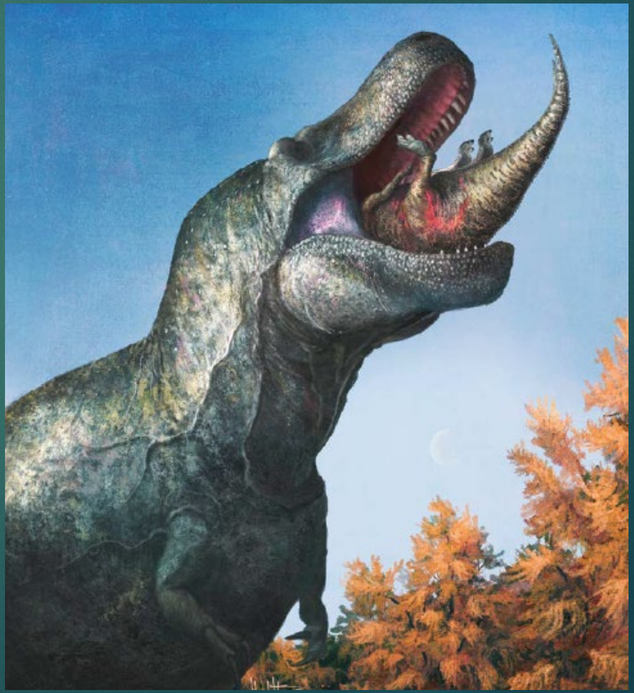
Brief Scientific Update
April 2023

Charles J Vella, PhD

Facelift for *T. rex*: analysis suggests teeth were covered by thin lips

- Crocodiles and Komodo dragons provide evidence to support the idea of a scaly cover over the teeth of dinosaur *Tyrannosaurus rex*.. The reconstruction of soft tissues around the jaws of *T. rex* strongly suggests that it resembled lizards with lips rather than lipless crocodilians. Enamel needs to stay hydrated



That asteroid at 65 Ma

Dinosaur-killing asteroid did not trigger a long 'nuclear winter' after all

- Dinosaur-killing asteroid did not trigger a long 'nuclear winter' after all.

- One spring day 66 million years ago, a 6-mile-wide asteroid smashed into the Yucatán Peninsula and upended life on Earth. This event, called the Chicxulub impact, triggered a mass extinction that wiped out 75% of species, including all non-avian dinosaurs.

- Study published March 22 in the journal Geology tells a different story. Found that there was no evidence for a long 'nuclear winter'.

- Analyzed bacteria fossilized in coal samples from before, during, and after the Chicxulub impact.

The Asteroid

- Found that in the millennia after the impact, the bacteria didn't seem to be bulking up for winter. Instead, they found a roughly 5,000-year warming trend that stabilized relatively quickly. These hot years may have been the result of super volcanoes belching CO_2 into the atmosphere in the millennia leading up to the Cretaceous period's abrupt end.
- This doesn't mean that an impact winter is off the table altogether, Sean Gulick, a geophysicist. The blanket of dust kicked up by the asteroid may have only lingered in the atmosphere for a decade or less — not noticeably changing global temperatures, but plunging Earth into darkness. If you just had months without the sun, it would be enough to kill most of the plants in the world.

The Asteroid

- With so many plants gone, herbivores would have struggled to find enough food to eat. As these species died, it would have sent shockwaves up the food chain, killing off large carnivores and other species that depended on them.

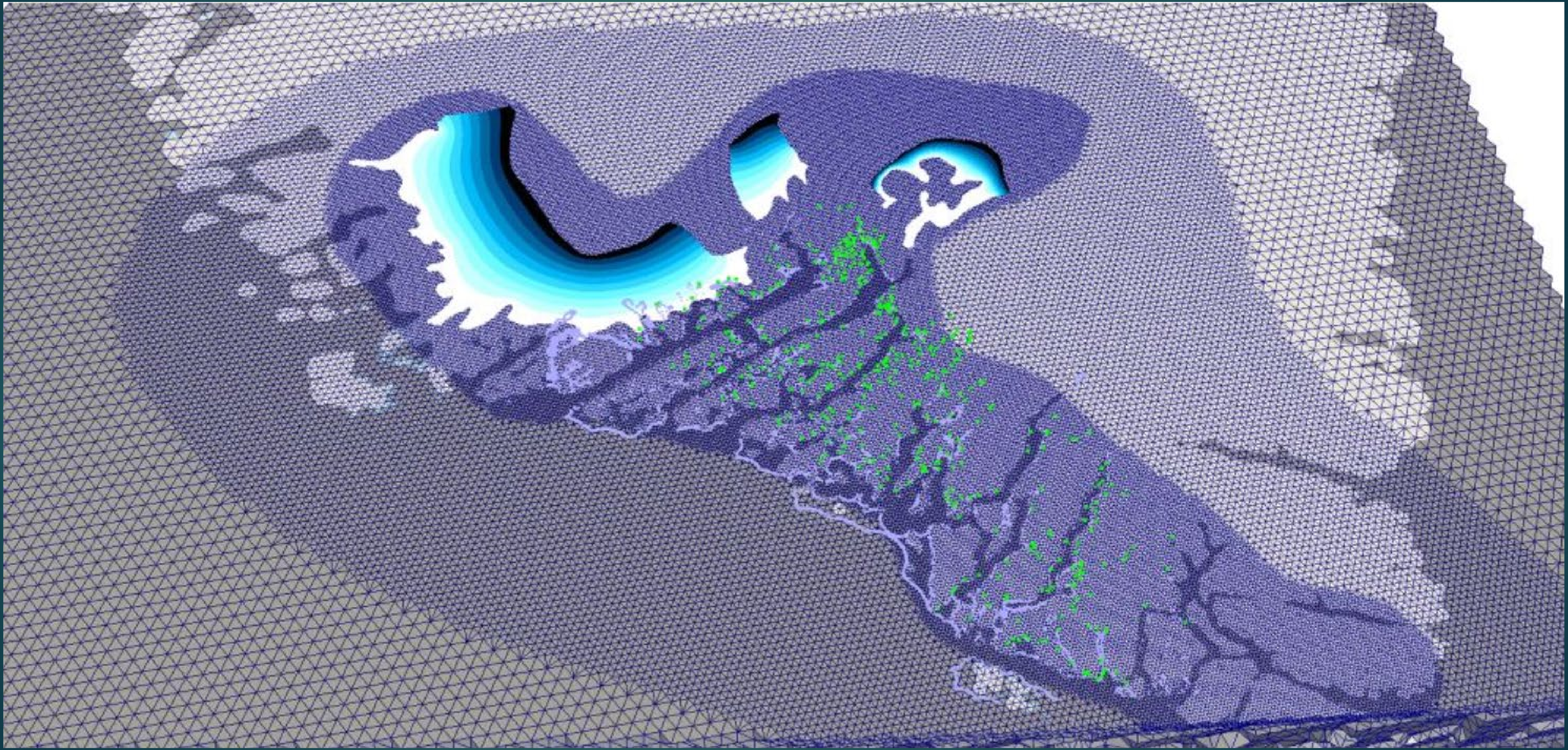
- O'Connor's team agreed that there likely was a short period of cold and darkness at the start of the end-Cretaceous extinction. But it doesn't seem to have set off a long-term cooling trend.

- Their findings indicate that Earth may be capable of rebounding from a climate-changing event faster than previously thought — but not without triggering a mass extinction.

Epic 11-foot-tall sea level rise drove Vikings out of Greenland

- Not even the mighty Vikings could stand against climate change.
- The Vikings first established a foothold in southern Greenland around A.D. 985 with the arrival of Erik Thorvaldsson, also known as "Erik the Red."
- At the time of the Vikings' arrival, Greenland was already inhabited by people of the Dorset Culture, an Indigenous group that preceded the arrival of the Inuit people in the Arctic.
- Ice sheet growth and sea level rise led to massive coastal flooding that inundated Norse farms and ultimately drove the Vikings out of Greenland by the 15th century.
- Around the 15th century, signs of Norse habitation in the region vanished from the archaeological record

Green dots= Viking sites; Blue = flooding area



Greenland flooding and Vikings

- Models showed that from about 1000 to 1400, rising seas around Greenland would have flooded Viking settlements by as much as 11 feet covering 204 square kilometers of coastal land. This flooding would have submerged land that the Vikings used for farming and as grazing pastures for their cattle.
- A perfect storm of external pressures — such as climate change, social unrest and resource depletion — may have spurred the Vikings to abandon their settlements for good

Hunter-gatherer admixture facilitated natural selection in Neolithic European farmers

- Genome-wide DNA from 677 individuals spanning Mesolithic and Neolithic Europe.
- Farmers contributed pigmentation gene: The region around the pigmentation-associated gene SLC24A5 shows the greatest overrepresentation of Neolithic local ancestry in the genome.
- Hunter gatherers donated immunity genes: the greatest overrepresentation of Mesolithic ancestry across the major histocompatibility complex, an immunity region.
- Study extends previous results that highlight immune function and pigmentation as targets of adaptation

Tom Davy, et al., 2023

Apes may have evolved upright stature for eating leaves, not fruit, in open woodland habitats

- The hominoid lineage underwent a major morphological change in the Miocene, acquiring strong hind legs and a more upright posture.

- The prevailing hypothesis pertaining to these changes has been that they were adaptive for foraging on fruit in the terminal branches of tropical forest trees.

- A pair of papers now argue that, instead, such changes may have been driven by adaptation to feeding on leaves in seasonally dry and open forests.

- .

Laura M. MacLatch, et al., 2023

Two studies

- Peppe *et al*. used new data from fossil mammal study sites and found that the expansion of grassy biomes dominated by grasses with the C4 photosynthetic pathway in eastern Africa likely occurred more than 10 million years earlier than prior estimates.
- MacLatchy *et al*. looked at fossils of the earliest ape in this region at this time, *Morotopithecus*, and found isotope evidence of the consumption of water-stressed vegetation and postcranial morphology indicative of strong hind limbs similar to modern apes.
- Together, these papers suggest that early hominoids emerged in a dryer and more irregular environment than was previously believed

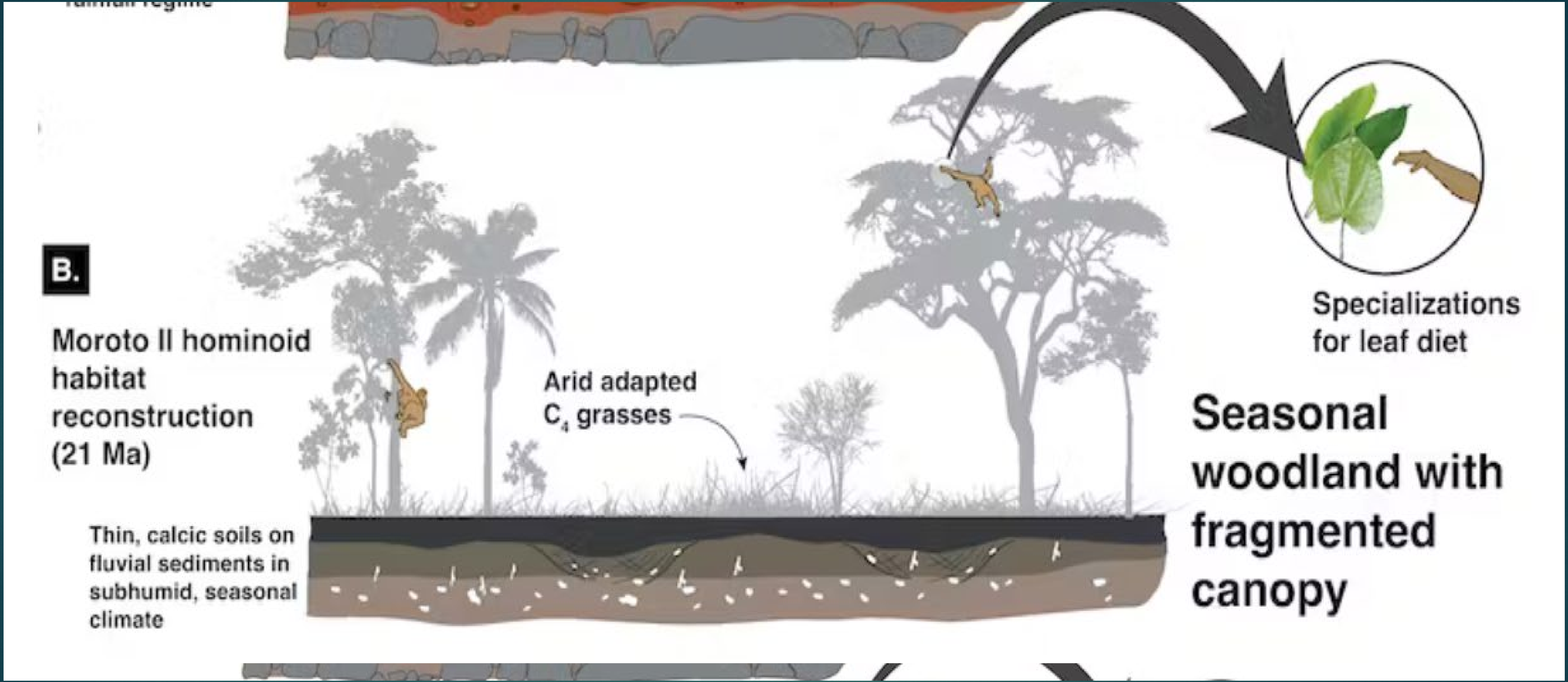
Apes and trees

- Historical theory: our ape ancestors evolved an upright torso in order to pick fruit in forest canopies, but new research suggests a life in open woodlands and a diet that included leaves drove apes' upright stature.
- Pushes back the origin of grassy woodlands from between 7 million and 10 million years ago to 21 million years ago, during the Early Miocene.
- Fruit grows on the spindly peripheries of trees. To reach it, large apes need to distribute their weight on branches stemming from the trunk, then reach out with their hands toward their prize. This is much easier if an ape is upright because it can more easily grab onto different branches with its hands and feet. If its back is horizontal, then its hands and feet are generally underneath the body, making it much harder to move outward to the smaller branches of a tree—especially if the ape is large bodied.
- This is how modern-day apes reach fruit, and, it's been theorized, that's why apes evolved to be upright,

Leaves in the ape diet

- New theory: early apes ate leaves and lived in a seasonal woodland with a broken canopy and open, grassy areas. Suggest this landscape, instead of fruit in closed canopy forests, drove apes' upright stature.
- Found that the apes were eating leaves. The second surprise was that they were living in woodlands
- Study led by MacLatchy focuses on a 21-million-year-old site called the Moroto site in eastern Uganda. Evidence to recreate the ancient environment of Miocene ape Morotopithecus. Had a stiff lower back, good for climbing upright in the trees.

(A) Forested ecosystem traditionally believed to be the habitat of early apes, which ate fruit at the ends of tree branches



(B) New perspective of grassy woodland ecosystem reconstruction, where early apes lived in open habitats and fed on leaves.

Rain and aridity

- The plants living in this landscape were what's called "water stressed," meaning they lived through seasonal periods of rain and of aridity. This also means that at least part of the year, apes had to rely on something other than fruit to survive.

- Together, these findings indicate that Morotopithecus lived in an open woodland punctuated by broken canopy forests composed of trees and shrubs.

Morotopithecus fossils

Three fossilized bones from Morotopithecus: a vertebra, part of a jaw, and a femur.
L. MacLatchy and J. Kingston

Implications of an open woodland at 21 Ma

- If open woodland environments were present at least 10 million years before bipedalism evolved, we need to really rethink human origins

- The first clue that these ancient apes were eating leaves was in the apes' molars. The molars were very "cresty": they were craggy, with peaks and valleys. Molars like this are used for tearing fibrous leaves apart, while molars used for eating fruit are typically more rounded

- The apes and other mammals had been eating water stressed C_3 plants that are more common in open woodland or grassy woodland environments today.

- C_3 plants are primarily woody shrubs and trees while C_4 plants are arid-adapted grasses. Use different photosynthesis pathways.

C_4 grasses

- C_4 grasses lose less water during photosynthesis than C_3 trees and shrubs do. Today, C_4 grasses dominate seasonally dry savanna ecosystems that cover more than half of Africa.
- But scientists hadn’t thought the levels of C_4 biomass measured at Moroto had evolved in Africa until 10 million years ago. Our data suggests it happened twice as far back in time, 21 million years ago.
- This evidence dramatically contradicts the traditional view of ape origins – that apes evolved upright torsos to reach fruit in forest canopies.
- Instead, *Morotopithecus*, the earliest known ape with upright locomotion, consumed leaves and inhabited an open woodland with grassy areas.

2nd study: Apes lived in a C_4 ecosystem at 21 Ma

- The second paper, Peppe *et al*., uses a set of environmental proxies to reconstruct the vegetation structure from nine fossil ape sites across Africa, including the Moroto site, during the Early Miocene. These proxies revealed that C_4 grasses were "everywhere" during that time period.
- These environments are open, and they're open with C_4 grasses.
- C_4 grasses and open habitats were important parts of the early Miocene landscape and that early apes lived in a wide variety of habitats, ranging from closed canopy forests to open habitats like scrublands and wooded grasslands with C_4 grasses.
- These grasses are widespread, and open seasonal woodland ecosystems were integral in shaping the evolution of different mammalian lineages, including how different ape lineages evolved.

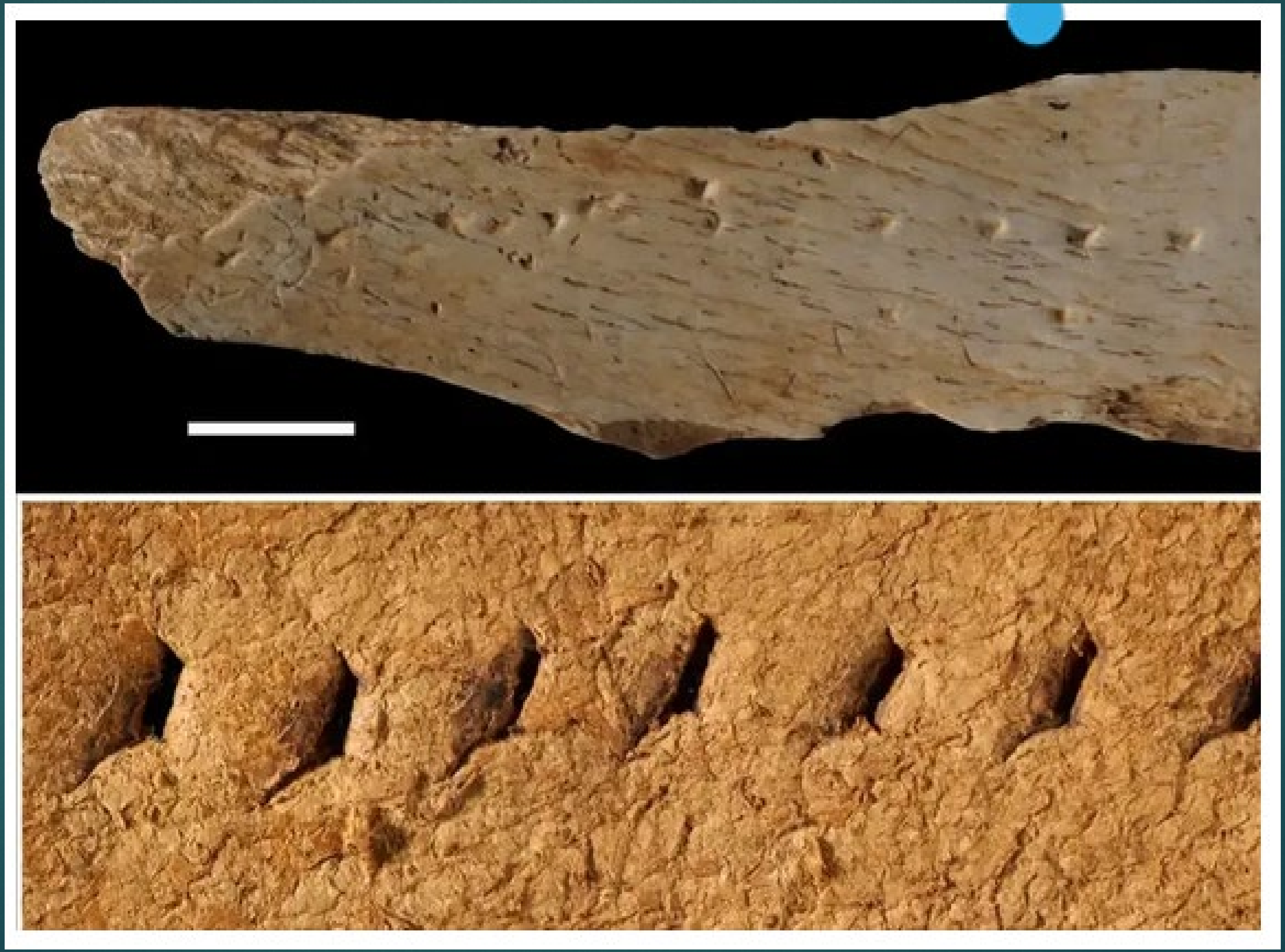
A 39,600-Year-Old Bone Fragment Indicates Humans Were Making Leather Clothes

- A study of an ancient bone with evenly spaced notches suggests that it was used by early humans to make holes in leather clothing.
- A 39,600-year-old bone fragment with strange indentations has been found in Spain. Researchers believe that the bone was used as a punch board for making holes in leather, which suggests that humans were wearing leather clothes in Europe 39,000 years ago. This is the earliest evidence of humans making leather clothes, and it provides new insights into how early humans adapted to cold climates.

Leather clothes

- The bone fragment was found at the Canyars Cave site in Spain. The bone fragment is made from the hip bone of a large mammal, and it has a series of evenly spaced indentations on one side. They display a remarkable uniformity in morphology, distance, and alignment.
- The researchers believe that these indentations were made by a tool with a sharp point, and that they were used to make holes in leather.

This 39,600-year-old bone has puncture marks consistent with leatherworking.



UP Dihedral Burin

Leather working

- The researchers also found evidence that the leather was tanned, which means that it had been treated with chemicals to make it more durable. This suggests that early humans had a sophisticated understanding of leather-working, and that they were able to produce high-quality leather clothing.

- Aurignacian hunters-gatherers used this technology to produce leather works and probably tailored clothes well before the introduction of bone eyed needles in Europe 15,000 years later.

Sahelanthropus tchadensis, TM266: Hominin? Or hominoid?

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

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

Has been virtually remodeled

Foramen magnum shape and forward positioning indicate bipedalism

Did camel herders rebury Toumai facing Mecca?

Two contradictory studies: *Sahelanthropus* was and wasn’t a hominin.

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

2023: *Sahelanthropus* is the earliest known knuckle-walking ape. A hominid, not a hominin.

- 2023 Study: found that the distinctive forelimb morphology of the African knuckle-walking apes is present in the forelimb of the 7-million-year-old *Sahelanthropus tchadensis*.
- Ulna is normally a straight bone in the arm. Only chimpanzees and gorillas exhibit robust and forward-curving ulna shafts, which are thought to serve as an adaptation to knuckle-walking. Curvature in the ulna signals more terrestrial quadrupedal postures

Marc Meyer, et al., 2023

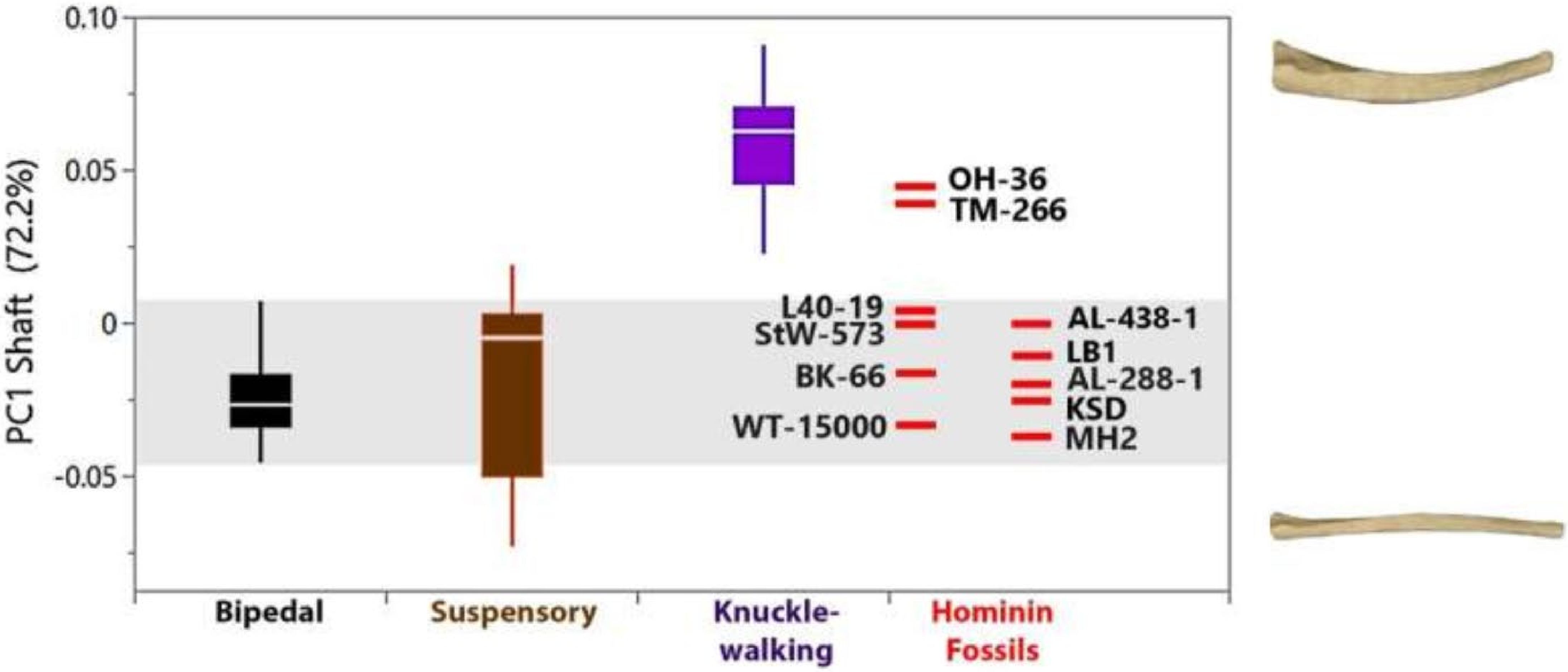
Lateral view of ulna of S. tchadensis; normally a straight bone

Knuckle-walking in *Sahelanthropus*? Locomotor inferences from the ulnae of fossil hominins and other hominoids

- Sahelanthropus: Propose 2 theories - (1) that this species represents the earliest known knuckle-walking African ape and was not a hominin, or (2) that if this species was a facultatively bipedal (capable of walking), like chimps and gorillas it was a habitual knuckle-walker.

- While new research from the leg and arm bones of this species strongly refute the idea that Sahelanthropus was an early biped, the new evidence indicating that it was a knuckle-walking Miocene ape shifts it to a uniquely privileged evolutionary position.

The shape of the ulna shaft in knuckle-walking African apes is distinctive



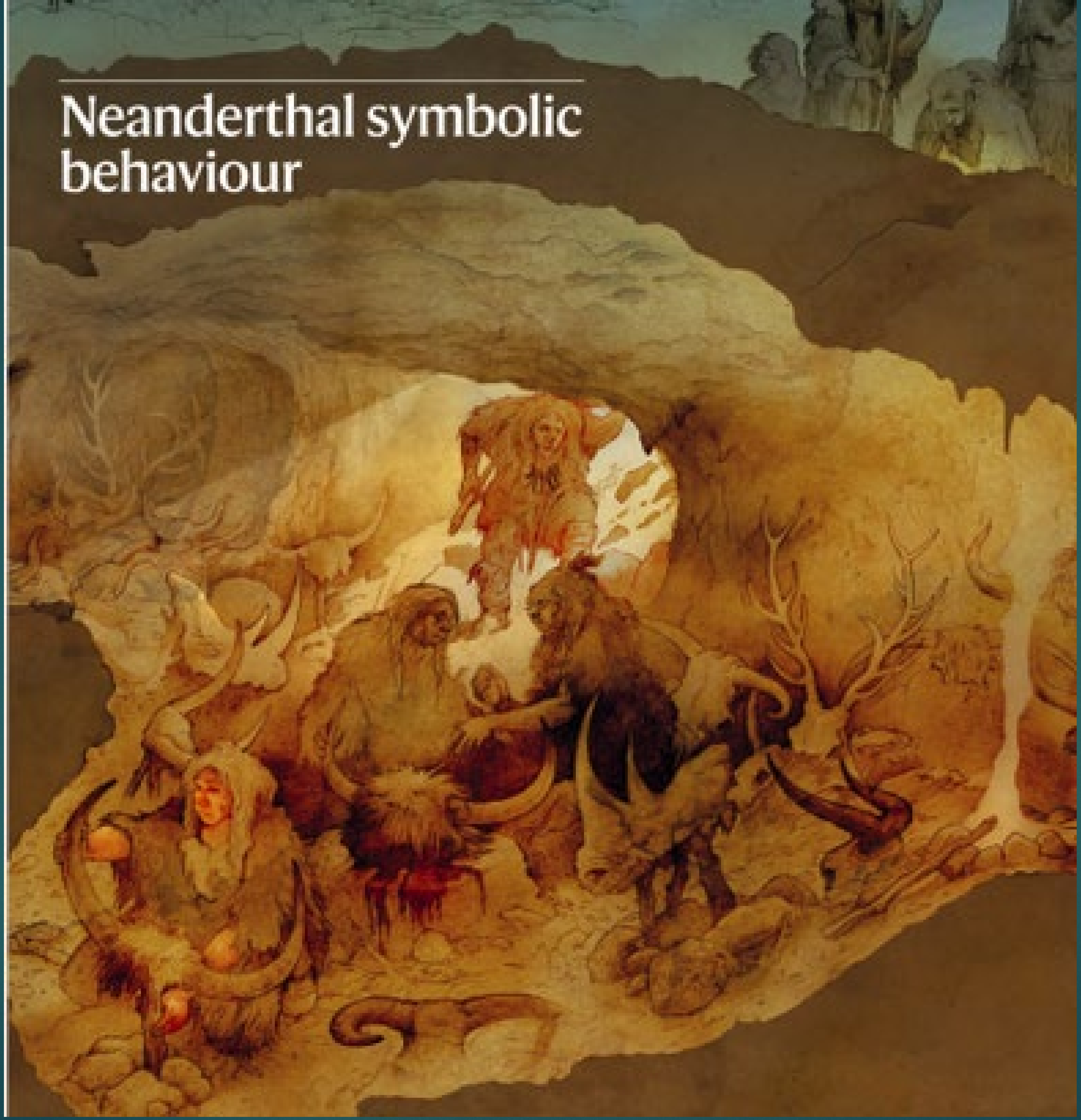
The shape of the ulna shaft in knuckle-walking African apes is distinctive. Credit: Figure from Meyer et al,...

S. tchadensis: represents a late Miocene hominid with knuckle-walking adaptations

- Study compared the relative influence of locomotion, taxonomy, and body mass on ulna contours in Homo sapiens (*n* = 22), five species of extant apes (*n* = 33), two Miocene apes (*Hispanopithecus* and *Danuvius*), and 17 fossil hominin specimens including *Sahelanthropus*, *Ardipithecus*, *Australopithecus*, *Paranthropus*, and early *Homo*.
- Ulna shafts significantly correlate with type of locomotion. African apes' ulna shafts are more robust and curved than Asian apes and are unlike other terrestrial mammals, curving ventrally rather than dorsally.
- Because this distinctive curvature is absent in orangutans and gibbons, it is likely a function of powerful flexors engaged in wrist and hand stabilization during knuckle-walking, and not an adaptation to climbing or suspensory behavior.

Sahelanthropus = A knuckle-walking hominid

- The *Sahelanthropus tchadensis* fossils differ from other hominins by falling within the knuckle-walking morphology, and thus appear to show forelimb morphology consistent with terrestrial locomotion.
- Along with its associated femur, the TM 266 ulna shaft contours and its deep, keeled elbow socket comprise a suite of traits signaling African ape-like quadrupedalism.
- This study supports the growing body of evidence indicating that *S. tchadensis* was not an obligate biped, but instead represents a late Miocene hominid with knuckle-walking adaptations.



Why were Ns collecting large horned animal heads?

A Neandertal trophy cave

Nature Human Behavior
March 2023

N trophy collection

- The discovery and interpretation of the archaeological material from level 3 of Cueva Des-Cubierta (Madrid), accumulated in a two-meter-deep deposit between 43 and 70 ka has been published.
- An astonishing accumulation of 35 megafauna skulls (bison, aurochs, deer, rhinoceros) stands out in this set.
- It has been interpreted as a possible accumulation of hunting trophies or another ritual action carried out by Neanderthals continuously at different times.

Enrique Baquedano …Tom Higham, et al., 2023

Steppe bison (2 meter tall, 2000 lb) - hunting trophy?

A symbolic Neanderthal accumulation of large herbivore crania

- Examination of the possible behavior of Neanderthal groups at the Cueva Des-Cubierta (central Spain) via the analysis of the latter’s archaeological assemblage.

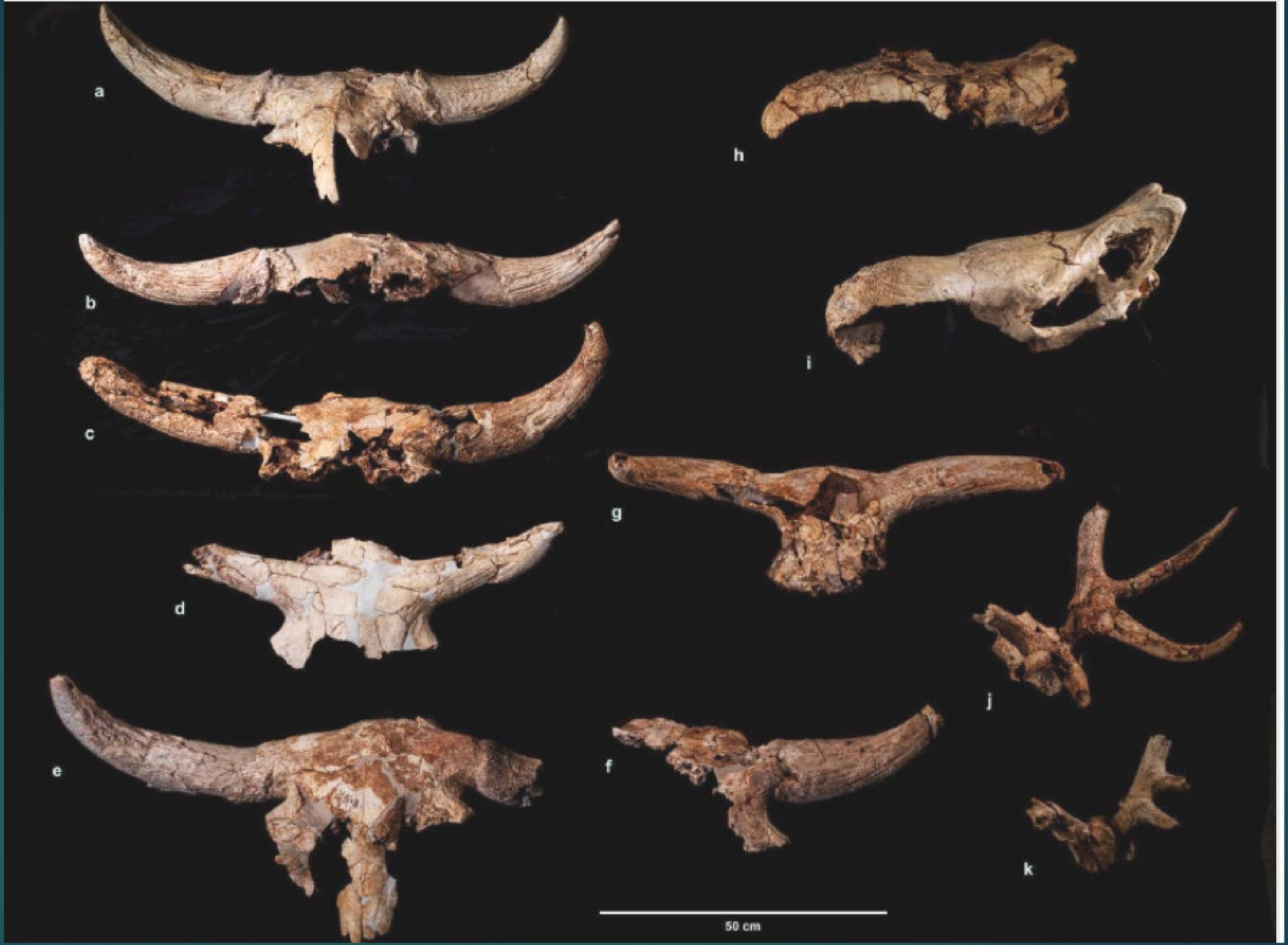
- Alongside evidence of Mousterian lithic industry, Level 3 of the cave infill was found to contain an assemblage of mammalian bone remains dominated by the crania of large ungulates, some associated with small hearths.

- The scarcity of post-cranial elements, teeth, mandibles and maxillae, along with evidence of anthropogenic modification of the crania (cut and percussion marks), indicates that the carcasses of the corresponding animals were initially processed outside the cave, and the crania were later brought inside.

Enrique Baquedano …Tom Higham, et al., 2023

A symbolic Neanderthal accumulation of large herbivore crania

- A second round of processing then took place, possibly related to the removal of the brain.
- The continued presence of crania throughout Level 3 indicates that this behavior was recurrent during this level’s formation.
- This behavior seems to have no subsistence-related purpose but to be more symbolic in its intent.



Some of the best preserved crania from the Uncovered Cave Level 3: a,b,c,d,e,f = Bison priscus; g = Bos primigenius; h,I = Stephanorhinus hemitoechus; j,k = Cervus elaphus

Hunting trophies

- Studies involving modern hunter-gatherer groups have shown that the heads of large animals are usually discarded and not taken back to camp, since they are heavy and of lower use as food.
- The introduction of the crania, and not of other parts of the carcasses of greater nutritional interest, into the Cueva Des-Cubierta thus seems to have been deliberate and not related to subsistence. Rather, it seems more related to their symbolic use.

Hunting trophies

- Today, the accumulation and display of large mammal skulls in the form of hunting trophies is linked to sport hunting.
- Similar practices been documented for the most recent hunter-gatherer societies. Indeed, cultures worldwide have invested animal skulls with a strong symbolic content and have protected or displayed them with due attention.

Cueva Des-Cubierta as a hunting shrine

- In the present case, the fact that the crania all belong to species with cranial appendages (unshed antlers in the case of the deer) suggests that they may represent trophies.
- Their concentration in a small space also suggests that the accumulation might be considered a hunting shrine.
- However, other interpretations cannot be ruled out, such as a link with ritual and fire (given the proximity of the evidence of the latter's use), some expression of the symbolic relationship between Neanderthals and the natural world, or some kind of initiatory rite or propitiatory magic.

N repeat behavior: Cultural phenomenon

- The finding of crania, thermoaltered materials and lithic elements throughout, along with the continued presence of the tools necessary for that exploitation over the entirety of Level 3, indicates that the site's Neanderthal occupants repeated the same type of behavior over a long period (years, decades, centuries or even millennia).

- The intentional deposition of large mammal crania over the time that Level 3 formed suggests the transmission of this behavior between generations, which would be consistent with its interpretation as a cultural phenomenon.

- The accumulation of crania in the Cueva Des-Cubierta reported here provides further evidence of Neanderthal symbolism associated with the animals these humans hunted.

++++ Paleogenetics, Pt. 15

Americas, Pt. 2

April 2023

Beware of binary opinions

- Anthropologists have long been acutely sensitive to the racism (& distortion of evolution) dripping from the binaries–
  - ancestral and modern
  - primitive and advanced,
  - simple and complex,
  - savage and civilized,
  - backward and advanced,
  - progressive and retrograde,
  - developed and underdeveloped,
  - higher and lower,
  - secular and religious,
  - traditional and modern.
- Yet tragically these binaries continued to be deployed to justify the genocide of indigenous America, the African slave trade, colonialism by white empires, and today the war on Islam.

Reich, 2018: All humans are mixtures

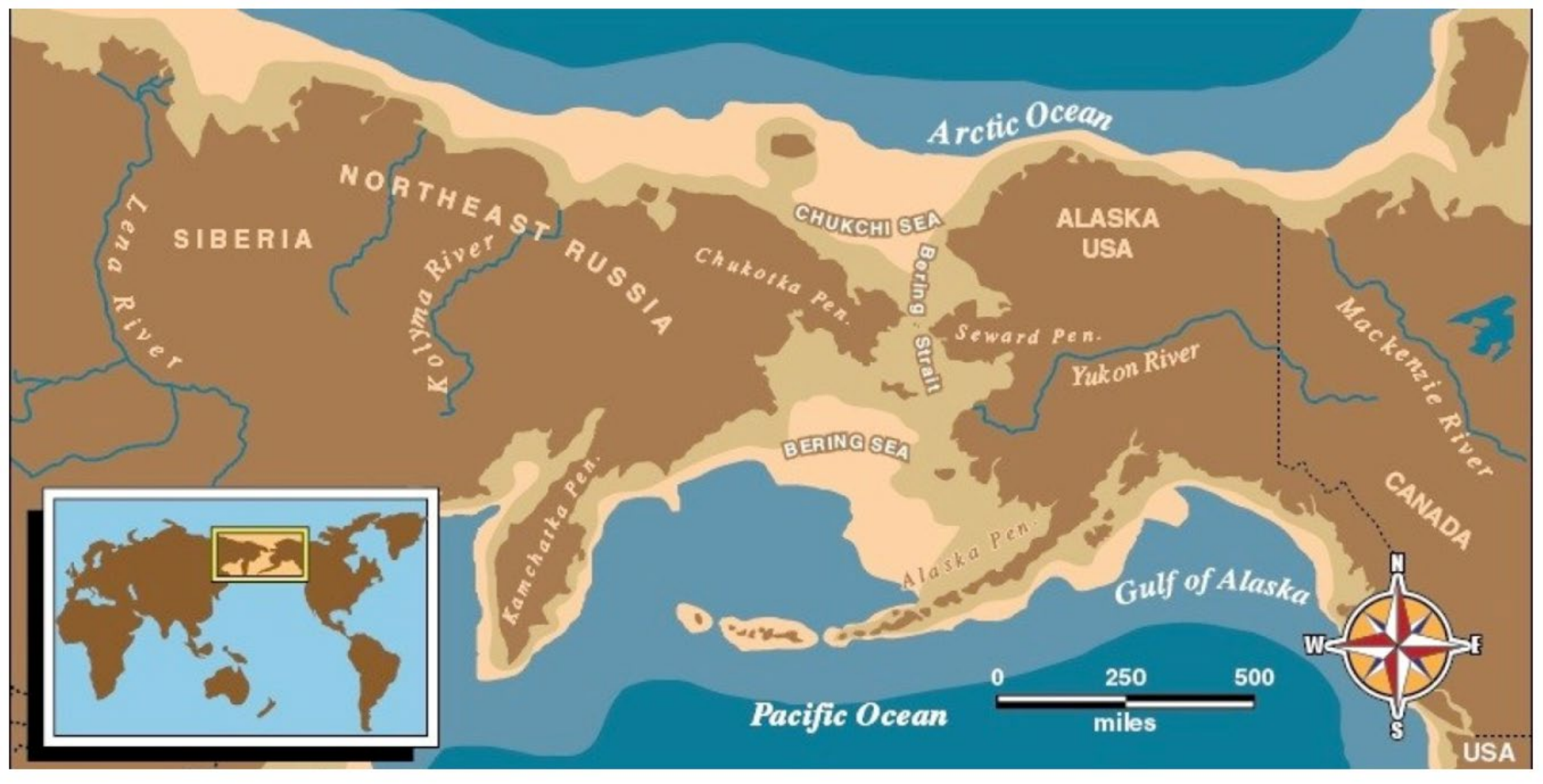
- David Reich's Core message: almost all human individuals and populations are mixtures resulting from multiple population migrations and gene flow.
- Almost no populations today in one geographic location were there in far past. Human populations have repeatedly turned over.
- Mixing is in human nature, and not a single population is –or could be—"pure".
- Continuous gene flow is the norm, not the exception, in the history of our species.
  - "Mixture is fundamental to who we are. We need to embrace it, not deny it occurred."

AMHs: Bering Land Bridge

AMHs: LP Population Expansion: The Americas

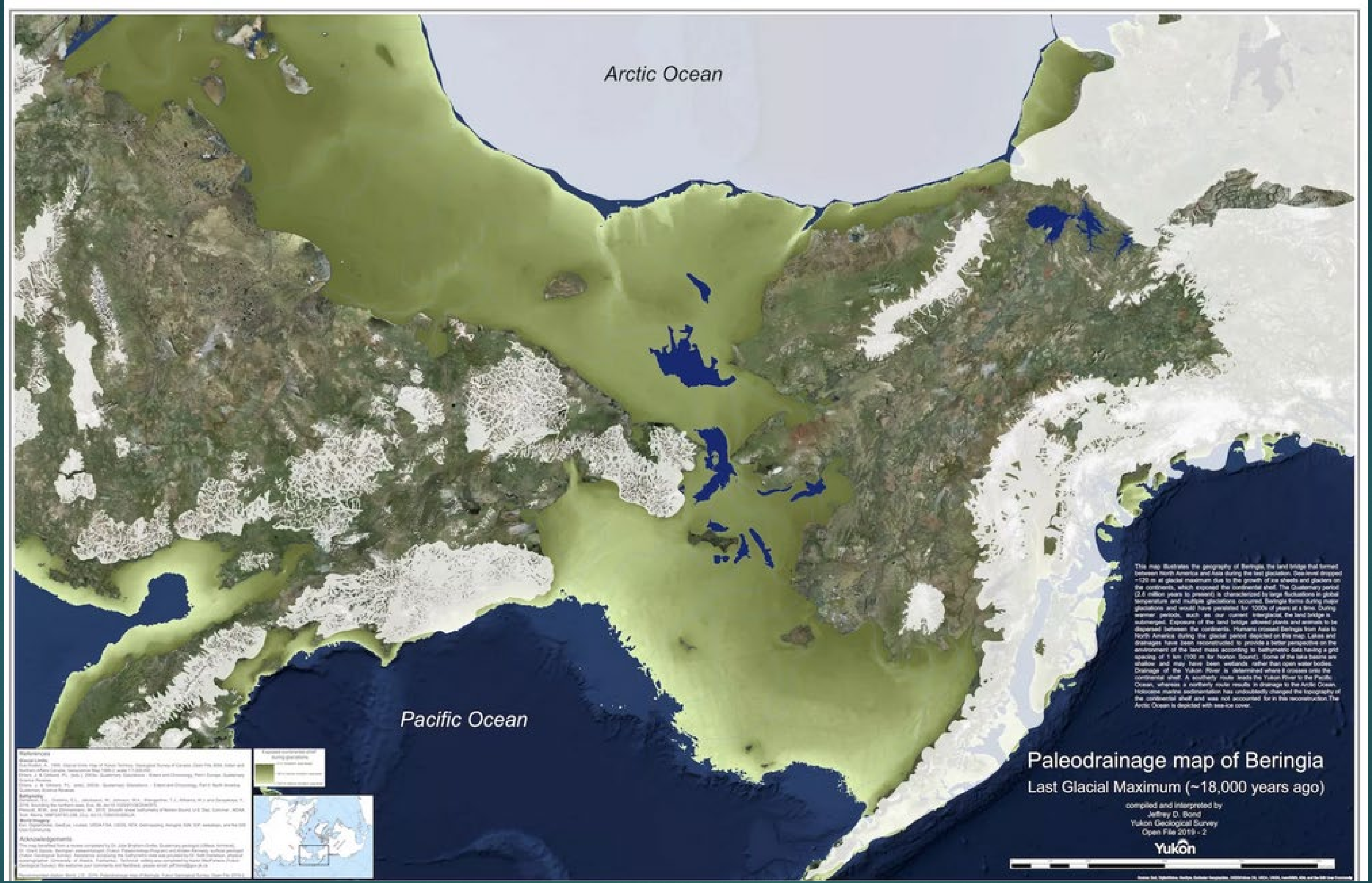
- Last Glaciation: 26 to 11 Ka
- Canada, Alaska, Northern US covered by Laurentide glacier, 3 miles thick in places
- The barrier: Laurentide Ice Sheet = giant wall of ice up to 2 miles tall from coast to coast in S Canada and N US region. For millennia, it was an impenetrable barrier
- Beringia: 1000 km wide land bridge across the Bering Strait between Asia and America; caused a 100 meter drop in sea level. Ice began to melt circa 14 Ka; land bridge severed by 10 Ka.

Bering Land Bridge/Bergenia



Historical theory: a small human population of at most a few thousand arrived in Beringia from eastern Siberia during the Last Glacial Maximum before expanding into the settlement of the Americas sometime after 16,500 years age. This would have occurred as the American glaciers blocking the way southward melted, but before the bridge was covered by the sea about 11,000 years ago.

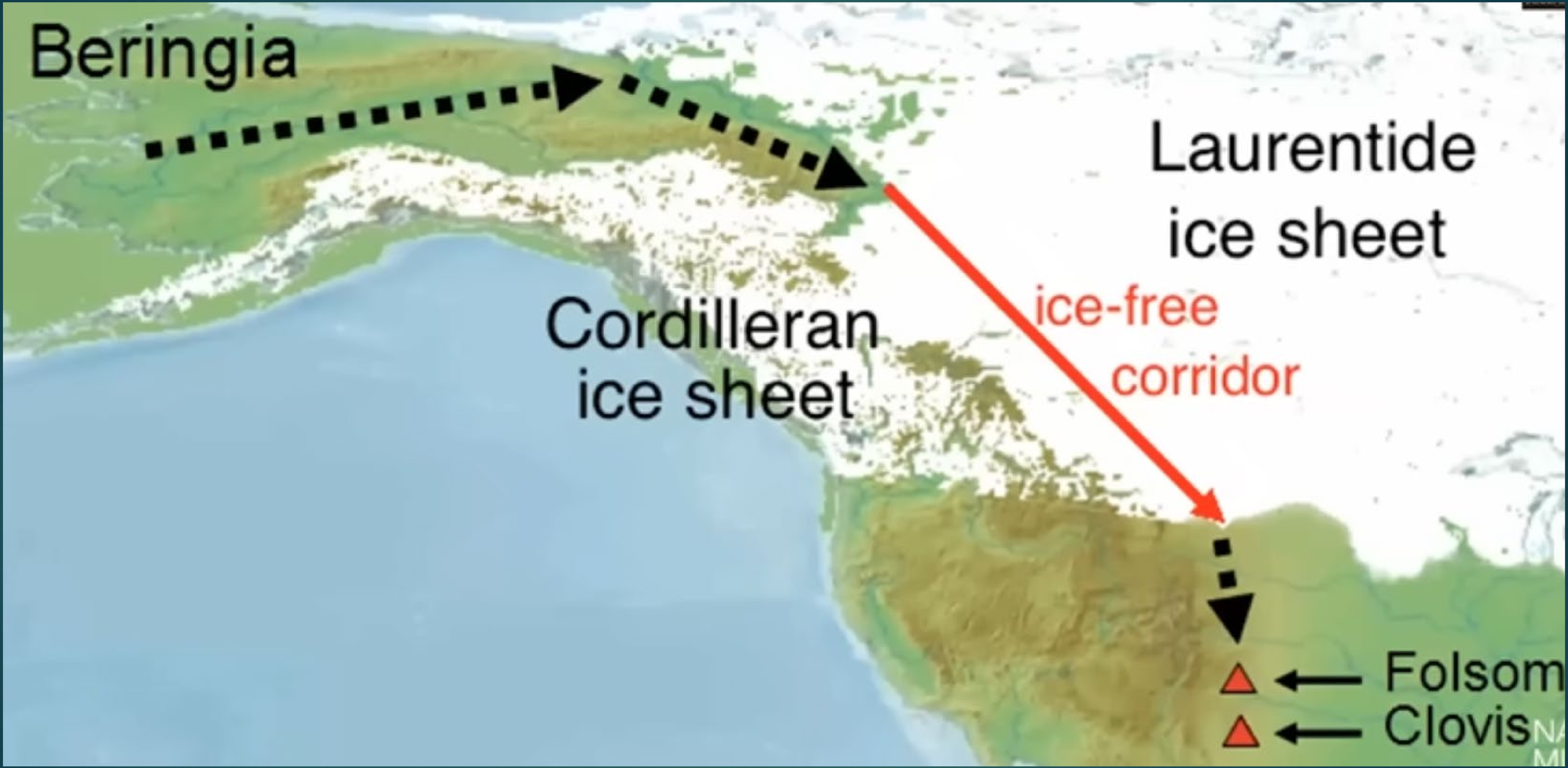
Bering Land Bridge formed much later than originally thought



Tim Stephens, 2022

Bering Land Bridge: formed 35,700 ya

- Researchers reconstructed the sea level history of the Bering Land Bridge from 46,000 years ago and found that it didn't emerge until around 35,700 years ago, which is less than 10,000 years before the last ice age (Last Glacial Maximum (LGM));
- Land bridge consisted of steppe/tundra; supported herds of horses, mammoths, and other Pleistocene fauna
- Some studies suggest people may have lived in Beringia throughout the height of the ice age.
- The growth of the ice sheets, which led to a subsequent drop in sea levels, occurred later in the glacial cycle, with the Bering Strait being open and flooded from at least 46,000 to 35,700 years ago
- As Earth warmed and its ice sheets began melting, the bridge became inundated around 11,000 to 13,000 years ago as it disappeared under the Bering Strait


Beringia
Laurentide ice sheet
Cordilleran ice sheet
ice-free corridor
Folsom
Clovis

Massive Beringia Ice Wall led to coastal migration

- There are two main hypotheses as to how people first migrated to North America.
  - The older idea suggested that people made this journey when a Beringia corridor was relatively free of ice.
  - The more recent theory suggested that travelers made their way on watercraft along the Pacific coasts of Asia, Beringia and North America.

- New study: An icy barrier up to 300 stories high — taller than any building on Earth — may have prevented the first people from entering the New World over the land bridge that once connected Asia with the Americas.
- These findings suggest that the first people in the Americas instead arrived via boats along the Pacific coast.

Massive insurmountable Ice Wall: no interior passage

- New investigation of 64 geological samples taken from six locations spanning 745 miles (1,200 kilometers) along the zone where the ice-free corridor was thought to have existed.
- Examined boulders that glaciers once carried far from their original homes. They analyzed how long these rocks were exposed on Earth's surface — and thus how long they sat on ice-free ground
- The new findings suggest that the ice-free corridor did not fully open until about 13,800 years ago.
- Ice sheets may have been 1,500 to 3,000 feet (455 to 910 m) high in the area where they covered the ice-free corridor. Compare: the tallest building in the world, the Burj Khalifa in Dubai, stands about 2,722 feet (829.8 m) high.

Clovis vs pre-Clovis

- Clovis theory: Based on stone tools dating back as much as 13,400 years, archaeologists had long suggested that Clovis people were the first to migrate from Asia to the Americas.

- In 2020, discovery of stone artifacts in central Mexico that were at least 26,500 years old.

- In 2021, 60 ancient footprints in New Mexico suggested humans were there about 23,000 years ago,

- Recent estimates suggested the ice-free corridor did not open until about 14,000 to 15,000 years ago, which would mean that the earliest Americans may have relied on a coastal route instead of an overland one.

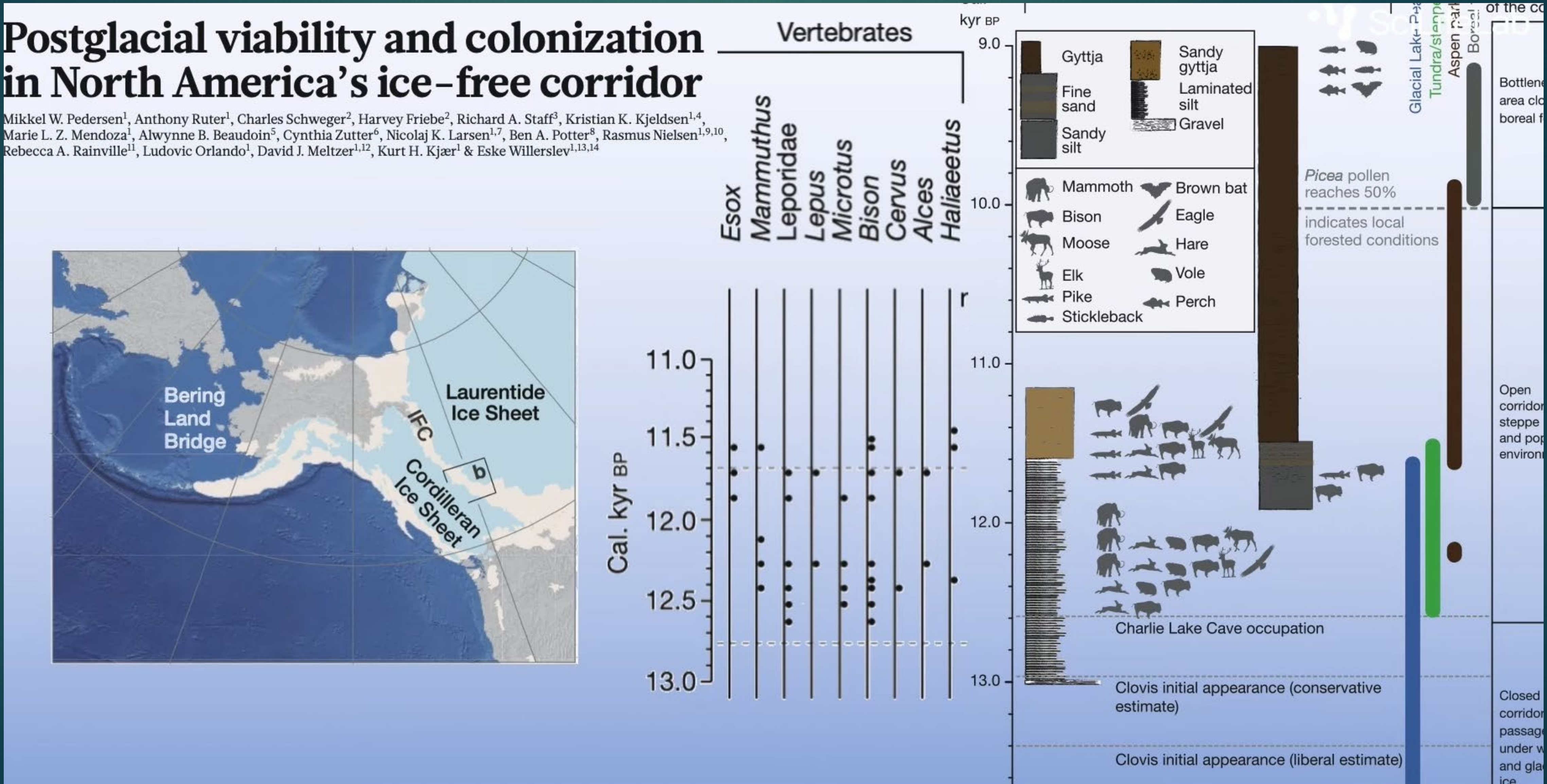
Bering Land Bridge was only passable during 2 brief windows

- During the last ice age, the coastal route from Asia to North America was so treacherous, humans likely crossed over only during 2 time windows, when environmental factors were more favorable for the long and dangerous journey, a new study finds.
  - The first window lasted from 24,500 to 22,000 years ago, and
  - the second spanned from 16,400 to 14,800 years ago,
- The researchers developed climate models. Their models revealed the 2 time windows
  - the first 2,500-year-long window and
  - the second 1,600-year-long span — for year-round coastal migration,
  - which would have enabled a favorable coastal route when the inland route was blocked.

Bering Bridge

- During those two windows, summer kelp forests would have helped keep travelers fed.
- Coastal sea ice during the winter during those periods also may have supported migration; when stuck on the shoreline, sea ice can be relatively flat and stable, so ancient hunters could have walked on it and captured seals, whales and other prey to survive those winters.

Proved no ice-free corridor: only opened at 12,600 years ago; therefore only coastal route prior



Postglacial viability and colonization in North America's ice-free corridor

Mikkel W. Pedersen[1], Anthony Ruter[1], Charles Schweger[2], Harvey Friebe[2], Richard A. Staff[3], Kristian K. Kjeldsen[1,4], Marie L. Z. Mendoza[1], Alwynne B. Beaudoin[5], Cynthia Zutter[6], Nicolaj K. Larsen[1,7], Ben A. Potter[8], Rasmus Nielsen[1,9,10], Rebecca A. Rainville[11], Ludovic Orlando[1], David J. Meltzer[1,12], Kurt H. Kjær[1] & Eske Willerslev[1,13,14]

AMHs: LP Population Expansion: The Americas

- Native American peoples have numerous oral histories of their origins.
- President Thomas Jefferson theorized about the Asiatic origins of Native Americans.
- The population source and route are undisputed. Timing of migration has been the debate.
- Oldest unequivocal sites date to 13-12 Ka; older sites may be absent
- Antiquity of human occupation south of Alaska has been hotly debated for decades

Peopling The Americas

- Historically the leading theory for decades held that a single group of hunters from East Asia swept into the Americas after the LGM on the trail of big game animals and gave rise to all Native Americans.
- First Americans were Siberian UP people who extended their range eastward, just like saiga antelope, yak, and other N Asian species
- New genetic studies have shown that the process of populating the Americas was far more complex than previously understood. Significantly, we now know that multiple ancient populations contributed to the ancestry of Indigenous peoples, not just one.

Jennifer Raff, SCAmer, 2021

Clovis First model

- For much of the 20th century, the so-called Clovis First model of Indigenous origins dominated the field of archaeology.

- These fluted Clovis spearpoints appeared abruptly south of where the ice sheets were around 13,000 years ago, sometimes in association with the remains of megafauna such as mastodons, mammoths and bison.

- People migrated from Siberia to North America across the now submerged Bering Land Bridge after the LGM, moving swiftly down a corridor along the eastern Canadian Rocky Mountains, then spread rapidly southward to populate South America in about 1,000 years.

Folsom fluted point in situ between ribs of Bison antiquus.

Sept 1927 at type site in Folsom NM.

It was the first proof that NAs had arrived in North America

Projectile points from Vail, ME kill and camp sites

Clovis biface cache

Rare quartz crystal biface

Clovis toolkit, incl. bone shaft wrench

Clovis points: 13 Ka

But then Monte Verde, SA, 14 Ka

Monte Verde, Chile, 14 Ka – one of first pre-Clovis sites

Monte Verde: The Door Opens

- Evidence Seafaring People: 14,500 years ago
- 10+ types of seaweed from Pacific Coast, food and medicine, 60 foot shelter structure, Wooden slabs for grinding, Human footprints
- Extinct elephant species with butchered bones
- Normally accepted dating: 14.2 Ka
- A Controversial Age: Oldest layer carbon dated, found with human tools, is 30,000 years old.

Non-Clovis discovery & Ancient East Asians

- Then archaeological sites predating the first appearance of Clovis tools came to light; i.e. Monte Verde in southern Chile, which dates to 14,200 years ago.

- The artifacts found there—tools made of stone, wood and bone—are nothing like the Clovis toolkit. So non-Clovis people reached South America first.

Beringia

- Home to future Native Americans in Beringia - Ancient North Siberians interbreed with East Asians – 25 Ka.

- Two origin groups: 63% of First Peoples = East Asian; 37% Ancient North Siberians.

- Southern central Beringia, now under 164 feet water, was coast 50-11 Ka.

Native Americans ancestors: Ancient East Asians & Siberians

- 1) Approximately 36,000 years ago, a group of people living in what is now East Asia became increasingly isolated.
- By about 25,000 years ago, they were genetically distinguishable from the ancestors of contemporary East Asians.
- This isolated group of Ancient East Asians contributed the majority of ancestry to all Native Americans.
- 2) Another ancestral branch of hunter gatherers emerged around 39,000 years ago and lived at the Yana Rhinoceros Horn site in northeastern Siberia 31,600 years ago. = in the western part of Beringia.

Ancestral Branches: Ancient North Siberians & Mal’ta child

- Genetics of 2 baby teeth of this genetic group, the Ancient North Siberians, who thrived in extremely challenging environments.

- The Ancient North Siberians spread throughout northern and central Siberia. Remains of a child who lived at a site known as Mal’ta document their presence in south-central Siberia 24,000 years ago.

- There is essentially no archaeological record in northeastern Siberia between around 29,000 and 15,000 years ago

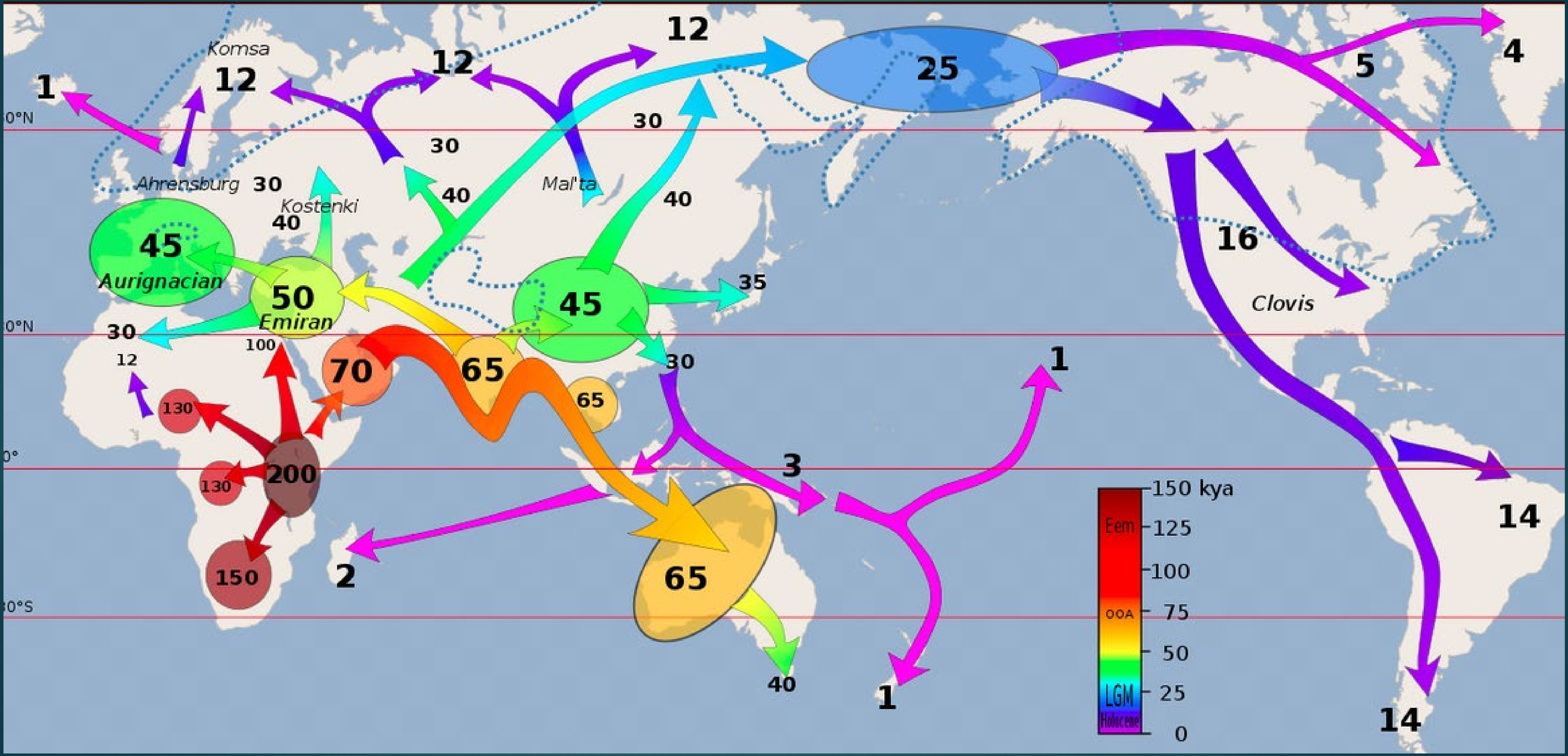
Ancient East Asians and Ancient North Siberians

- Two main branches of the First Peoples' ancestry—the Ancient East Asians and the Ancient North Siberians—converged around 25,000 to 20,000 years ago and interbred, shortly after the start of the LGM.
- They were initially isolated for several thousand years during the LGM; where this refugium was during the LGM is debated.
- The two ancestral population split into at least two branches between about 22,000 to 18,100 years ago.
  - 1 - Ancient Beringians have no known living descendants.
  - 2 - Ancestral Native Americans, gave rise to First Peoples south of the Laurentide and Cordilleran ice sheets.

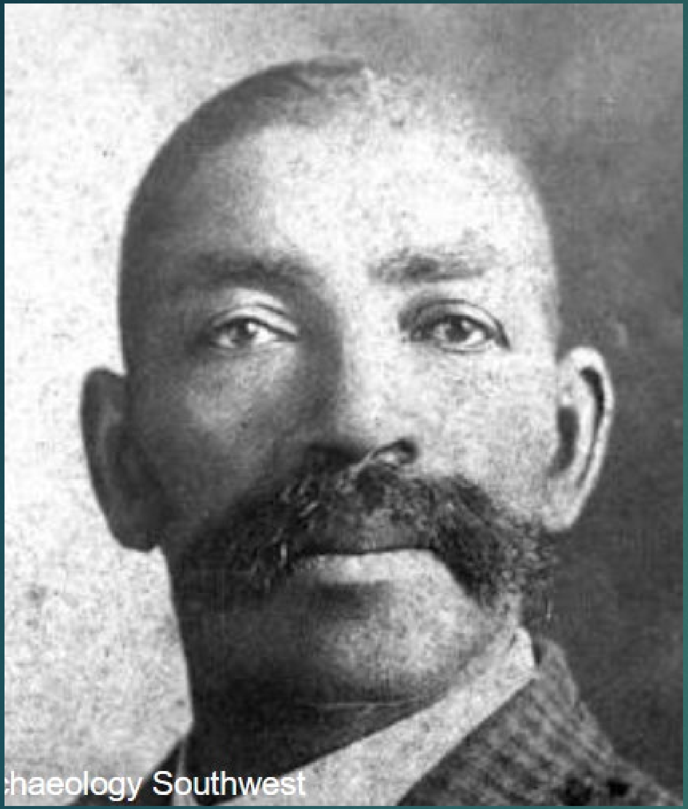
Native American Ancestry

- Please note:
- The following discussion is about aDNA and genetics of Native Americans ancestry
- Indigenous Native American identity is not necessarily about scientific genetics, but rather about political citizenship, culture, kinship, and daily, lived experience as part of an Indigenous community.
- Native Americans have their own origin stories.

Standard model of Out of Africa migrations



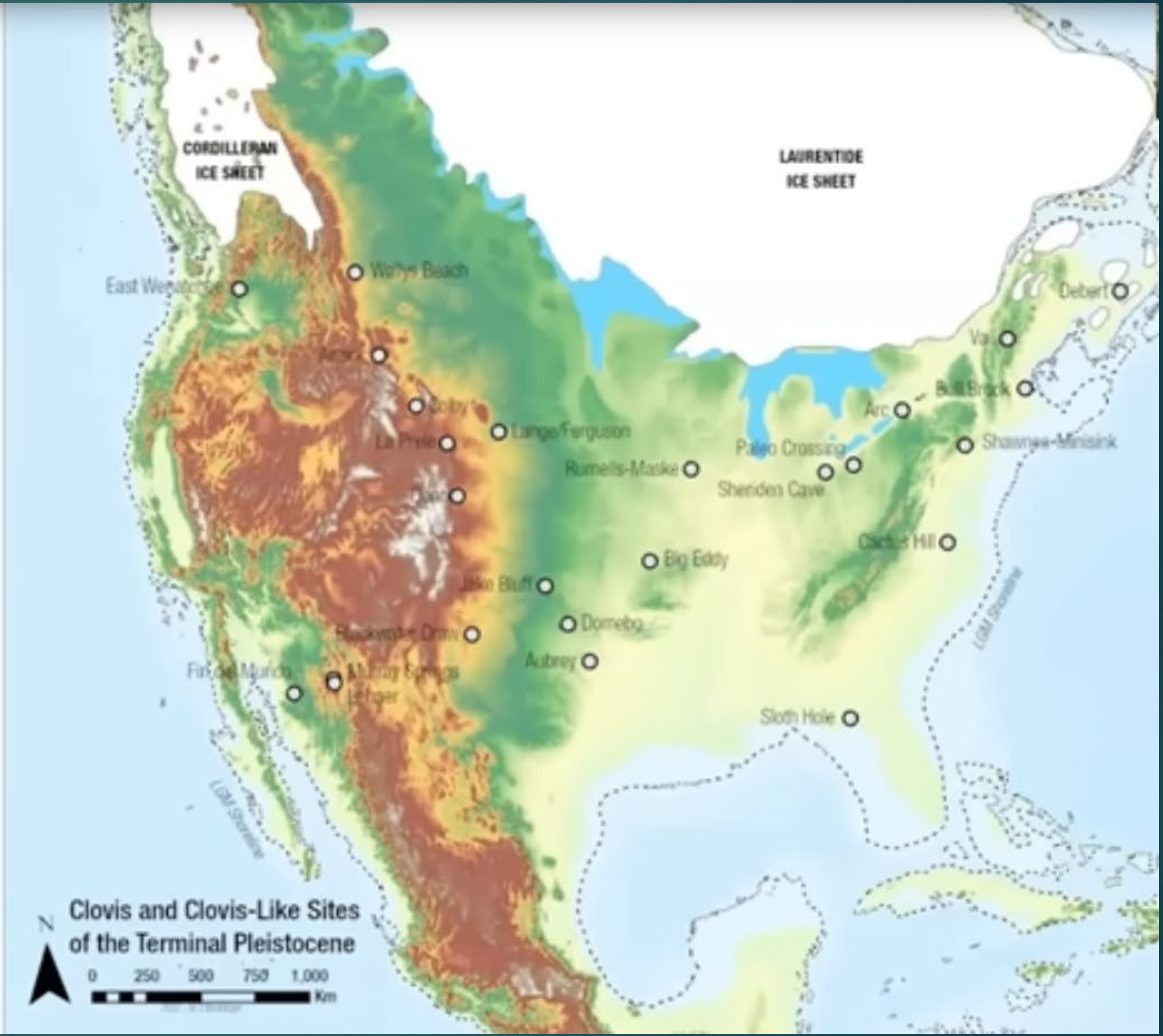
George McJunkin: an AA cowboy & amateur archeologist



In 1908, George McJunkin, an AA cowboy & amateur archeologist, found giant extinct bison bones at Folsom, NM; and then in 1926, first Clovis point was discovered there; and later bisons with embedded points. Later near Clovis, NM, older points were found; named Clovis points. In 1950s, C14 dating = 12,900 for appearance of Clovis people and 1000 years later, extinction of megafauna.

Clovis Sites

https://commons.wikimedia.org/w/index.php?curid=32583959



Solutrean theory

- The Solutrean theory is untrue; theory that UP individuals, who lived in Europe from 20-18 Ka with Solutrean lithics (which look like Clovis points) came across Atlantic;
- PaleoAmerican theory: All genomic studies rule out the possibility that the First Peoples mixed with Europeans or Africans or any other populations before 1492.
- There is no European DNA in NAs; no genetic evidence for transatlantic migrations; Norse people in Newfoundland c 1000 CE left no genetic trace, but lots of archeology

Origin. A Genetic History of the Americas
- Jennifer Raff, 2022

- Accepted historical theory:
  - the first humans in America were the Clovis people with their distinctive spearheads around 13 Ka, having crossed the Bering Land Bridge after the last Ice Age.
  - Clovis period was brief—13,050 to 12,750; Raff: all the megafauna—some 70 species—had been hunted to extinction.
  - Predominance of Clovis First model for 50 years.

- Conservative entry into America estimate for first people – 15-14 Ka, more likely 17-16 Ka and perhaps even as early as 30,000–20,000 years ago

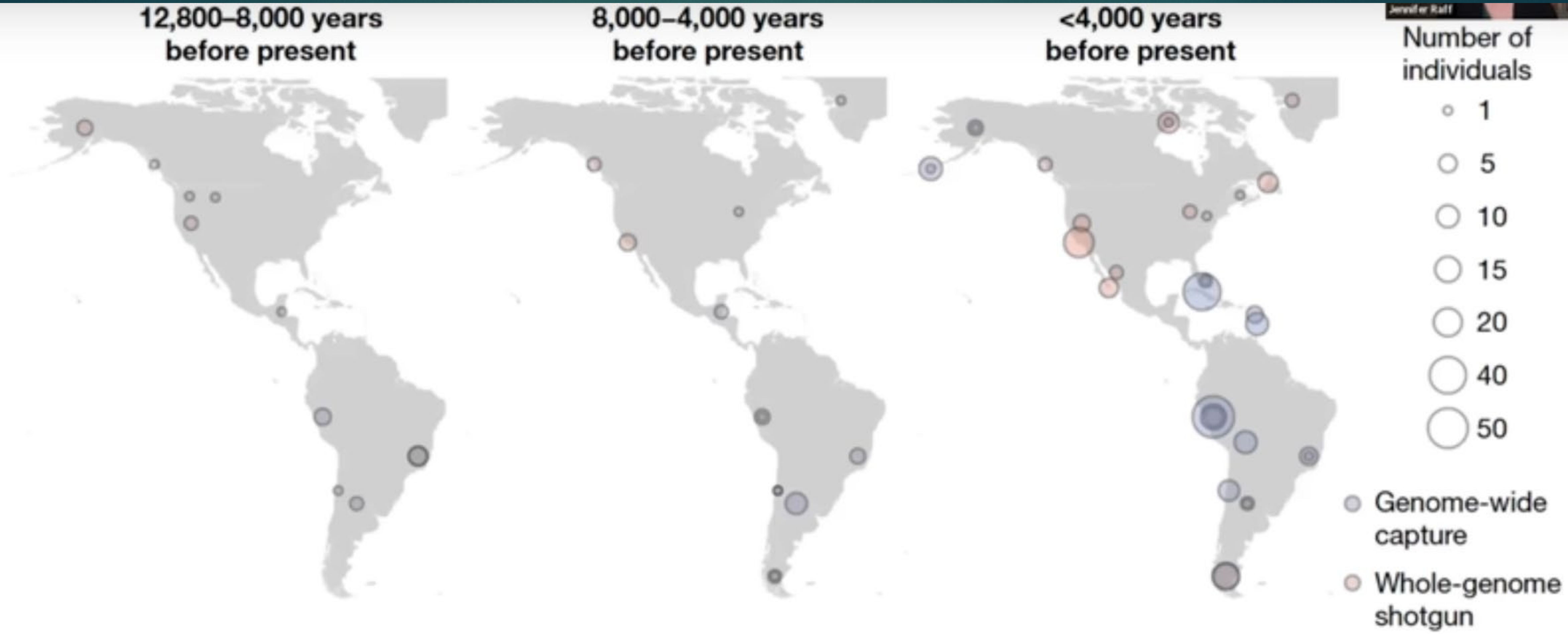


Figure 1 from Willerslev and Meltzer, 202

Now multiple pre-Clovis sites identified

- Monte Verde, Chile (in 1970s) – 14.6 Ka. (1997 expedition confirmed)
- Meadowcroft site, Pa (in 1974) – 16 Ka,
- Cactus Hill (VA) 16.9-15 Ka,
- Paisley Caves (OR) 14 Ka,
- Buttermilk Creek (TX) 15 Ka. - pre-Clovis tools,
- Page-Ladson (FL) 14.5 Ka,
- Huaca Prieta (Peru) 14-5-13.5 Ka,
- Cooper’s Ferry (ID) – 16 Ka

Western Stemmed tradition: Cooper's Ferry, ID; 11.4 Ka or older; genetically similar to Clovis Anzick individual; 2 lithic traditions by same group

Coastal Migration Theory: The Theory Preferred by Geneticists

- At 65,000 years ago, humans reached Australia by boat. MHs were capable of using boats for travel; suitable for island hopping.
- Implications: That technology could have been used to travel the coast, island hopping, to the Americas.
- The "Kelp Highway" Hypothesis: coastal migrations would have encountered the same kinds of marine coastline from Beringia to Chile.
- The Cordilleran Ice Sheet receded from the coast 17,000. People could have lived there.
- The Humboldt Current off the Pacific coast of South America is one of the planets richest marine currents. It has low salinity and high biodiversity
- Early fishing villages off the coast of Peru are thought to have developed early because of the vast richness of the Humboldt Current.

Coastal migration

- There has never been any archaeological evidence whatsoever showing that anyone moved from Beringia through the interior corridor to the Plains or Great Lakes area. No vegetation in corridor until 12.6 Ka.
- The Cordilleran ice sheet melted back from the Pacific coast around 17,000 years ago, meaning that people could have lived along the coast, eating kelp, waterfowl, fish, shellfish, and marine mammals, and periodically going inland for hunting and gathering animals and plants that had survived the LGM south of the ice sheet.
- After Monte Verde evidence, coastal highway became major theory. Humans were using boats to travel to Australia by 75,000 to 62,000 years ago

Kelp Highway

- Kelp highway or Coastal migration hypothesis: coast open by 16 Ka; the ice-free interior corridor, not until 12.6 Ka. Rapid movement south – by boat – leaping over regions. "Kelp Highway" Alaska to Tierra del Fuego – evidence of eating kelp 14 Ka at Monte Verde. Migration along west coast could have happened as early as 30-25 Ka.

- We have no direct evidence that the earliest peoples in the Americas had maritime adaptations. We know that people were making and using watercraft by 13,000 years ago because of the presence of a person's remains dating from that period on Santa Rosa Island off coast of Southern California.

Earlier migrations

- Barring the possibility that there was some as-yet-undiscovered path through the ice wall, people could only have migrated before 26,000 years ago or after 19,000 years ago. Currently the weight of evidence leans more toward the post-19,000-year side, but there are some sites in South America that have been recently discovered dated to as old as 30,000 years ago,

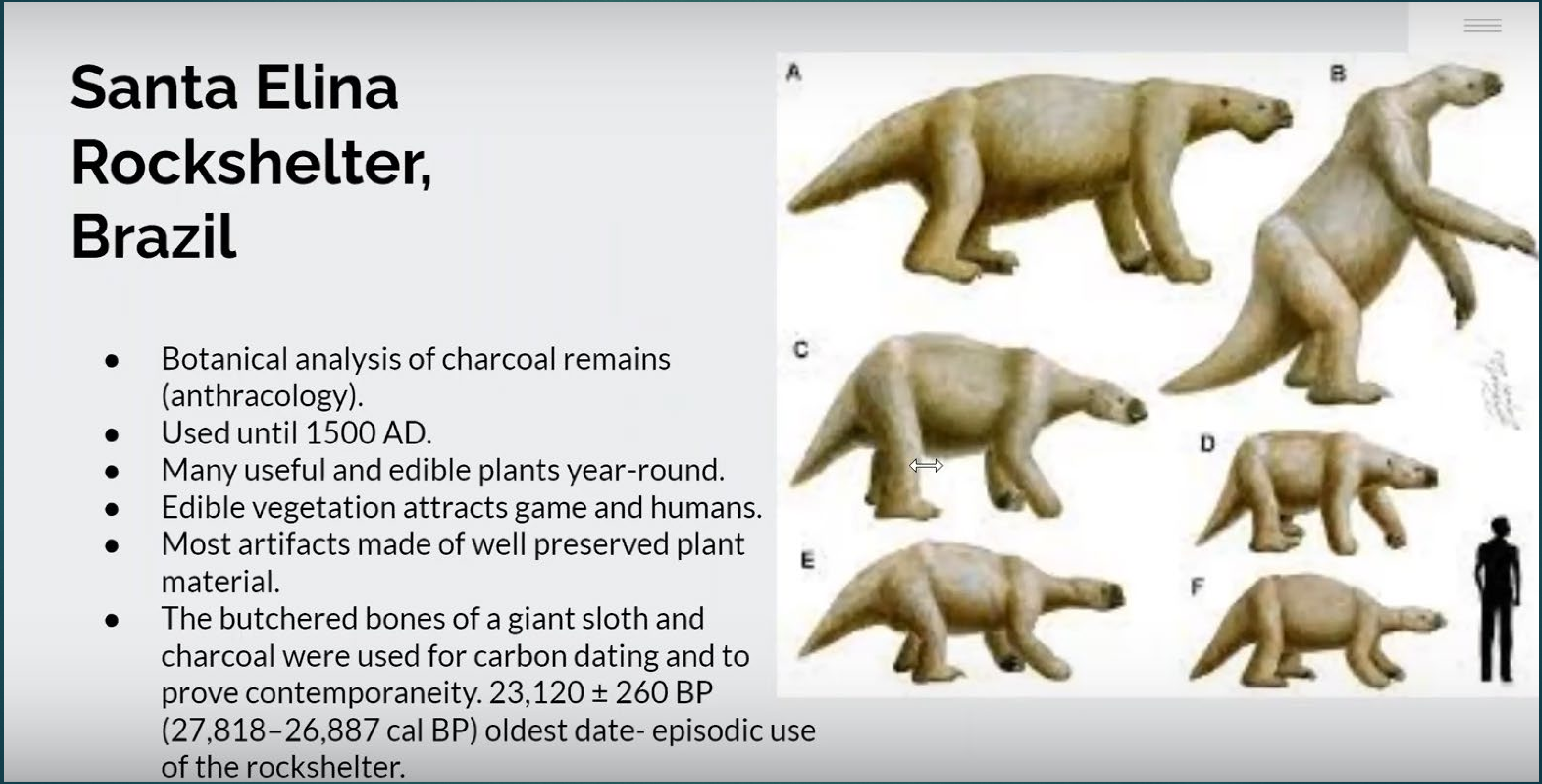
- The footprints at the White Sands Locality 2 site provide even stronger evidence (if their 23,000-to-21,000-year dates are accurate) that at least some people were in North America during the LGM.

- Depending on how early their initial migration was, the interior route may have been a plausible pathway for them

Archeological Evidence hints at earlier entry into the Americas

- Bluefish and Monte Verde sites aren’t alone.
- Genetics DO NOT line up with Clovis First.
- Clovis Lithic Tradition continuity is not what is expected from people encountering new environments. It would not be so uniform. Different lithics for hunting different animals and harvesting different vegetation.
- At this time, genetics do not support the idea that other earlier hominins populated the Americas first
- Genetics does support an earlier peopling than Clovis, of fully modern humans.
- 20,000 ya-easily. 30,000- we are still looking at evidence.

Santa Elina Rockshelter, Brazil: 26-27 Ka



Santa Elina Rockshelter, Brazil

- Botanical analysis of charcoal remains (anthracology).
- Used until 1500 AD.
- Many useful and edible plants year-round.
- Edible vegetation attracts game and humans.
- Most artifacts made of well preserved plant material.
- The butchered bones of a giant sloth and charcoal were used for carbon dating and to prove contemporaneity. 23,120 ± 260 BP (27,818–26,887 cal BP) oldest date- episodic use of the rockshelter.

White Sands, NM, footprints, 21-23 Ka

Lithics

- Stone tool industries of Beringia – different cultures present?
  - Dyuktai (Swan Point) – 14.2 Ka
  - Denali – 12-6 Ka,
  - Nenema – 13.6-12.7 Ka,
  - Mesa – 13 Ka.
- Migration back into north Asia after LGM – 18-15 Ka – Dyuktai tools

Native American mtDNA = Pre-Clovis

- Mitochondrial haplogroups present in pre-contact First Peoples include the following:
    - South of the Arctic: A2 B2 X2a, possibly X2g C1b, C1c, C1d, C1d1, C4c D1, D4h3a.
    - In circum-Arctic peoples: A2a, A2b, D2a, D4b1a2a1a.
    - Geneticists sometimes use "A, B, C, D, X" as a shorthand for these haplogroups
- Mitochondrial haplogroups coalesce much earlier than 13,000 years. Earlier than Clovis theory postulates.
- All mitochondrial lineages commonly found in populations below the Arctic Circle share common ancestors between about 18,400 and 15,000 years ago (via mtDNA molecular clock calc.).

DNA

- This close agreement suggests that these haplotypes were all present in the initial founder population(s).

- Mitochondrial lineages within Siberian and Native American populations show that their ancestral populations became isolated from each other between about 25,000 and 18,400 years ago.

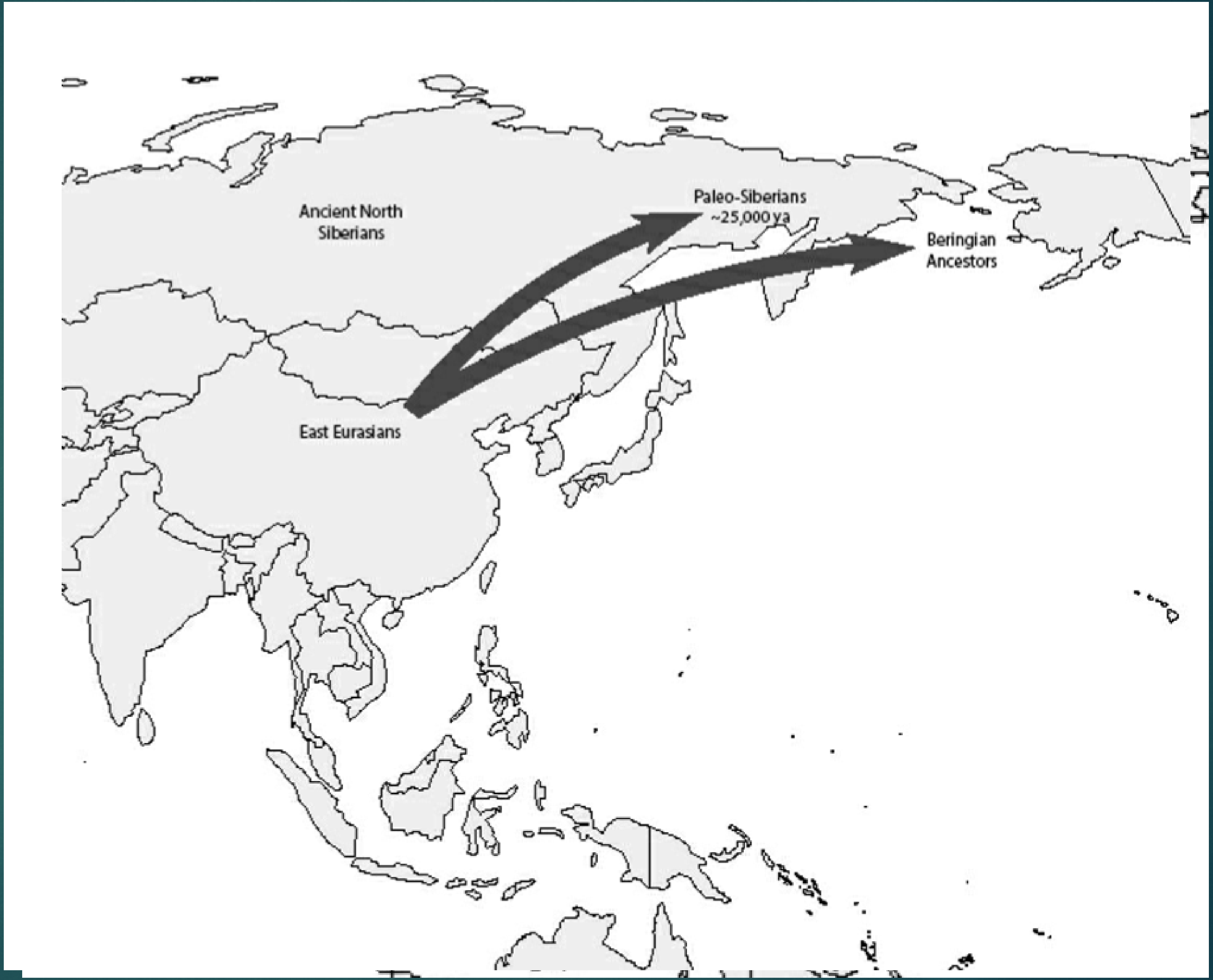
- From this genetic diversity, one can estimate the effective female population size (Ne) of the founding population to be approximately 2,000.

NA mtDNA = proof of NA’s Siberian ancestry

- Many Native Americans possessed mitochondrial (A, B, C, D, X) and Y chromosome haplogroups (C and Q), clearly sharing common ancestry with haplogroups from Asia.
- Together, mitochondrial and Y chromosome DNA from contemporary Native American populations gave a clear signal that they were the descendants of a Siberian population that had split from a larger group in northeast Asia and then had been isolated from other peoples for many thousands of years.
- Ancient DNA researchers confirmed this model by finding the same lineages within ancient Native Americans.
- They found no evidence for ancestry from any other source in populations predating European contact.

Original groups:
East Eurasians &
Ancient North
Siberians

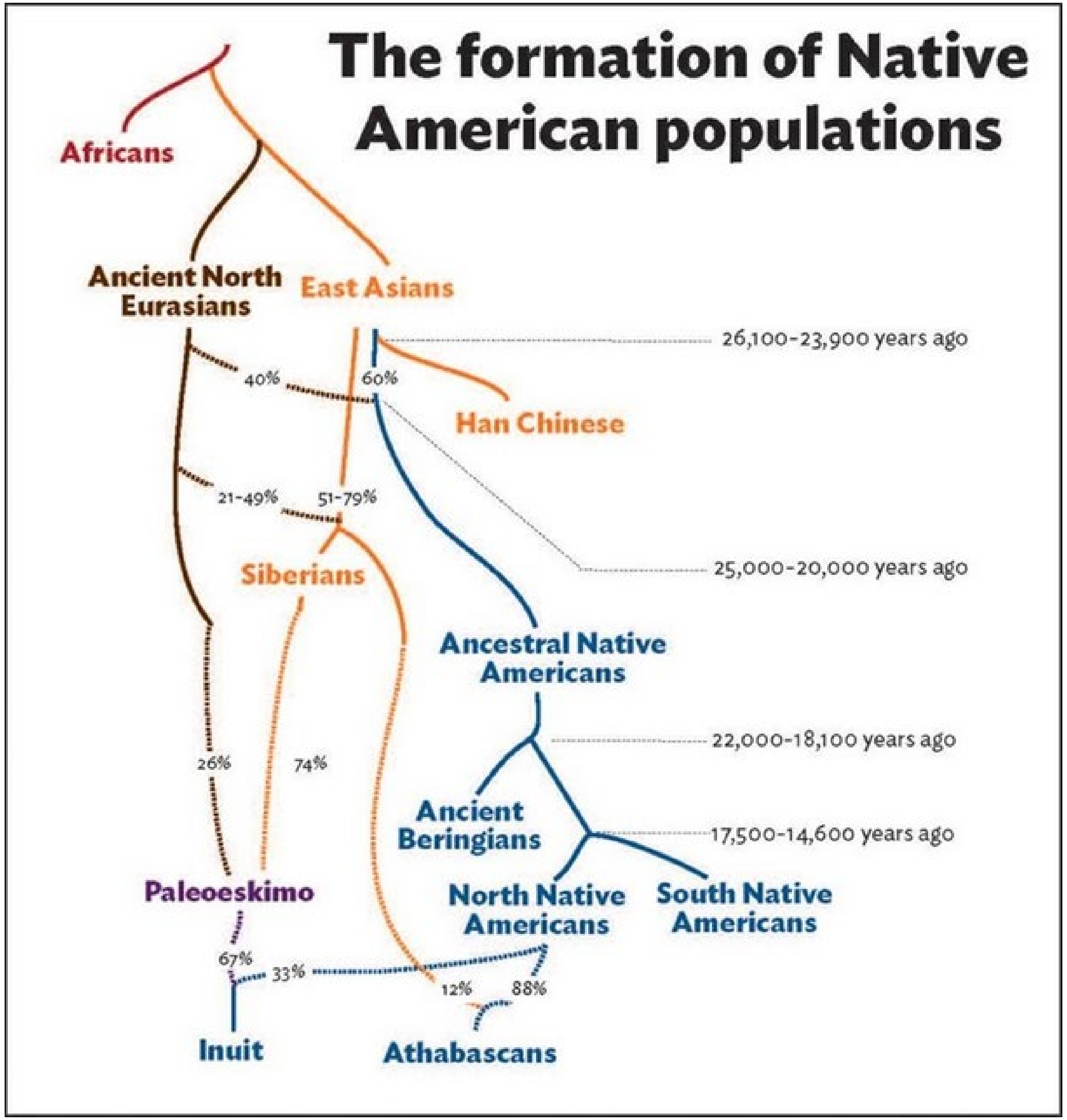
ANS = Mal’ta
child-ancestral
to NAs & Western
Eurasians & Europeans



NA lineages

- Split into three lineages in Beringia:
  - Ancestral Native Americans (First Peoples in America) (ANA)
  - Ancient Beringians (stayed there)
  - ghost Population Y

- Further split of Ancestral Native Americans –
  - major branch – Southern Native Americans (SNA) – US and central and S. America. The largest group.
  - Other branch – Northern Native Americans (NNA) – include Algonquians, Na-Dine, and others.
  - Split (15.7 Ka) occurred south of ice sheets (Ancient Beringians equally related to both groups).



A diagram showing the genetic timeline of Native American populations.

DIAGRAM COURTESY BEN POTTER, ESKE WILLERSLEV

Living Native Americans descend from two major ancestral groups.
The northern branch includes a number of communities in Canada, such as the Athabascans, along with some tribes in the United States like the Navajo and Apache. The southern branch includes the other tribes in the United States, as well as all indigenous people in Central America and South America

Both the Anzick Child and Kennewick Man belonged to the southern branch.

Her ancestors — and those of all Native Americans — started out in Asia. Estimate those two lineages split about 36,000 years ago.
The population that would give rise to Native Americans originated somewhere in northeast Siberia,

Dogs: same mtDNA divergences as Native Americans

- A notable corollary to the NA population divergences is seen in the genetic history of their dogs, which were possibly domesticated in Siberia or Beringia in the late Pleistocene.
- American dogs are descendants of Siberian dogs.
- Show mtDNA lineage splits in their dogs from there and into the Americas that roughly coincide with the major splits within the dispersing human populations.
- It is not surprising that their divergences parallel one another.

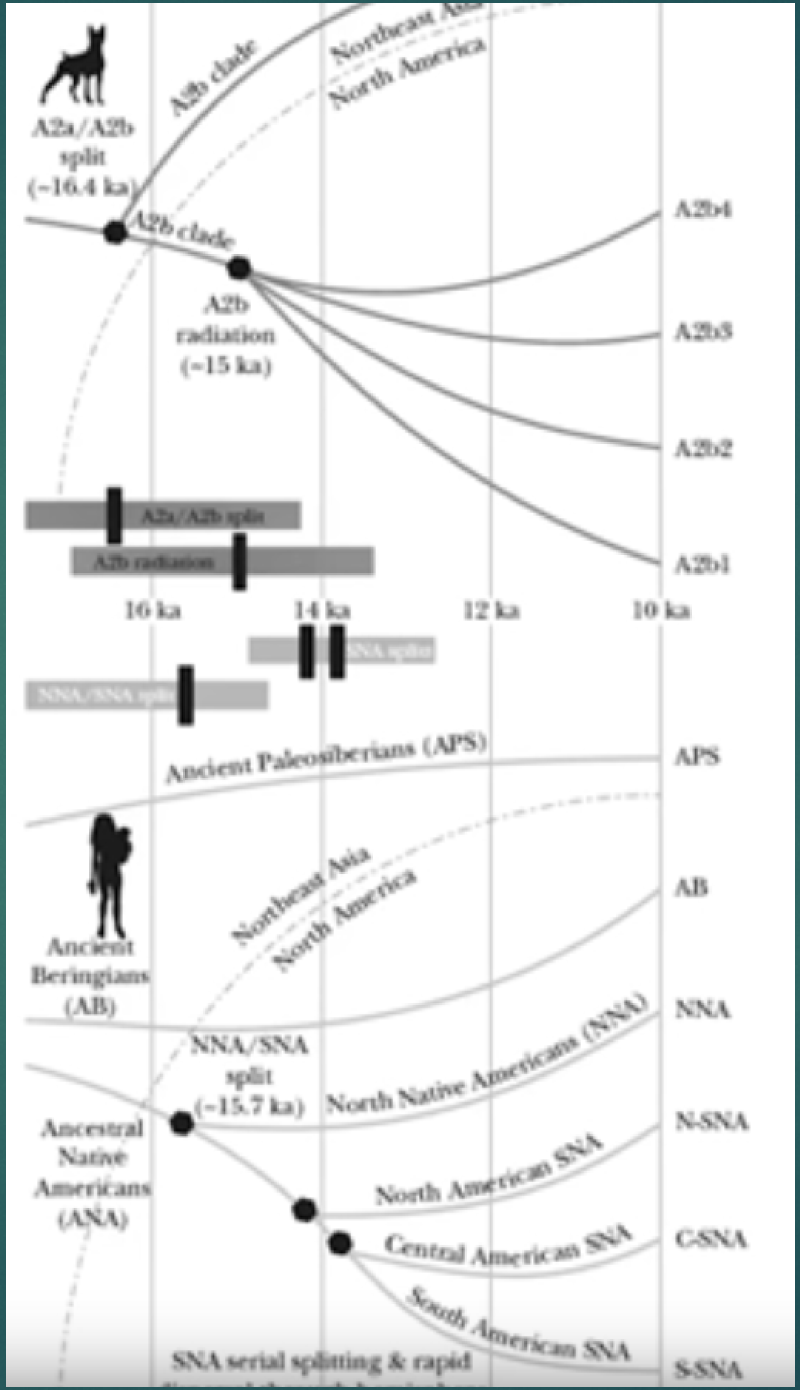
Their dogs came too.

- A dog bone from Wrangel, Alaska is dated to 10 Ka, making its owner the oldest dog known in the Americas. Its genome related to oldest 23 Ka Siberian dogs

- That's a clue that dogs—and their humans—left Siberia and entered the Americas thousands of years before North America's glaciers melted.

- Dog mitochondrial genomes rapidly diversify into the four lineages found in ancient North American dogs at nearly the exact same time as the NNA/SNA split: also about 15,000 years ago.

4 Dog divergences matches NA divergences: branching patterns and timing match



Rapid dispersal after split

- Following the split between the NNA and SNA branches, people belonging to the SNA clade dispersed throughout North and South America very rapidly.
- We can see just how rapid this movement must have been when we compare the genomes of the most ancient peoples in the Americas.
- Despite being on different continents, 6,000 miles apart, the genomes of the Anzick-1 child, an ancient man from Spirit Cave in Nevada (10,700 years ago), and five people from the Lagoa Santa site in Brazil (~10,400 to 9,800 years ago) are very closely related to each other.
- Between 15,000 and 13,000 years ago the ancestors of Central and South Americans diverged from populations in North America. Their movement southward was along the coast, rather than by inland routes.
- .

Denisovan & Neanderthal DNA in Native Americans

- High incidence of Type 2 diabetes (T2D) in Native Americans due to N alleles – SLC16A11 and SLC16A13 – (associated with hepatic lipid metabolism) probably was beneficial to early Native Americans eating meat at high elevations.

- Denisovan genes TBX15 and WARS2 gave Native Americans physical traits, fat distribution, hair pigment – adaption to living above Arctic Circle.

Ancestral Branches

- A. Ancient North Siberians contributed ancestry to First Peoples, among other populations. DNA from this group has been recovered from the Mal’ta and Yana Rhinoceros Horn sites.
- B. An isolated subgroup of East Asians contributed the majority of ancestry to the First Peoples.
  - Ancient East Asians and the Ancient North Siberians converged ~25 Ka. Exactly where they encountered each other is unknown.
  - Might have met in eastern Siberia. Other possible meeting spots include central and northern Beringia and eastern Eurasia.

Ancestral Branches

- C. The ancestral population that resulted from this merger went on to split into two branches between 22 Ka and 18 Ka ago.

- One of these branches, the Ancient Beringians, has no known living descendants. The sites of Upward Sun River and Trail Creek Cave document their presence in Alaska.

- D. The other branch, known as the Ancestral Native Americans, gave rise to the First Peoples south of the Laurentide (Canada & eastern US) and Cordilleran (Western Canada & US) ice sheets.

Native Americans: hx of multiple branching

- This branch of Ancestral Native Americans was probably itself subdivided into multiple distinctive groups during the LGM.
- After the LGM, Ancestral Native Americans moved southward and split into at least three branches.
- The first branch - a single genome from a woman who lived on the Fraser Plateau in British Columbia about 5,600 years ago.
- The other two branches encompass all the currently known genetic diversity of populations south of the ice sheets.
  - 1 – smaller Northern Native Americans branch includes the ancestors of Algonquian, Na-Dené, Salishan and Tsimshian peoples.

Native Americans

  - 2 - The Southern Native Americans branch includes the ancestors of Indigenous peoples distributed broadly throughout South America, Central America and much of North America.

- Experts disagree over when, where and how these populations dispersed into the continents. To date, there are three major competing scenarios for this process.
  - Scenario 1 - The most conservative archaeologists stand by what is essentially an updated version of the Clovis First model.
  - Swan Point site in central Alaska is the key to understanding the peopling of the Americas. Dated to about 14,100 years ago, it is the oldest uncontroversial site in eastern Beringia, and its stone tool technology is said to show clear links to the Diuktai culture in Siberia, as well as Clovis tools.

- **Scenario 1: A Late Peopling:**
- Some archaeologists maintain that the people who made distinctive spearheads initially found in Clovis, N.M., and later discovered at sites such as Anzick in Montana were the first humans to establish themselves successfully in the Americas.
- The Swan Point site in Alaska figures importantly in their argument because it contains stone tools that appear to link the older Diuktai culture in Siberia to the Clovis culture in North America. Proponents of this so-called Clovis First model hold that people entered the Americas well after the Last Glacial Maximum, traveling down the ice-free corridor that formed as glaciers retreated.
- These researchers reject pre-Clovis sites as invalid or unrelated to contemporary First Peoples.

Native Americans – Dispersals: Clovis vs pre-Clovis

- The Clovis First theory claims NA ancestors did not migrate across the Bering Land Bridge into Alaska until between 16,000 and 14,000 years ago. They maintain that Clovis represents the first successful establishment of humans in the Americas, with people traveling down the so-called ice-free corridor that formed as glaciers retreated,
- Under this model, sites predating Clovis are either rejected as invalid or attributed to people who did not contribute culturally or biologically to subsequent Indigenous populations.
  - Scenario 2: Other archaeologists emphasize the importance of pre-Clovis evidence, including remains found half a world away from central Alaska at the Page-Ladson site in northern Florida - 14,450-year-old mastodon bones and broken knife.

Native Americans – Dispersals: Pre-Clovis coastal route

- On balance, the evidence suggests that the first humans to enter the Americas did not take the ice-free corridor in.
- The most likely alternative route is via boat along the western coast, which would have become accessible about 17,000 to 16,000 years ago. A coastal route also fits genetic evidence for the Southern Native American expansion better.
- The best-supported models for population history currently show that the Southern Native American group diversified rapidly into regional populations throughout North, South and Central America between about 17,000 and 13,000 years ago.
- Travel by water along the coast would better explain the speed and timing of these population splits than the slower overland route would. Latest geology studies back up coastal route theory.

Native Americans - Dispersals

- One variant of this early coastal peopling scenario allows that humans may have been present in the Americas during or even slightly before the LGM, perhaps as early as 20,000 to 30,000 years ago.
- Evidence of pre-LGM occupation comes from several sites in Mexico and South America, including Pedra Furada in northeastern Brazil. But many archeologists remain skeptical about these sites
  - Unlikely Scenario 3: The third major scenario is radically different. A small group of scholars believes that people reached this part of the world at an extremely early date.
  - This claim rests in large part on 130,000-year-old mastodon remains excavated from the Cerutti Mastodon site in California. Damage patterns on the bones were interpreted as the result of butchering. Stones found at the site were interpreted to be manufactured tools. Claim First people to arrive were probably *Homo erectus.* Most reject this scenario. Unsupported by genetics.

- **Scenario 2:** An Early Coastal Peopling
- Other archaeologists place great importance on pre-Clovis sites, arguing that they document human presence throughout the Americas well before Clovis technology appeared and before the ice-free corridor opened up.
- These scholars contend that people probably instead traveled by boat along the western coast starting around 17,000 years ago or possibly as early as 20,000 to 30,000 years ago, if the controversial claims for evidence of such ancient human activity at Pedra Furada and Chiquihuite Cave are to be believed.

Americas

- As things stand in 2023, most archeologists and geneticists agree that humans were established in the Americas by at least 14,000 to 15,000 years ago, but they disagree on exactly which pre-Clovis sites are legitimate and therefore how early people may have entered the continents

- There are perhaps several dozen publicly available complete genomes from contemporary and ancient Indigenous peoples. These genomes are unevenly distributed; most are from Central and South America and the northern parts of North America.

- However, only a few complete genomes from the present-day U.S., the result of Indigenous peoples' justified distrust in researchers

The Americas

- Oldest known American skeletal remains, 11-8 Ka:
  - Some North American skulls resemble S Asian, Ainu people of S Japan, or Polynesians
  - South American remains, more like Australian or Sub-Saharan African
  - Indicative of complex migration pattern from NE Asia

- Kennewick Man from WA state, 1998:
  - ownership controversy;
  - DNA proved it was Native American (mtDNA haplogroup X2a and the Y DNA haplogroup Q-M3); but only tested one local NA group

The Americas

- Historic Native Americans derive overwhelmingly from northeast Asians, who share same mtDNA and Y Dna chromosomes haplotypes

- Striking similar in derived “Asian” form of skulls, featuring broad, short braincases; broad, flat faces with high, frontally directed cheekbones; narrow noses

- High frequency of “Sinodonty” dental traits; shovel shaped crown in upper incisors; upper 3rd molars unusually small; lower first molars with extra third root, and 5 cusped lower 2nd molars; very different from SE Asian and Polynesian dental pattern

Settlement of the America

- Indigenous peoples of the Americas have been linked to Siberian populations by linguistic factors, the distribution of blood types, and genetic DNA

- The common occurrence of the mtDNA Haplogroups A, B, C, and D among eastern Asian and Native American populations has long been recognized, along with the presence of haplogroup X.

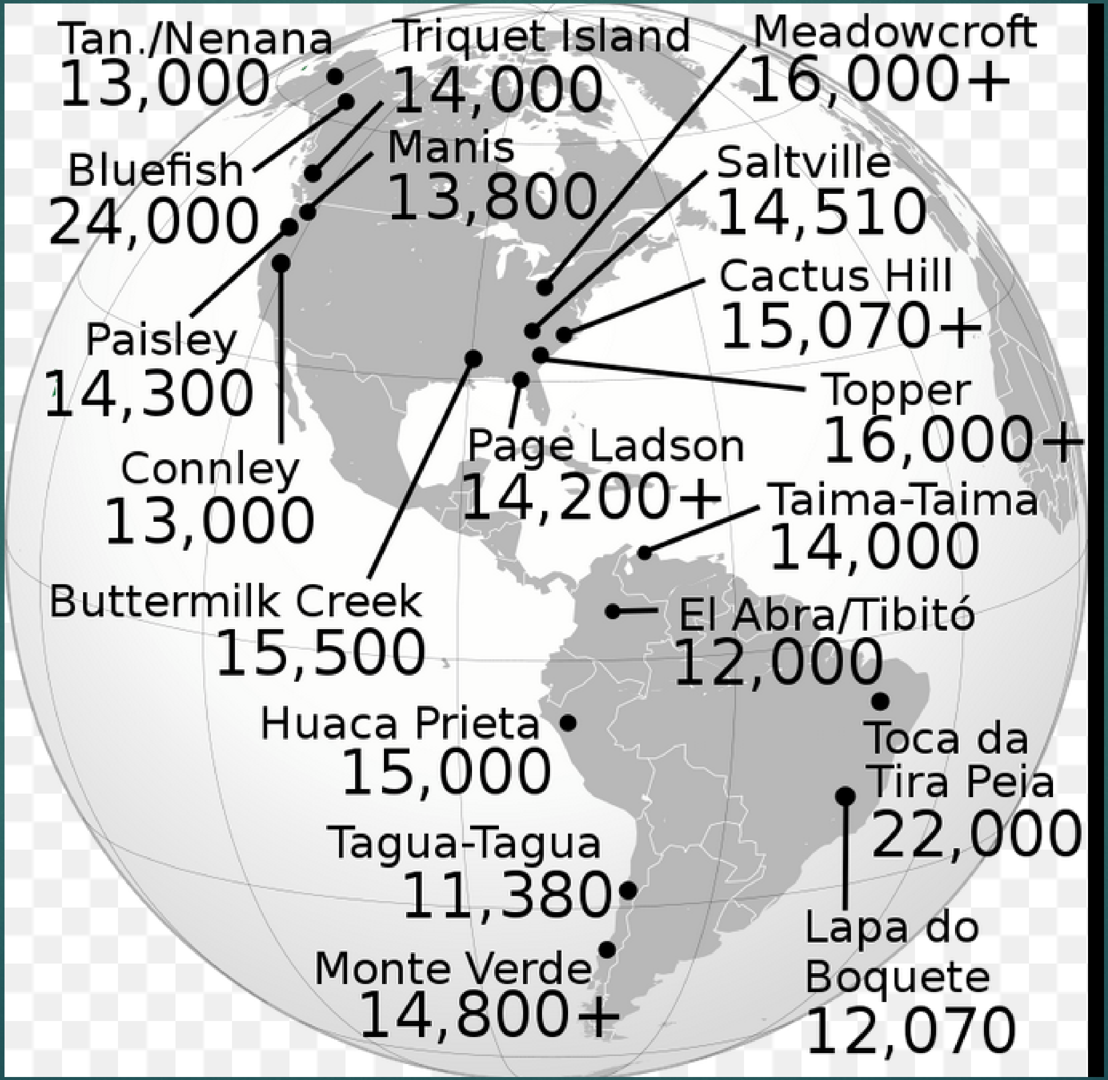
Sampling bias

- 90% of Indigenous peoples were wiped out after colonial contact. All those people took their genetic stories with them, lost to pestilence and colonial violence.
- So much shoreline evidence is underwater.
- There is often a Eurocentric narrative about all civilization.
- Because of issues with blood quantum labeling of Indians in the United States and the unsanctioned use of their DNA material by western scientists, many living Indigenous people of this continent have no wish to participate in genetic research, especially without reconciliation. Their genomes are largely unknown.
- We have built over many NA sites.
- Rainforest soil acidity leaves nothing behind.

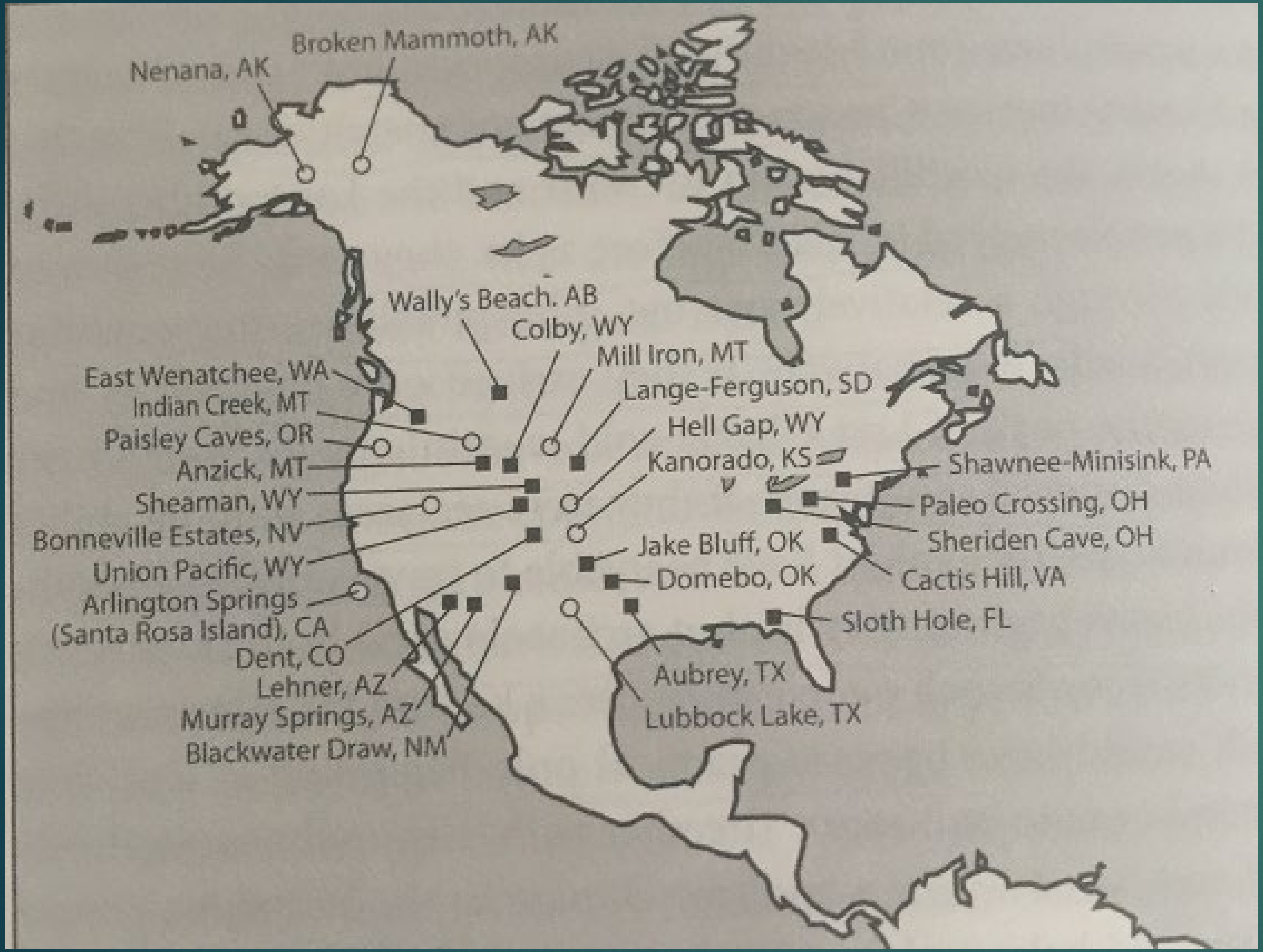
NA attitudes toward genetics research

- Issue of genetic studies and Native American belief in their origin stories: While accepting NA rights to their own religious beliefs, this is a form of religious anti-evolution thinking, similar to Creationism. [But read Raff on this issue.]
- NA refusal to participate in genetics studies, based on historical mistreatment by geneticists, is problematic because it excludes NAs from potential benefits of genomics research (such as genomic medicine, the use of genomics for repatriation claims, etc.).
- Genetics studies can be used to argue against tribal histories, potentially threaten sovereignty, or dispute cultural identities. They can be used in ways that benefit outside researchers at the expense of tribal members and potentially reveal stigmatizing information.
- Genetics researchers mending relationships with Indigenous groups is way of the future..

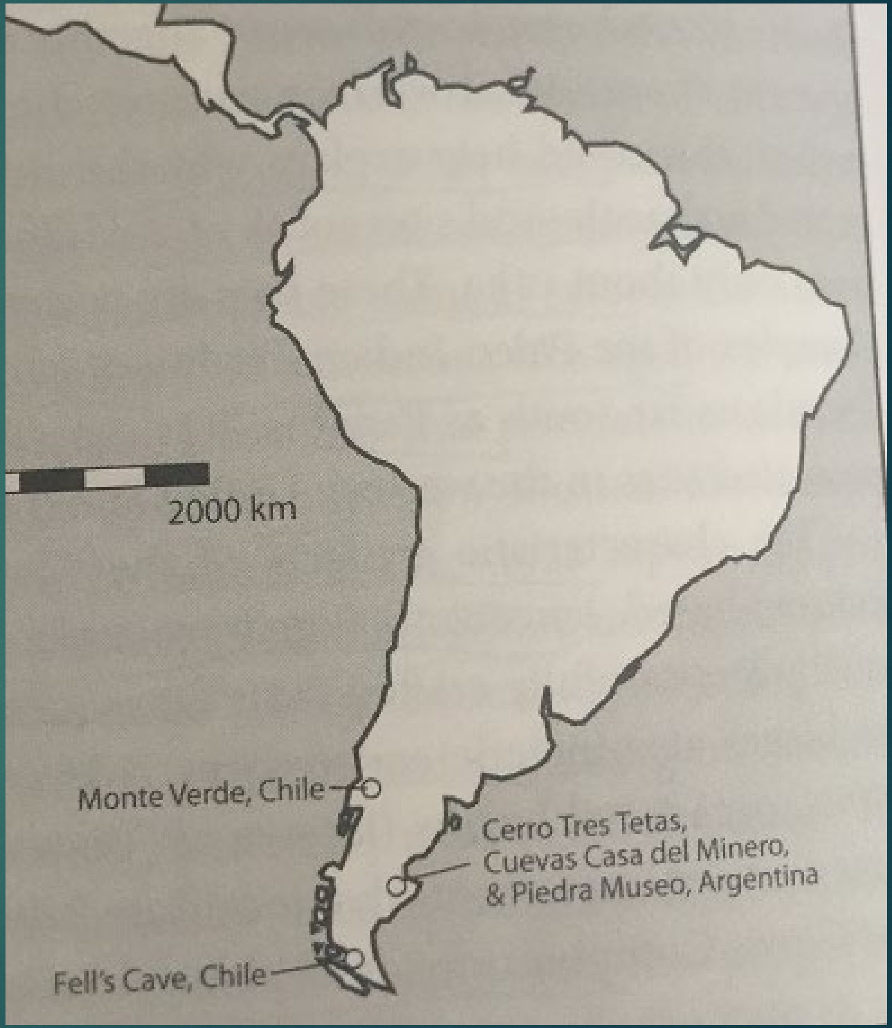
Map of the earliest securely dated sites showing human presence in the Americas, 16–13 ka for North America and 15–11 ka for South America



AMHs: Clovis Culture locations



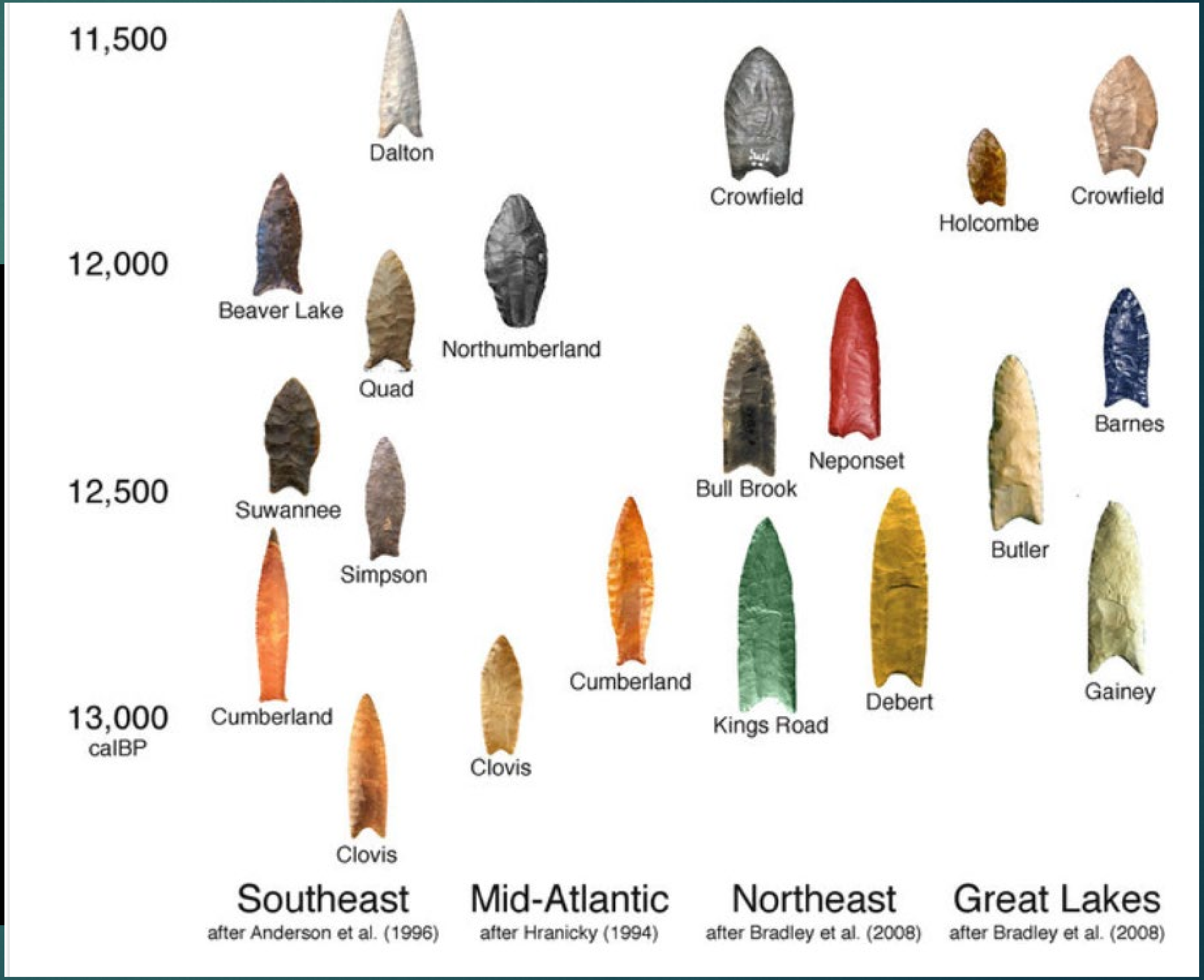
Pre-Clovis sites



Clovis Culture onward

- The "Clovis first theory" refers to the 1950s hypothesis that the Clovis culture represents the earliest human presence in the Americas, beginning about 13,000 years ago
- Clovis people did not migrate to South America; but other groups reached its tip by 14 Ka
- Evidence of pre-Clovis cultures has accumulated since 2000, pushing back the possible date of the first peopling of the Americas to 33,000 years ago
- Characteristic artifacts of Clovis Complex were bifacial, concave-based, lanceolate, fluted projectile points

Clovis points: first American invention?



Clovis points:

13,300 to 12,800 years ago

Mammoth & Mastodon hunters

Megafauna extinction

- North American Megafauna Extinction:
  - Historical theory: Ecological shock of human arrival (combined with climate change to present interglacial) may explain why North America lost 35 large mammal genera (mammoths, horses, camels);
  - 80% of its total between 12 and 10 Ka; More in South America

  - Recent research: Climate change, not human population growth, correlates with Late Quaternary megafauna declines in North America; evidence that decreases in global temperature correlated with megafauna population declines.

- Mathew Stewart, W. C. Carleton & H. S. Groucutt, 2021

Folsom points:

smaller;
no more
Mammoth

75 species
disappeared

Human vs
climate change
theories

Pre-Clovis Claims

- Serious pre-Clovis site contenders south of ice sheet are mostly in South America
    - Monte Verde, Chile, 14.5 Ka (now 18.5 Ka)
    - Los Toldos Cave in Argentine Patagonia at 12.6 Ka
    - Tagua-Tagua in central Chile, 11.4 Ka
    - Taima-Taima, Venezuela, 13 Ka
    - Pedra Furada, Brazil, over 20 Ka

- Mostly based on stone tool datings.

5 Archeological remains of Native Americans

- 1. Footprints in New Mexico, 21-23 Ka:
- A group of fossilized footprints of children & adolescents was preserved on the shore of an ancient lake in today's White Sands National Park - 21,000 and 23,000 Ka, probably over a period spanning a few thousand years.
- When ice sheets blocked Beringia

2. Radiocarbon dates in Idaho

- The archaeological site of Cooper's Ferry, Idaho, sits in a valley at a bend of the Lower Salmon River. This would have been an excellent place to live, with resources close at hand. Excavations at the site have uncovered evidence of hearth fires, animal butchery, and stone toolmaking, the earliest of which were dated in 2019 to around 15,000–16,000 years ago.
- This find supports the idea that the first people who traveled over the Beringia land bridge moved down the Pacific coast, probably in boats, following the rich hunting and fishing grounds of the kelp forests just off the coastline.
- Ice sheets covered most of the North American continent at this time; only once people reached the mouth of the Columbia River (some 300 miles northwest of the Lower Salmon River) would they have been able to move inland.

3. Ancestral human genomics in Alaska

- A young girl’s remains were found during archaeological excavations of a burial in present-day Alaska within a hearth feature dating back 11,500 years.
- A community now called Upward Sun River, in central Alaska, named the girl, who was about 3 years old at the time of her death, Xach’itee’aanenh T’eede Gaay, which loosely translates to “Sunrise Girl-Child.”
- While Xach’itee’aanenh T’eede Gaay was related to contemporary Indigenous peoples, she was part of a previously unknown lineage that split from modern Native Americans about 20,000 years ago.
- This suggests that her group lived in isolation in Beringia, Siberia, or North America for a long time, crossing the land bridge to North America earlier than thought and over a much longer time span than previously assumed.

4. Stone tools in the Channel Islands

- Archaeologists have uncovered ancient implements such as barbed stone points that were used for hunting and fishing on Santa Rosa Island in the Channel Islands, off the coast of California, some 8,000–13,000 years ago. These tools were made from local stone and are of a shape that is distinctive to the region, and they are totally different from Clovis points.
- Also some of the oldest basketry from the Pacific coast of North America and crescent-shaped arrow tips thought to be specifically made for waterfowl hunting, as the half-moon–shaped tips would skip and skim across the water to their targets.

Curved arrow tips found in the Channel Islands could have been made to skip across the water.

5. Fossilized feces in Oregon

- In 2008, human coprolites, or fossilized feces, found at the site of Paisley caves in Oregon were radiocarbon dated to 14,300 years ago. That is astonishingly old.
- The sample also provided DNA that matches genetic patterns common to present-day Indigenous peoples in the Americas and some inhabitants in Eastern Asia.
- Ancestral populations likely used the Beringia land bridge to travel east to new territories, but more than 1,000 years before the appearance of Clovis technology.

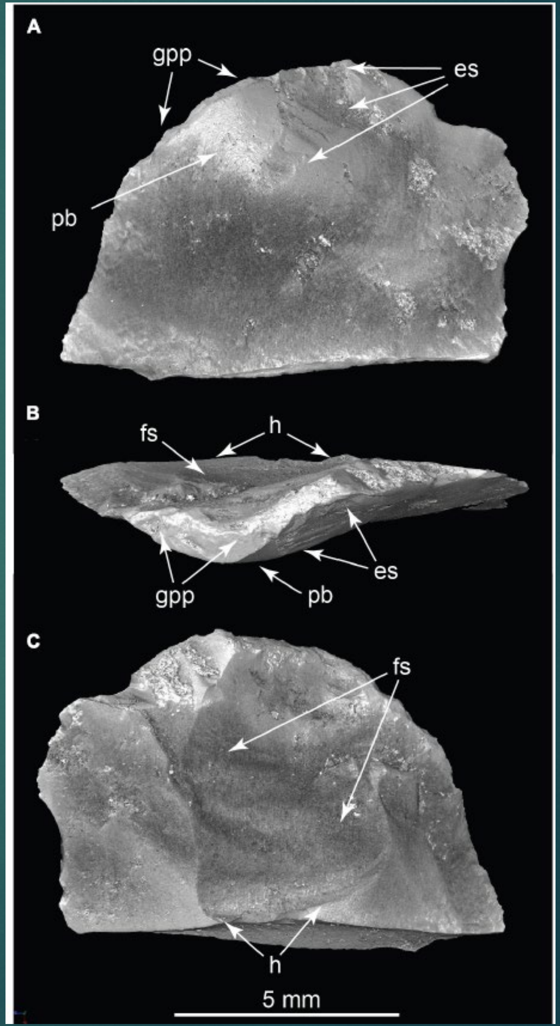
2023 study: Human occupation of the north American Colorado plateau ~37,000 years ago

- Description of Hartley, MT, mammoth locality, which dates to 38,900–36,250 Ka (from bone collagen). They accepted the standard view that elaborate stone technology of the Eurasian Upper Paleolithic was introduced into the Americas by arrival of the Native American clade 16,000 KA.
- It follows that if older cultural sites exist in the Americas, they might only be diagnosed using nuanced taphonomic approaches. We employed computed tomography (CT and mCT) and other state-of-the-art methods that had not previously been applied to investigating ancient American sites.
- This revealed multiple lines of taphonomic evidence suggesting that two mammoths were butchered using expedient lithic and bone technology, along with evidence diagnostic of controlled (domestic) fire.
- Independent genetic evidence of two founding populations for humans in the Americas, which has already raised the possibility of a dispersal into the Americas by people of East Asian ancestry that preceded the Native American clade by millennia.

Rowe, T. B., et al., 2023

Butchered mammoth bones in MT at ~37 Ka: raises the possibility that humans first arrived in North America 17,000 years earlier than previously thought.

© Timothy Rowe et al. / The University of Texas at Austin



Chert Microflakes

Pre-LGM American sites: MHs in America 20-33 Ka

- Recent archeological discoveries placing humans in the Americas during or before the Last Glacial Maximum (LGM), between 20-33 Ka. A growing record of probable human occupation sites in the Americas that predate arrival of the Native American clade by millennia.
  - Multiple in situ human footprints from New Mexico that date from 22,860 to 21,130 Ka
  - Footprints from Argentina that date to 30,000 Ka
  - Simple stone tools discovered in Chiquihuite Cave, Mexico, date from 26,500 to 19,000 KA and represent a previously unknown tradition
  - At Coxcatlan Cave, Mexico, re-dating butchered small mammals associated with minimally worked stone tools established a 33,448 to 28,279 Ka

Pre-LGM American sites: MHs in America 20-33 Ka

- Simple flaked stone artifacts are known from numerous ancient South American sites. These include Toca da Tira Peia, Brazil, which dates to 20,000 Ka, and Vale da Pedra Furada, Brazil, which dates to 24,000 Ka
- Older artifacts dating to 32,000 Ka are also reported from this site.
- At Toca do Serrote das Moendas, Brazil, faunal remains associated with human bones were dated to between 29,000 and 24,000 Ka.
- And at Arroyo del Vizcaíno, Uruguay, a fossil-rich 30,000 years old megafaunal locality with cut-marked bones

Beringian Standstill

- Reich: all Native Americans descend from single common stem populations circa 13 Ka; 2/3 East Asia and 1/3rd north Eurasian

- The prevailing model for ancestry of stem population is known as the Beringian Standstill (or Pause or Incubation), which was originally conceived of based on classical genetic markers and fully developed by the analysis of mtDNA.

- This model states that the ancient Beringians must have experienced a long period of isolation from all other populations.

- Estimates for the length of this isolation vary, but the lower end is ~7,000 years. During this period they developed the genetic variation uniquely found in Native American populations.

2013: 24,000 ya Mal’ta Child

- Genome of 24,000 ya Mal’ta boy, from shores of Lake Baikal, Siberia
- Descent from early Asians and proto-Europeans (1st wave)
- Only genome related to American Native Americans: Related to modern South Americans
- This finding helps explain why some Native Americans have similar genetic signatures to Europeans; both groups got DNA from the Mal’ta child’s people, who were ancestral to the Yamnaya who migrated into Europe.
- When Willerslev's team sequenced the genome of a 24,000-year-old Siberian boy from Mal'ta in 2013, it found no genetic connection to anyone living in Central Asia today. But the Mal'ta boy was related to Kennewick Man and Native Americans, suggesting that he represented an ancient source population for migrations of Paleoindians to the Americas.

Eske Willerslev, et al. 2013

Siberian Mal’ta genome

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

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

- The Mal’ta lineage is basal to all western Eurasian Paleolithic genomes

- Mal’ta lineage persisted locally through the LGM.

2014: Anzick child – oldest Native American Genome

- 12.6 Ka – S. central Montana – Anzick-1 (2 yo) and Anzick-2 (8 yo) – oldest known person aDNA in America – from Southern Native Americans (SNA)
- First full genome of earliest Native American. Part of the Clovis culture; is an ancestor to all Native Americans
- Discovered in 1968 on Anzick family land, under cache of Clovis flints; with bone tool
- Compared with Canadian & Latin American indigenous DNA (but not USA)
- Mix of Mal'ta & other Asian DNA; Ancestor of Central & South American Indians (equally); closer to them than to Canadian Indians or Kennewick Man

Eske Willerslev, et al. 2014

America: Anzick-1

- Archaeological evidence supports a human presence in the Americas at least by 14,500 Ka.

- All present-day Native Americans can trace part of their ancestry to a single population that existed at least by 12,600 Ka.

- The Solutrean hypothesis of a European origin was dispelled by the sequencing of a 12,600 Ka Anzick individual

- This individual, known as Anzick-1, falls within present-day Native American diversity and was more closely related to present-day populations from Central and South America than to geographically closer populations from North America.

Population Y

- Population Y (for Ypikuera, a Tupi speaking population) –
  - Amazonians share alleles with Australians, New Guineans, Onge from Andaman Island.
  - DNA signal also in west coast S. Americans; as early as 10.4 Ka, long before Europeans there 1492. Signal is also in Tianyuan Cave, China individual (40 Ka).
  - Probably ancient population in Asia gave rise to alleles in both Australasians and First Peoples before leaving Alaska – shows spotty genetic drift.

- Could Pop Y be at White Sands Locality 2 site? – 23-21 Ka – footprints?

Reich's other theory for Popul Y was population preceded First people – 17-16 Ka.

Population Y

- Some physical anthropologists studying the shapes of human skeletons had for years been asserting that there are some American skeletons, dating to before ten thousand years ago, that do not look like what one would expect for the ancestors of today’s Native Americans.
- The most iconic case is Luzia, an approximately 11,500-year-old skeleton whose remains were found in Lapa Vermelha, Brazil, in 1975.
- Many anthropologists find the shape of her face more similar to those of indigenous peoples from Australia and New Guinea than to those of ancient or modern peoples of East Asia, or Native Americans.
- This puzzle led to speculation that Luzia came from a group that preceded Native Americans.

Two South American populations

- Pontus Skoglund, 2017: compare all possible pairs of populations from the Americas that had First American ancestry to all possible pairs of populations outside the Americas, including indigenous people from Australasia (including Andaman Islanders, New Guineans, and Australians) and other populations hypothesized by some anthropologists to be related to Paleoamericans.
- *** He found two Native American populations, both from the Amazon region of Brazil, that are more closely related to Australasians than to other world populations.

SA population

- Skoglund later found weaker signals of genetic affinity to Australasians, but still probably real, in other Native American populations ringing the Amazon basin.

- He estimated that the proportion of ancient ancestry in these populations was small—1 to 6 percent—with the rest being consistent with First American ancestry.

Ghost Y Population

- Showed that these patterns could not arise as a result of recent migrations from Asian populations—while Amazonians had their strongest affinity to indigenous people from Australia, New Guinea, and the Andaman Islands (compared to East Asians as a baseline), they were not particularly close to any of them.

- Polynesian migration from the Pacific across to the Americas was contradicted by the genetic data.

Ghost Y Population

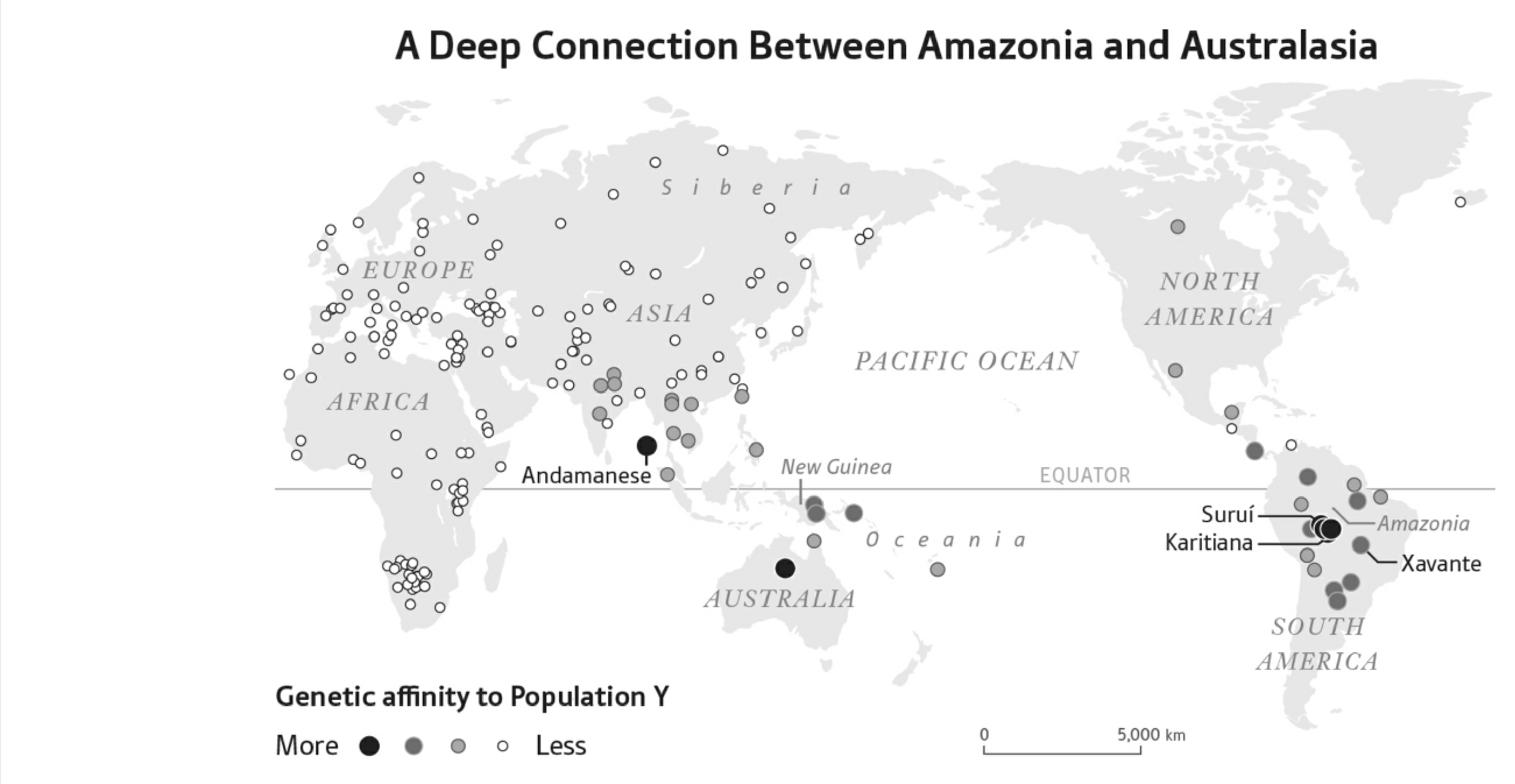
- *** It really looked like evidence of a migration into the Americas of an ancient population more closely related to Australians, New Guineans, and Andamanese than to present-day Siberians.
- Concluded this was evidence of a “ghost” population: a population that no longer exists in unmixed form.
- *** Called this “Population Y” after the word *ypykuéra,* meaning “ancestor” in Tupf, the language family of the populations with the largest proportions of this ancestry.

Population Y = ghost population

- The Population Y geographic distribution is largely limited to Amazonia, providing yet more evidence for an ancient origin.
- The fact that Population Y ancestry is restricted to difficult terrain far from the Bering link to Asia is perhaps what one would expect from an original pioneering population that was once more broadly distributed and was then marginalized by the expansion of other groups.
- Most recent ancestors: Tupi in Brazilian state of Rondonia

Y population

- The ancestral population that contributed this signal was termed a "genetic ghost population" and given the name "Population Y" (Skoglund et al., 2015).
- Population Y was estimated to have occupied eastern Asia 50,000 years ago (Reich, 2018).
- Additional aDNA support came from a 40,000 years old human bone from Tianyuan cave


A Deep Connection Between Amazonia and Australasia

Despite extraordinary geographic distance, populations in the Amazon share ancestry with Australians, New Guineans, and Andamanese to a greater extent than with other Eurasians. This may reflect an early movement of humans into the Americas from a source population that is no longer substantially present. Represented in northeast Asia.

Population Y

- How and when Population Y ancestry reached South America has been explained by an alternative hypotheses (Skoglund et al., 2015; Reich, 2018).
- The first is that Population Y contributed ancestry to the Native American clade before its dispersal south from Beringia.
- Some of the Native Americans then carried this ancestry as they dispersed down the west coast and into South America.

Source of Population Y

- However, several recent aDNA analyses that included a 45,000 years old human genome from Ust'-Ishim, Siberia, 32,000 years old human genomes from the Yana RHS site, and younger ancient Asian genomes, revealed complex patterns of dispersal, admixture, and turnover among West Eurasian and East Asian populations in the occupation of Siberia and western Beringia.
- Marine Isotope Stage 3 (MIS 3, ca. 50,000 – 30,000 cal BP) was evidently a time of rapid expansion of modern humans across Eurasia, but no Population Y ancestry was detected by any of these studies (Sikora et al., 2019).

Very early dispersal of Population Y

- The second hypothesis is that unmixed descendants of Population Y dispersed directly to the Americas during pre-LGM time, predating the Native American arrival by millennia (Skoglund et al., 2015; Reich, 2018).
- This early population was later displaced by the Native Americans except in South America, where it mixed with Native Americans and left a discernable signal in every major living linguistic group.
- This second theory now seems the more likely, because the first hypothesis alone fails to explain archeological sites that predate Native American arrival.

Population Y got there first

- If Population Y spread through parts of South America before the First Americans, then it seems likely that after this initial peopling, the First Americans advanced into nearly all of the territories the Population Y people had already visited, replacing them either completely or only partially, as in Amazonia.
- Population Y ancestry may have survived better in Amazonia than it did elsewhere because of the relative impenetrability of the Amazonian environment.
- This could have slowed down the movement of First Americans into the region enough to allow people living there to mix with the new migrants rather than simply being replaced.

2% Population Y ancestry today

- It is likely that Population Y was already mixed with large amounts of First American-related ancestry when it started expanding into South America.

- Our estimate of around 2 percent Population Y ancestry in the current Suriri population is based on the assumption that Population Y traversed the entirety of Northeast Asia and America without mixing with other people it encountered.

- If we allow for the likelihood that there was mixture with populations related to First Americans on the way, the proportion of Population Y in the Surui could be as high as 85 percent and still produce the observed statistical evidence of relatedness to Australasians.

Skip

Posth et al. 2018 (no Popul Y evidence) vs Moreno-Mayar et al. 2018 (Popul Y evidence) papers debate over Population Y

"Peopling of the Americas as inferred from ancient genomics".
Eske Willerslev, et al. Nature (2021)

- A review of previous genomic studies, similarly concluded that all Native Americans descended from the movement of people from Northeast Asia into the Americas.
- These Ancestral Americans, once south of the continental ice sheets, spread and expanded rapidly, and branched into multiple groups, which later gave rise to the major subgroups of Native American populations.

First Peoples

- Descendants of First Peoples—over the next 15,000 years—experienced varying degrees of isolation, admixture, continuity and replacement
- All ancient individuals in the Americas, save for later-arriving Arctic peoples, are more closely related to contemporary Indigenous American individuals than to any other population elsewhere.
- Challenges the claim, based on anatomical evidence, that there was an early, non-Native American population in the Americas.

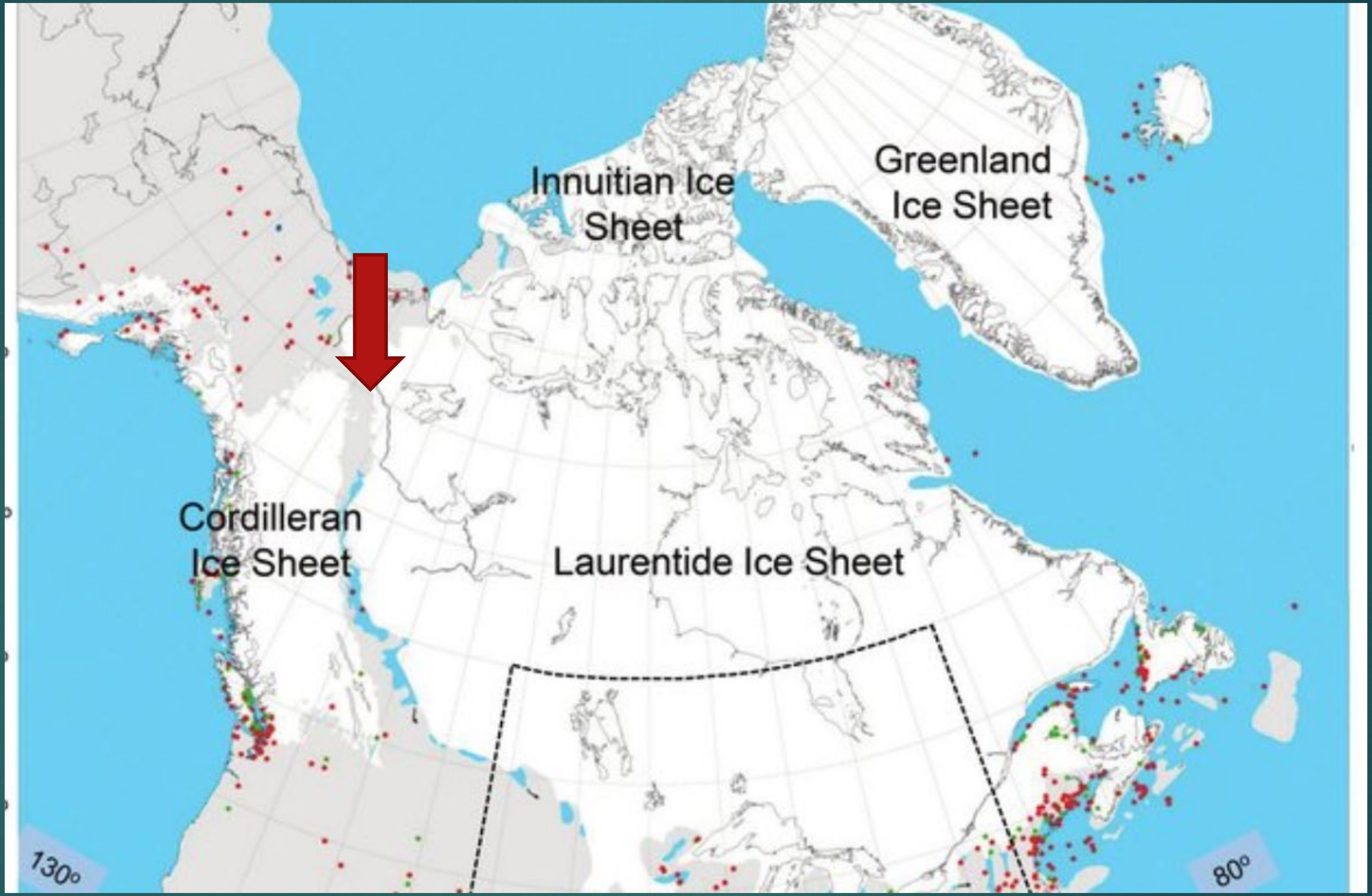
Siberia and Beringia

- The earliest secure archaeological evidence of AMHs in northeast Asia dates to around 32 ka at the Yana RHS site, NE Siberia
- Ice Sheets culminate in Last Glacial Maximum (LGM) approximately 23–19 ka.
- Sea levels in the north Pacific fell around 50 m below their present level, the continental shelf in the Bering Strait region became dry land, creating an approximately 1,800-km-wide (measured north–south) land bridge—the central portion of the region known as Beringia—that linked Asia and America; ice free, steppe/tundra; from 30 to 12 Ka
- After 12 ka, groups could no longer walk from Siberia to America; needed boats

Arrivals

- Earliest currently accepted archaeological evidence for the arrival of ancestral Native American populations (around 15.5–15 ka);
- Paleo-Inuit arrived about 5.5 ka
- The earliest archeological presence of people in eastern Beringia dates to 14.2 ka at the Swan Point site in Alaska.
- However, this cannot date the first peoples’ arrival, as humans were already in North and South America by around 15.5–15 ka—the so-called ‘pre-Clovis’ period
- The earliest substantial and widespread human presence—the Clovis archaeological complex in North America and contemporaneous groups in South America—appears around 1,500 years later.

Classic image of Cordilleran and Laurentide Ice Sheets and the Corridor



Recent data indicates inland ice-free corridor was in fact not passable

Coastal route due to absence of interior route south

- Traditional theory: people travelled through an ice-free corridor that opened in postglacial times along the eastern flank of the Rocky Mountains.
- Current geological evidence shows that the corridor was not fully ice-free until around 15–14 ka, and by ancient DNA from both fossil bison and lake sediments, indicating that the plants and animals that hunter-gatherers would have needed for food along the roughly 1,500-km route were not available in the corridor region until about 13 ka. Thus, this route would not have been viable early enough for the first peoples' travels.
- The absence of an interior route suggests that the first peoples moved south along the Pacific coast.
- Glacial ice blocked that route as early as around 23 ka, but with the post-LGM retreat long reaches were ice-free after 17 ka and, by 16–15 ka, the coast was largely clear and supported the resources necessary for human travelers. A coastal route would have enabled people to reach the Americas south of the continental ice sheets well before the earliest currently accepted archaeological presence

Ancient North Siberians

- Genomes from individuals at the Yana RHS site, and the Mal’ta site (dated to 24 ka), show that Siberia was occupied by a population designated ‘Ancient North Siberian’ (ANS) individuals.

- ANS ultimately disappeared as a separate population, traces of their genetic legacy occur in later ancient and some present-day groups, most notably Native American populations

ANS & East Asian Gene Flow

- ~23–20 ka: there was gene flow between an Ancient North Siberian group and an East Asian group
- Gene flow between these populations ultimately gave rise on separate occasions to at least two distinct lineages.
  - 'Ancient Paleo-Siberians', formed the ancestral population of present-day groups of northeast Siberia, such as the Chukchi & Koryak.
  - The other lineage became the basal Native American branch, whose descendants ultimately crossed to the Americas.
- Where and when the basal American branch emerged remains uncertain; most likely before ~21–20 ka

Beringian Standstill Model: period to develop genetic diversity

- Native American individuals have only ANS and East Asian ancestry.
- They were isolated during the LGM.
- This LGM isolation is in keeping with the Beringian standstill model, which proposes that dispersal into the Americas did not happen immediately, but instead followed an extended pause, possibly in the region of the land bridge.
- Ancestors of Native Americans did not rush across Beringia and disperse across the Americas. Instead, they lingered there for thousands of years, their genes acquiring increasingly distinctive variations.

Beringian Standstill model

- From that isolated population, several lineages emerged:
  - 1 unsampled population A (UPopA), a ‘genetic ghost’ of which little is currently known,
  - 2 ‘Ancient Beringians’
  - 3 ‘Ancestral Native Americans’ (ANA)
- Only ANA ultimately crossed into North America
- First to split off were the Ancient Beringians.
- About 15,700 years ago the northern and southern branches of the Native American tree split

Ancient Beringians disappeared

- Although the Ancient Beringian individuals crossed into Alaska, they evidently did not continue farther south. At some point after around 9 ka, this population disappeared;

- There were successive internal splits within the Ancient NA lineage.
  - The first at around 21–16 ka when the ‘Big Bar’ lineage branched off from the ANA line
  - and then at about 15.7 ka, when there was a split between Northern Native American (NNA) and Southern Native American (SNA) populations.

Dispersal patterns of NNA and SNA groups

- The dispersal patterns of NNA and SNA groups, once south of the continental ice sheets, were quite different.
- NNAs appear to have remained in northern North America.
- NNA groups shifted further northward, as they are presently in Alaska and the Yukon
- Clovis Culture falls on the SNA branch

Southern Native Americans: rapid descent

- SNA populations rapidly spread southward, into North and South America.
- The rapidity of the SNA dispersal matches what was long suspected of early movements based on the near-contemporaneity of the earliest archaeological sites in North and South America
- There was repeated splitting within the SNA lineage as groups made their way south, which in turn led to considerable ancestry variability in ancient South Americans

Solutrean theory?: No. All NAs had NE Asian ancestry

- To date, there is no genetic evidence that any population from a region other than northeast Asia was an important source of America’s first peoples.
- The controversial claim that the first peoples came from Europe via the North Atlantic, based on an ostensible similarity in stone-tool technology between the Solutrean culture of Pleistocene Europe and Clovis in North America, was undermined by the genome of the Anzick Clovis child, which sits squarely on the SNA branch of Ancestral Native American peoples.
- No ancient or present-day genome (or mtDNA or Y chromosome marker) in the Americas has shown any direct affinities to Upper Palaeolithic European populations

Paleoamerican theory is wrong

- Similarly rejected is the assertion that ancient and more-recent skeletons with distinct crania—so-called 'Paleoamericans'—had different ancestry, possibly related to European, Aboriginal Australian, Japanese Ainu or Polynesian populations, and thus were only distantly related to present-day Native American groups.

- All 'Paleoamericans' sequenced to date, including those from early in the peopling process (for example, individuals from the Spirit Cave, Nevada, USA, dated to 10.7 ka), Lagoa Santa (Brazil, dated to 10.4 ka) and Kennewick (Washington, USA, dated to 9 ka)), have Native American genetic ancestry. No evidence of European or Pacific migrations.

- Willerslev: with the exception of the later arriving Paleo-Inuit and Inuit Thule groups, all ancient human genomes from the Americas have closer affinities to contemporary Native American peoples than to any other present-day populations worldwide

Willerslev: Population Y debate

- Willerslev dismissed the existence of an hypothetical distinct non-Native American population (suggested to have been related to Indigenous Australians and Papuans), sometimes called "Paleoamerican".
- The authors explained that these previous claims were based on a misinterpreted genetic echo, which was revealed to represent early East-Eurasian geneflow (close but distinct) to the 40,000 BC old Tianyuan lineage) into Aboriginal Australians and Papuans.

Willerslev reversed himself about Population Y: more evidence recently

- But the Australasian signal has recently been detected in present day Native American individuals who inhabit the Pacific coast region of South America.

- It is inferred that the Australasian signal was introduced by a population that entered the Americas via the Pacific coast, but the absence of that signal from ancient individuals in that region, and also from Central and North America, remains unexplained.

NA teeth: shoveling

- The incisors of Indigenous peoples of the Americas very often have a morphology known as shoveling: an indentation that you can feel as you rub your tongue along the inside surface.
- This shoveling trait is also found at high frequencies among East Asian populations, but it is uncommon among other groups around the world.
- It was one of the clues that physical anthropologists used to infer a connection between Native Americans and Asiatic peoples, before it was possible to sequence their DNA.
- Shoveling has no use but is genetic, based on V370A gene which leads to increased ability to absorb vitamin D via increased mammary ductal branching,

Paleo-Inuit

- Arrival of Paleo-Inuit: between 9 and 5.5 ka; related to ancient Siberians; extended across the Arctic from Alaska to Greenland; the first to people the regions above the Arctic Circle.
- The earliest Paleo-Inuit cultures appear in the archaeological record of far northern North America and Greenland around 5.2 ka; and disappear around AD 1500.
- Additionally, there is evidence of back migration from the Americas to Siberia, in the genetic composition of ancient Ekven (around 2 ka) and contemporary Chukchi peoples

Paleo-Inuit

- The Paleo-Inuit represent a population dispersal into the Americas from Siberia that is altogether independent of other Indigenous American peoples.
- Paleo-Inuit individuals = carry same mtDNA haplogroup (D2a193)
- They are followed and eventually replaced by people of the Thule culture (previously, Neo-Inuit), who are generally considered to be the ancestors of present-day Inuit and Iñupiat.

Thule Culture

- The Thule culture developed in coastal Alaska by the year 1000 and expanded eastward across northern Canada, reaching Greenland by the 13th century. Met the Vikings. Were skilled hunters of whales and other marine mammals. They introduced the dog sled and the umiaq, They were ancestral to the Inuit.
- Genetically, the Thule are a mix of Paleo-Inuit-related groups and Native American peoples.
- The Native American component in Inuit derives from NNA groups.
- A subgroup of the Thule culture were the Saqqaq culture.

Paleo-Inuits Into the Americas

- There has been recurrent bidirectional *gene* flow across Beringia

- In 2010, sequencing of a 4,000-year-old Paleo-Inuit from the now extinct Saqqaq culture.

- The Saqqaq existed in southern Greenland -4,500 to 2,800 years ago, before it was superseded by the Thule culture, which represents the ancestors of today's Inuits.

- These results were qualitatively consistent with a migration from Siberia into the Americas -5,000 years ago that was distinct from the movements that founded modern-day Amerinds, Inuit and Na-Dene

2010: 4000 year old Saqqaq man from Greenland

- First analysis of whole genome of an ancient human; based on hair sample found in 1986
- Migration of people across the continent, from Siberia to Greenland, some 5,500 years ago.
- Greenlander belonged to a Paleo-Inuit culture called the Saqqaq
- The Paleo-Inuit Saqqaq and the Inuit appeared to be genetically distinct from each other.
- Closest living relatives were the Chukchis, people who live at the easternmost tip of Siberia. His ancestors split apart from Chukchis some 5,500 years ago
- No traces of the Saqqaq people have been found in North America
- Brown eyed, thick hair, dry ear wax

An artist's impression of "Inuk." Nuka Godfredsen

Paleo-Inuit did not die out

- In 2017, Pavel Flegontov et al. confirmed that the Paleo-Inuit lineage did not die out, and instead lives on in the Na-Dene.

- Evidence for recent common ancestors between the ancient Saqqaq individual and present-day Na-Dene.

- The ancestry of present-day speakers of Inuit-Aleut languages is as a mixture of lineages related to Paleo-Inuits and First Americans.

Two ancestral populations

- 2017 Reich: there were just two ancestral lineages that contributed all Native American ancestry apart from that in Population Y: the First Americans and the Paleo-Inuits.

- All Native Americans excluding Amazonians with their Population Y ancestry can be described as mixtures of two ancestral populations related differentially to Asians.

- Mixtures of these two ancestral populations produced the three source populations that migrated from Asia to America and that are associated with Inuit-Aleut languages, Na-Dene, and all other languages.

Caribbean Islands

- There were at least two major episodes of population movement onto the Caribbean Islands.
- An archaic group arrived first, circa 6 Ka.
- Sometime after about 2.5 ka, Ceramic Age peoples arrived from northern South America, from a source population that includes Amazon groups.
- The genomic record also confirms that having passed through a substantial bottleneck, populations increased steeply in the millennia after their arrival,

Caribbean - Reich

- With a pre-conquest population of 10s of thousands, what happened to Indigenous Americans after Europeans arrived amounted to genocide: the systematic obliteration of individuals and of their culture and community
- The numbers of deaths in both absolute and relative terms are horrific. According to a 1540 census, the number of Indigenous people in Hispaniola had dropped to 250 people. It dropped to zero in later counts.
- Genetic legacy of pre-contact Caribbean people did not disappear: They contributed an estimated 14 percent of the DNA of living people from Puerto Rico, 6 percent of that in the Dominican Republic and 4 percent of that in Cuba

Geography of Na-Dene Languages

Tlingit

Most widely spoken Na-Dene language today is Navajo.

After the First Americans: the Na-Dene

- Question of the origin of speakers of Na-Dene languages, who live along the Pacific coast of North America, in parts of northern Canada, and as far south as Arizona in the United States.

- The overwhelming consensus among linguists is that these languages stem from an ancestral language no more than a few thousand years old, and that their dispersal over this vast range in northwestern America must have been driven at least in part by migrations.

Na-Dene

- In an astonishing development in 2008, the American linguist Edward Vajda documented a deeper connection between Na-Dene languages and a language family of central Siberia called Yeniseian, once spoken by many populations, though today only the Ket language of the Yeniseian family is still used on a day-to-day basis.

- These results suggest that despite the enormous distance, a relatively recent migration from Asia gave rise to Na-Dene speakers in the Americas.

Genetic Evidence of at Least Four Prehistoric Migrations to America: 15-10 Ka

- There were at least two migrations that left a human legacy as far as South America and at least two whose impact was limited to northern North America.
  - 1 Split from closest Eurasians - 23,000 years ago
  - 2 Source of Population Y -- Timing of entry unknown
  - 3 Migration out of Asia forms the Paleo-Inuit lineage. 5,000 ya
  - 4 A final wave from Asia contributes to the Neo-Inuits and displaces the Paleo-Inuits. 1,000 ya

New Mexico Ghost footprints: 21 to 23 Ka

- In September 2021, a study revealed that 60 human footprints in White Sands National Park in New Mexico dated to between 21-23 Ka, making them the oldest "unequivocal evidence" of humans in the Americas.

- Less than a mile (1.6 kilometers) away from where the tracks were uncovered, a previous research group uncovered a hunter-gatherer camp dating to 12,000 years ago, where the humans who left the prints might have lived.
- The site included an ancient fireplace, stone tools used for cooking, a pile of more than 2,000 animal bones and charred tobacco seeds, which are the earliest evidence of tobacco use in humans.

Americas: Anzick child and Kennewick Man

- In 2014, the Anzick child, the oldest and the only Clovis-associated human genome from the Americas (found in Montana, United States), which belonged to an individual who lived about 12.6 kyr ago, was published.
- Clovis population from which the genome came was directly ancestral to many contemporary Native Americans.
- Similarly, analysis of the genome sequence of the roughly 9.5-kyr-old Kennewick Man skeleton found in the state of Washington in the United States, which was previously thought to be closely related to the Ainu and Polynesians on the basis of cranial morphology, determined that he was most closely related to contemporary Native Americans.

Americas

- Modern Siberians are the closest relatives of Native Americans outside of the Americas.
- 24-ka Mal’ta skeleton suggests that Native Americans are derived from a mixture of populations that are related to the Mal’ta lineage as well as one or more unknown East-Asian lineages.
- Because the Clovis-associated genome and contemporary Native Americans contain similar amounts of the Mal’ta genetic signature (14–38%), the admixture event happened more than 12.6 kyr ago.
- However, whether it took place inside or outside the Americas remains unclear.

Americas – Paleo-Inuit and Inuits

- The <u>Inuit of the American Arctic</u>: originated from a migration separate to that of other Native Americans.
- Question: Did first people to inhabit the Arctic, the <u>now extinct Paleo-Inuit culture</u>, which appeared about 5 kyr ago in the Americas, represent the ancestors of the present-day Inuit or an independent founder population from Siberia.
- Sequencing of Saqqaq DNA from a 4000 y-old tuft of hair from Greenland showed that the population the individual belonged to had migrated from Siberia to the North American Arctic independently of the Native American and Inuit migrations.
- The <u>group then survived in the Arctic for about 4 kyr by reinventing their subsistence strategies and technology</u> but were eventually replaced by the Inuit around 700 yr ago.

America: North vs South

- Diversification of Native American mitochondrial lineages around 12 – 18 Ka suggests that northern and southern lineages diverged during this time.

- Native American lineage must have split from Siberian ancestors around 25,000 Ka at the earliest (more likely around 20 Ka or later) and at least before the divergence of northern and southern Native American lineages (13-18 Ka).

- However, a genetic affinity between Amazonian and Australo-Melanesian populations (Population Y) suggests that we still do not have the full picture of the ancestry of the first Americans.

Americas

- Population Y: The expansion into the Americas was done by different populations, with some subpopulations retaining greater affinity to an unknown northeastern Asian population related to present-day Australo-Melanesians.

- Discovery that the ~40,000-year-old Tianyuan individual from eastern China also had affinity to the Amazonian populations supports the presence of ancient subgroups in Siberia contributing to the Amazonian and Australo-Melanesian connection

2014:
Naia, Hoyo Negro Adolescent, HN5/48

- Near-complete human skeleton of a 15 to 16 years old female with an intact cranium and preserved DNA found with extinct fauna in the Hoyo Negro submerged cave on Mexico’s Yucatan Peninsula.
- This skeleton dates to between 13,000 and 12,000 kya and has Paleoamerican craniofacial characteristics and a Beringian-derived mitochondrial DNA (mtDNA) haplogroup (D1) (which only occurs in the Americas but originated in Asia.).

James C. Chatters, et al., *Science*, 2014

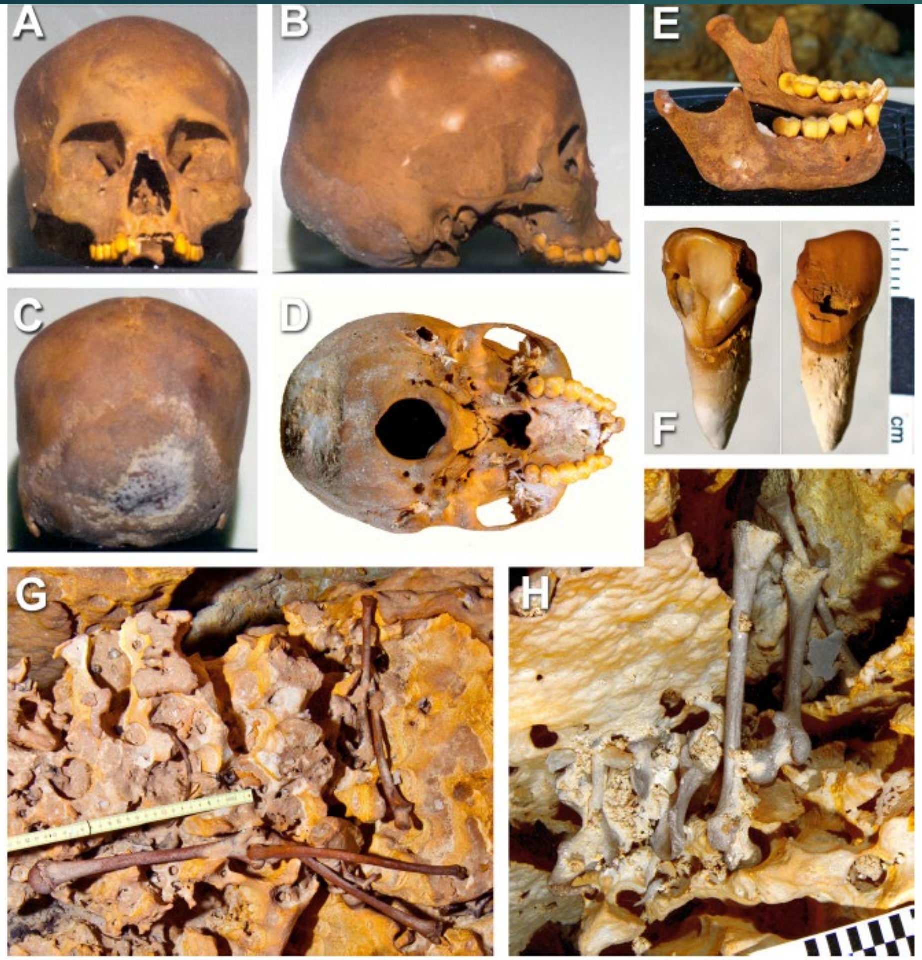


Figure S7. Portions of the human skeleton HN5/48, including the skull (A-E), upper first incisor (F) arms and associated ribs and vertebrae (G) and the pelvic girdle (H). The cranium is shown in anterior (A), left lateral (B), posterior (C) and basal (D) views. Note the lack of projecting zygomatics and the proportionate shortness of the upper face (A, B), the angle formed by the occipital bones (B), and the parabolic dental arcade (D). The upper right third molar (B, D) is fully erupted, whereas the upper left has emerged but is not yet in occlusal position. Lower third molars, however, appear to be impacted. Note the well-developed shoveling and three large carious lesions in F. Scales are metric. All photos except F taken underwater by Roberto Chávez-Arce; (G) and (H) were taken in situ.

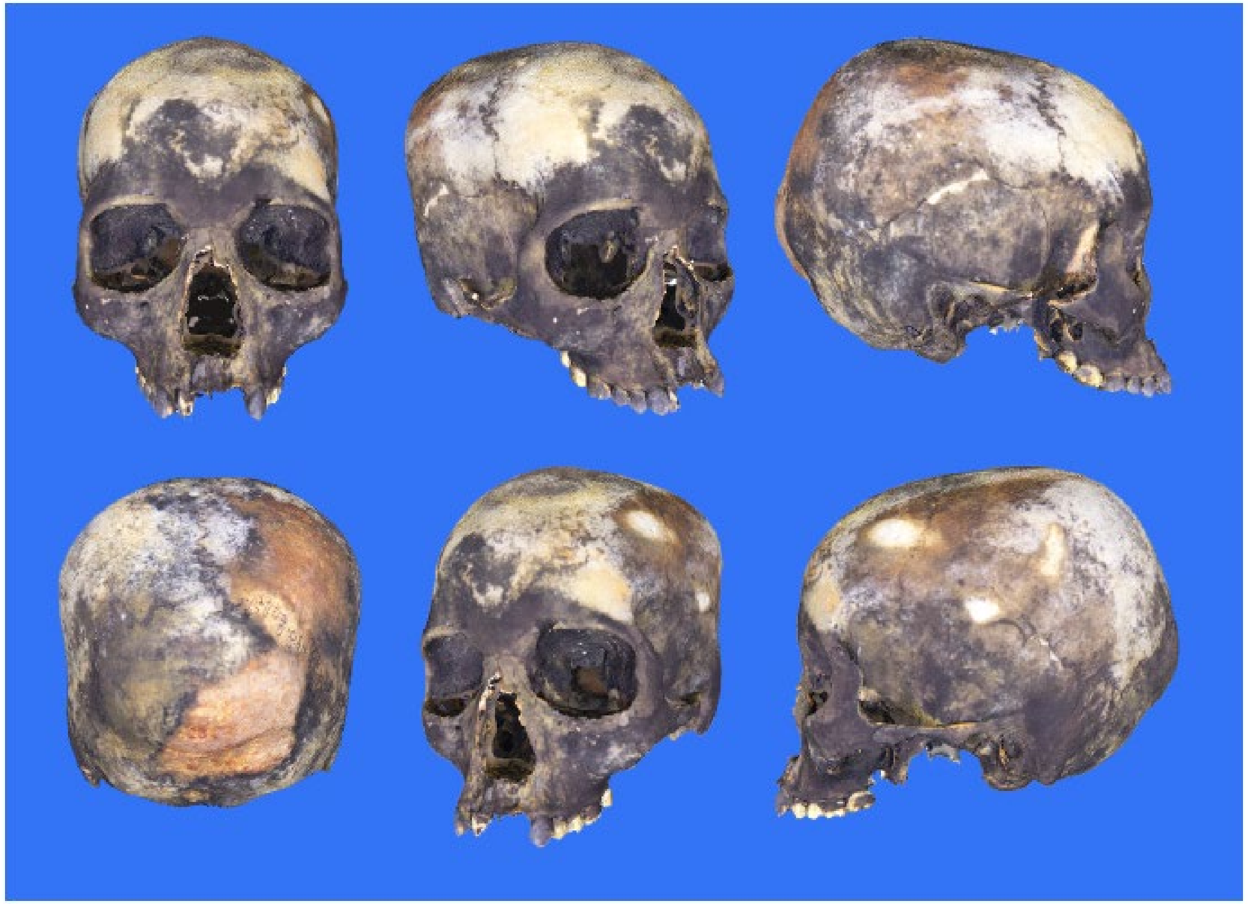


Figure S8. Multiple views of the skull of HN5/48 taken as screen grabs of a digital 3-D model produced from photographs. On screen, the model has a strong parallax effect, which is particularly evident in front and ¾ views. Color here differs from that seen in other figures due to a redox reaction caused by temporary protective underwater storage in a closed vessel. It has since reverted to its original color. Model by Ann Jaskolski and Corey Jaskolski from photos by Roberto Chávez-Arce.

Reconstructing the Deep Population History of Central and South America - 2018

- Cosimo Posth[1], Nathan Nakatsuka[2], Iosif Lazaridis[3], Pontus Skoglund[4], Swapan Mallick[5], Thiseas C Lamnidis[6], Nadin Rohland[3], Kathrin Nägele[6], Nicole Adamski[7], Emilie Bertolini[8], Nasreen Broomandkhoshbacht[7], Alan Cooper[9], Brendan J Culleton[10], Tiago Ferraz[11], Matthew Ferry[7], Anja Furtwängler[12], Wolfgang Haak[6], Kelly Harkins[13], Thomas K Harper[14], Tábita Hünemeier[15], Ann Marie Lawson[7], Bastien Llamas[9], Megan Michel[7], Elizabeth Nelson[16], Jonas Oppenheimer[7], Nick Patterson[17], Stephan Schiffels[6], Jakob Sedig[3], Kristin Stewardson[7], Sahra Talamo[18], Chuan-Chao Wang[19], Jean-Jacques Hublin[18], Mark Hubbe[20], Katerina Harvati[21], Amalia Nuevo Delaunay[22], Judith Beier[23], Michael Francken[23], Peter Kaulicke[24], Hugo Reyes-Centeno[21], Kurt Rademaker[25], Willa R Trask[26], Mark Robinson[27], Said M Gutierrez[28], Keith M Prufer[29], Domingo C Salazar-García[30], Eliane N Chim[31], Lisiane Müller Plumm Gomes[15], Marcony L Alves[31], Andersen Liryo[32], Mariana Inglez[15], Rodrigo E Oliveira[33], Danilo V Bernardo[34], Alberto Barioni[35], Veronica Wesolowski[31], Nahuel A Scheifler[36], Mario A Rivera[37], Claudia R Plens[38], Pablo G Messineo[36], Levy Figuti[31], Daniel Corach[39], Clara Scabuzzo[40], Sabine Eggers[41], Paulo DeBlasis[31], Markus Reindel[42], César Méndez[22], Gustavo Politis[36], Elsa Tomasto-Cagigao[24], Douglas J Kennett[10], André Strauss[43], Lars Fehren-Schmitz[44], Johannes Krause[16], David Reich[45]

Genomic evidence for ancient human migration routes along South America's Atlantic coast

- Found a distinct relationship between ancient genomes from Northeast Brazil, Lagoa Santa, Uruguay and Panama, representing evidence for ancient migration routes along South America's Atlantic coast.
- Also detect greater Denisovan than Neanderthal ancestry in ancient Uruguay and Panama individuals.

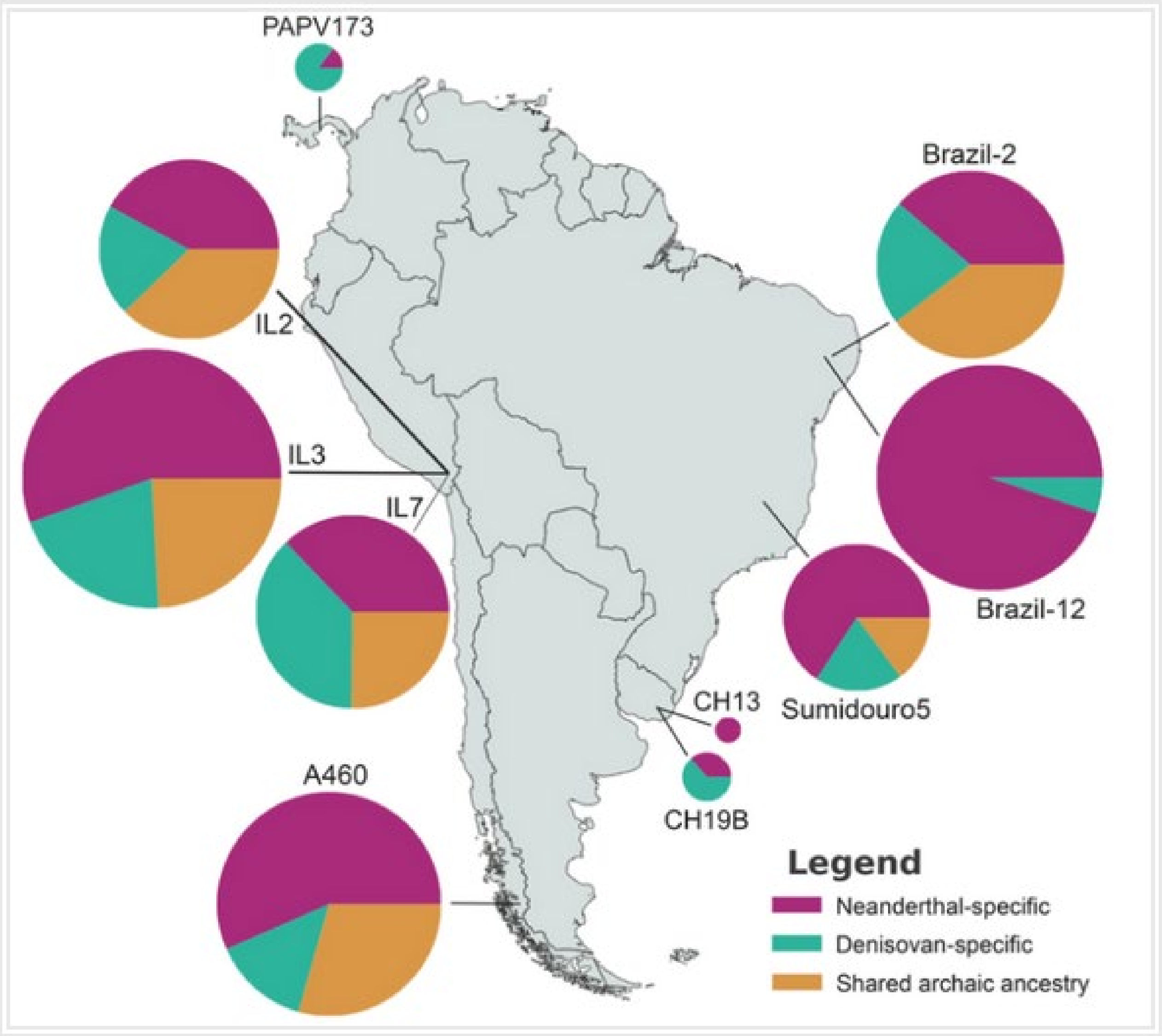
- The first southern North American groups entered South America and spread through the Pacific coast settling the Andes (yellow arrow).
  At least one population split occurred soon after, branching the first groups that settled the Atlantic coast (green arrow) from the groups that gave rise to the ancient populations of Southern Cone.
  New Migrations may have then emerged along the Atlantic Coast, with a possible origin around Lagoa Santa, heading north toward Northeast Brazil and Panama, and south to Uruguay.

South American Migration routes

- Many unanswered questions still persist. While there is archaeological evidence for a north-to-south migration during the initial peopling of the Americas by ancient Indigenous peoples, where these ancient humans went after they arrived has remained elusive.
- Have discovered migrations in the opposite direction along the Atlantic coast.

South American migrations

- Evidence of Neanderthal ancestry within the genomes of ancient of individuals from South America
- Human movements closer to the Atlantic coast eventually linked ancient Uruguay and Panama in a south-to-north migration route –3,270 miles apart. Dated to 1000 years ago
- This new model reveals that the settlement of the Atlantic coast occurred only after the peopling of most of the Pacific coast and Andes.



Neanderthal and Denisovan genetic trace in South America.

Credit: Florida Atlantic University

Most complete genetic evidence to date of complex migration routes in Ancient Central and South America

N and D genetic traces

Australasian and Denisovan signals

- Found strong Australasian (Australia and Papua New Guinea) genetic signals in an ancient genome from Panama.
- Still don’t know how these ancestral genomic signals appeared in Central and South America without leaving traces in North America.
- Also detected greater Denisovan than Neanderthal ancestry in ancient Uruguay and Panama individuals.
- The admixture must have occurred a long time before, perhaps 40,000 years ago.

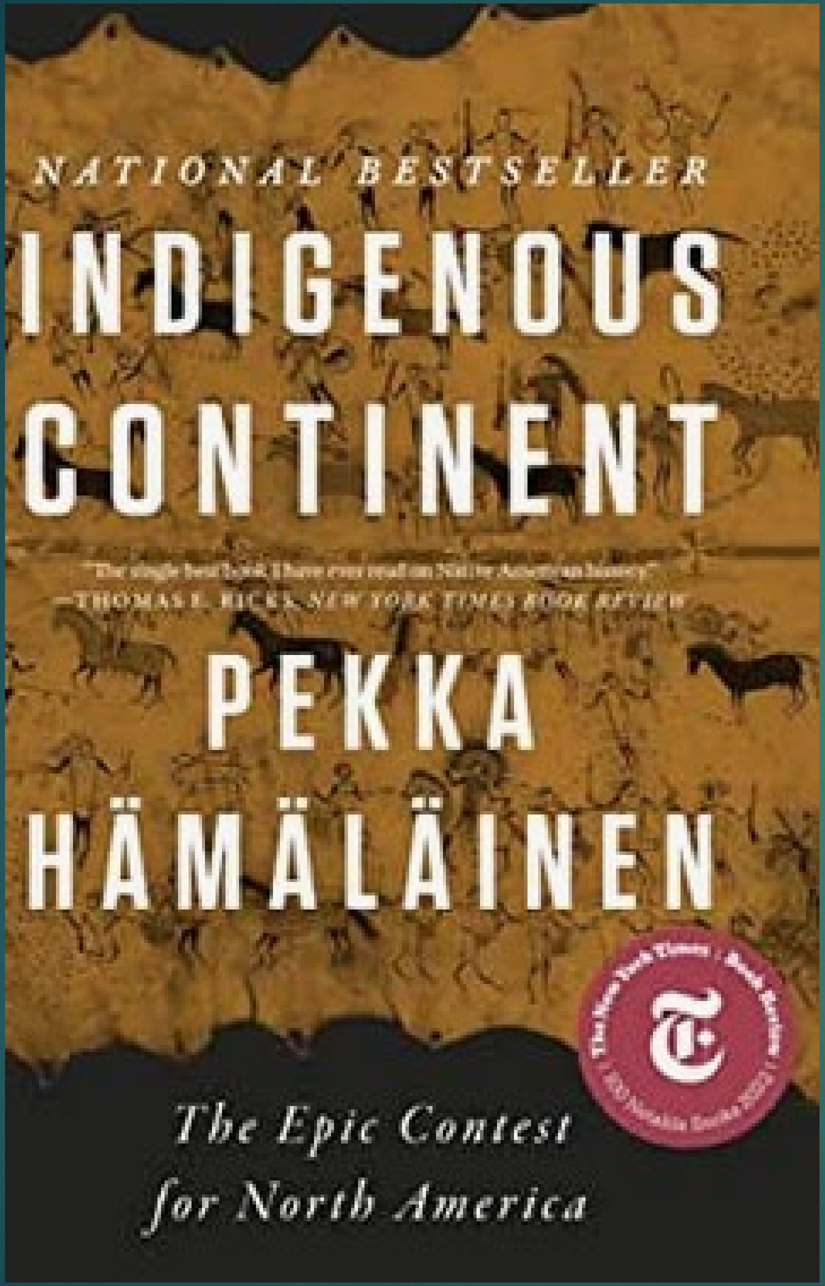
Migration patterns

- Results suggest that at least one population split probably occurred not long after the first SNA groups reached the southern portion of the Americas.
- Hypothesize that this split took place around the Andes, later giving rise to ancient Southern Cone populations and the first groups that settled the Atlantic coast.
- The split occurred at least 10 000 years ago. Conjecture that new migrations may have then emerged along the Atlantic coast,
- .
- Hypothesis proposing that human movements closer to the Atlantic coast eventually linked Uruguay and Panama in a south-to-north migration route. The migrations along the Atlantic coast apparently left no trace in the populations closer to the Pacific,

New Ancient DNA Discoveries Show some Native Americans Returned to Siberia

- Although the progenitors of today's Native Americans originated in Asia, the migration was not one-way
- According to a study from 2019, genetic and linguistic data demonstrated that humans who lived in northwest Alaska between 2,200 and 500 years ago may have somehow crossed across the Bering Sea into Siberia. It was not known, however, whether this gene flow of Native American heritage back into Asia was typical or an anomaly
- Given the current data, repeated backflow is the most plausible scenario.

K. Wang, et al., 2023



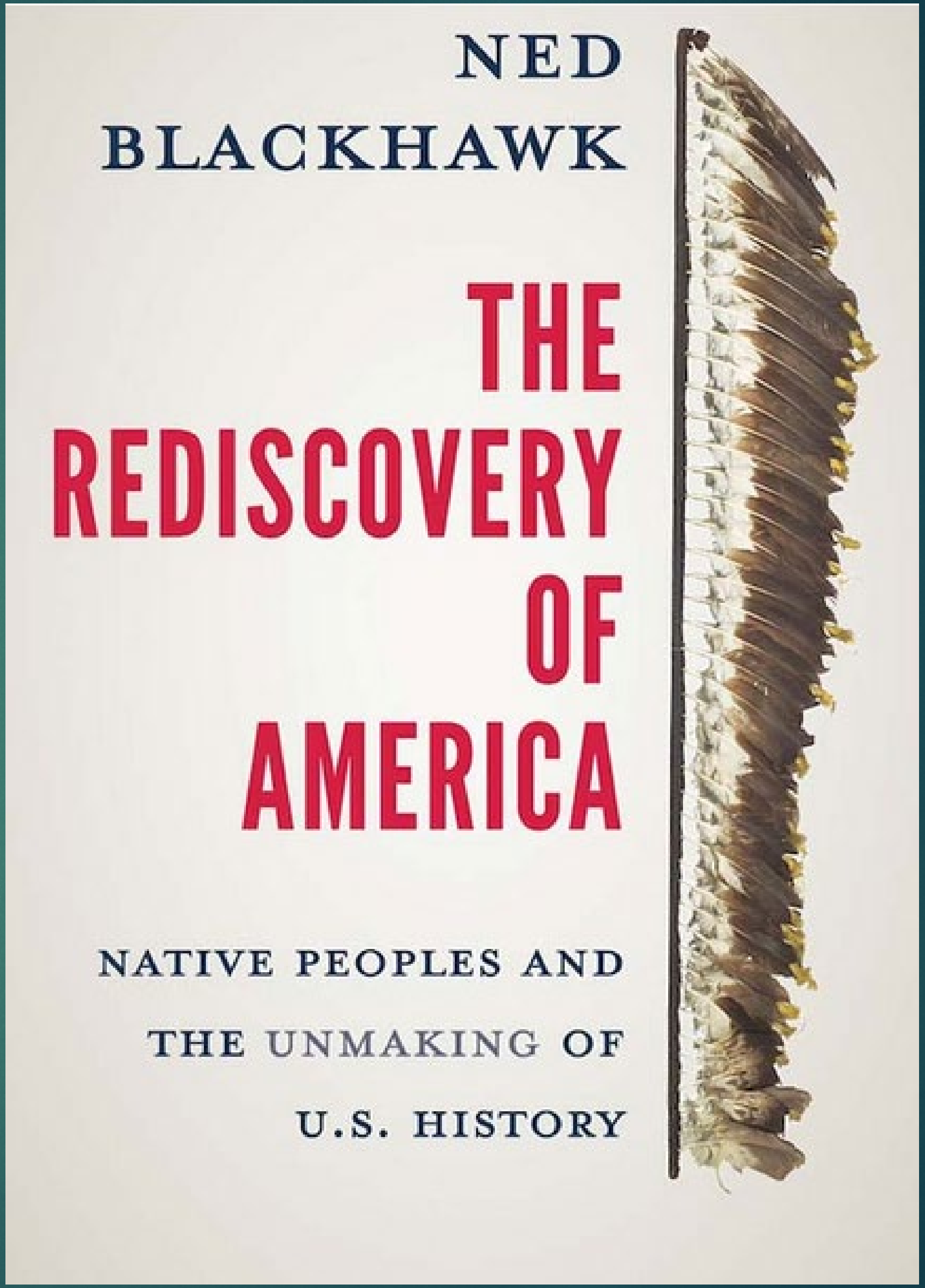
NATIONAL BESTSELLER

INDIGENOUS CONTINENT

"The single best book I have ever read on Native American history."
—THOMAS E. RICKS, NEW YORK TIMES BOOK REVIEW

PEKKA HÄMÄLÄINEN

The Epic Contest for North America



NED BLACKHAWK

THE REDISCOVERY OF AMERICA

NATIVE PEOPLES AND THE UNMAKING OF U.S. HISTORY

The horse and Native Americans

The horse in America

- Scattered across the prairie east of the Colorado Front Range are rings of ancient stones. The rings were used to anchor tipis, and they measure barely 2 meters across. The tiny footprint comes as a surprise to modern Pawnee, whose traditional tipis are big enough to fit whole families.

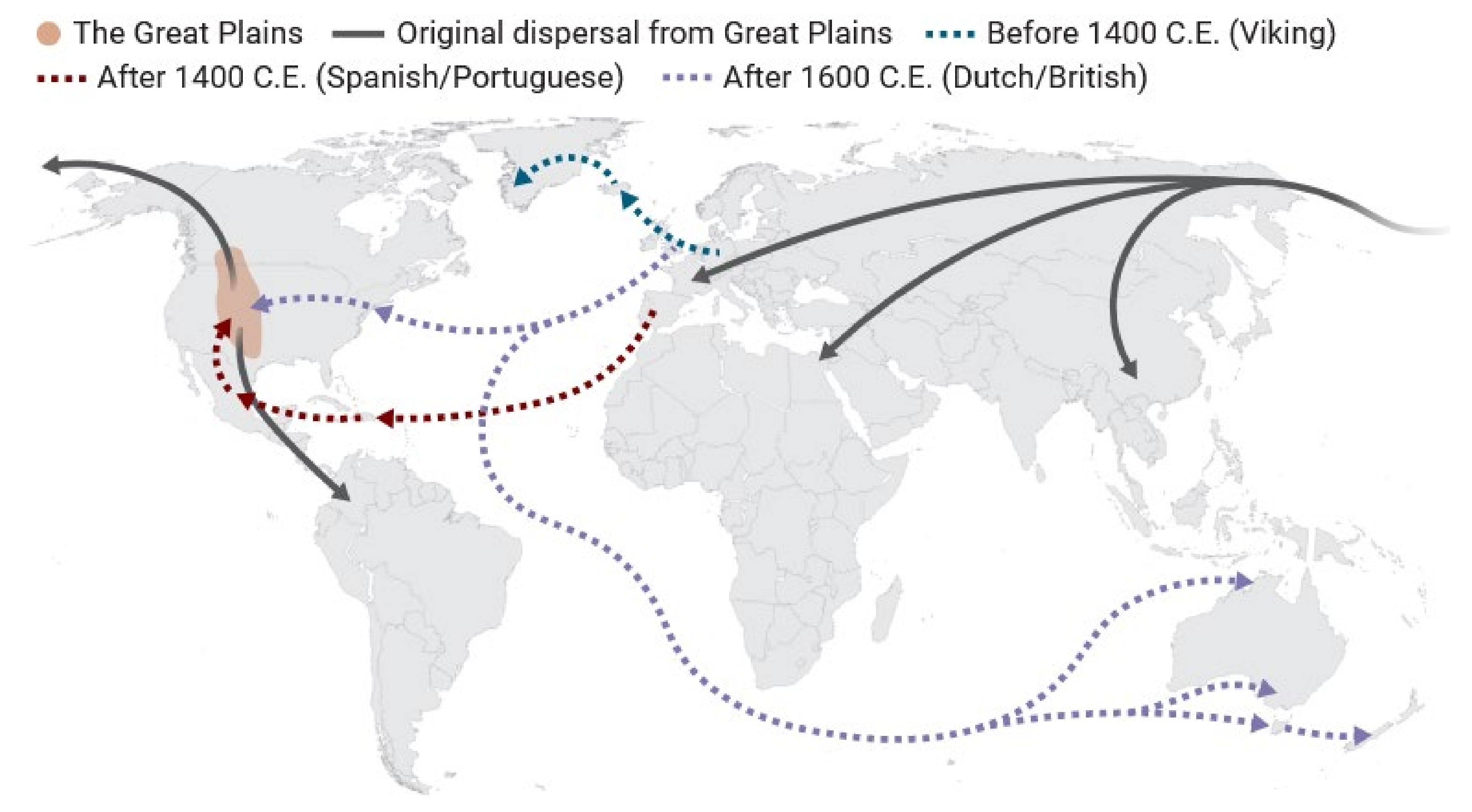
- The change resulted from the introduction of the horse. For millennia, the Pawnee had relied on dogs to haul their belongings on bison hunting trips; when they acquired horses, the impact was immediate and dramatic. They allowed NAs to carry more gear, pull more food, have bigger tipis.

Horse Nation - Andrew Curry, 2023

The horse in America

- For Native peoples on the Great Plains grasslands that stretch from the Rocky Mountains to the Missouri River, horses took on a central economic and military role, enabling bison hunting on a large scale and raiding across vast distances.
- The introduction of this technology, of horses, changed Great Plains cultures

Horses evolved millions of years ago in North America and, after spreading to Eurasia and Africa, went extinct in their homeland at the end of the last ice age. Spanish and British colonizers brought them back.



The Horse in America

- Centuries ago, the Americas were apparently horseless—even though *Equus* had evolved in the Americas more than 4 million years ago, spreading west from there into Eurasia and Africa.
- When the ancestors of Native Americans entered North America toward the end of the last ice age, more than 14,000 years ago, they would have encountered herds of wild horses.
- From the archaeological evidence—cutmarks on bones found at a handful of sites—it seems early Americans hunted horses and used their bones as tools, but did not domesticate or ride them.
- And by 5000 years ago at the latest, the fossil record suggests, North America's horses were gone.
- Along with nearly 40 other species of megafauna, from saber-toothed tigers and mammoths to camels, they were wiped out by hunting, climate change, or both.

The Horse

- It wasn't until 1519 C.E., when Spanish conquistador Hernán Cortés made landfall on the Gulf Coast of Mexico, that horses entered the Americas again. His 16 horses stunned local people, and the shock helped him defeat the Aztec Empire just 2 years later.
- In the centuries that followed, the horse spread once again across the continent, this time as a status symbol, means of transport, and hunting companion rather than prey. In the process, it set off massive human migrations, as some Native groups shifted to more mobile lifestyles.
- Historians have tended to date the widespread adoption of the horse by Native peoples to the 18th century, when the first European travelers recorded its presence in the central and northern Plains.
- 2023 new study: based on archaeological evidence, radiocarbon dating, isotope analysis, and ancient DNA, Shield Chief Gover and dozens of other researchers conclude that horses had made it that far north up to a century earlier. The study shows they had begun to spread within a few decades after the Spanish introduced them to the Southwest in the 16th century.

Pueblo revolt

- Historical theory: Based on written sources, many historians have tended to compress the adoption of the horse by tribes throughout the Great Plains and Rocky Mountains into a pivotal half-century, beginning in 1680 with a bloody revolt against Spanish rule by Pueblo people in New Mexico and ending with the first European accounts of horses on the northern Plains.

- After the uprising, the story goes, the Pueblos sold thousands of horses that had belonged to the expelled Spanish to neighboring tribes. What historians argue is that the Pueblo Revolt pushes a volume of horses, enough to transform tribes far to the north.

- In the aftermath of the Great Southwestern Rebellion, the horse frontier moved rapidly outward from New Mexico along the ancient Indigenous trade routes,

Controversy

- Adoption was facilitated by contact with the Spanish, who employed Pueblo people to herd horses and other livestock in New Mexico in the early 1600s.
- Native accounts contradicted the timeline centered on the Pueblo Revolt, suggesting some tribes had acquired horses much earlier, but oral tradition was discounted. The end result has been to discredit the antiquity of the relationship between Native people and horses.
- As a result, many horse remains found on the Great Plains wound up in paleontological collections rather than archaeology labs. Just a handful had been radiocarbon dated.

Horses earlier in time

- Dates of horse remains from sites in Wyoming and Nebraska, for example, show people far beyond the Spanish frontier were breeding, feeding, herding, and caring for horses—and probably riding them—beginning sometime after 1550, and had thoroughly incorporated them into their societies by 1650 at the latest.
- The results showed horses on the Great Plains in the historic period were closely related to horses in Spain at the same time.
- By the 1770s, however, genetic signatures from British breeds began to filter into the region, and horses there today show a mix of both Spanish and British ancestry (and no link to horses the Vikings are known to have taken as far as Greenland).
- No DNA has been found of the horses that had lived in the Americas in the ice age or right after.

Native American oral traditions

- In Pawnee, the word for “horse” translates as “new dog.”
- Other Indigenous languages, too, reflect an initial unfamiliarity with the beasts: Blackfeet called them “elk dogs,” Comanche “magic dogs,” the Assiniboine “great dogs.” Even in language, it shows up as ‘what is this?!’”.

Horses from South America

- Another 2023 study: looked at the DNA of horses from across North America. Found that the horses in the American West were more closely related to horses from South America than to horses from the East Coast.
- This suggests that the horses in the West arrived from South America, and that they did so before the Spanish arrived in North America.
- The researchers believe that Native Americans may have been responsible for bringing the horses to the West. They may have acquired the horses from South America, and then transported them north along trade routes.
- This new study suggests that the history of horses in North America is more complex than we thought.

Contact Info

- Charles J. Vella, PhD
- www.charlesjvellaphd.com
- charlesvella@comcast.net
- 415-939-6175