groups took place. That merger produced a lineage that would give rise to living people in West Africa and East Africa, as well as the people who expanded out of Africa.

Stem1 and Stem2

- It's possible that climate upheavals forced Stem1 and Stem2 people into the same regions, leading them to merge into single groups.

- Even after these mergers 120,000 years ago, people with solely Stem1 or solely Stem2 ancestry appear to have survived. The DNA of the Mende people showed that their ancestors had interbred with Stem2 people just 25,000 years ago. Stem2 was somewhere around West Africa

- Dr. Scerri speculated that living in a network of mingling populations across Africa might have allowed modern humans to survive while Neanderthals became extinct. In that arrangement, our ancestors could hold onto more genetic diversity, which in turn might have helped them endure shifts in the climate, or even evolve new adaptations. This diversity at the root of our species may have been ultimately the key to our success.

A weakly structured stem for human origins in Africa – A. P. Ragsdale, et al., 2023

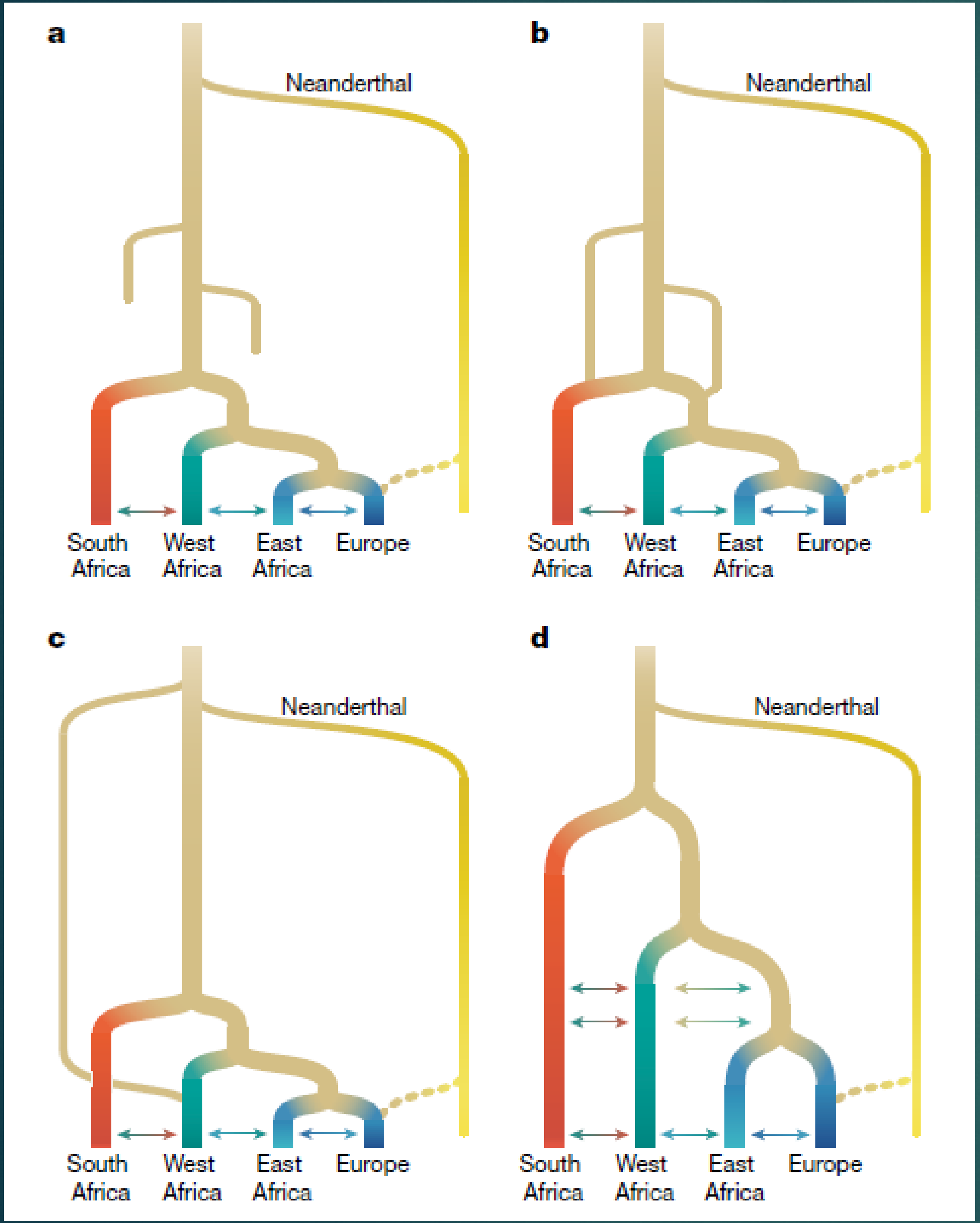
- Despite broad agreement that Homo sapiens originated in Africa, considerable uncertainty surrounds specific models of divergence and migration across the continent.
- We infer detailed demographic models for populations across Africa, including eastern and western representatives, and 44 newly sequenced whole genomes from Nama (Khoe-San) individuals from southern Africa.
- We infer a reticulated (networked) African population history in which present-day population structure dates back to MIS 5 (130-80 Ka). The earliest population divergence among contemporary populations occurred 120,000 to 135,000 years ago and was preceded by links between two or more weakly differentiated ancestral Homo populations connected by gene flow over hundreds of thousands of years.

A weakly structured stem for human origins in Africa

- Such weakly structured stem models explain patterns of polymorphism that had previously been attributed to contributions from archaic (ghost) hominins in Africa.

- In contrast to models with archaic introgression, we predict that fossil remains from coexisting ancestral populations should be genetically and morphologically similar

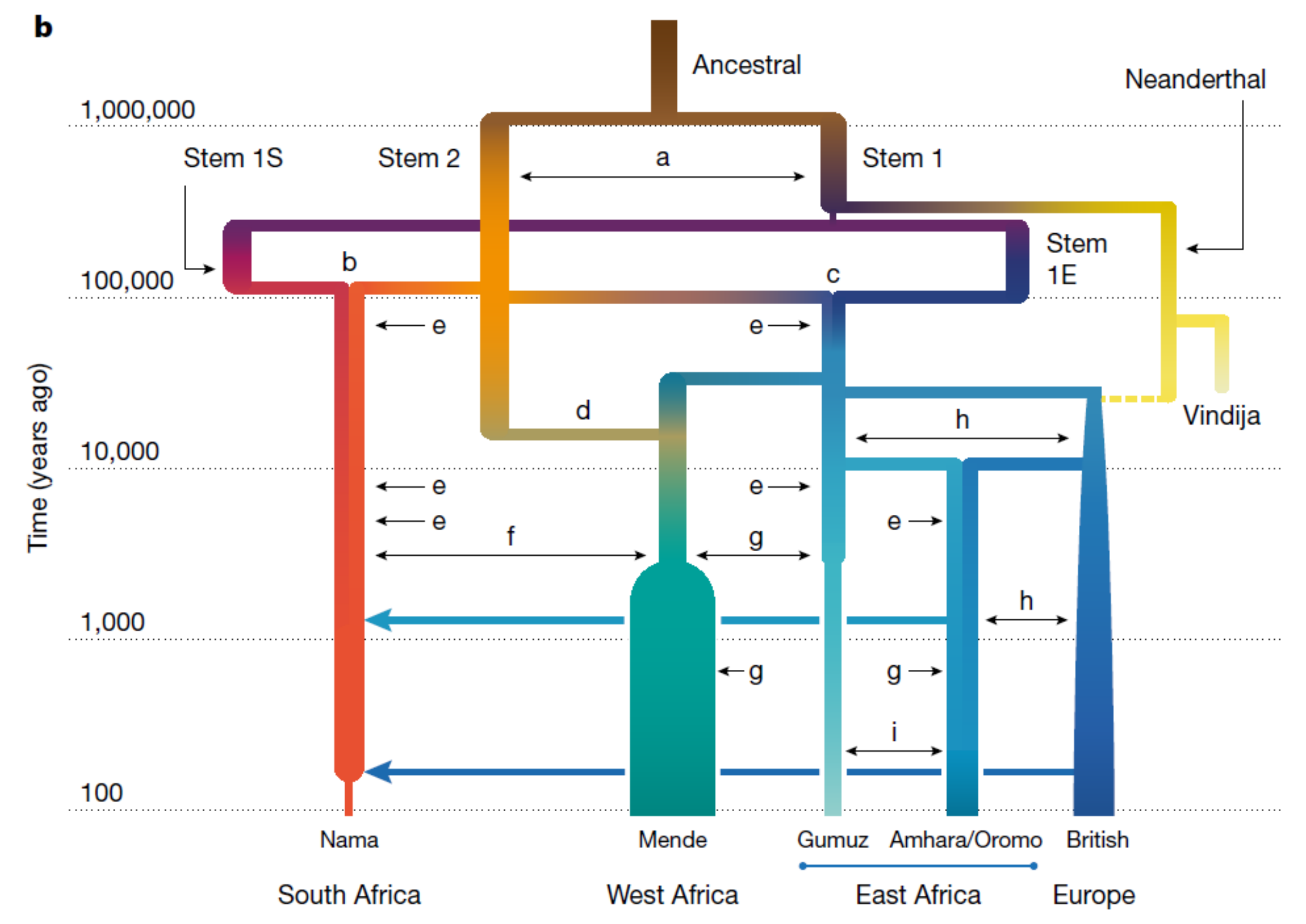
- Only an inferred 1–4% of genetic differentiation among contemporary human populations can be attributed to genetic drift between stem populations.



- Proposed conceptual models of early human history in Africa.

- A. Recent expansion,
- B. Recent expansion with regional persistence,
- C. Archaic admixture,
- D. African multiregional.

- The models have been designed to translate models from the paleoanthropological literature into genetically testable demographic models.



A weakly structured stem best describes two-locus statistics. **a**,**b**, In the two models of early population structure, continuous migration (**a**) and multiple mergers (**b**), models that include ongoing migration between stem populations out perform those in which stem populations are isolated. Most of the recent populations are also connected by continuous, reciprocal migration that is indicated by double-headed arrows . These migrations last for the duration of the coexistence of contemporaneous populations with constant migration rates over those intervals. The merger-with stem-migration model outperformed the continuous migration model. The letters a–i represent continuous migration between pairs of populations

Mergers

- The Middle to Late Pleistocene was a critical period of change. During the late Middle Pleistocene, the multiple-merger model indicates three major stem lineages in Africa, tentatively assigned to southern (stem 1S), eastern (stem 1E) and western/central Africa (stem 2).
- Stem 1S contributes 70% to the ancestral formation of the Khoe-San. The extent of the isolation at 400 ka between stem 1S, stem 1E and stem 2 suggests that these stems were not proximate to each other.
- Models with a period of divergence, isolation and then a merger event out-performed other models with bifurcating divergence and continuous gene flow.

Mergers

- We observed two merger events.
  - The first, between stem 1S and stem 2, resulted in the formation of an ancestral Khoe-San population around 120 ka.
  - The second event, between stem 1E and stem 2 about 100 ka, resulted in the formation of the ancestors of eastern and western Africans, including the ancestors of people outside Africa.
- Evidence for archaic hominin admixture in Eurasia has bolstered the plausibility of archaic hominin admixture having also occurred in Africa.
- Previous work that sought to explain patterns of polymorphism inconsistent with a single-origin model therefore focused on archaic hominin admixture as an alternative model, by referring to additional (ghost) branches required to fit the data as archaic and assuming (or inferring) deep divergences.

Contrasting ancestral structure models

- A weakly structured stem model better captures the apparently inconsistent patterns of polymorphisms.

- Preferring models of a weakly structured stem to archaic-admixture models has a range of implications.

- With a weakly structured stem, there is no need to posit that an archaic hominin population in Africa remained reproductively isolated from the ancestral human lineage for hundreds of thousands of years before the initiation of gene flow. Instead, there would simply have been continuous or recurrent contact between two or more groups present in Africa.

Models

- This potentially allows predictions of their model to be related to the fossil record. Some *H. sapiens* fossils, such as those from Iwo Eleru in Nigeria (13 ka), Ishango in the Democratic Republic of Congo (20–25 ka) and Nazlet Khater in Egypt (35–40 ka), have morphological features that may reflect recent gene flow from archaic hominins, and have been used in support of previously inferred archaic admixture scenarios.

- The weakly structured stem model is not incompatible with archaic admixture having occurred in the ancestry of these fossils, but would imply, by contrast, that such individuals are unlikely to have contributed much ancestry to contemporary humans.

Overturns previous beliefs that a single African population gave rise to all humans.

- Contributions from archaic hominins were unlikely to have significantly affected *Homo sapiens’* evolution.

- The most morphologically divergent fossils are unlikely to represent branches that contributed appreciably to contemporary human ancestries.

- Homo sapiens evolved from multiple diverse populations across Africa,

Climate effects

- Shifts in wet and dry conditions across the African continent between in 140 ka and 100 ka may have promoted these merger events between divergent stems.
- After these merger events, the stems subsequently fractured into subpopulations which persisted over the past 120 ka.
- These subpopulations can be linked to contemporary groups despite subsequent gene flow across the continent.

Stem 2 in western Africa

- We also find that stem 2 continued to contribute to western Africans during the Last Glacial Maximum (26 ka to 20 ka), indicating that this gene flow probably occurred in western and/or central Africa.
- Such an interpretation is reinforced by differential migration rates between regions; that is, the gene flow from stem 2 to western Africans is estimated to be five times that of the rate to eastern Africans during this period.
- End Ragsdale et al.

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