Science Update, November 2022

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Finland: a burial of a child and her dog

Finland: a burial of a child and her dog

- A Stone Age burial in Finland holds the remains of a child, as well as an assortment of grave goods, bird feathers, canine hairs and plant fibers, giving archaeologists insight into burial practices from that time period.
- First discovered in 1991 in Majoonsuo, an archaeological site near the town of Outokumpu in eastern Finland, the grave contains the teeth of a child, who, based on a dental analysis, died between the ages of 3 and 10.
- Feathers of waterfowl that could have been used to create a bed of down feathers for the child; they also found a single falcon feather fragment.
- At the base of the burial lay 24 fragments of mammalian hair. While many of the hairs were badly degraded, the researchers determined that three came from a canine, possibly a wolf or a dog that may have been laid at the feet of the child as part of the burial. It's also possible that the canid hairs came from clothing, such as footwear crafted from dogskin or wolfskin, worn by the child.
- Because soil in this area of Finland is highly acidic, the archaeologists were surprised at how well some of the organic remains have lasted over the centuries.

CRISPR cancer trial success paves the way for personalized treatments

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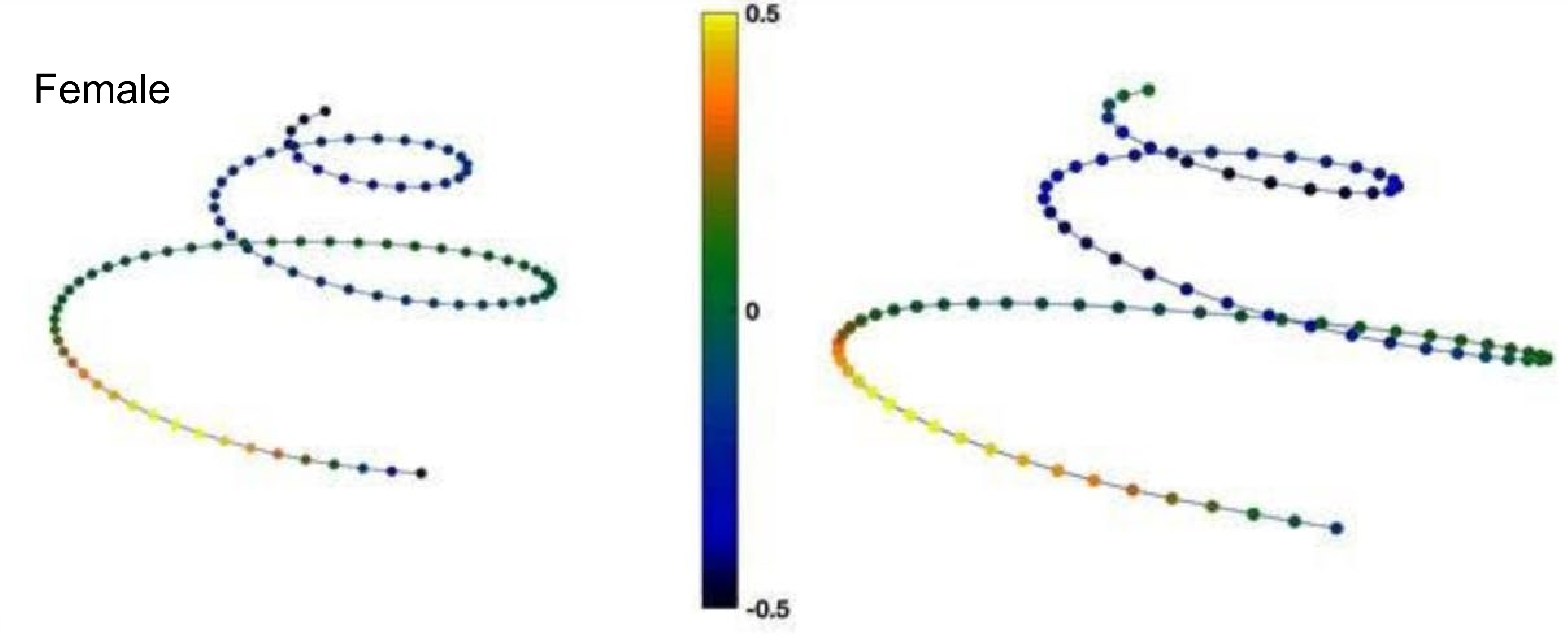
- Most complicated therapy ever’ tailors genome-edited immune cells to attack tumors.
  A small clinical trial has shown that researchers can use CRISPR gene editing to alter immune cells so that they will recognize mutated proteins specific to a person’s tumors. Those cells can then be safely set loose in the body to find and destroy their target.
- It is the first attempt to combine two hot areas in cancer research: gene editing to create personalized treatments, and engineering immune cells called T cells so as to better target tumors. The approach was tested in 16 people with solid tumors, including in the breast and colon.
- UCLA: mutations that are found in the tumor but not in the blood. This had to be done for each person in the trial. took blood samples from each participant and used CRISPR genome editing to insert the receptors into their T cells

The Shape of the Cochlea is an Indicator of Sex: inner ear accommodation for female ability to hear higher pitch



Average female (left) and male (right) shapes for the cochlear spiral curve, whose torsion has been coded on a coloured scale. While the two forms are oriented in the same way, the geometric differences are visible. Credit: C. Samir, A. Fradi, and J. Braga

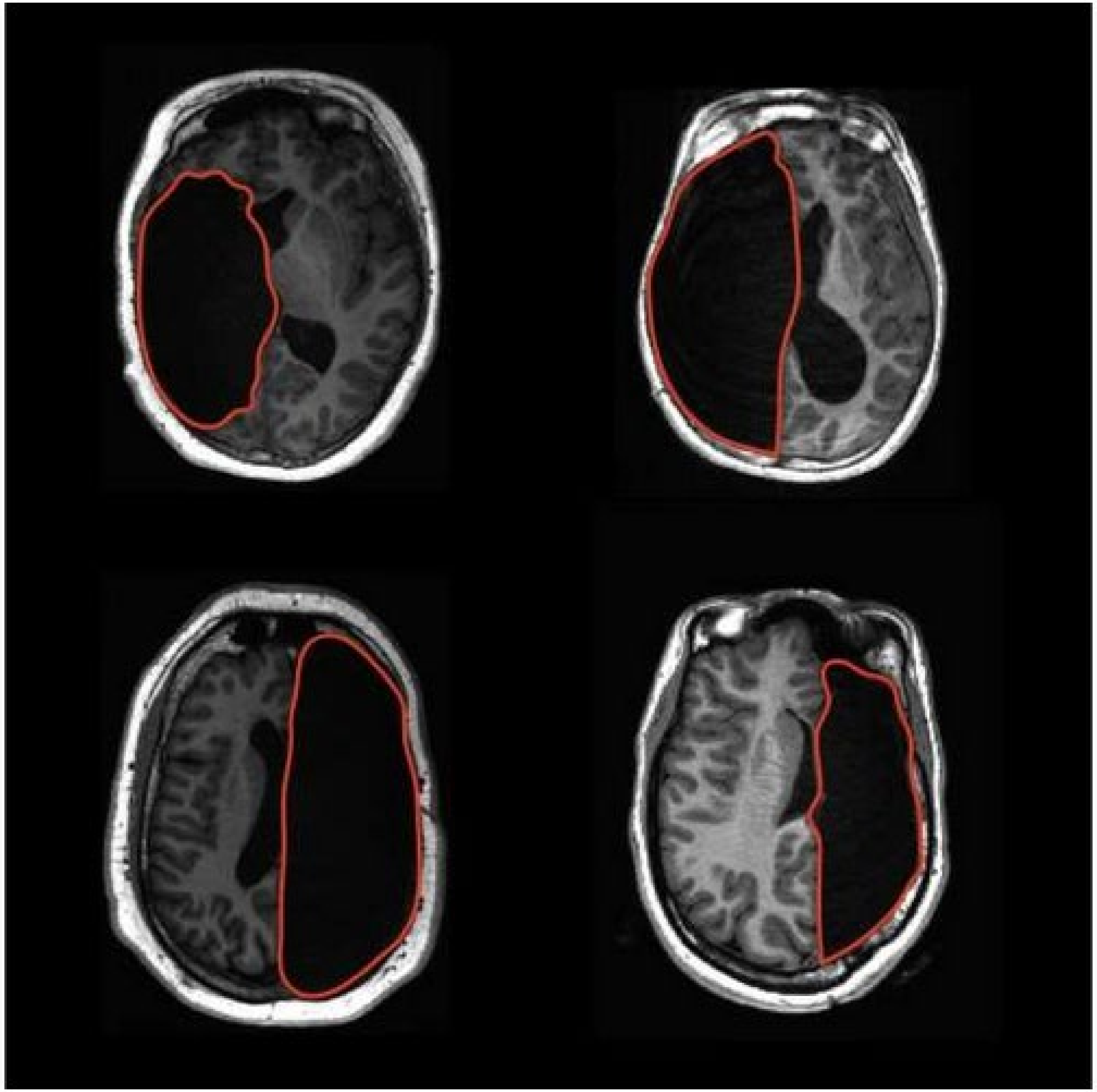
One in ten older Americans has dementia, according to first nationally representative study in more than 20 years

- In the first nationally representative study of cognitive impairment prevalence in more than 20 years, Columbia University researchers have found almost 10% of U.S. adults ages 65 and older have dementia, while another 22% have mild cognitive impairment.
- People with dementia and mild cognitive impairment are more likely to be older, have lower levels of education, and to be racialized as Black or Hispanic.
- Men and women have similar rates of dementia and mild cognitive impairment.
- Based on data on 3,500 individuals (mean age of 76) enrolled in the nationally representative Health and Retirement Study, an ongoing longitudinal nationally representative study of people 51 years and older with staggered entry dates from 1992 to 2022 and follow-up ranging from 4 to 30 years

Jennifer J. Manly, et al., 2022

Disparities in Dementia

- Rates of dementia and mild cognitive impairment rose sharply with age: 3% of people between 65 and 69 had dementia, rising to 35% for people age 90 and over.
- Every 5-year increase in age was associated with higher risk of dementia
- First accurate study of Blacks and Hispanics: higher risk of developing cognitive impairment because of structural racism and income inequality
- Each additional year of education was associated with a decrease in risk of dementia



Top row: Removal of the left hemisphere. Bottom row: Removal of the ...

Complete hemispherectomy—or a surgical removal of one hemisphere to control epileptic seizures—during childhood.

Study of 40 hemispherectomy patients

Brain plasticity

- An unprecedented study of brain plasticity and visual perception has found that people who, as children, had undergone surgery removing half of their brain, correctly recognized differences between pairs of words or faces more than 80% of the time. Considering the volume of removed brain tissue, the surprising accuracy highlights the brain's capacity—and its limitations—to rewire itself and adapt to dramatic surgery or traumatic injury.
- Neuroplasticity is a process that allows the brain to change its activity and rewire itself, either structurally or functionally, in response to changes in the environment. And even though brain plasticity peaks early in development, our brains continue to change well into adulthood.
- As humans age, the two halves of our brains, called hemispheres, become increasingly specialized. Even though this division of labor is not absolute, the two hemispheres adopt distinct chief responsibilities: The left hemisphere matures into the primary place for reading printed words, and the right hemisphere matures into the primary place for recognizing faces.

Hemispherectomies

- Astoundingly, the single remaining hemisphere supported both word recognition and facial recognition functions. The average accuracy exceeded 80%.
- In direct comparisons between matching hemispheres in patients and controls, patients' accuracy on both face and word recognition was comparable regardless of the hemisphere removed.

Genetics of Height

- Study of 5.4 million people revealed that over 12,111 genetic variants have an influence on height differences among those with European ancestry
- Common variants associated with height made up about 20% of genome and were clustered in regions linked to medical conditions affecting skeletal growth.
- Each of 12 K variants is found in more than 1% of population. Can explain 40% of height differences
- Each genetic variant was a single nucleotide polymorphism
- 20% of other 60% due to environment; 40% due to less common variants

Evidence for the cooking of fish at 780 Ka at Gesher Benot Ya’aqov, Israel

- Scientists have found the earliest known evidence of cooking at an archaeological site in Israel. The detailed study of fish teeth unearthed at the Gesher Benot Ya’aqov site, situated on the edge of the ancient lake Hula, revealed that some of our early ancestors — most likely Homo erectus — were able to cook fish.
- Hula lake would have been shallow, and it might have been easy to catch large fish like the extinct Luciobarbus longicep, which could grow up to 6.5 feet (2 meters), by hand.
- The shift to eating cooked meals meant humans expended less energy on the intensive work of searching for and digesting fresh, raw food, freeing up more time in which to develop new social and behavioral systems.

I. Zohar, et al., 2022

H. erectus ate cooked fish

- Layers of sediment where Acheulean stone tools were found were associated with a high number of fish teeth from two particular species (Luciobarbus longiceps and Carasobarbus canis) that were part of the carp family but now extinct.
- The fish were cooked at temperatures between 392 and 932 degrees Fahrenheit (200 and 500 degrees Celsius); it is clear that they were not cooked directly in fire and were not thrown into a fire as waste or as material for burning
- The team was also able to determine that fish were a regular part of the diet — they weren't just a seasonal treat or a last resort when other sources of food were scarce. The researchers did this by looking at the geochemical composition of oxygen and carbon isotopes in the enamel of the teeth to figure out during which season the fish died. The results suggested that they were cooked and eaten year round.

Earliest Prior Cooking date

- Until this study, the earliest hard evidence of the use of fire to cook was by Neanderthals and Homo sapiens, who cooked starchy roots in what’s now South Africa about 170,000 years ago.

Last Glacial Maximum

- Around 30,000 years ago, a cooling event caused huge glaciers to start to grow in the northern hemisphere.
- Known as the Last Glacial Maximum, these icesheets extended their reach over much of northern Europe, forcing surviving plants, animals and any humans into the south.
- This would last for around 10,000 years, until a pronounced warming on the continent brought about momentous change.
- By 14,000 years ago, the Late Glacial Interstadial (warming) was in full swing. This warm period opened up many of the previously uninhabitable regions

Skeleton of Cheddar Man, 1st Englishman?

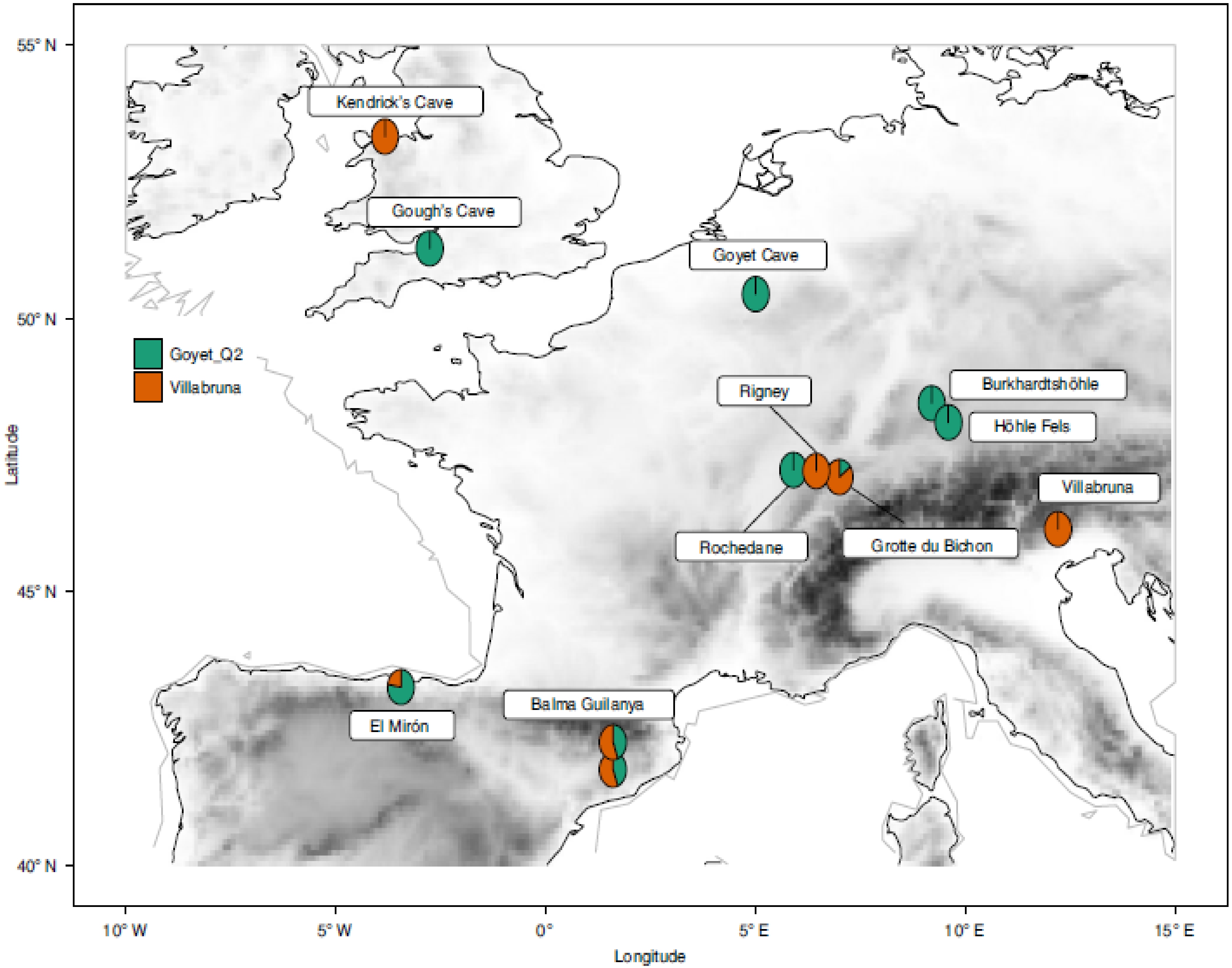
Cheddar Man: Mesolithic Britain's blue-eyed boy

Ancient DNA from Cheddar Man, a Mesolithic skeleton found in 1903 at Gough's Cave in Cheddar Gorge,

Cheddar Man lived around 10,000 years ago and is the oldest almost complete skeleton of our species, *Homo sapiens*, ever found in Britain.

Had dark skin and most of them had pale colored eyes, either blue or green, and dark brown hair; lactose intolerant

Britain was attached to continental Europe


Kendrick's Cave
Gough's Cave
Goyet Cave
Goyet_Q2
Villabruna
Rigney
Burkhardtshöhle
Höhle Fels
Villabruna
Rochedane
Grotte du Bichon
El Mirón
Balma Guilanya
55° N
50° N
45° N
40° N
Latitude
10° W
5° W
0°
5° E
10° E
15° E
Longitude

Post glacial Britain at 14 Ka

- Oldest DNA reveals two distinct populations in late Ice Age Britain.
- The two populations lived only around 1,000 years apart, and yet were found to be genetically and culturally distinct from each other.
- Following the peak of the last Ice Age, human populations in Europe went on the move, incl. to Britain
- DNA was retrieved from ancient human remains discovered in Gough's Cave, Somerset, and then compared to other human remains found in Kendrick's Cave, Wales.
- Prior study of Cheddar Man, that western hunter-gatherers were in Britain by around 10,500 years ago, but we didn't know when they arrived in Britain

S. Charlton, et al. 2022

Britain: 2 genetically different groups in late Glacial period

- The Gough’s Cave individual shows clear affinity to Goyet Q2 ancestry, whereas the Kendrick’s Cave individual shows affinity to Villabruna (WHG).
- A Late Upper Palaeolithic individual from Gough’s Cave probably traced all its ancestry to Magdalenian-associated individuals closely related to those from sites such as El Mirón Cave, Spain, and Troisième Caverne in Goyet, Belgium.
- The Kendrick’s Cave individual traces its ancestry to groups who expanded across Europe during the Late Glacial and are represented at sites such as Villabruna, Italy.
- Furthermore, the individuals differ not only in their genetic ancestry profiles but also in their mortuary practices and their diets and ecologies,

New Chinese *H. erectus*

New Chinese *H. erectus,* 1 Ma

- A new human skull fossil in Central China's Hubei province. Finding could be the best-preserved skull fossil of *Homo erectus* from about 1 million years ago ever found in the hinterland of the Eurasian region

- Well-preserved fossil was found on May 18 in an excavation site known as Xuetangliangzi in the Yunyang district of Shiyan city.
- Skull has not been fully excavated from the ground yet, but the part that has been exposed, including the frontal bone, eye sockets and left cheekbone and temporal bone, indicate that the skull's structure is intact. Features the typical characteristics of *Homo erectus;* named the No 3 skull of Yunxian Man
- The Xuetangliangzi site is well known because of a milestone discovery of two hominid crania, in 1989 and 1990. The two fossils, dating from 800,000 to 1.1 million years ago, were named by scientists the No 1 and No 2 skulls of Yunxian Man (Yunyang district was then known as Yunxian county). However, when unearthed, the two fossils were found to be severely deformed.

Unearthing Neanderthal population history using nuclear and mitochondrial DNA from cave sediments

- To date, complete or partial nuclear genome sequences have been recovered from the skeletal remains of only 23 archaic hominin individuals
- Sediments from caves contain hominin mitochondrial and nuclear DNA that can be enriched, sequenced, and analyzed to reveal the genetic histories of past occupants even in the absence of their skeletal remains.
- Although DNA sequencing from hominin skeletal remains allows the association of ancient populations with specific places in time and space, many archaeological sites lack associated hominin remains, limiting the scope of genetic analyses.
- Even when ancient hominin remains are found, they often do not cover the full time span of a site or sampling them for DNA may not be possible.

Benjamin Vernot, et al., 2021

Don’t need fossils: Dirty DNA

- The fossil record is particularly sparse for Pleistocene hominins, leaving large gaps in our understanding of the genetic histories of archaic and early modern humans.
- Study developed a set of probes for hybridization capture that targets 1.6 million ancestry informative positions in the hominin nuclear genome, specifically at loci with high mammalian sequence divergence.
- Then developed computational methods to deplete residual microbial and faunal DNA sequences.
- This work demonstrates that detailed genetic analyses are now possible for many more archaeological sites than previously thought, with DNA from abundant sediments allowing dense time-series studies that are independent of the fossil record.

Dirty DNA

- Applied these methods to explore the history of Neanderthal populations in western Europe and southern Siberia using sediment samples from three Pleistocene caves: 1 - Galería de las Estatuas, a site in northern Spain. with 40 thousand years of Neanderthal occupation but that is genetically unexplored,
- 2 - Chagyrskaya and 3 - Denisova Caves, which have previously yielded high-coverage genomes of two Neanderthals and one Denisovan hominin.
- In total, we recovered Neanderthal or Denisovan mtDNA from >60 sediment samples and nuclear DNA from 30 of these.

Dirty DNA

- For Chagyrskaya and Denisova Caves, our phylogenetic results from sediment DNA were consistent with previously published results from skeletal remains, confirming the accuracy of our approach.
- At Galería de las Estatuas, we recovered Neanderthal DNA from layers spanning nearly the entire stratigraphy, and identified a population turnover ~100,000 years ago accompanied by a loss of mtDNA diversity.
- Associated this turnover with two putative radiations in Neanderthal history.

mtDNA and nuclear DNA in sediments

- To date, complete or partial nuclear genome sequences have been recovered from the skeletal remains of 23 archaic hominin individuals: 18 Neanderthals from 14 sites across Eurasia (mostly in Europe), four Denisovans, and the offspring of a Neanderthal mother and a Denisovan father (Denisova 11). Although numerous Paleolithic sites have been excavated, relatively few have yielded skeletal remains of hominins, which are often concentrated in one or a few strata
- Presence of mtDNA genome: from Estatuas pit layer 4 was most similar to the mtDNA of the ~120 ka old Neanderthal from Hohlenstein-Stadel (HST), Germany, which falls basal to all other known Neanderthal mitochondrial genomes
- Presence of nuclear DNA: All showed significant levels of C-to-T substitutions in DNA fragments overlapping our targeted SNPs, consistent with the presence of ancient nuclear DNA

2 Neandertal population divergences

- The apparent clustering of branching times suggests two distinct radiations of Neanderthal populations:
  - Mezmaiskaya 1, Vindija 33.19, Chagyrskaya 8, and Estatuas pit II/layer 2 and pit I/layers 2 and 3 diverged from each other ~100 to 115 ka ago,
  - whereas the Altai, HST, Scalding, and Estatuas pit I/layer 4 Neanderthals and the lineage leading to Vindija 33.19 and Chagyrskaya 8 diverged from each other ~135 ka ago.
  - These radiation events therefore occurred during the early part of the Late Pleistocene and may be associated with changes in climate and environmental conditions during the last interglacial.

Sediment DNA

- Results also show that the recovery of hominin DNA from sediment may not be limited to population samples.
- It may be possible in the future to also assess heterogeneity in the genetic composition of past populations based on the analysis of sediment DNA.
- However, the presence of Neanderthal DNA in layer 7 of Chagyrskaya Cave highlights the need to evaluate evidence for post-depositional mixing of sediments when assigning DNA sequences from sediment to specific layers, as is common practice when interpreting finds of artifacts, skeletal remains, and other archaeological materials.

Extinction of Neandertals: sex? -- C. Stringer & Lucile Crété, 2022

- How the Neanderthals died out remains one of the biggest mysteries in human evolution.
- A new theoretical paper by C. Stringer & L. Crété proposes that *Homo sapiens* may have been responsible for the extinction of Neanderthals not by violence, but through sex instead. Making love, not war.
- Early MH dispersals:
  - Fossils from Apidima Cave (Greece) suggests an earlier dispersal of our species that reached Europe more than 200 ka ago; data from ancient DNA suggesting gene flow between the early H. neanderthalensis and H. sapiens lineages during the time span of the later Middle Pleistocene.
  - New data from sites like Zlatý kůň (Czechia), Bacho Kiro Cave (Bulgaria), Grotta del Cavallo (Italy) and Grotte Mandrin (France) indicate that there were pre-Aurignacian dispersals that potentially placed H. sapiens populations alongside the persisting Neanderthals. While some of these populations can be related to later Eurasians, others seem to represent now-extinct lineages of H. sapiens.

Neandertal extinction: absorption into H. sapiens populations

- Furthermore, it is now known from a growing body of genetic data that this co-existence of H. neanderthalensis and H. sapiens was accompanied by bouts of interbreeding between the two species.
- This paper reviews the growing evidence for early dispersals of H. sapiens into Europe and discusses how these populations might have interacted with each other, and the social backdrop of these genetic exchanges.
- It is suggested here that a continuing absorption of Neanderthal individuals into H. sapiens groups could have been one of the factors that led to the demise of the Neanderthals.

Locations


Ust'Ishim
[=/> 45 ka]
La Cotte de St Brelade
[< 48 ka]
Zlatý Kůň
[> 40 ka]
Grotte Mandrin
[~ 54 ka]
Peștera cu Oase
[=/> 40 ka]
Bacho Kiro
[~ 44 ka]
Grotta del Cavallo
[~ 43 ka]
Apidima
[=/> 210 ka]
Misliya [~ 180 ka]
Qafzeh [~ 100 ka]
Skhul [~ 100 ka]
Jebel Irhoud
[~ 300 ka]
0
1,000
2,000 km

Basal vs Derived nomenclature

- Since 2019, a succession of publications that demonstrate a longer-term potential co-existence of early H. sapiens and late Neanderthals not only in western Asia, as previously observed, but also in Europe.
- More-over, ancient DNA evidence shows that this overlap was accompanied by multiple episodes of interbreeding between these populations, in Europe as well as in Asia.
- Fossils like Jebel Irhoud 1 and Omo Kibish 2 represent basal *H. sapiens* (bHs), while on the parts preserved Omo Kibish 1 could be described as a derived *H. sapiens* (dHs).
- Equally, early members of the Neanderthal lineage such as those from the Sima de los Huesos could be called basal Neanderthals (bHn), while fossils like La Ferrassie 1 and Forbes' Quarry would be referred to as derived Neanderthals (dHn).
- Scrapping the 'archaic' vs. 'modern' dichotomy would also end the vague labelling of 'archaic' introgression,

Last Common Ancestor (LCA) of N and MH

- Sima at 430 ka pushes back when the divergence between the Neanderthal and *H. sapiens* lineages began about 600 ka ago
- LCA of N and MH usually thought of as H. heidelbergensis; but Kabwe cranium of *H. rhodesiensis* has shown that this specimen could be dated to only about 300 ka, much younger than the expected age for an ancient African ancestor of ours (Grün et al. 2020).
- Moreover, recent studies of the facial shape of *H. rhodesiensis* fossils suggest that they have a derived zygomaxillary morphology, and thus they are less likely to represent our ancestors (Lacruz et al. 2019).
- Therefore, in our view, there is currently not enough evidence to establish the exact nature of our LCA with the Neanderthals from about 600 ka, nor where it lived.

H. sapiens evolved in Africa over same time scale as Neandertals evolved in Eurasia

- If our line of evolution stretches back to about 600 ka, where are the equivalents of the SH fossils that should document the early evolution of our species?
- Until recently, many scientists argued that the human fossils Omo Kibish 1 and Herto from Ethiopia, dated between about 150–200 ka, represented the earliest known members of our species. Both these fossils have globular braincases and reduced brow sizes, and Omo Kibish 1 has been also shown to have a *sapiens*-like hipbone, as well as a greater antiquity (233 ka) than estimated previously. If these Ethiopian specimens represent dHs, there seems to be a large temporal gap between them and our much more ancient common ancestor with the Neanderthals.
- It has been argued that other African fossils, such as Florisbad (South Africa) and Eliye Springs (Kenya), might represent more plesiomorphous *H. sapiens* populations that existed earlier on our lineage, but the evidence is incomplete and not well-dated.

Early H. sapiens

- In 2017, fossils and archaeological discoveries from Jebel Irhoud, Morocco, dating to about 300 ka
- The Jebel Irhoud fossils display some ancestral features such as a longer, lower braincase, strong brow ridges, and a large face and teeth, as one might expect at around 300 ka.
- Yet, the delicate cheekbones and retracted face look more derived, as do details of the skulls and teeth, and the shape of the jawbones.
- Associated evidence of the controlled use of fire and the sophistication of the stone tools from Jebel Irhoud also suggest complex behaviors in these putative early members of our lineage

Other African species at 300 Ka

- At least three human species existed across the African continent at 300 Ka.
  - *H. sapiens* was probably present in Morocco,
  - *H. rhodesiensis* persisted at Kabwe in Zambia.
  - *H. naledi* existed in southern Africa.

- Early *H. sapiens* from sites like Eliye Springs and Guomde (Kenya), Florisbad (South Africa), Omo Kibish 2 (Ethiopia), and Ngaloba. These show great variation and different combinations of ancestral and more derived traits, which do not suggest an orderly, sequenced evolution of dHs features, or may even question their assignment to the *H. sapiens* lineage

Pan-African model

- Instead, Chris Stringer and several other researchers now favor a more complex pan-African model for the evolution of our species, where our ancestors were diverse in form and scattered across much of the African continent. Influenced by ever-changing climates, regional lines of evolution waxed and waned, sometimes reticulating, sometimes going their separate ways, and sometimes disappearing altogether.
- What are called ‘modern humans’ are the eventual result of a blending of these different ancestral populations over a period of hundreds of thousands of years in Africa.

(Hublin et al. 2017; Scerri et al. 2018; Stringer 2002, 2016).

One way gene flow: no MH DNA in late Ns, only N into MH

- There is no evidence of *Homo sapiens* DNA in Late Neanderthal genomes dating to between 40-60,000 years ago; only of N DNA in dHs
- It is possible this is due to the process of hybridization itself, as some species are only capable of producing offspring in certain directions.
- The lack of mitochondrial DNA from Neanderthals in living humans has been suggested as evidence that only male Neanderthals and female *Homo sapiens* could mate, but there is also some evidence that male hybrids may have been less fertile than females.
- ***With fewer Neanderthals breeding with each other and group sizes already small and scattered due to the environment, hybridization outside of Neanderthal family groups could have helped push the species into decline. At the moment, however, there isn't enough evidence to decide either way.

Early dispersals of H. sapiens from Africa

- Don't know if the apparent one-way gene flow from N to dH is because it simply wasn't happening, that the breeding was taking place but was unsuccessful, or if the Neanderthal genomes we have are unrepresentative.
- As more Neanderthal genomes are sequenced, we should be able to see whether any nuclear DNA from *Homo sapiens* was passed on to Neanderthals and demonstrate whether or not this idea is accurate.
- DHs started a significant dispersal from Africa about 60 ka and Neanderthal populations disappeared about 20 ka later.
- Were those two events connected, and what happened when the two species met?

Earlier MH fossils

- MH and Ns exchanged some genes about 250 ka ago, perhaps when early *H. sapiens* made brief forays into Eurasia.
- The spread of prepared core (Levallois) technology around this time might reflect such contact, and fossil remains
- Apidima Cave in Greece, where the back part of a *sapiens*-like braincase has been dated to at least 210 ka.
- The more complete Apidima 2 cranium showed shape similarities to Neanderthal crania like La Chapelle-aux-Saints (France),

(Petr et al. 2020; Posth 2017).

Early MH in Europe

- Apidima 1 partial cranium showed features closer to those observed on *H. sapiens* fossils from the last 130 ka.
- New dating analyses were unexpected, placing Apidima 2 at a minimum of 170 ka and Apidima 1 at a minimum of 210 ka; Apidima 1 exhibits features typical of dHs.
- These results suggest a new scenario whereby there was an early *H. sapiens* population in Greece by 210 ka, perhaps related to comparable groups in the Levant, and which was subsequently replaced by a Neanderthal population by about 170 ka.
- If the Apidima analyses are correct (for an alternative view see Rosas and Bastir 2020 = a female N), *H. sapiens* entered Europe over 150 ka earlier than previously thought.

Other earlier MH excursions from Africa

- Signs of other early excursions of *H. sapiens* from Africa as indicated by remains in Israel from sites like Skhul, Qafzeh, and Misliya dating from over 100 ka.
  - Skhul and Qafzeh remains, which we regard as dHs, date from about 100–130,
  - a partial upper jaw with a complete series of teeth on the left side was published from Misliya Cave, and assigned to derived *H. sapiens*, with a minimum age estimate of ~174 ka.
  - a partial mandible and braincase, have been recovered and published from the site of Nesher Ramla in Israel.

Other earlier MH excursions from Africa

- Dispersals of dHs prior to 60 ka in regions ranging from southern China to Sumatra to northern Australia

- Analyses of extant genomes outside of Africa suggest that the main dispersal of *H. sapiens* started about 60 ka ago, and the subsequent disappearance of the Neanderthals about 20 ka later could well relate to that event.

Early Dispersal

- Important new evidence has emerged from sites like Bacho Kiro Cave in Bulgaria, Zlatý kůň Cave in Czechia, Grotta del Cavallo in Italy, and Grotte Mandrin in France, that seemingly push that arrival dates even further back.
- Additionally, beyond Europe but without archaeological associations, a partial human femur from a male *H. sapiens* individual was discovered at Ust'Ishim (Omsk Oblast, Russian Federation), dated to ~45 ka, and whose genome sequence indicated Neanderthal gene flow into his ancestors about 7–13 ka before he lived.
- Two deciduous teeth from Grotta del Cavallo were identified as representing *H. sapiens* based on their morphology, a key discovery in revealing a previously unidentified spread of *H. sapiens* through the northern Mediterranean region.

Europe at 40 Ka

- Bacho Kiro, dated to between about 46–42.5 ka, indicate an early *H. sapiens* population in eastern Europe. these individuals had Neanderthal ancestors only a few generations back.
- The recency of Neanderthal ancestry is similar to that estimated for the ~37–42 ka old Oase 1 individual from Romania, but whereas the Oase male was unrelated to later Eurasians, the Bacho Kiro genomes showed links to East Asians, including the ~40 ka old skeleton from Tianyuan Cave, China.
- This hints at an early Eurasian dispersal of *H. sapiens* that either occurred after the time of the Zlatý kůň female and Ust'Ishim male, or was a completely separate event.
- What is also remarkable about the Bacho Kiro evidence is that it falsifies a common notion about the earliest dispersals of *H. sapiens* into Europe, which are usually assumed to have occurred during brief climatic ameliorations in Marine Isotope Stage 3.
- The archaeological and faunal records at Bacho Kiro show that these dHS were already coping with life in colder environments some 44 ka, something that may speak to the adaptability of our species, but which might also reflect the part-Neanderthal biological and cultural heritage of these people.

La Cotte de St. Brelade, Isle of Jersey: Not N, but N-MH hybrids?

- During the last Ice Age, the island of Jersey was connected to France. Excavations between 1911 and 1920 at the site of La Cotte de St Brelade on Jersey found more than 20,000 stone tools from the Middle Paleolithic (an industry associated with the Neanderthals in Europe), as well as the bones of Ice Age megafauna such as mammoth and woolly mammoths..
- In 1910–1911, thirteen human teeth were also discovered, and because they were large, with robust roots, they were identified as Neanderthal.
- In the last few years, researchers have re-examined these teeth: there were at least two individuals represented. Second, while all the teeth had some Neanderthal traits and their size was consistent with being Neanderthal, several of the teeth lacked features normally found in these ancient humans, while other aspects of their shape looked much more typical of our species, *H. sapiens*.
- It is known from recent dating work at the site that these teeth are probably less than 48 ka old, meaning they might represent some of the youngest Neanderthal remains known to date. However, given that it is also known that *H. sapiens* overlapped with Neanderthals in some parts of Europe from more than 40 ka ago and that these populations interbred at times, perhaps the unusual combinations of features in these individuals indicate that the Jersey population had a dual Neanderthal-*sapiens* ancestry. This is something that could be tested if ancient DNA is preserved in the teeth.

Early dispersals in Europe

- 2022 French study: further evidence of multiple *H. sapiens* dispersals, with a deciduous upper molar from Layer E at Grotte Mandrin in the Rhône Valley (France) identified morphologically as *H. sapiens* and dated between ~57–52 ka.
- These discoveries at Grotte Mandrin raise further questions about possible genetic and cultural contacts during this time period, and about possible dispersal routes from western Asia to the Rhône Valley along the northern Mediterranean coast.
- This wealth of new data adds to a growing picture of multiple dispersals of early *H. sapiens* into Neanderthal territories in Europe prior to 40 ka, at various times. However, some of these were seemingly brief and transient occupations (for example at Grotte Mandrin), perhaps due to fluctuating environments linked to unstable climates,
- We should perhaps instead imagine small rivulets of people, ebbing and flowing through time. Some of these early range expansions of *H. sapiens* (for example, the populations represented by the Ust'Ishim, Zlatý kůň, and Oase genomes) apparently had no later descendants in Eurasia, indicating that these individuals represent now-vanished lineages of our species..

What happened when Ns and MHs encountered each other

- The long debate about whether Neanderthals and *H. sapiens* interbred has finally been resolved by the availability of ancient DNA, and models such as Recent African Origin with Hybridization, and Assimilation, now look to be the most appropriate for the observed data.
- If gene exchanges between the populations were widespread and the derived traits of *H. sapiens* spread more gradually through demic diffusion, Assimilation will eventually prove the more applicable,
- whereas evidence that the indigenous populations were predominantly absorbed by dispersing *H. sapiens* in a replacement process would favor Recent African Origin with Hybridization.

N phenotype: lots unknown

- Differences in pelvic and ribcage anatomies suggest clearly distinct physiologies as well as physiques, and there is no precise knowledge of the external appearance of Neanderthals in terms of body, facial, and head hair distribution, and the exact form of elements such as the external ears, eyes, nose, and lips.
- The brow ridge, ubiquitous in adult Neanderthals, is a much-debated structure, but recent research suggests it may have had a signaling function in earlier humans, which could have persisted in Neanderthals and was lost in dHs.
- This implies that dHs replaced that function with other signals, perhaps in the eyebrows or other facial expressions, or perhaps in a repertoire that involved language or symbolic displays, which might have included cultural adornments such as piercings and tattoos.

MH-N differences and similarities

- When the lineages of *H. sapiens* and *H. neanderthalensis* began to encounter each other some 60 ka ago in Eurasia, there could have been both similarities and differences (most unknowable to us) in appearance, verbal and gestural communication, expression, general behavior, and perhaps even smell, that would have impinged on how they perceived each other at first contact, thus affecting the mechanisms of mate recognition.

- Would they have seen each other as people, and thus potential allies, mates, or enemies, or even as the next meal?

N-MH differences

- In addition, although the Neanderthals were clearly intelligent and surely had spoken language, language distinctions that developed along the Neanderthal and *H. sapiens* lineages would probably have far exceeded any that exist today.

- Genetic data suggests that cognition and vocal tract anatomy were also distinct in *H. sapiens*, which could have heightened contrasts between the two species of humans.

- Whatever the scale of differences between *H. neanderthalensis* and *H. sapiens* at a species level, it is known from a growing body of genetic data that members of their respective populations must have interbred on many occasions, and those matings produced fertile offspring, even though there might have been some level of hybrid infertility in the male line.

N and MH Differences

- So, what was the social milieu that led to these sexual encounters?
- Females of both pre-reproductive and reproductive age have at times been seized from their social groups among recent hunter-gatherer and pastoralist populations (Hrdy 2009).
- Opportunistic and often covert couplings solicited by individual males or females may take place away from regular partners in gorillas and chimpanzees, as well as in *H. sapiens.*
- More structured movements of partners among recent hunter-gatherers vary according to local demographic conditions, and thus may also have developed between Neanderthal and *H. sapiens* groups at times.

Evidence only in MHs, not Ns, of interbreeding

- What is intriguing at the moment is that there are several actual or possible examples of interbreeding between late Neanderthal and *H. sapiens* groups that were deciphered from the fossil record, but all of them so far (apart from the equivocal La Cotte example) are evidenced from *H. sapiens,* not Neanderthal, fossils.

- Is this because of a sparser genetic record from late Neanderthals, or is this an indication that hybrids within Neanderthal social groups were rarer, or were not viable?

Evidence only in MHs, not Ns, of interbreeding

- ***If a larger sample of genomes from the critical 40–45 ka period maintains the present pattern of Neanderthal DNA entering *H. sapiens* gene pools, but not the reverse, then this might provide a mechanism for the demise of Neanderthal populations.

- *** If fertile Neanderthals were regularly being absorbed into *H. sapiens* groups (by whatever mechanisms) during that time period, they were effectively also being removed from Neanderthal gene pools, and such a consistent drain of prime-age individuals is not something that could have been sustained for long in small hunter-gatherer groups.

MHs absorbed N populations?

- ***Perhaps dispersing *H. sapiens* groups acted like sponges in absorbing pockets of late Neanderthals and maybe that, as much as anything else, led to the eventual demise of the Neanderthals as a viable population.
- Recent progress in the recovery of environmental DNA from cave sediments promises to revolutionize our understanding of population relationships on the ground as *H. sapiens* and *H. neanderthalensis* groups interacted with each other.
- Few European sites in the time period between 40–60 ka contain human fossils, but many more of them could contain traces of human presence in the form of mitochondrial and nuclear genomic material in sediments.

MHs absorbed N populations?

- Research so far demonstrates that sediment DNA can identify humans at the species and individual levels, and this could potentially map the co-existence of different populations, their sex, their kinship relations, and the extent of intermixture between the different populations.

- Evidence that Neanderthal ancestry was probably a significant liability that hurt the fitness of early human–Neanderthal hybrids.

- At the time when Neanderthals first encountered anatomically modern humans, their long period of inbreeding made them at least 40% less fit than the modern humans who migrated into Eurasia to join them.

Love, not War

- Assuming that Neanderthals passed this fitness disadvantage down to their hybrid children, the fraction of Neanderthal ancestry in the human population is predicted to have decreased over time, as it was eliminated by natural selection.
- According to population genetic theory and simulations, Neanderthals may at one time have contributed around 10% of the human gene pool, though the contribution has been reduced to levels of only around 2–3% today.
- It is possible that Neanderthals did not truly die off at all, but simply melted together with the human species.
- One could perhaps argue that Neanderthals did not disappear due to warfare or competition—but due to love.

Neandertal Families

Neanderthal family found in El Sidrón cave in Spain

- 2010 study: The remains of 12 Neandertal individuals were found at the El Sidrón site (Asturias, Spain), consisting of three men, three women, three teenage boys and three children, including one infant. . Dated to 49 Ka.
- These individuals represent all or part of a contemporaneous social group of Neandertals, who died at around the same time and later were buried together as a result of a collapse of an underground karst.
- The 12 individuals stem from three different maternal lineages, accounting for seven, four, and one individual(s), respectively, based on mtDNA.
- .

El Sidrón cave in Spain

- Although the three adult males carried the same mtDNA lineage, each of the three adult females carried different mtDNA lineages.

- Neandertal groups not only were small and characterized by low genetic diversity but also were likely to have practiced patrilocal mating behavior

- Patrilocality: The genetic data suggested that while the three adult males in the group shared the same maternal lineage, the three adult females had different maternal origins.

El Sidrón site

- At least in this Neanderthal family, the women came from outside the group, while the men remained within the family group on reaching maturity.
- These Neanderthals were almost certainly killed and cannibalized by another Neanderthal group, not by animal scavengers.
- Geological analysis of the soils in that area suggests that the bones fell into the cave through a vertical shaft, in a massive water-driven deposit, probably resulting from a flood event

A Neandertal female from Chagyrskaya Cave

- 2020 Study: Sequenced the genome of a female Neandertal from Chagyrskaya Cave in the Altai Mountains, Russia, to 27-fold genomic coverage. This Neandertal was more related to Neandertals in western Eurasia, than to Neandertals who lived earlier in Denisova Cave, which is located about 100 km away.

- About 13% of the Chagyrskaya genome is spanned by homozygous regions. This is consistent with the fact that Siberian Neandertals lived in relatively isolated populations of less than 60 individuals. In contrast, a Neandertal from Europe, a Denisovan from the Altai Mountains, and ancient modern humans seem to have lived in populations of larger sizes.

F. Mafessoni , et al., 2020

Neandertal Whole Genome Sites = 13

First Known Family of Neanderthals Found in Russian Cave

- 2022 - Skov *et al.* Study: Analyzing fossils from a cave in Russia, scientists have found the first known Neanderthal family: a father, his teenage daughter and others who were probably close cousins, found alongside stone tools and butchered bison bones. The new discovery came from a Siberian cave called Chagyrskaya in 2007.
- The family, part of a band of 11 Neanderthals found together in the cave, most likely died together, possibly from starvation.
- Neanderthals at the easternmost edge of their range hunted migrating bison, and retreated to Chagyrskaya Cave to enjoy their spoils. Their living space was cramped, but occupation was probably only seasonal.
- 90,000 stone artefacts and butchered bison bones have been found in this cave, along with the largest collection of Neanderthal remains known for north Asia.

L. Skov, etc. 2022

Carl Zimmer, 2022

Genetic insights into the social organization of Neanderthals

- In 2020, Dr. Pääbo and his colleagues published the first DNA findings from Chagyrskaya: a collected from a Neanderthal genome from a woman's finger bone. Her genes showed that she was more closely related to Neanderthals more than 3,000 miles away in Croatia than those just 65 miles away in another cave known as Denisova.
- That kinship suggests that the Neanderthals in Siberia did not belong to a single population. They expanded east from Europe at least twice — first to Denisova, then tens of thousands of years later to Chagyrskaya.
- This 2022 study: DNA from 11 individuals: six adults and five children. All rested in the same layer of sediment in the cave.
- Descendants of a late expansion of eastern European Neanderthals into Siberia, distinct from the earlier occupants of Denisova Cave, only 100 kilometers to the east

Chagyrskaya Cave

Genetic insights into the social organization of Neanderthals

- 2022 Skov study: genetic data for 13 Neanderthals from two Middle Palaeolithic sites in the Altai Mountains of southern Siberia: 11 from Chagyrskaya Cave and 2 from Okladnikov Cave—making this one of the largest genetic studies of a Neanderthal population to date.
- Obtained genome-wide nuclear data, as well as mitochondrial and Y-chromosome sequences.
- Some Chagyrskaya individuals were closely related, including a father–daughter pair and a pair of second-degree relatives, indicating that at least some of the individuals lived at the same time.

Chagyrskaya Cave and Okladnikov Cave fossils

Neanderthal teeth and bones from Chagyrskaya Cave (A, B) and Okladnikov Cave (C) i

Chagyrskaya Cave

- Members of a nuclear family — a father and his adolescent daughter — as well as a male–female pair of second-degree relatives (share about 25% of their DNA).
- They found that the father had two types of mitochondrial DNA — a characteristic known as heteroplasmy — that were shared by two other adult males from the cave, suggesting that they were all from the same maternal lineage. Heteroplasmies usually vanish after a few generations, so the three probably lived around the same time. Also identified members of another Neanderthal family: a male and female who were second-degree relatives, such as cousins.
- A male individual who was a maternal relative of the aforementioned father was also identified, owing to a genetic phenomenon called heteroplasmy.
- These different versions coexist for only a few generations, and thus individuals who share a heteroplasmy are expected to be recently related along the female line. Skov *et al.* speculate that these men might have shared a grandmother,

Inbred Ns

- The Chagyrskaya genomes, like that of an earlier Neanderthal from Denisova, contain signatures of inbreeding, in the form of long stretches of identical DNA inherited from each parent
- 30% of these individuals’ genomes had long segments of homozygosity, suggesting that the Chagyrskaya Neanderthals were part of a small, inbred, community.
- In addition, the Y-chromosome diversity is an order of magnitude lower than the mitochondrial diversity, a pattern that we found is best explained by female migration between communities.
- The genetic data presented here provide a detailed documentation of the social organization of an isolated Neanderthal community at the easternmost extent of their known range.

Eastern Ns

- Genome-scale data have been reported for the skeletal remains of 18 individuals from 14 archaeological sites spanning Neanderthal history across large parts of their known geographical range, which extends as far east as the Altai Mountains in southern Siberia.

- Multiple distinct Neanderthal populations existed over time and space

- Previous studies on the social organization of Neanderthal communities have suggested that Neanderthals probably lived in small communities.

- In addition, partial mitochondrial DNA (mtDNA) sequences from six adult Neanderthals have been used to suggest that Neanderthals were likely patrilocal.

Chagyrskaya

- Chagyrskaya: an unprecedented haul of Neanderthal Y chromosomes (six in total), which were notably lacking in diversity
- The maternally inherited mitochondrial genomes were vastly more diverse than were the Y-chromosome, explained by a steady influx of females from different Neanderthal communities. Patterns observed in genetic diversity would occur if more than half of women in small communities were born elsewhere.
- Carles Lalueza-Fox, of El Sidrón study: this social structure was present in most Neanderthals. Evidence that females left their own families. This makes Lalueza-Fox wonder whether it was mobile Neanderthal women who encountered — and mated with — *Homo sapiens* in other parts of Eurasia

A Neandertal family

- The Neanderthal occupation deposits at Chagyrskaya Cave accumulated between 59,000 and 51,000 years ago;
- Okladnikov Cave dated to 44 Ka.
- Neanderthals from Chagyrskaya Cave and from Denisova Cave (Denisova 5, the ‘Altai Neanderthal’) belonged to different populations.
- A first-generation offspring (Denisova 11) of a Neanderthal mother and a Denisovan father (Denny) revealed that the Neanderthal mother was more similar to Chagyrskaya 8 than she was to other Neanderthals

Denisovan DNA at Chagyrskaya

- Gene flow between Neanderthals and Denisovans in the Altai Mountains has been observed in the nuclear genome of an individual (Denisova 11) who lived 79 to 118 Ka and had a Neanderthal mother and a Denisovan father.
- Amount of Denisovan ancestry in Chagyrskaya 8 Neandertal is around 0.09% and that the admixture event occurred 24 ± 14 years before Chagyrskaya 8 lived.
- The high amounts of homozygosity in all individuals indicate that the local community size of the Chagyrskaya Neanderthals was small.

Patrilocality

- The amount of homozygosity is also similar to the amount found in the genomes of present-day mountain gorillas, an endangered species that lives in small communities of 4–20 individuals
- Suggest that these small Neanderthal communities were predominantly linked by female migration
- Several scenarios could account for the greater diversity of maternal lineages, including the possibility that a subset of men fathered most children.
- But, through modelling, the authors found that their data are best explained by female-biased migration between communities of about 20 individuals, with more than 60% of women being born elsewhere.

N family

- All 13 newly sequenced individuals shared most variants with the high-coverage female genome from Chagyrskaya Cave (Chagyrskaya 8) and were more similar to the ~50 Ka Neanderthal genome from Vindija Cave (Vindija 33.19) in Croatia than to the 91 to 130 Ka Altai Neanderthal (Denisova 5) from Denisova Cave
- Two of the fossils shared 50% of their DNA, implying they had to be first-degree relatives. One came from a broken vertebra that appeared to belong to an adult male. The other came from a tooth that seemed to come from a teenage female. If these estimated ages were accurate, then the specimens could have come from siblings, or from a father and his daughter.
- The Chagyrskaya man and the girl had different mitochondrial DNA, ruling out a sibling relationship. Proves that this was in fact a father and a daughter.

A family

- Other fossils offered hints of other familial relationships.

- The father proved to be a close relative of two other adult males at Chagyrskaya. And an adult woman and a boy also shared enough DNA that they were likely related.

- The kinship of the Neanderthals suggested that they all died at once. If they had died at different times, that would mean the group would have returned to the same cave over many years to bury each member — a scenario Dr. Skov considers very unlikely.

- Speculated that the band's bison hunts failed one year, leading to starvation.

Chagyrskaya and Okladnikov Caves

- None of the 11 Neanderthals at Chagyrskaya showed any genetic link to the Neanderthals of the Denisova Cave.
- Discovered a connection to a third cave nearby known as Okladnikov. Two Neanderthal fossils found at Okladnikov have genetic links to Chagyrskaya.
- The Y chromosomes shared by the males were fairly similar. The mitochondrial DNA passed down from mothers to their children, on the other hand, was very diverse. An example of patrilocality.
- Conclusion that among Neanderthals, it was the women who moved from band to band. estimate that 60 percent of women in any community actually come from other communities,

N family

- Lack of diversity most likely means that Neanderthals in Siberia lived in small bands of 20 people or fewer.
- It also means that the entire population of Neanderthals in Siberia was very low — perhaps fewer than a thousand.
- Findings raise questions as to whether the characteristics of the Altai communities are related to
  - their isolated geographical location at the easternmost extremity of the known range of Neanderthals (especially because the population size at Vindija Cave was probably larger),
  - or whether they are characteristic of Neanderthal communities more broadly.

More to come…

- The Chagyrskaya family is likely to grow.
- Only one-third of the cave has been excavated so far, and Skov and his colleagues have analyzed less than one-quarter of the Neanderthal remains already discovered.
- Skov hopes that future studies can build more complete Neanderthal family trees — and perhaps find the teenage girl’s mother. “She’s probably also in there,” he says.

Black Death

Black Death

- During the Industrial Revolution, the pigmentation of peppered moths (*Biston betularia*) changed in a matter of decades, with natural selection favoring darker moths that were better camouflaged against soot-covered surfaces.
- This is a classic example of what evolutionary biologists have long known — that natural selection can happen rapidly, given the right conditions.
- Klunk *et al., 2022:* report that even humans can adapt at remarkable speed. But riding the evolutionary bullet train might come at a cost.

Black Death: Were there protective variants?

- Bubonic plague is a deadly infectious disease caused by the pathogenic bacterium *Yersinia pestis*, which is spread by rodents.

- In the fourteenth century, a wave of bubonic plague dubbed the Black Death killed up to 50% of people in Europe, making it the deadliest pandemic recorded in modern European history.

- Klunk *et al.* asked a simple question — was the Black Death so deadly that it triggered an episode of natural selection in the genomes of infected individuals? In other words, did survivors carry specific genetic variants that made them more likely to survive than those who were killed?

Black Death

- Tracked genetic variants that had become more common during the pandemic. People who carried them survived more often than those who did not; and left more descendants who inherited the protective genetic variants.
- In turn, these descendants would have had more protection during subsequent waves of disease, which occurred every few years for the next four centuries.
- Found that a striking number of genetic variants were selected for in genes that govern immune defense against pathogens.
- In just a few generations, 245 genetic variants that might potentially be protective against the plague became more common.

Fast evolution of immune variants

- Found that the four that became most common were selected for at a speed and an intensity never observed before in human genomes.
- Individuals who carried some or all of these variants probably had immune defenses that responded efficiently to *Y. pestis*, and, as a result, had much better odds of surviving infections.
- It is worth noting that such rapid and strong selection is highly unlikely to occur for human traits other than immune defense. No other set of traits is under such strong evolutionary pressure.

Genes that might have aided survival during the Black Death are now linked to autoimmune disorders.

- Four DNA variants in particular seem to have become more common after the Black Death, and might have contributed to survival.
- But the protection afforded by those variants could have come at a cost:
  - two of them are associated with an increased risk of autoimmune disorders, such as Crohn's disease and rheumatoid arthritis.

Black Death

- Looked at genetic variation in more than 200 DNA samples isolated from the bones or teeth of individuals who lived before the plague, died from it or lived one or two generations later.
- Found four DNA variants that seemed to have been selected for during the Black Death in samples from both the United Kingdom and Denmark.
- One variant affected the expression of a gene called *ERAP2*. People with the variant produce a full-length version of an RNA molecule that encodes the ERAP2 protein; those who lack it make a shorter version of the RNA.
- Having two copies of *ERAP2,* was strongly associated with surviving the plague.

Black Death immunity variants also have negative effects

- Having a full-length, fully functional ERAP2 protein might have improved immune protection during the Black Death. Laboratory studies backed up this idea: macrophages expressing the longer version of ERAP2 were able to keep *Yersinia pestis* from replicating more effectively than were macrophages expressing the truncated version.
- But the protective *ERAP2* gene variant is also a known risk factor for Crohn's disease.
- Another of the variants is associated with rheumatoid arthritis and another autoimmune condition, systemic lupus erythematosus

What is the leading cause of death in pregnant women in the US

- Homicide
- Women in the U.S. are more likely to be murdered during pregnancy or soon after childbirth than to die from the three leading obstetric causes of maternal death (high blood pressure disorders, hemorrhage, or sepsis)
- Majority of these pregnancy-associated homicides are linked to the lethal combination of intimate partner violence and firearms; and are entirely preventable.
- Reports suggest the U.S. has a higher prevalence of lifetime and past-year intimate partner violence than other high-income countries, and homicides by an intimate partner in the U.S. are overwhelmingly committed using firearms. Recent estimates indicate that firearms were used in 68% of homicides around pregnancy between 2008 and 2019, with black women at substantially higher risk of being killed than White or Hispanic women.

Mosquito magnets: Subject 33, was four times more attractive to mosquitoes than the second-place participant and 100 times more than the least appealing participant: produced carboxylic acids, used by bacteria on human skin to produce unique body odors; production of a chemical tied to smell

Evolution of bipedalism

- **Jeremy DeSilva** is a paleoanthropologist at Dartmouth College. His research focuses on the evolution of bipedalism. He is author of *First Steps: How Upright Walking Made Us Human* (HarperCollins, 2021).
- In a lifetime, the average person will take about 150 million steps—enough to circle Earth three times.
- Long before our ancestors evolved large brains and language, even before they tamed fire or made stone tools, they started doing something no mammal had done before: walking on two legs. Skeletal adaptations for traveling upright are evident in fossils of the very oldest hominins
- It allowed our predecessors to expand their home ranges and diversify their diets, and it transformed the way we give birth and parent our children. This peculiar mode of locomotion was foundational to virtually all the other characteristics that make humans unique.

Many forms of bipedalism

- We now know that various hominin species living in different environments throughout Africa, sometimes contemporaneously, evolved different ways to walk on two legs.
- Our modern stride was not predetermined, with each successive ancestor marching closer to a particular end goal (evolution has no plans, after all). Rather it's one of many forms of upright walking that early hominins tried out—and the version that ultimately prevailed.
- Bipedalism evolved multiple times at the base of the hominin family tree, perhaps for different reasons, in different hominins living in slightly different environments throughout Africa.

Fossil footprints from Laetoli, Tanzania, show that two different hominin species walked bipedally in this area 3.66 million years ago.

The Site G trackway is thought to have been made by *Australopithecus afarensis*.

Two or three, perhaps even four, individuals had walked stride for stride through the muddy ash, leaving 69 stunningly humanlike footprints

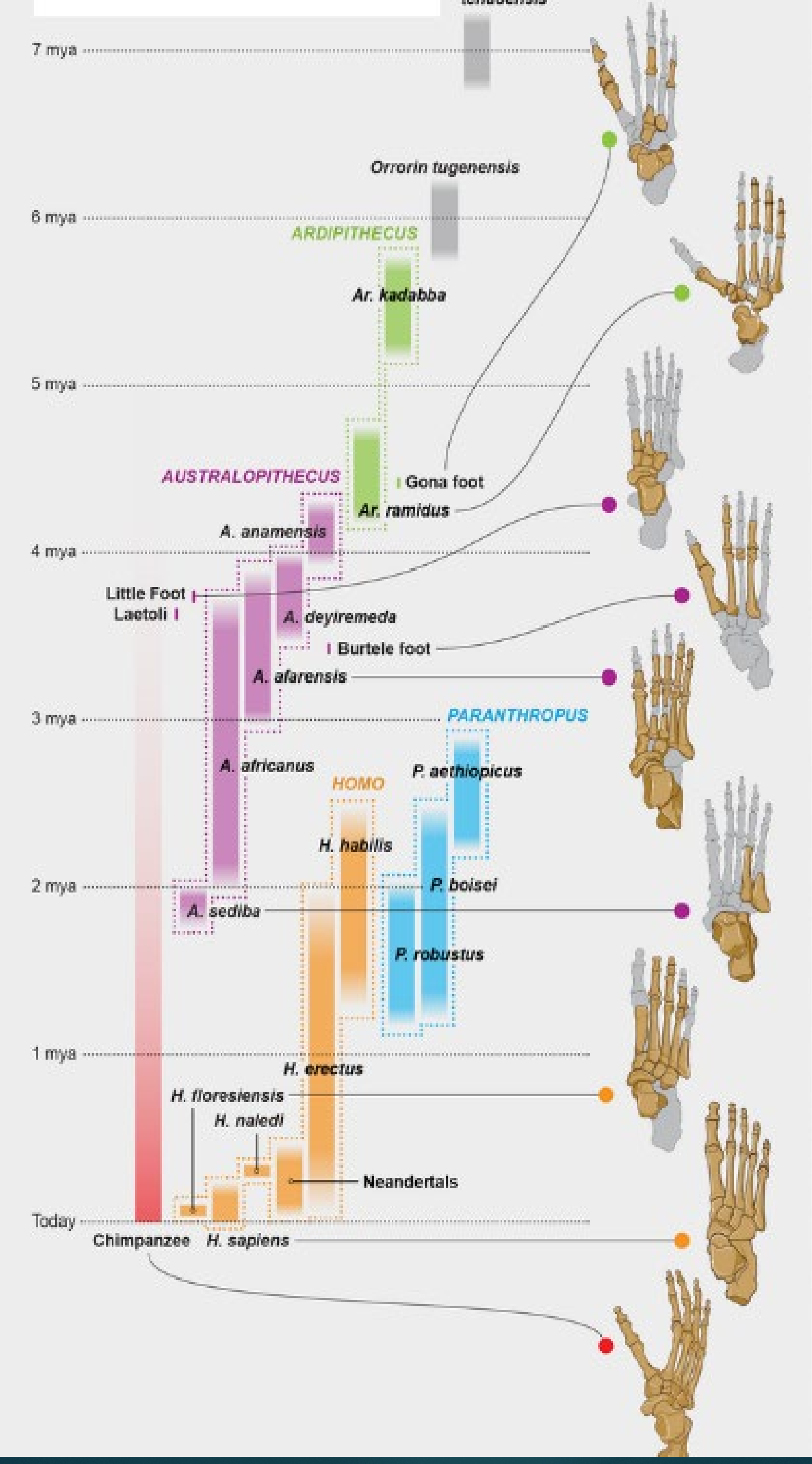
The Site A trackway was made by a different, as yet unidentified hominin.

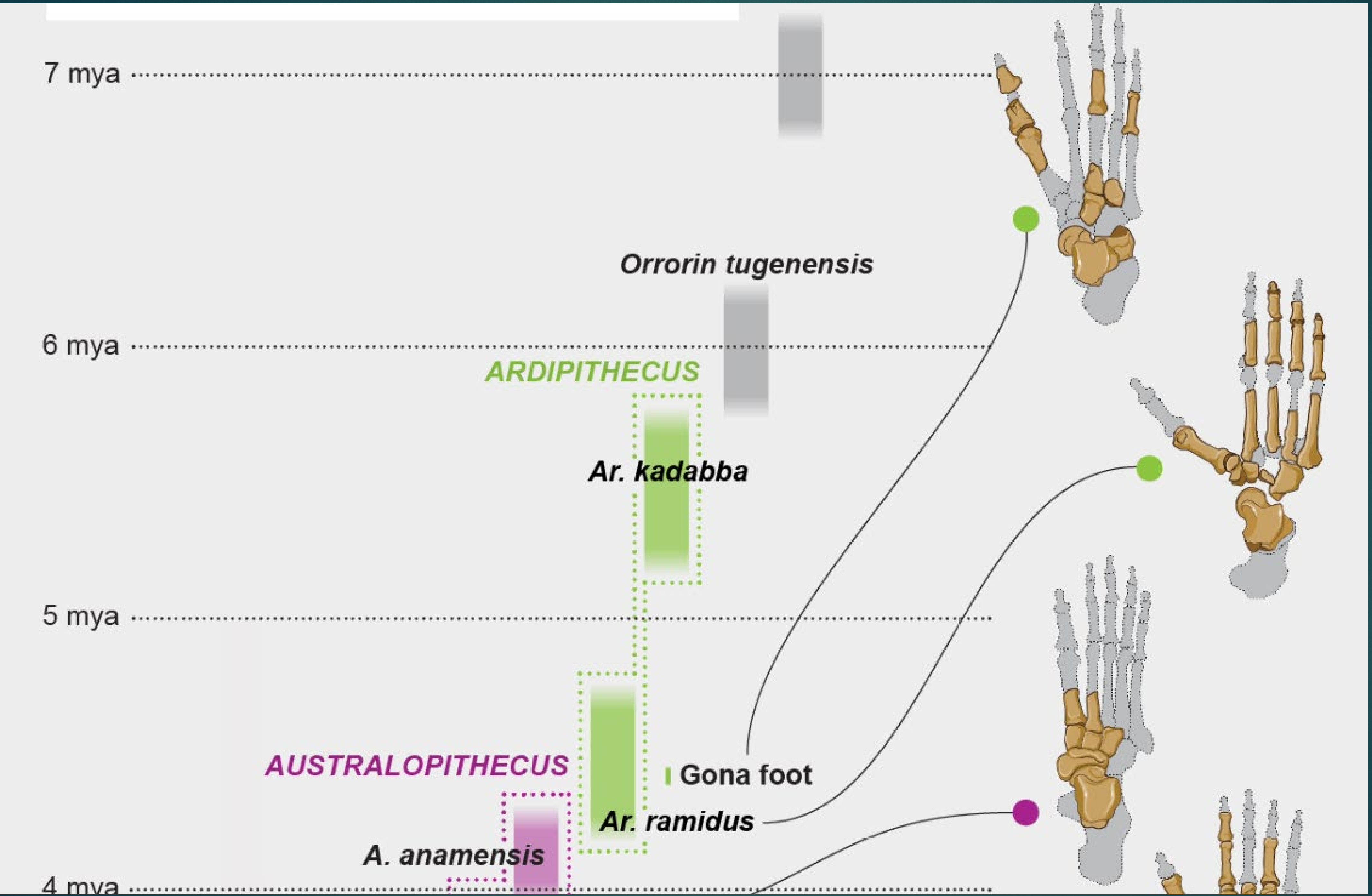
2 kilometers west of Site G

Originally thought to be bear tracks

Walk these ways

- Upright walking was long thought to have evolved in linear, sequential fashion, with each successive ancestor looking more like us in posture and stride. But discoveries made over the past two decades have upended that view.
- Paleoanthropologists now know that for most of the time over which humans have been evolving, multiple hominin species with different ways of walking upright overlapped in time and space.
- For example, three hominin species belonging to three different genera—*Paranthropus, Australopithecus* and *Homo*—all roamed South Africa's Cradle of Humankind region two million years ago, each with a distinct gait.
- Some hominins, such as *Australopithecus sediba* and *Homo naledi,* even possessed adaptations to life in the trees long after other hominins were fully committed to life on the ground.

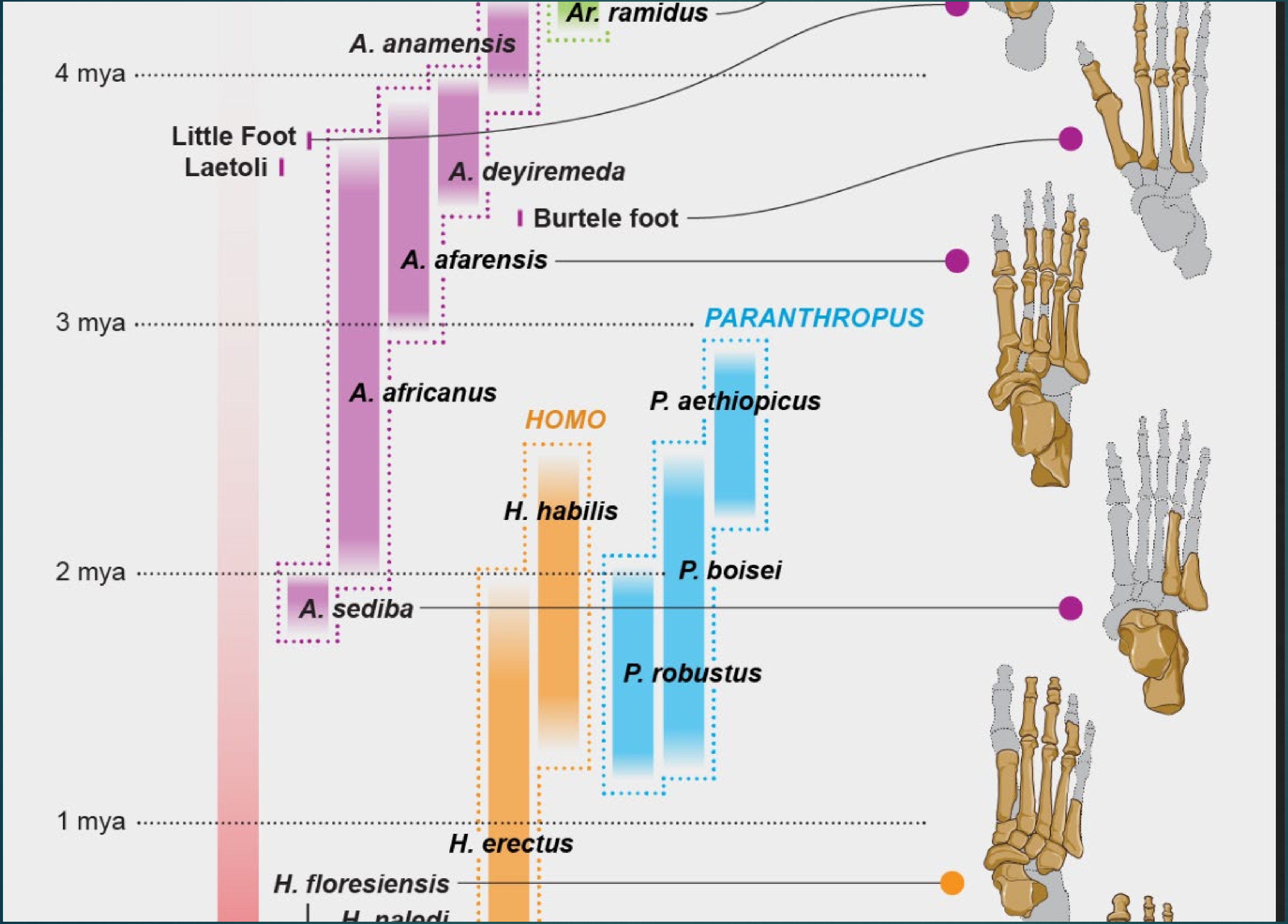

7 mya
Orrorin tugenensis
6 mya
ARDIPITHECUS
Ar. kadabba
5 mya
AUSTRALOPITHECUS
Gona foot
Ar. ramidus
A. anamensis
4 mya
Little Foot
Laetoli
A. deyiremeda
Burtele foot
A. afarensis
3 mya
PARANTHROPUS
A. africanus
HOMO
P. aethiopicus
H. habilis
2 mya
P. boisei
A. sediba
P. robustus
1 mya
H. erectus
H. floresiensis
H. naledi
Neandertals
Today
Chimpanzee
H. sapiens



Australopithecus

Ardipithecus
Ramidus

A. prometheus
Little Foot

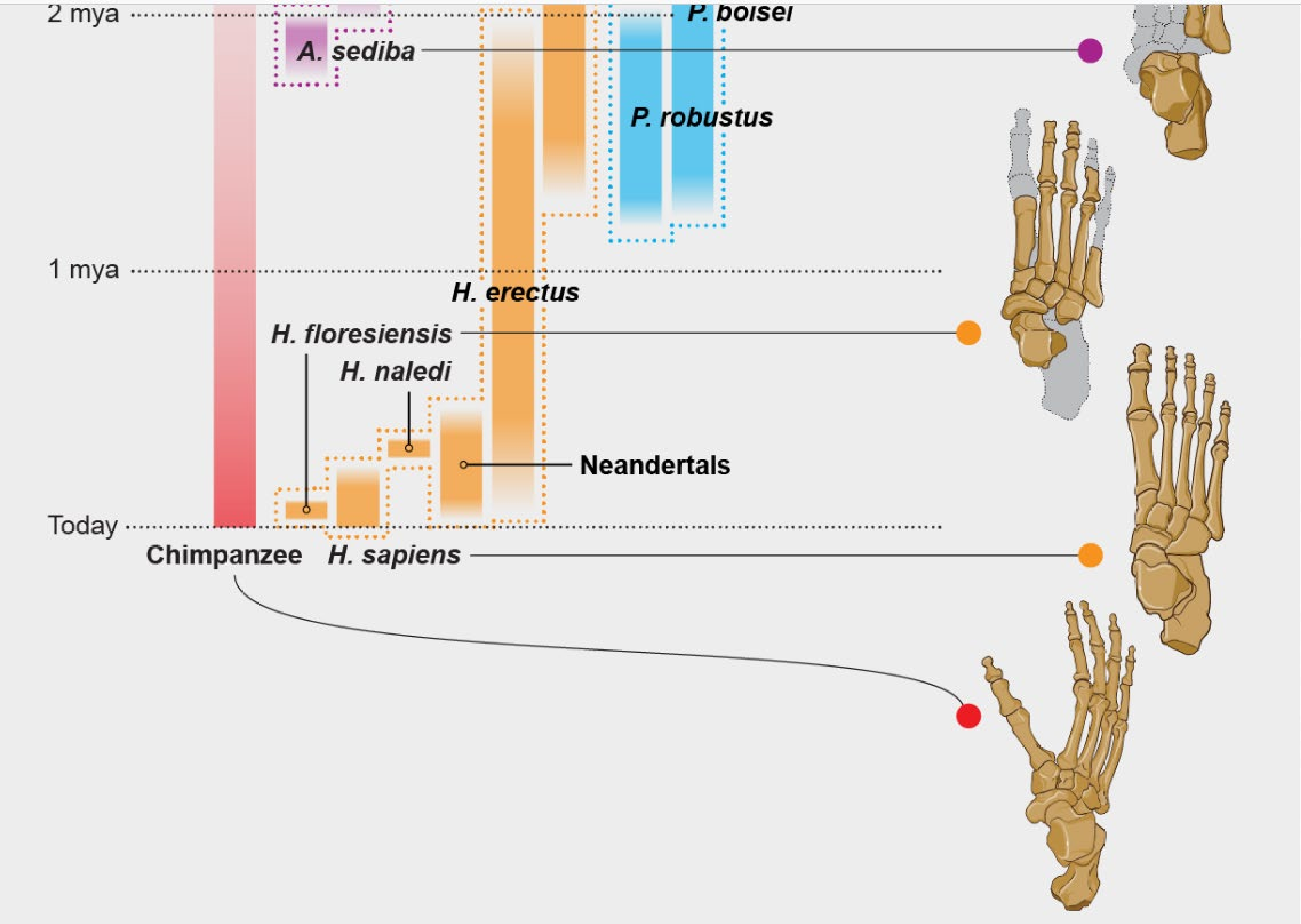


Burtele foot

A. afarensis

A. sediba

H. floresiensis



H. floresiensis

Homo sapiens

Chimpanzee

Site G – A. australopithecus

Site A – hominin?: short & wide; big toe sticks out to the side

Site A

- Site A footprints were short and wide, the big toe stuck out to the side a bit, and there was some evidence the walkers had a more flexible middle portion of the foot.
- Because it is thought that the footprint layer at Laetoli captures at most a few days of activity, this is the best evidence we have that different Pliocene hominin species not only were contemporaries but shared the same landscape

Evolution of walking

- According to the traditional view, hominins started out with a chimplike foot built for grasping tree branches.
- This foot evolved into a transitional foot capable of both grasping and walking, as seen in *Ardipithecus ramidus* at 4.4 Ma
- Lucy, the *A. afarensis* individual who lived in Hadar, Ethiopia, some 3.2 million years ago, had a foot which has a big heel and a stiff midfoot that were better adapted to life on the ground. With the emergence of our own genus, *Homo*, roughly a million years later, the foot became even better suited to terrestrial locomotion, evolving shorter toes and a high arch.

DeSilva study: 2 million year period = 5 foot morphologies

- Five different foot morphs, possibly indicating five distinct ways of walking upright.
- Between Ardi and Lucy are three other uniquely shaped feet.
  - first belongs to an Ardi-type creature, about the same age as that fossil, from Gona, Ethiopia
  - second comes from a 3.67-million-year-old hominin from Sterkfontein, South Africa, dubbed "Little Foot"
  - third is a strikingly primitive foot from a site called Burtele in Woranso-Mille, Ethiopia, that dates to 3.4 million years ago.
- **Although** all five of these hominin feet exhibit both apelike and humanlike features, these traits occur in a completely different combination in each foot and do not follow the predicted pattern of becoming less apelike and more humanlike over time.

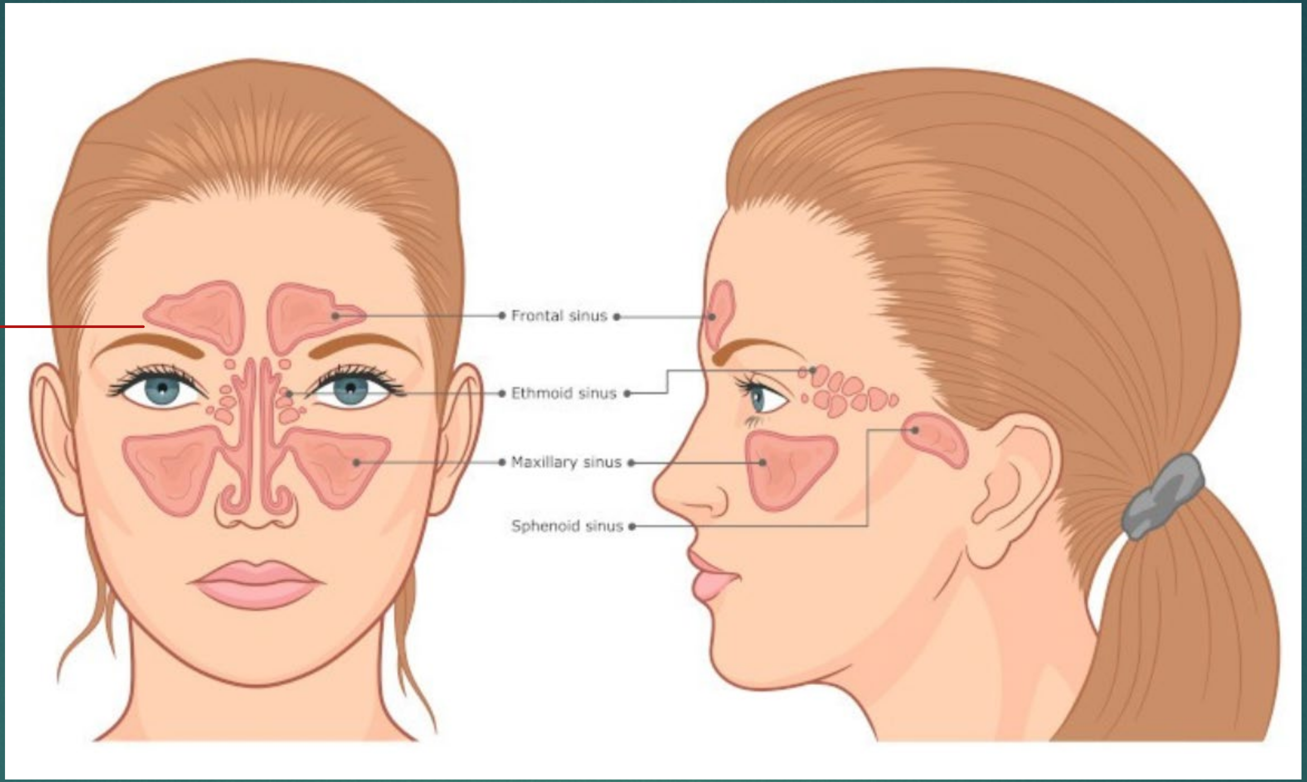
Australopithecus sediba (left) had adaptations to both terrestrial and arboreal locomotion; heel bone was apelike; tiny *Homo floresiensis* (right) had large, flat feet that might have required taking small, high steps.

Walking in the trees

- Possible that the ape from which the ancestors of humans, chimpanzees and gorillas split was not a knuckle-walker at all but more upright, using hand-assisted bipedalism to "walk" through the trees.
- In that case, the unique hominin adaptation would be not bipedal walking per se but rather bipedal walking *on the ground*.
- If more fossils continue to support this hypothesis, then rudimentary bipedalism might turn out not to be a new form of locomotion at all; it may be an old one co-opted for a new environment as our ancestors shifted from an arboreal to a terrestrial existence.

Frontal sinuses and human evolution

Frontal sinuses



Sinuses are air-filled spaces within the bones of the skull that are lined with a mucous membrane. Humans have four types of sinuses: the maxillary sinuses under the eyes, the ethmoidal sinuses between the eyes and nose, the sphenoidal sinuses to the outside of the eyes, and the frontal sinuses. Unknown function.

Antoine Balzeau, et al., 2022

Sinuses

- 2022 Study: Sinuses: the small cavities, located just above the nose, are linked to the size of the frontal lobe. Examined 94 fossil hominins from over 20 species
- Correlates with the development of the frontal lobe in fossil hominins. Within our genus, *Homo*, sinuses can be used to tease apart the relationships between different species.
- In early hominins and non-human apes, the size and shape of frontal sinuses is directly related to the amount of space available for them to grow into.
- The maxillary and frontal sinuses, in primates, are only found in humans and our closest relatives, the chimpanzees and gorillas.

Sinuses

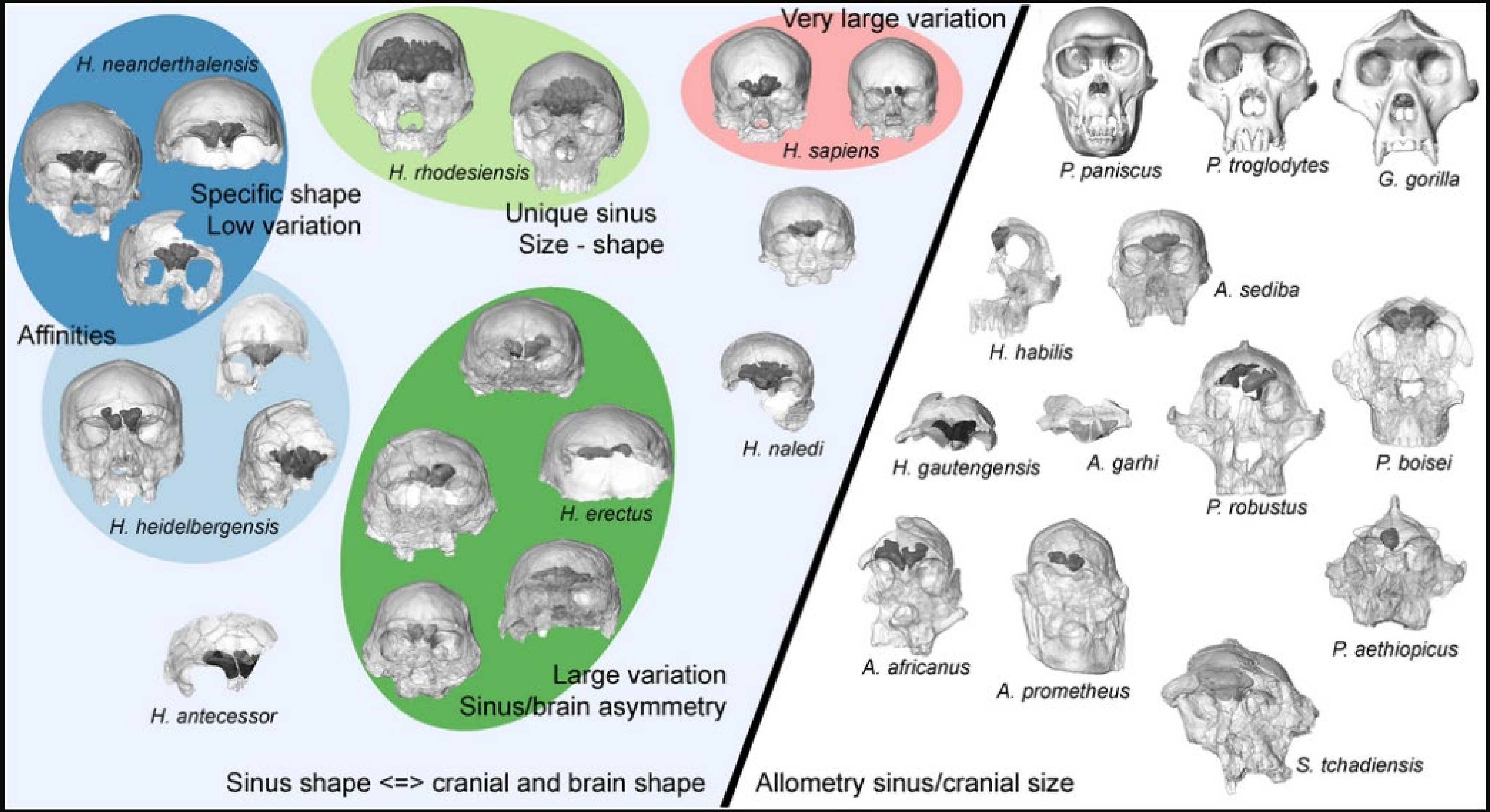
- While sinus size was not able to distinguish between early species of hominins, such as *Australopithecus*, it could separate more recent *Homo* species in the past two million years.

- The study found that species such as *Homo erectus*, *Homo neanderthalensis* and *Homo sapiens* have distinct ranges of sinus size, which researchers suggest could be linked to evolutionary constraints caused by the development of characteristics such as larger brains.

- This relationship was also seen for Middle Pleistocene (770 to 120 Ka) hominins whose identity is currently uncertain, including in specimens associated with the controversial species *Homo rhodesiensis*.

Sinuses

- 'Three crania, which I believe represent *Homo rhodesiensis*, stand out as very different from the others,' Chris Stringer says. 'Their sinuses are much bigger than their relatives and we don't know why. It could represent that they're a specialized group.'
- 'They have very large brow ridges which have been suggested as having a role in social signaling, and large sinuses would reduce the weight of these.'
- Meanwhile, the sinuses of *Homo naledi* were similar to those of *Homo erectus*. This supports *H. naledi*'s human status
- Study found links between these sinuses and the size of the frontal lobe from *Homo erectus* onwards. The size of the sinuses are consistent with the development of a short extension of the brain's left lobe relative to the other, a feature that most humans have today and may be associated with the dominant hand.



Weak constraint on sinus development from surrounding anatomical structures and large frontal superstructures providing potential space for expansion give the sinuses the opportunity to develop isometrically with endocranial size

Sinus size and brain size: potential utility in taxonomic analyses.

- With regard to the relationship between sinus size and endocranial size, early hominins, including *Sahelanthropus* and various species of *Australopithecus* and *Paranthropus*, plot comfortably within the range of variation observed for *Pan* and *Gorilla* and at some distance from the distribution of *Homo* individuals
- Our results suggest that frontal pneumatization develops in *Homo* species in relation to new and variable constraints related to factors such as the integration between the vault and the upper face, brain, and frontal sinuses.
- These groups of *Homo* share a reduced antero-posterior extension of the sinuses compared to early hominins and show variation in the extension of the sinuses in the lateral and vertical directions, depending on taxon. These differences may be an indirect consequence of the differences in cranial morphology between taxa, and of different evolutionary trajectories.

Sinuses

- Despite its relatively small brain size, *H. naledi* does not follow the pattern of frontal pneumatization seen in other small-brained hominins but is in the center of the range of variation observed for *H. erectus*.
- High levels of variation in sinus size and shape are visible among Middle Pleistocene hominins, particularly because of the huge pneumatization of Bodo, Broken Hill 1, and Petralona.
- These individuals are unique in terms of the size and shape of their sinuses, which might support their grouping in a separate taxon that could be called *Homo rhodesiensis* due to the presence of the holotype of the species in the group (i.e., Broken Hill 1)
- When relative dimensions are considered, the *H. heidelbergensis* fossils are slightly further outside the range of *H. neanderthalensis.*

Sinuses

- There is no clear support for a functional or a climatic origin of *H. neanderthalensis* pneumatization.
- On the basis of this multiple evidence, we, therefore, propose that the long-standing hypothesis that the frontal sinuses of *H. neanderthalensis* are an adaptation to cold climate, should be definitively rejected.
- We propose then that climate does not seem to directly explain the development of frontal sinuses in our species
- A more anterior, lateral extension of the right frontal lobe of the brain, as reflected by the endocranial cast, compared to the contralateral side is a general pattern in hominins that becomes consistent in *H. erectus*, *H. heidelbergensis*, *H. neanderthalensis*, and *H. sapiens*. This asymmetry is a well-known feature of *H. sapiens*

Sinuses

- Conclude that large frontal superstructures induce weak constraints related to the position of the face and the brain and give the sinuses the opportunity to expand allometrically in all directions into the available space in the genera *Gorilla*, *Pan*, *Sahelanthropus*, *Australopithecus*, and *Paranthropus*.
- In later hominins, new and variable constraints related to developmental integration between the cranium, brain, and frontal sinuses as well as the timing of growth and development of all these structures result in limitations in the opportunistic expansion of the sinuses into the osseous structures of the frontal bone.
- This different condition results in a lower antero-posterior extension of the sinuses compared to early hominins and *Pan*/*Gorilla*. However, differences in sinus shape and size are also observed among later *Homo* species,