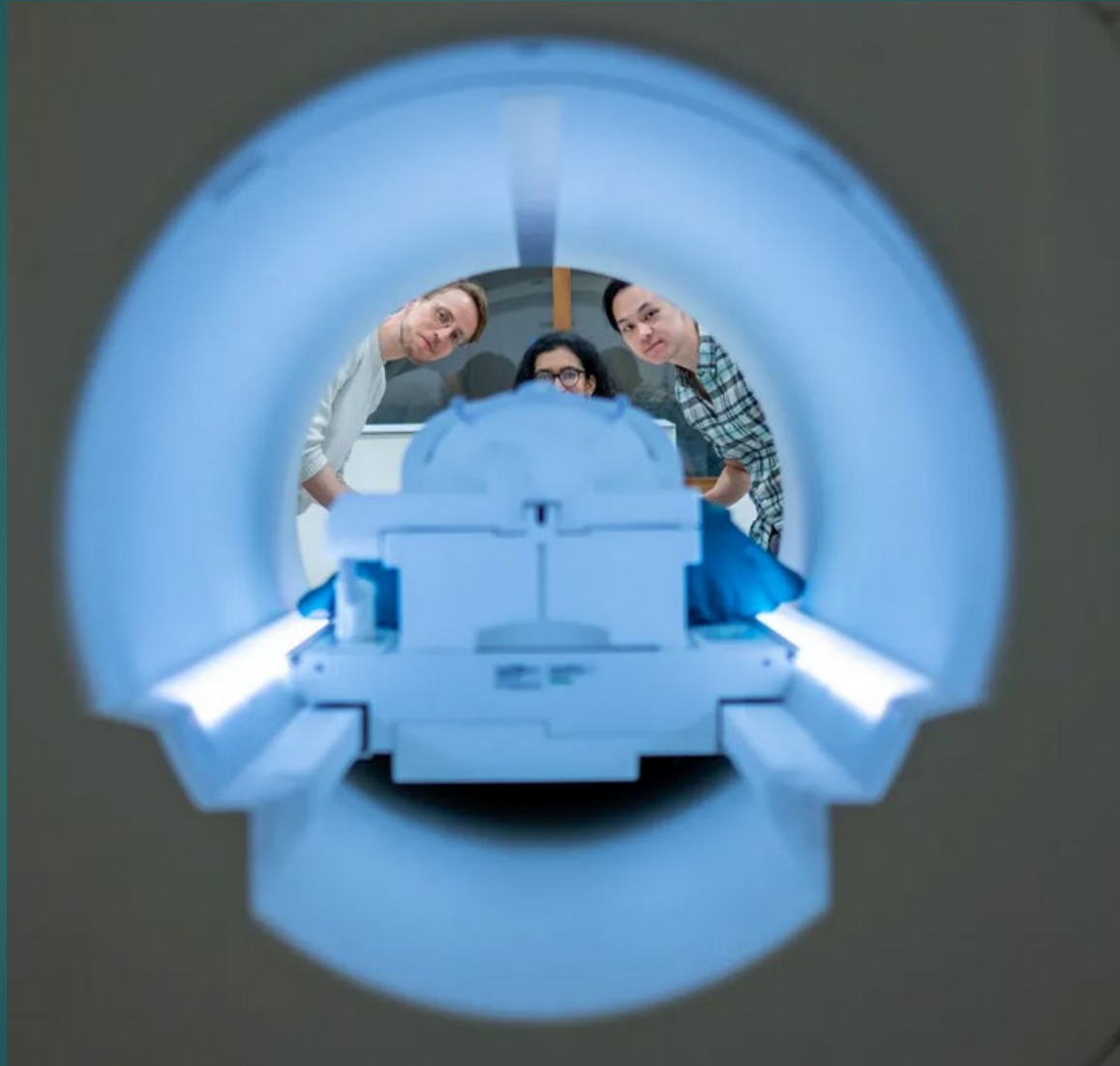


Scientific Update,  
May 2023

**Sperm whales sleep vertically** for 15 minutes at a time; 1 hemisphere sleeping at a time; 1 eye open, 1 closed



# Brain Activity Decoder Can Reveal Stories in People's Minds



Researchers trained their semantic decoder on dozens of hours of brain activity data from participants, collected in an fMRI scanner.

# Semantic reconstruction of continuous language from non-invasive brain recordings

- ▶ A new artificial intelligence system called a semantic decoder can noninvasively translate a person's brain activity — while listening to a story or silently imagining telling a story — into a continuous stream of text via fMRI imaging.
- ▶ The system developed by researchers at The University of Texas at Austin might help people who are mentally conscious yet unable to physically speak, such as those debilitated by strokes, to communicate intelligibly again.
- ▶ Patient must be trained on constant streams of words (podcasts) or images (like large language programs that create ChatGPT), which learns where these are uniquely stored in your brain

# Examples: decoder exactly reproduces some words and phrases and captures the gist of many more

## Actual stimulus

*i got up from the air mattress and pressed my face against the glass of the bedroom window expecting to see eyes staring back at me but instead finding only darkness*

*i didn't know whether to scream cry or run away instead i said leave me alone i don't need your help adam disappeared and i cleaned up alone crying*

*that night i went upstairs to what had been our bedroom and not knowing what else to do i turned out the lights and lay down on the floor*

*i don't have my driver's license yet and i just jumped out right when i needed to and she says well why don't you come back to my house and i'll give you a ride i say ok*

## Decoded stimulus

i just continued to walk up to the window and open the glass i stood on my toes and peered out i didn't see anything and looked up again i saw nothing

started to scream and cry and then she just said i told you to leave me alone you can't hurt me anymore i'm sorry and then he stormed off i thought he had left i started to cry

we got back to my dorm room i had no idea where my bed was i just assumed i would sleep on it but instead i lay down on the floor

she is not ready she has not even started to learn to drive yet i had to push her out of the car i said we will take her home now and she agreed

Exact

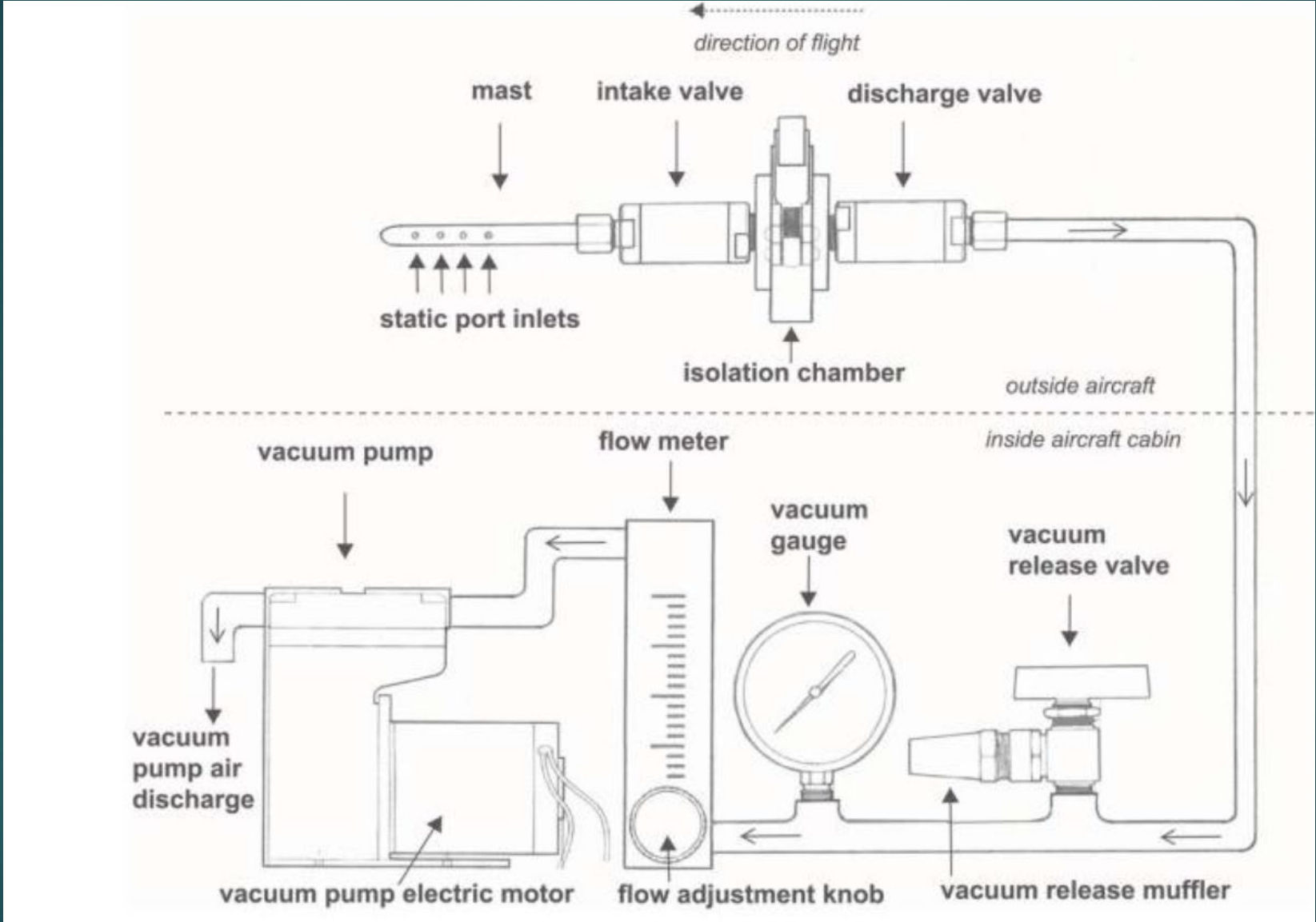
Gist

Error

# Reading thoughts

- ▶ Later, provided that the participant is open to having their thoughts decoded, **their listening to a new story or imagining telling a story allows the machine to generate corresponding text from brain activity alone.**
- ▶ **Model can decode continuous language for extended periods of time with complicated ideas**
- ▶ **Current protection:** Results for individuals on whom the decoder had not been trained were unintelligible, and if participants on whom the decoder had been trained later put up resistance — for example, by thinking other thoughts — results were similarly unusable.
- ▶ **Researchers think this work could transfer to other, more portable brain-imaging systems, such as functional near-infrared spectroscopy (fNIRS).**

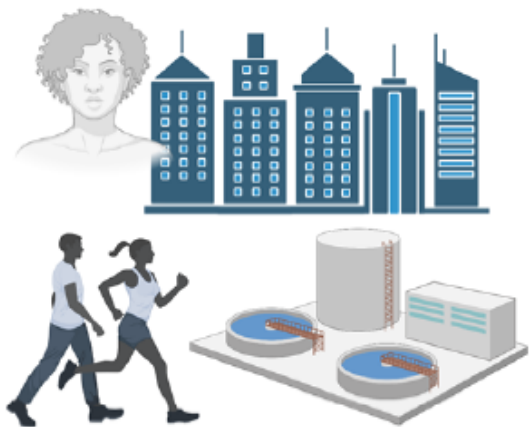
# Environmental Air DNA probe



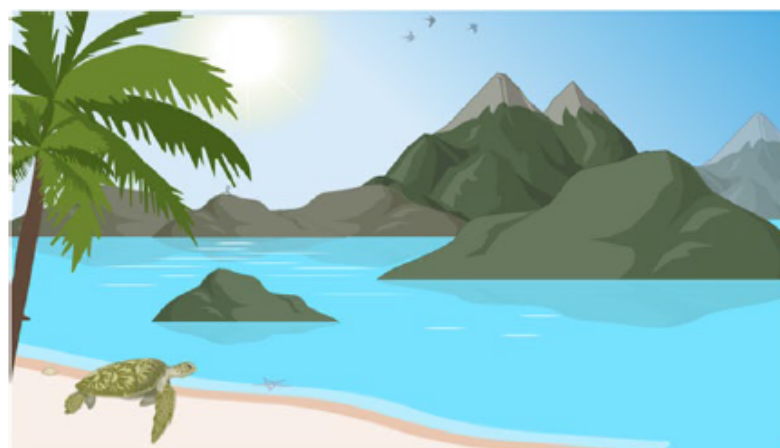
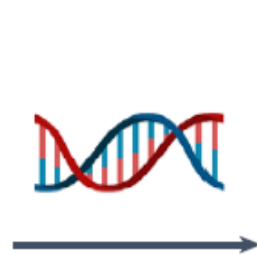
# Environmental DNA: ability to capture your DNA in the air or from footprints on beach

**a**

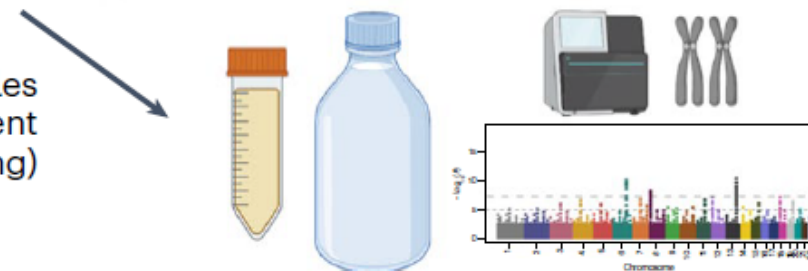
Human DNA as genetic bycatch from pathogen and wildlife eDNA studies



1. Human activities release DNA into the environment (direct, wastewater, landfill and so on).



2. Extraction of DNA from environmental samples recovers all DNA present in the environment (soil, aquatic or air sampling)



3. Untargeted shotgun sequencing recovers reads from all organisms for which eDNA was present in a sample, including human.



# DNA in air: airborne genetic material

- ▶ Through the use of their sampling probe and high throughput metagenomic sequencing, the researchers discovered the **widespread presence of prokaryotic and eukaryotic eDNA in the atmosphere**, reaching thousands of meters into the planetary boundary layer in the southeastern US. Notably, the study detected chicken, cow, and human eDNA at all altitudes flown, including an astonishing 8,500 feet above the ground.
- ▶ The researchers identified various common plant-based allergens from grasses, weeds, and trees, as well as from species not typically reported in the air, such as garlic, revealing a **diverse array of airborne genetic material**.

**Inadvertent human genomic bycatch** and intentional capture raise beneficial applications and ethical concerns with environmental DNA – L. Whitmore et al. 2023

- ▶ **Study of turtle cancers**: The team **found long stretches of quality human DNA in the ocean and rivers** surrounding the Whitney Lab, both near town and far from human settlement, as well as in sand from isolated beaches. Including from footprints in the sand
- ▶ **“Human genetic bycatch (HGB)”**: Scientists and regulators must grapple with the ethical dilemmas inherent in accidentally—or intentionally—sweeping up human genetic information, not from blood samples but from a scoop of sand, a vial of water or a person's breath.
- ▶ In most cases the **quality is almost equivalent to if you took a sample from a person**. Because of the ability to potentially identify individuals, the researchers say that ethical guardrails are necessary for this kind of research.

# Human DNA is everywhere. That's a boon for science, and an ethical quagmire

- ▶ We cough, spit, shed and flush our DNA into all of these places and countless more. Human DNA can be found nearly everywhere
- ▶ DNA was of such high quality that the scientists could identify mutations associated with disease and determine the genetic ancestry of nearby populations. They could even match genetic information to individual participants who had volunteered to have their errant DNA recovered.
- ▶ **Environmental DNA (eDNA)** samples could benefit fields from medicine and environmental science to archaeology and criminal forensics. For example, researchers could track cancer mutations from wastewater or spot undiscovered archaeological sites by checking for hidden human DNA. Or detectives could identify suspects from the DNA floating in the air of a crime scene.
- ▶ **Current computer programs designed to screen for and filter out human DNA sequences reduced, but did not eliminate the problem; after filtering, the group could still identify as many as 11% of the samples.**

# eDNA

- ▶ Collected room air samples from a veterinary hospital. They recovered DNA matching the staff, the animal patient and common animal viruses.
- ▶ Found eDNA of fatal genetic disorder: tell the people nearby?
- ▶ Raises ethical dilemmas, from consent, privacy and surveillance to data ownership, requiring further consideration and potentially novel regulation
- ▶ China is already using mass collections of human DNA to help suppress minorities; use a DNA sample to create an image of a person's face; used for racial profiling and other state discrimination against Uighurs.

# Potential problematic implications of the capture of human genomic eDNA data

- ◆ Requirement of human-study-related ethical approvals for wildlife studies
- ◆ Lack of human subject consent/breach of privacy
- ◆ Public deposition of eDNA data including human genomic data
- ◆ Inadvertent location tracking
- ◆ Inadvertent genome harvesting Potential malicious applications:
- ◆ **Genome harvesting**—the ability to illegally/unethically harvest human genomic data from local populations/ethnic groups without their knowledge or consent
- ◆ Covert accumulation of human genetic data for malicious or commercial purposes
- ◆ Genetic surveillance—individual tracking (similar to forensics/ wildlife applications)
- ◆ **Genetic surveillance—unethical tracking/locating of ethnic groups/populations**
- ◆ Genetic surveillance—potential for involuntarily genetic surveillance from investigative applications, including the recovery of bystander shed genetic information or intentional overreach
- ◆ **Bio-piracy of human genetic data from populations and countries** (akin to flora/fauna genetic bio-piracy)

# Potential beneficial applications of human eDNA as the nascent field matures

- ▶ The **discovery of novel human genetic variation** can help redress the historical imbalance in human genomic databases not spanning the range of human diversity.
- ▶ **Population-based disease risk susceptibility** studies can be carried out particularly wastewater- or air-based when coupled with active pathogen surveillance.
- ▶ Human eDNA can be a new tool **in continual health monitoring and continual personalized medicine biomarker monitoring for chronic disease management initiatives** (particularly pertinent to somatic mutations, which arise spontaneously and can be drivers of life-threatening diseases such as cancer).
- ▶ It can enable sensitive quantification and source identification of **human effluent entering and polluting waterways** and aquifers (from septic tank leaching and release of improperly treated wastewater).
- ▶ **Forensic and criminal investigative applications can aid in solving crime.** Air eDNA holds particular novel promise.
- ▶ Human eDNA can assist in the **recovery of missing persons/ deceased remains** (particularly drone-enabled air eDNA in remote locations, especially if coupled with real-time eDNA detection technology and remote reporting).
- ▶ It can help **locate sites of archaeological importance** (cryptic human remains, such as sacrificial sites in remote bogs).
- ▶ It can serve as a roadmap for **future wildlife (fauna and flora) eDNA studies.**

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

- ▶ **New modeling study of complex origin of *H. sapiens*: rejecting the long-held argument that modern humans arose from one place in Africa during one period in time.**
- ▶ Analyzed the genomes of 290 living people: **four current groups** were used: 44 new sequenced genomes from the **Nama (Khoe-San from South Africa)**, 85 from the **Mende** (from Sierra Leone), 23 from the **Gumuz** (descendants of a group from hunter-gatherers from Ethiopia) and 46 from farmers from East Africa (**Amhara and Oromo from Ethiopia**, very similar genetically); also Europeans and a Neandertal

## 2 populations

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



# A new model of the origin of human evolution in Africa

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

## *H. naledi* not a relative

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

# Arose From Multiple Closely Related Populations

- ▶ The model suggests the earliest population split among early humans that is detectable in contemporary populations occurred 120,000 to 135,000 years ago, after two or more weakly genetically differentiated *Homo* populations had been mixing for hundreds of thousands of years.
- ▶ After the population split, people still migrated between the stem populations, creating a weakly structured stem.
- ▶ This offers a better explanation of genetic variation among individual humans and human groups than do previous models.

# Stem1 and Stem2 populations

- ▶ The researchers concluded that as far back as a million years ago, the ancestors of our species existed in two distinct populations. = Stem1 and Stem2.
- ▶ About 600,000 years ago, a small group of humans budded off from Stem1 and went on to become the Neanderthals. But Stem1 endured in Africa for hundreds of thousands of years after that, as did Stem2.
- ▶ If Stem1 and Stem2 had been entirely separate from each other, they would have accumulated a large number of distinct mutations in their DNA.
- ▶ Instead, found that they had remained only moderately different — about as distinct as living Europeans and West Africans are today. The scientists concluded that people had moved between Stem1 and Stem2, pairing off to have children and mixing their DNA.

# Khoe San at 120 Ka

- ▶ The model does not reveal where the Stem1 and Stem2 people lived in Africa. And it's possible that bands of these two groups moved around a lot over the vast stretches of time during which they existed on the continent. About 120,000 years ago, the model indicates, African history changed dramatically.
- ▶ In southern Africa, people from Stem1 and Stem2 merged, giving rise to a new lineage that would lead to the Nama (Khoe San) and other living humans in that region.
- ▶ Elsewhere in Africa, a separate fusion of Stem1 and Stem2 groups took place. That merger produced a lineage that would give rise to living people in West Africa and East Africa, as well as the people who expanded out of Africa.

# Stem1 and Stem2

- ▶ It's possible that climate upheavals forced Stem1 and Stem2 people into the same regions, leading them to merge into single groups. Some bands of hunter-gatherers may have had to retreat from the coast as sea levels rose. Some regions of Africa became arid.
- ▶ Even after these mergers 120,000 years ago, people with solely Stem1 or solely Stem2 ancestry appear to have survived. The DNA of the Mende people showed that their ancestors had interbred with Stem2 people just 25,000 years ago. Stem2 was somewhere around West Africa
- ▶ Dr. Scerri speculated that living in a network of mingling populations across Africa might have allowed modern humans to survive while Neanderthals became extinct. In that arrangement, our ancestors could hold onto more genetic diversity, which in turn might have helped them endure shifts in the climate, or even evolve new adaptations. This diversity at the root of our species may have been ultimately the key to our success.

# A weakly structured stem for human origins in Africa –

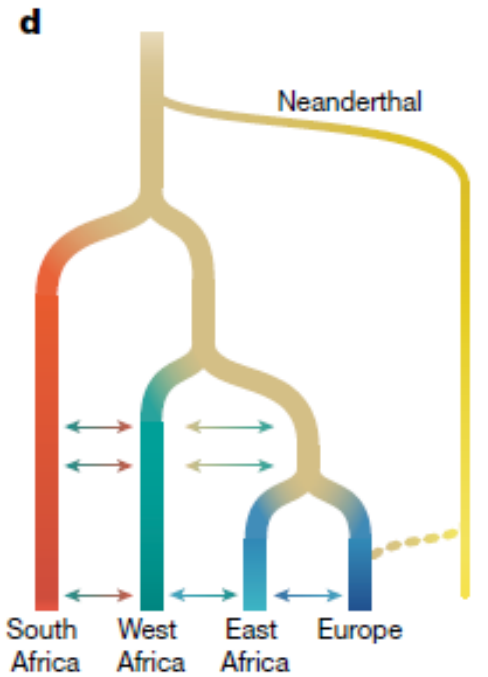
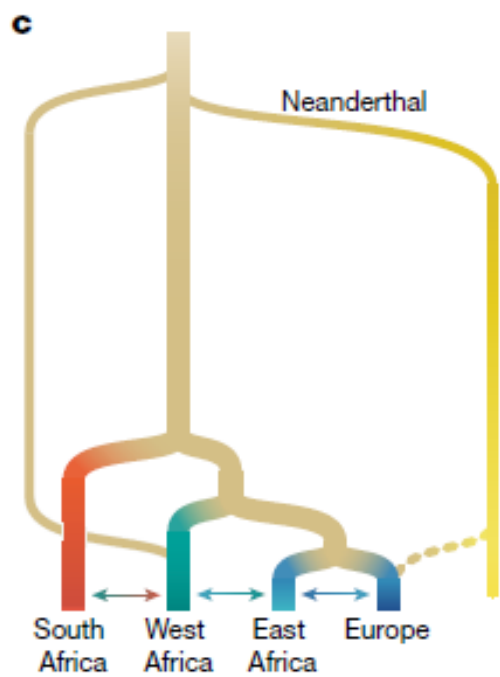
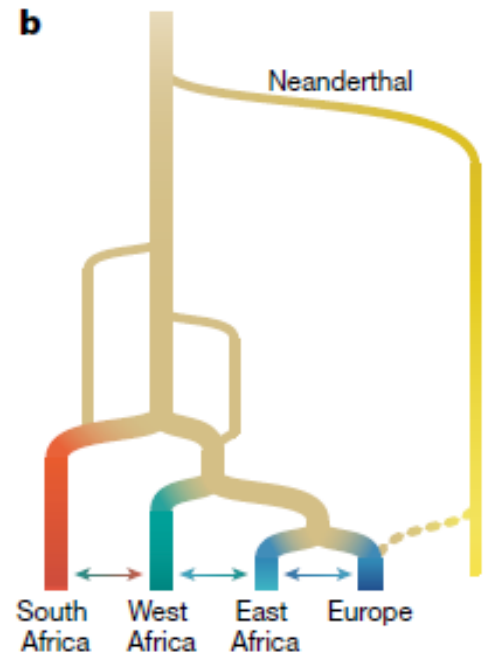
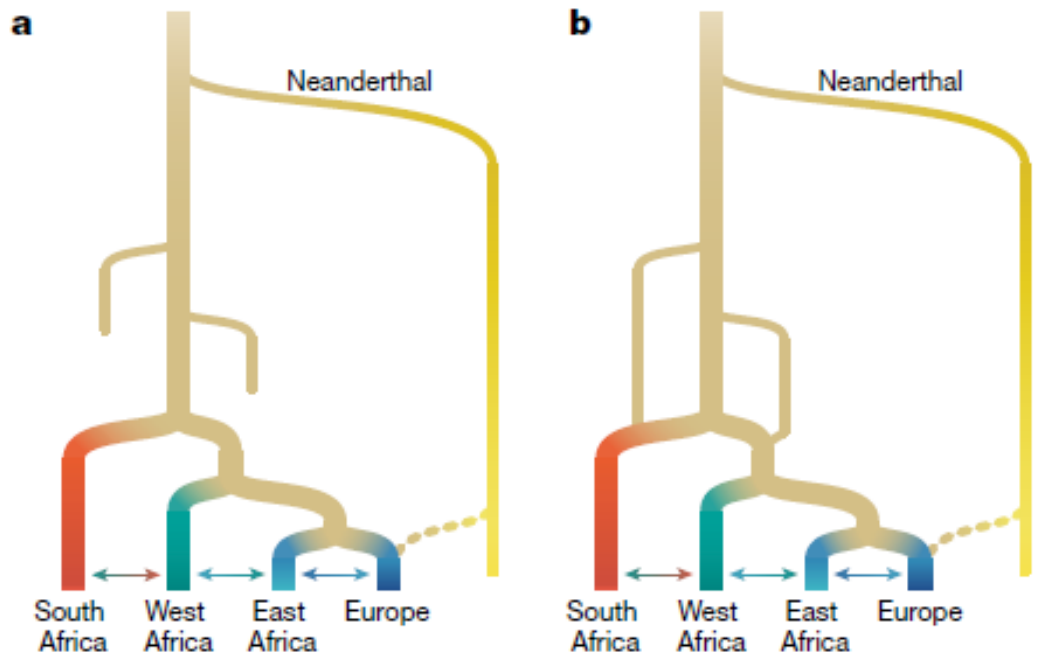
A. P. Ragsdale, et al., 2023

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

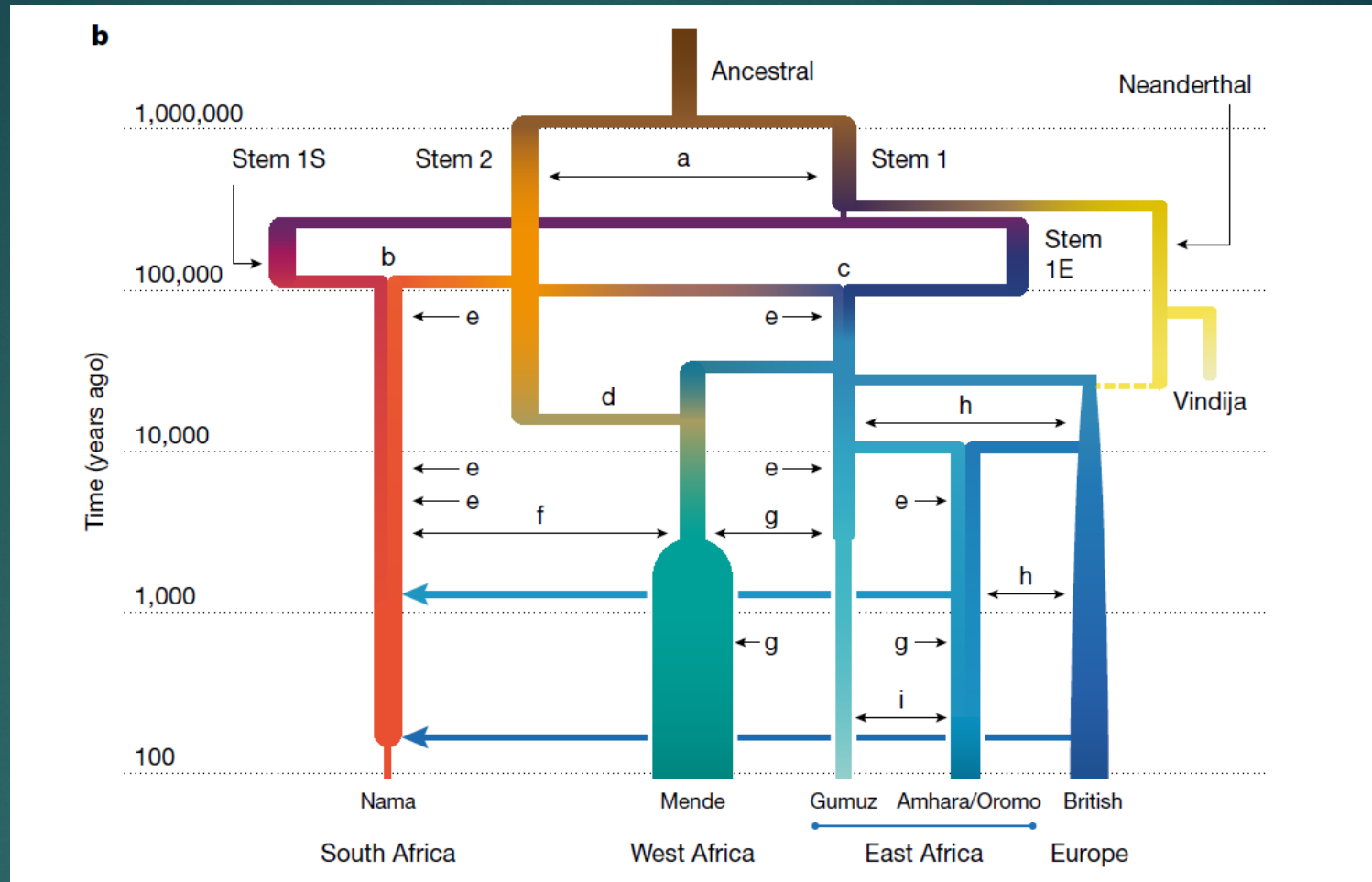
# A weakly structured stem for human origins in Africa

- ▶ Such weakly structured stem models explain patterns of polymorphism that had previously been attributed to contributions from archaic hominins in Africa.
- ▶ In contrast to models with archaic introgression, we predict that fossil remains from coexisting ancestral populations should be genetically and morphologically similar
- ▶ Only an inferred 1–4% of genetic differentiation among contemporary human populations can be attributed to genetic drift between stem populations.





- Proposed conceptual models of early human history in Africa.
- A. Recent expansion,
- B. Recent expansion with regional persistence,
- C. Archaic admixture,
- D. African multiregional.
- The models have been designed to translate models from the paleoanthropological literature into genetically testable demographic models.



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

# Mergers

- ▶ The Middle to Late Pleistocene was a critical period of change. During the late Middle Pleistocene, the multiple-merger model indicates three major stem lineages in Africa, tentatively assigned to southern (stem 1S), eastern (stem 1E) and western/central Africa (stem 2).
- ▶ Stem 1S contributes 70% to the ancestral formation of the Khoe-San. The extent of the isolation at 400 ka between stem 1S, stem 1E and stem 2 suggests that these stems were not proximate to each other.
- ▶ Models with a period of divergence, isolation and then a merger event outperformed other models with bifurcating divergence and continuous gene flow.
- ▶ We observed two merger events.
  - ▶ The first, between stem 1S and stem 2, resulted in the formation of an ancestral Khoe-San population around 120 ka.
  - ▶ The second event, between stem 1E and stem 2 about 100 ka, resulted in the formation of the ancestors of eastern and western Africans, including the ancestors of people outside Africa.

# Contrasting ancestral structure models

- ▶ Evidence for archaic hominin admixture in Eurasia has bolstered the plausibility of archaic hominin admixture having also occurred in Africa.
- ▶ Previous work that sought to explain patterns of polymorphism inconsistent with a single-origin model therefore focused on archaic hominin admixture as an **alternative model**, by referring to additional (ghost) branches required to fit the data as archaic and assuming (or inferring) deep divergences.
- ▶ A weakly structured stem model better captures the apparently inconsistent patterns of polymorphisms.
- ▶ Preferring models of a weakly structured stem to archaic-admixture models has a range of implications.
- ▶ With a weakly structured stem, there is **no need to posit that an archaic hominin population in Africa remained reproductively isolated from the ancestral human lineage** for hundreds of thousands of years before the initiation of gene flow. Instead, there would simply **have been continuous or recurrent contact between two or more groups present in Africa.**

# Models

- ▶ **Third**, multiple studies have shown a **correspondence between phenotypic differentiation**, usually assessed by measurements of the cranium, and genetic differentiation among human populations and between humans and Neanderthals.
- ▶ **This correspondence potentially allows predictions of our model to be related to the fossil record.** Some *H. sapiens* fossils, such as those from Iwo Eleru in Nigeria (13 ka), Ishango in the Democratic Republic of Congo (20–25 ka) and Nazlet Khater in Egypt (35–40 ka), have morphological features that may reflect recent gene flow from archaic hominins, and have been used in support of previously inferred archaic admixture scenarios.
- ▶ The **weakly structured stem model is not incompatible with archaic admixture having occurred in the ancestry of these fossils, but would imply, by contrast, that such individuals are unlikely to have contributed much ancestry to contemporary humans.**

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

- ▶ Contributions from archaic hominins were unlikely to have significantly affected *Homo sapiens*' evolution.
- ▶ The most morphologically divergent fossils are unlikely to represent branches that contributed appreciably to contemporary human ancestries.
- ▶ *Homo sapiens* evolved from multiple diverse populations across Africa.

# Climate effects

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

# Placental genes and schizophrenia

- ▶ The commonly shared view on the causes of schizophrenia is that genetic and environmental risk factors play a role directly and only in the brain, but these latest results show that placenta health is also critical.
- ▶ Schizophrenia genes influence a critical function of the placenta to sense nutrients in the mother's bloodstream, including oxygen, and exchange nutrients based on what it finds. The schizophrenia risk genes are more lowly expressed in the cells of the placenta that form the core of this maternal-fetal nutrient exchange, called trophoblasts, negatively affecting the placenta's role in nurturing the developing fetus.
- ▶ The paper also identifies several genes in the placenta that are causative factors for diabetes, bipolar disorder, depression, autism and ADHD. The scientists, however, found far more genetic associations with genes for schizophrenia than for any of these other disorders.



# Placenta and schizophrenia

- ▶ Also found interesting sex-based differences in the placenta risk genes. Different genes were associated with schizophrenia risk based on whether the placenta came from a male or female child.
- ▶ In pregnancies with male children, inflammatory processes in the placenta seem to play a central role. Previous research has shown males are more vulnerable than females to prenatal stress. Generally speaking, developmental disorders such as schizophrenia occur more frequently in men and boys.
- ▶ COVID-19 infection during pregnancy may be a risk factor for schizophrenia because of how infection affects the placenta.

# African DNA, or the lack thereof

- ▶ Only about 1% of genomic studies use data from people of African ancestry, and those data are mainly from African Americans
- ▶ Severe imbalance in representation of different populations in global DNA studies

# First human ‘Pangenome’



# First human 'pangenome' aims to catalogue genetic diversity

- ▶ Last complete human reference genome, mostly built on European data, known as T2T-CHM13, still doesn't reflect the genetic diversity of our species.
- ▶ More than 20 years after the first draft genome from the landmark Human Genome Project was released, researchers have published a draft human 'pangenome' — a snapshot of what is poised to become a new reference for genetic research that captures more of human diversity than has been previously available.

# Human Pangenome Reference Consortium

- ▶ The **draft genome**, published in *Nature* on May 10, was **produced by the Human Pangenome Reference Consortium**. Launched in 2019, the **international project aims to map the entirety of human genetic variation**, to create a comprehensive reference against which geneticists will be able to compare other sequences.
- ▶ Unlike human reference genome based on 1 person, **draft pangenome represents a collection of sequences from a diverse selection of 47 people from around the globe**, including individuals from Africa, the Americas, Asia and Europe. **Aims to analyze sequences from 350 people by mid-2024.**

# Pangenome project

- ▶ Human Pangenome Reference Consortium (HPRC) incorporated genomes collected from 47 individuals and their parents, with the whole group representing every continent except Antarctica.
- ▶ Added 119 million more base pairs—the building blocks of DNA—to the previously known 3.2 billion in GRCh38. The team also found 1115 new gene duplications.
- ▶ Reanalysis of 1000 Genomes Project data. Some collected from 1980s; different ethical rules then.
- ▶ Does not contain Native American samples.
- ▶ Open access of data; big Pharm can use it

# People from Polar Regions Have Bigger Brains

- ▶ CJV: Note Neandertal large eye orbits and larger occipital region.
- ▶ The higher in latitude a current person lives, the bigger his or her brain and eyeballs will be.
- ▶ The larger brains and eyeballs **lend** better visual acuity in areas that receive less sunlight than equatorial regions.
- ▶ The additional brain matter is needed for the extra visual processing.
- ▶ The increase in brain and eye size allows people to see better in places that receive less light than areas closer to the equator. The effect is most extreme at the poles.

# Bigger brains and eyes

- ▶ Someone living on the Arctic Circle would have an eyeball that is 20 percent larger than someone living on the equator per Robin Dunbar
- ▶ People living at high latitudes have greater visual acuity than those who live at the equator
- ▶ The whole point is that they need to have better vision to compensate for the lower light levels at high latitudes
- ▶ Found significant positive relationships between absolute latitude, orbital volume and brain size.
- ▶ Brain size isn't necessarily correlated with intelligence?



# Higher latitude and light exposure

- ▶ Larger brains of high latitude humans doesn't mean they're smarter, it just means they have increased the size of brain areas dedicated to vision, and this has increased brain size overall
- ▶ Only light exposure explained the size differences, even when climate was factored in.

# The causal influence of brain size on human intelligence

- ▶ **People with bigger brains tend to be smarter.** There exists a moderate correlation between MRI-measured brain size and the general factor of IQ
- ▶ **Highly significant within-family correlation between head circumference and intelligence performance (g)**
- ▶ **SNPs in the human genome that are associated with intracranial volume also tend to be associated with both years of education and IQ**

# The causal influence of brain size on human intelligence

- ▶ When the average number of cortical neurons is the measure of brain size, then humans are by far the top-ranked species
- ▶ Neuron number is causally correlated with g.
- ▶ Average level of g in human lineage has increased over the last several million years as a result of **evolution by natural selection**

# The human brain in numbers: a linearly scaled-up primate brain

- ▶ **Suzana Herculano-Houzel, 2008**: New methodology: brain converted to neuronal soup; computer count of number of nuclei
- ▶ Brain size can no longer be considered a proxy for the number of neurons in the brain; no assumptions about body–brain size relationships required.
- ▶ Human cerebral cortex:
  - ▶ holds only 19% of all brain neurons;
  - ▶ cerebellum = 81%; as in most mammals;
  - ▶ except elephants = 251 billion neurons in the cerebellum and only 5.6 billion neurons in the cortex.

# Suzana Herculano-Houzel, 2008

- ▶ Human brain = 86 billion neurons; 85 billion non-neuron cells
- ▶ Human cortex = 16 billion neurons; 19% of neurons;
- ▶ Human cerebellum = 69 billion neurons; 81% of neurons; 10% of brain mass
- ▶ Human Brain is a linearly scaled-up primate brain in its number of neurons with just the expected number of neurons for a primate brain of its size

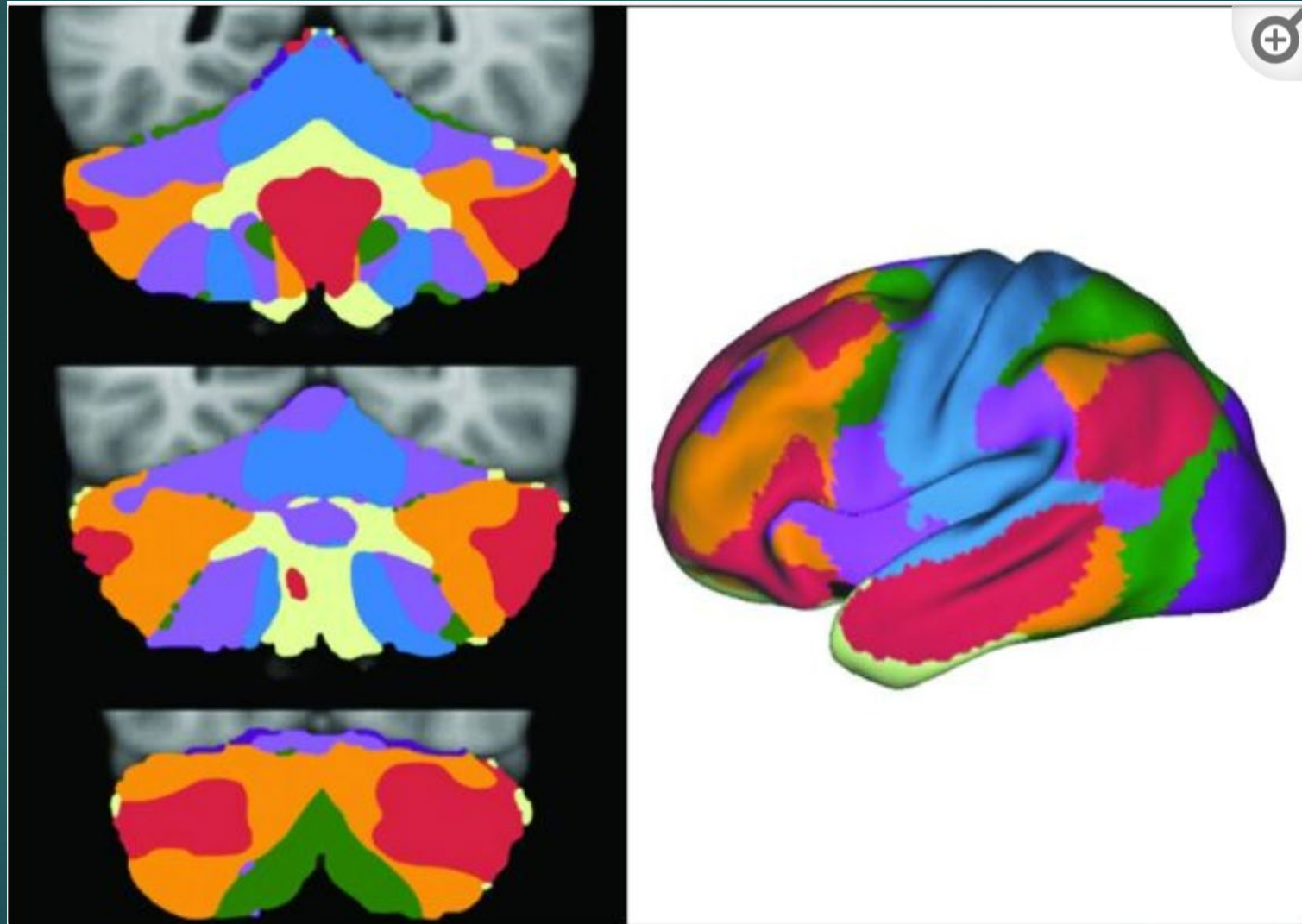
# Human neuron number

- ▶ The **cognitive abilities of a primate**, and of other mammals and birds for that matter, are **directly related to the number of neurons in its brain**.
- ▶ Oft quoted “there are 10× more glial cells than neurons in the human brain” is false.
- ▶ Glial cells in the human brain are at most 50% of all brain cells.

# Cerebellum: modern understandings of its functions

- ▶ Why did the lateral aspect of the human cerebellum, the cerebellar hemispheres, undergo enormous enlargement during the course of human evolution?
- ▶ Why did this lateral cerebellar growth seem to parallel the evolutionary enlargement of the prefrontal cortex?
- ▶ Study: Human evolution was, characterized by increasing technological complexity as well as social complexity. The cerebellum is particularly likely to have played a role in technological complexity, through its involvement in the learning of sensory-motor skills, imitation, and production of complex sequences of behaviors, such as those involved in making and using tools.
- ▶ It underpinned the evolution of humans' advanced technological capacities, which in turn may have been a preadaptation for language.

**Cerebellum:** associative learning with emotional tasks located in the medial zone (yellow). Motor tasks locate to the intermediate zone (orange), and cognitive tasks occupy most of the cerebellar hemisphere in the lateral zone (beige).





# Current concepts of functional anatomy of the cerebellum

- ▶ 2020 Study: The majority of the functions of the cerebellum are involved with non-motor association function. The cerebellum contributes to diverse distinct central nervous system functions including **motor**, **language**, **working memory**, **executive function**, **autonomic**, and **affect**.
- ▶ The majority of the cerebellum specializes in non-motor functions with **connectivity to multimodal association areas of cerebral cortex**
- ▶ Connectivity to association cerebral cortex. Overall, the size of regional connections between the cerebellum and cerebrum are relatively proportionate. Specific regions of the cerebellum have been found to participate in intrinsic connectivity networks of the brain such as the default mode, salience, and executive networks

# Functions of cerebellum

- ▶ **Language function** localizes to the right posterior lobe of the cerebellum. **Visuospatial function** localizes to the left posterior cerebellar hemisphere. **Working memory** function maps to the left posterior cerebellar hemisphere. **More than half of the cerebellar cortex is interconnected with association zones** of the cerebral cortex. **Executive functions** seem to be bilateral.
- ▶ In addition to its **direct role in motor control**, the cerebellum is necessary for several types of motor learning, most notably learning to adjust to changes in sensorimotor relationships.
- ▶ **Motor Specialty** = turning conscious actions into unconscious automatic actions including motor control and learning of motor coordination

# Cerebellum

- ▶ Cerebellum has been implicated in the regulation of many differing functional traits such as affection, emotion including emotional body language perception and behavior.
- ▶ The litany of other psychiatric disorders now associated with cerebellar pathology includes bipolar disorder, posttraumatic stress disorder, attention deficit autism spectrum disorders, and schizophrenia
- ▶ Cerebellum's function is best understood as predictive action selection based on "internal models" of the environment or a device for supervised learning

# No relative expansion of the number of prefrontal neurons in primate and human evolution

- ▶ Expansion of numbers of cortical neurons in human and nonhuman primate evolution occurred in a similar manner across the cortex, without an increase in the relative number of neurons in the prefrontal region, and without a relative increase in the number of cells in the prefrontal white matter.
- ▶ One thing that distinguishes the human brain from other primate brains is thus not the relative size of its prefrontal cortex but its absolute number of neurons.
- ▶ Prefrontal region of both human and nonhuman primates holds about 8% of cortical neurons
- ▶ The most distinctive feature of the human prefrontal cortex is its absolute number of neurons (1.3 billion), not its relative volume.

# No relative expansion of the number of prefrontal neurons in primate and human evolution

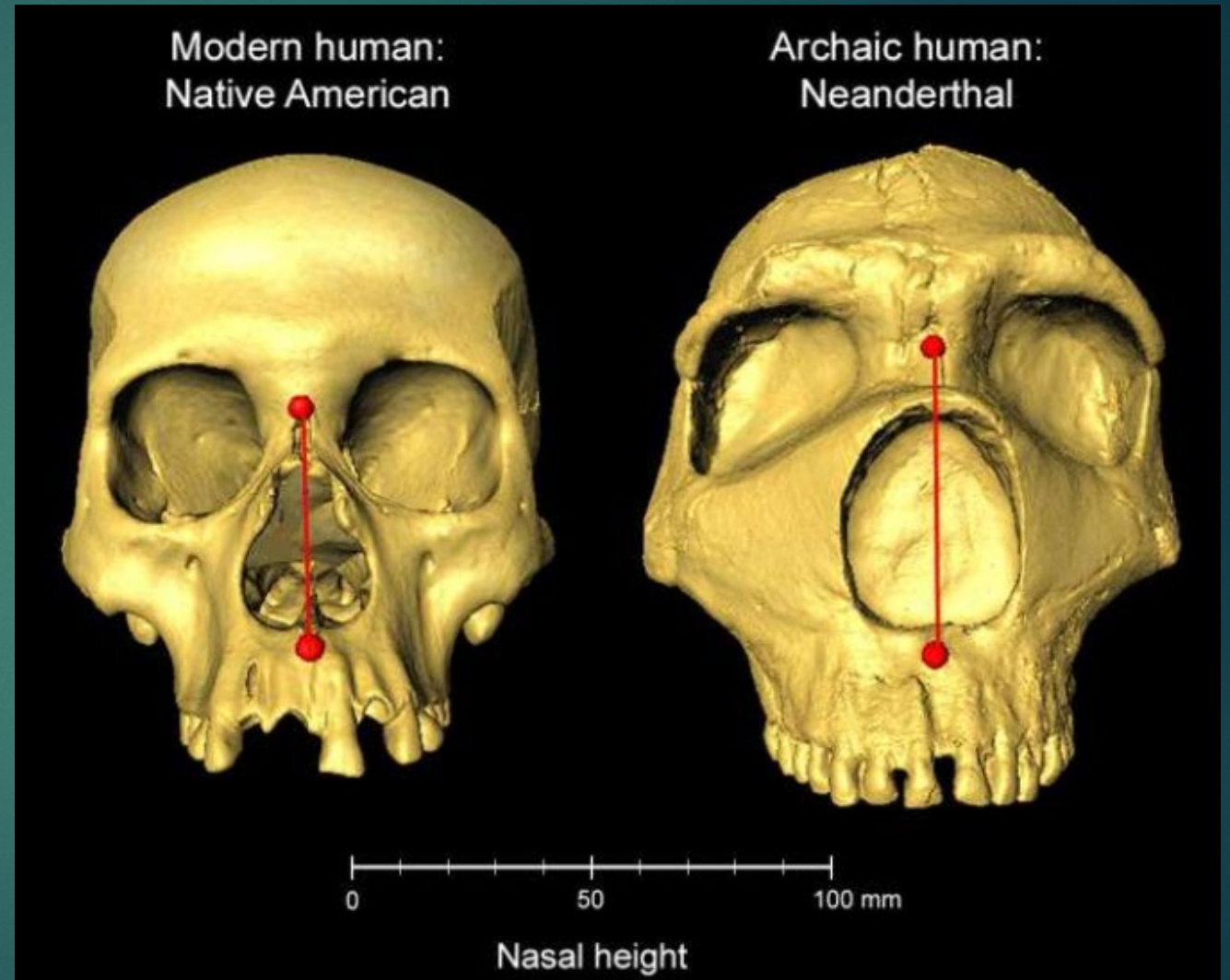
- ▶ Primate evolution did not involve a shift in the distribution of cortical neurons toward prefrontal regions.
- ▶ Our findings thus concur with the conclusion of Barton and Venditti that human frontal cortex is not proportionately larger than expected for a nonhuman primate of our cortical size, with no evidence of a relative enlargement of the human prefrontal white matter.
- ▶ We propose that the larger absolute number of neurons in human prefrontal, associative cortical regions is the main factor underlying the complexity of our cognitive abilities in comparison with other primates, and possibly all other mammals

# Are Bigger Brains Smarter? Evidence From UK Biobank

- ▶ A positive relationship between brain volume and intelligence has been suspected since the 19th century, and empirical studies seem to support this hypothesis
- ▶ New sample of adults from the UK Biobank that is about 70% larger than the combined samples of all previous investigations on this subject ( $N = 13,608$ )
- ▶ Robust association between total brain volume and fluid intelligence ( $r = .19$ ); found a positive relationship between total brain volume and educational attainment ( $r = .12$ ). These relationships were mainly driven by gray matter (rather than white matter or fluid volume)

# Nose shape gene inherited from Neanderthals

- 6,000 volunteers across Latin America, of mixed European, Native American and African ancestry
- 33 genome regions associated with face shape
- In one genome region in particular, called *ATF3*, the researchers found that many people in their study with Native American ancestry (as well as others with east Asian ancestry from another cohort) had genetic material in this gene that was inherited from the Neanderthals, contributing to increased nasal height.
- They also found that this gene region has signs of natural selection, suggesting that it conferred an advantage for those carrying the genetic material.



# Eli Lilly's Donanemab = a success; but safety issues

- ▶ Analysis of nearly 1,200 people Alzheimer's patients with high amyloid beta but low tau burden in the early stages of the disease, Donanemab slowed the progression of symptoms by 35 percent over a period of 18 months compared to placebo.
- ▶ Side effects included temporary swelling in parts of the brain, which occurred in 25% of patients, as well as microhemorrhages that occurred in 31 percent of patients on the treatment arm and 14 percent of patients in the placebo group. In 6 percent of people, it was symptomatic. The microhemorrhages known as ARIA-H occurred in 31 percent of people on drug. Most concerning, 1.6 percent of participants had serious ARIA. 3 deaths. Not due to anticoagulants.
- ▶ Major validation of the theory that removing amyloid beta does improve the course of the disease
- ▶ These are the strongest phase 3 data for an Alzheimer's treatment to date



## Complex requirements for any anti-amyloid Tx:

- ▶ **Diagnosis:** at UCSF, not just doctor's decision; require committee approval for Tx
  - ▶ PET, CSF = biomarker of AD (BA presence)
  - ▶ Cognitive testing (MMSE < 22); memory problem
  - ▶ must be MCI dx (cognitive difficulties, but still functionally independent); not a full dementia dx (incompetent without help)
- ▶ **IV Infusions** every 2 weeks
- ▶ **MRIs 4 x a year:** to monitor ARIA sx's (brain swelling or microbleeds)
- ▶ **Cost** = \$26,500/year; if FDA gives full approval, then Medicare pays 80%; you = \$5000; + 20% of cost of MRIs; currently won't pay except for study

# Anti-amyloid Alzheimer's drugs create brain atrophy

- ▶ Review of 31 published clinical trials of so-called anti-amyloid Alzheimer's drugs. Indicate they can cause brain atrophy
- ▶ It also links the brain shrinkage to the brain swelling, which often presents without symptoms.
- ▶ Trial participants taking these Alzheimer's drugs often developed more brain shrinkage than when they were on a placebo
- ▶ Eisai = greater cortical volume loss on lecanemab relative to placebo, those reductions may be due to antibody clearing the protein beta amyloid from the brain, and reducing inflammation. But that's sheer speculation
- ▶ Lecanumab recorded a 28% greater brain volume loss relative to placebo after about 18 months. This translated to a loss of an extra 5.2 milliliters (mL) in brain matter. Also increase in the size of brain ventricles (by 36%)
- ▶ Higher rate of ARIA also generated a bigger average increase in the size of the ventricles.

# Internet usage and the prospective risk of dementia

- ▶ Dementia-free adults aged 50 to 65 for a maximum of 17 (median=7.9) years using the Health and Retirement Study.
- ▶ In 18,154 adults, regular internet usage was associated with approximately half the risk of dementia compared to non-regular usage,
- ▶ The difference in risk between regular and non-regular users did not vary by educational attainment, race-ethnicity, sex, and generation.
- ▶ Regular internet users experienced approximately half the risk of dementia than non-regular users. Being a regular internet user for longer periods in late adulthood was associated with delayed cognitive impairment, although further evidence is needed on potential adverse effects of excessive usage.

## 29 Ka Denisovan pendant



Archaeologists wore gloves, masks, and coveralls when they excavated the pendant, and they put it in a plastic bag without removing the sediment clinging to it, which reduced contamination.

# 25 Ka tooth pendant from Denisova Cave: a bath removes DNA



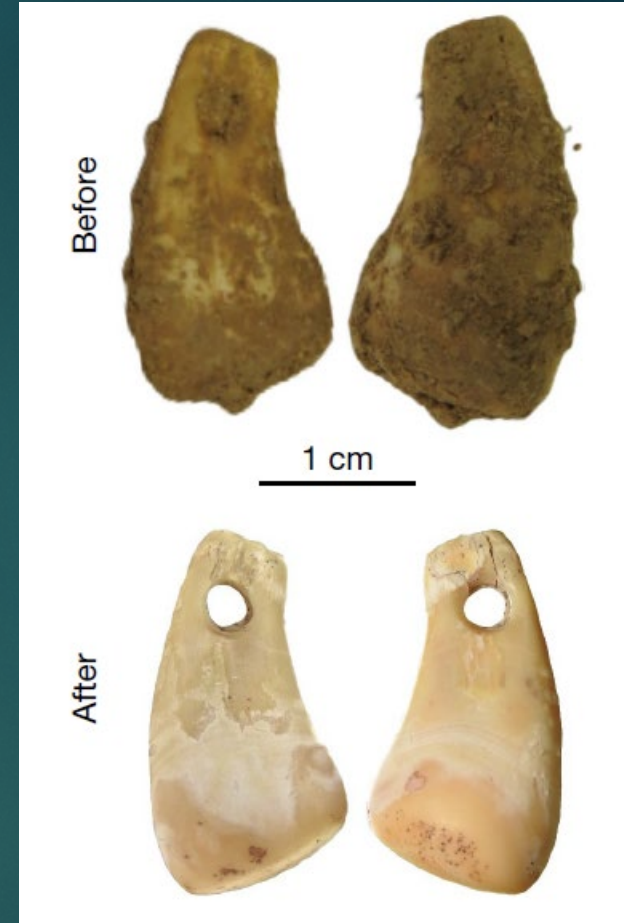
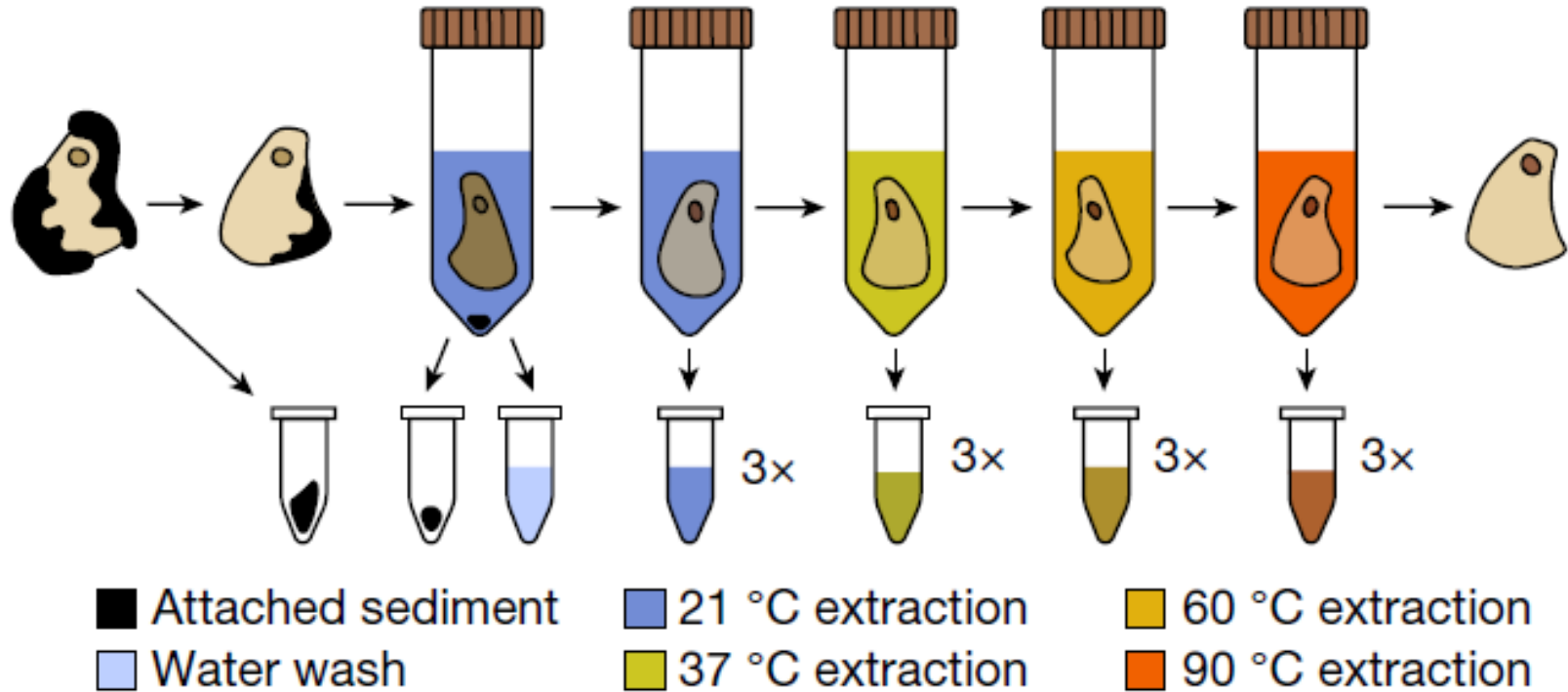
Both the woman and the deer, a species of elk (*Cervus canadensis*) known as wapiti, lived sometime between 19,000 and 25,000 years ago and that the woman was of Siberian heritage.

## 25 Ka pendant at Denisova Cave: increasingly warmer baths

- ▶ Retrieval of human DNA from a Paleolithic pendant (pierced deer tooth contained a single hole) and discovered that it belonged to a Siberian woman who lived roughly 19 to 25,000 years ago.
- ▶ This is the first-time scientists have successfully isolated DNA from a prehistoric artifact using a newly developed extraction method: increasingly warm salt solution baths; unlike other methods, does not destroy the artefact.

# New DNA bath methodology: 5 years of trial and error with different chemicals and methods

a



Teeth are ideal because they are porous and absorb DNA; they contain hydroxyapatite, which is known to adsorb DNA and reduce its degradation by hydrolysis and nuclease activity

# Don't contaminate your finds

- ▶ Only tells you the last person to handle an artefact, not maker.
- ▶ “Please, please, please wear gloves and face masks if you want to look at the DNA of the people who were making these things and using them.”
- ▶ Final answer to whether Neanderthals or modern humans made the famous Châtelperronian ornaments in France?



We now know which parts of the genome are important in building a mammal.

- ▶ 11 new papers in the journal Science: Zoonomia Project = 240 mammal genomes. One elephant, 43 primates, 53 rodents and more than 100 other creatures sampled; represents less than 1 percent of all living mammals.
- ▶ By pinpointing parts of the mammalian genome that have been conserved, remained the same through tens of millions of years of evolution, helping to identify the most crucial parts of our shared genetic makeup, those where change can spell disaster.
- ▶ Largest genome= Screaming hairy armadillo = 5.3 billion base pairs. Smallest = bent-wing bat, with 2 billion base pairs. Humans = 3 billion base pairs.

# Zoonomia

- ▶ Comprehensive analysis using Zoonomia data shows two events — the breakup of the continents more than 100 million years ago and the dinosaur-killing asteroid afterward — each sparked a round of mammal diversification.
- ▶ Studied more than 10,000 short sections of genetic code that are found in all other mammals but not in humans. Genetic deletions became conserved in all humans. These deletions created new genetic encodings that eliminated elements that would normally turn genes off. These 10,000 genetic deletions specific to humans and linked some of them to the function of neurons.
- ▶ Some key deletions take place near genes that have been linked to distinctly human diseases, such as schizophrenia and bipolar disorder

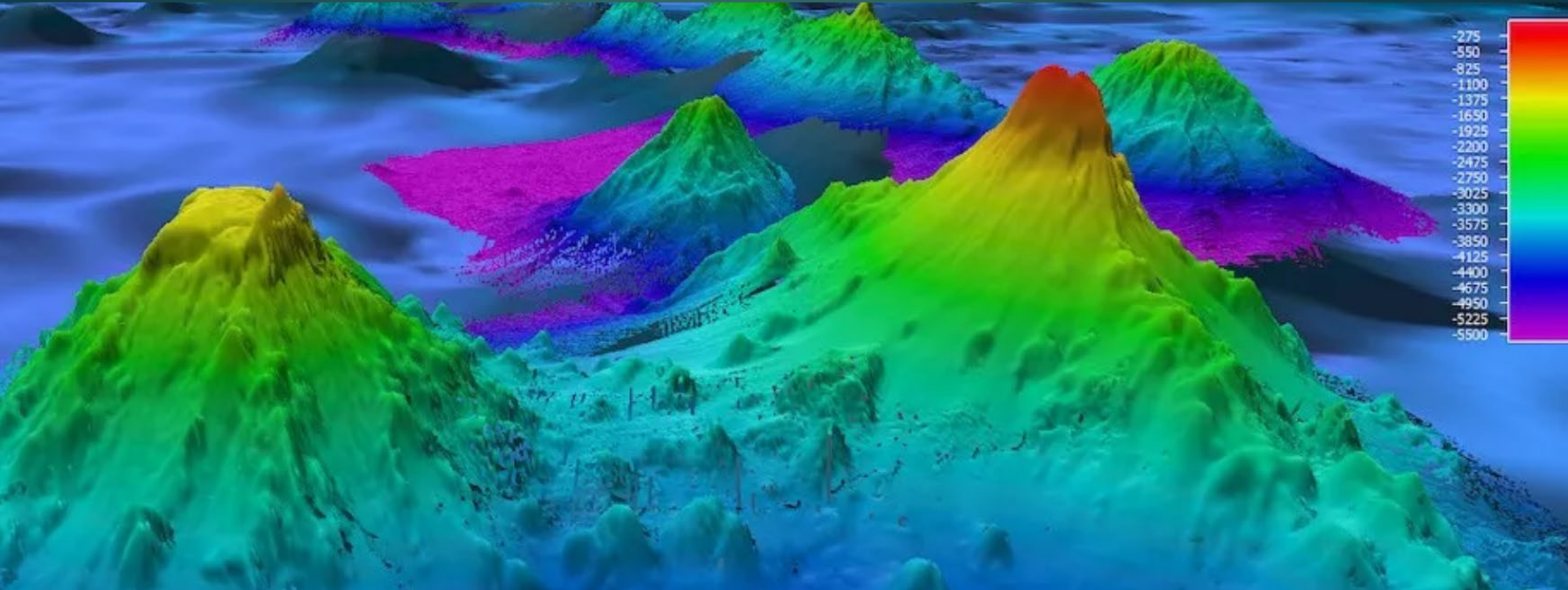
# Zoonomia

- ▶ 10% of the human genome is highly conserved across species, with many of these regions occurring outside of protein-coding genes; regulatory DNA. More than 4,500 elements are almost perfectly conserved across more than 98% of the species studied.
- ▶ Most of the conserved regions—which have changed more slowly than random fluctuations in the genome—are involved in embryonic development and regulation of RNA expression.
- ▶ Regions that changed more frequently shaped an animal's interaction with its environment, such as through immune responses or the development of its skin.
- ▶ Identified a few exceptional traits in the mammalian world, such as extraordinary brain size, superior sense of smell, and the ability to hibernate during the winter.

# Zoonomia

- ▶ Less than 5% of all mammalian species have reference genomes,
- ▶ Conservation analysis: species with **historically low populations are most likely to go extinct**. Mammals with fewer genetic changes at conserved sites in the genome were at greater risk for extinction
- ▶ Famous sled dog Balto, who was reported to have led a team of sled dogs in the final leg of the race to carry a life-saving serum to Nome, Alaska, in 1925. Not a wolf; no genetic recessives of modern dogs

# 19,000 new volcanos discovered underwater

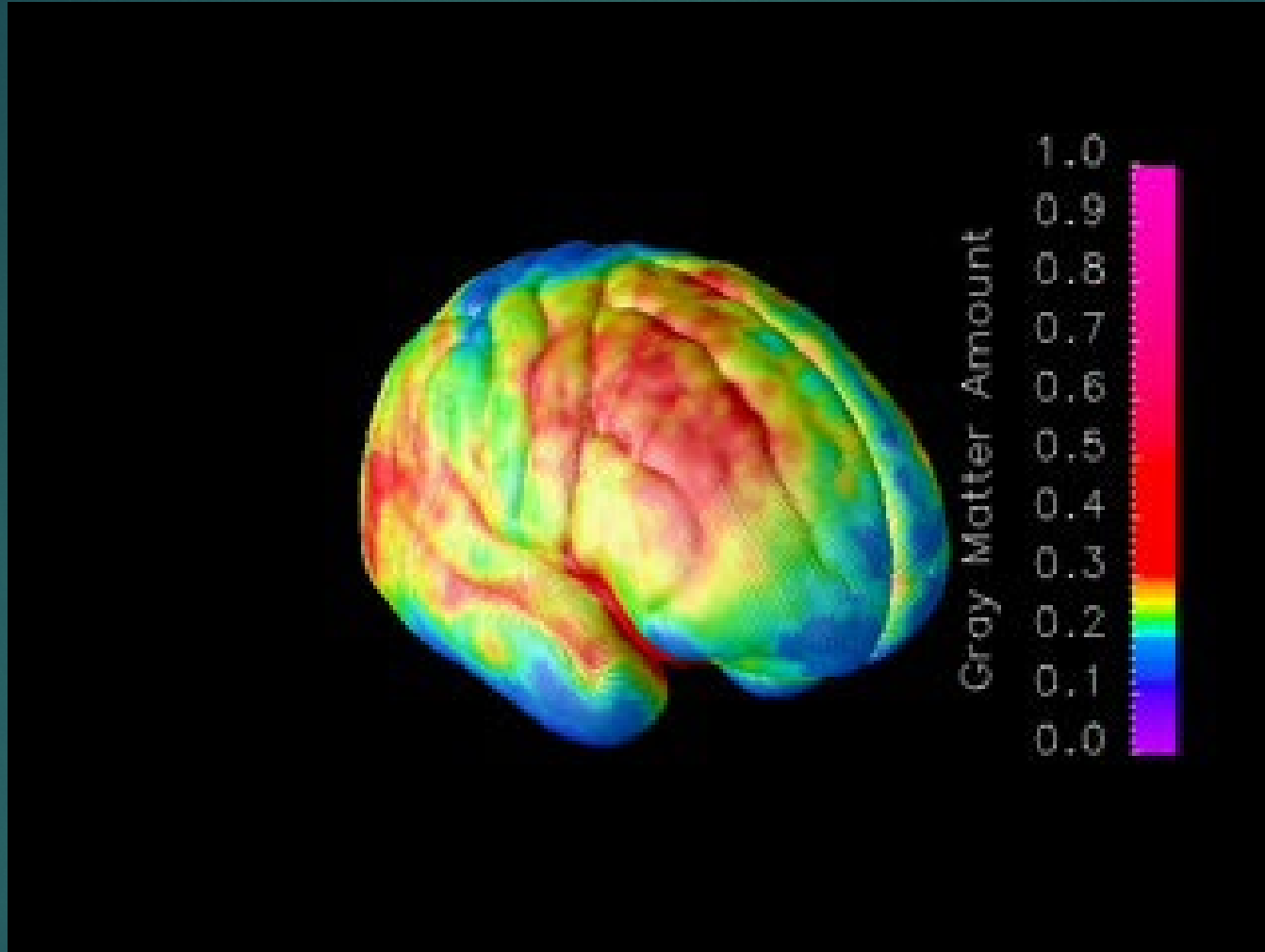


A 2011 sonar census found more than 24,000 seamounts, or undersea mountains formed by volcanic activity. However, there are more than 27,000 seamounts that remain uncharted by sonar, according to the Science article.

# Great Brain Pruning



## Teen Brain: age 5 to 21 = normal pruning



Lose 50% of all synaptic connections;  
Motor areas first, frontal last

# Innate Immune System: Complement pruning

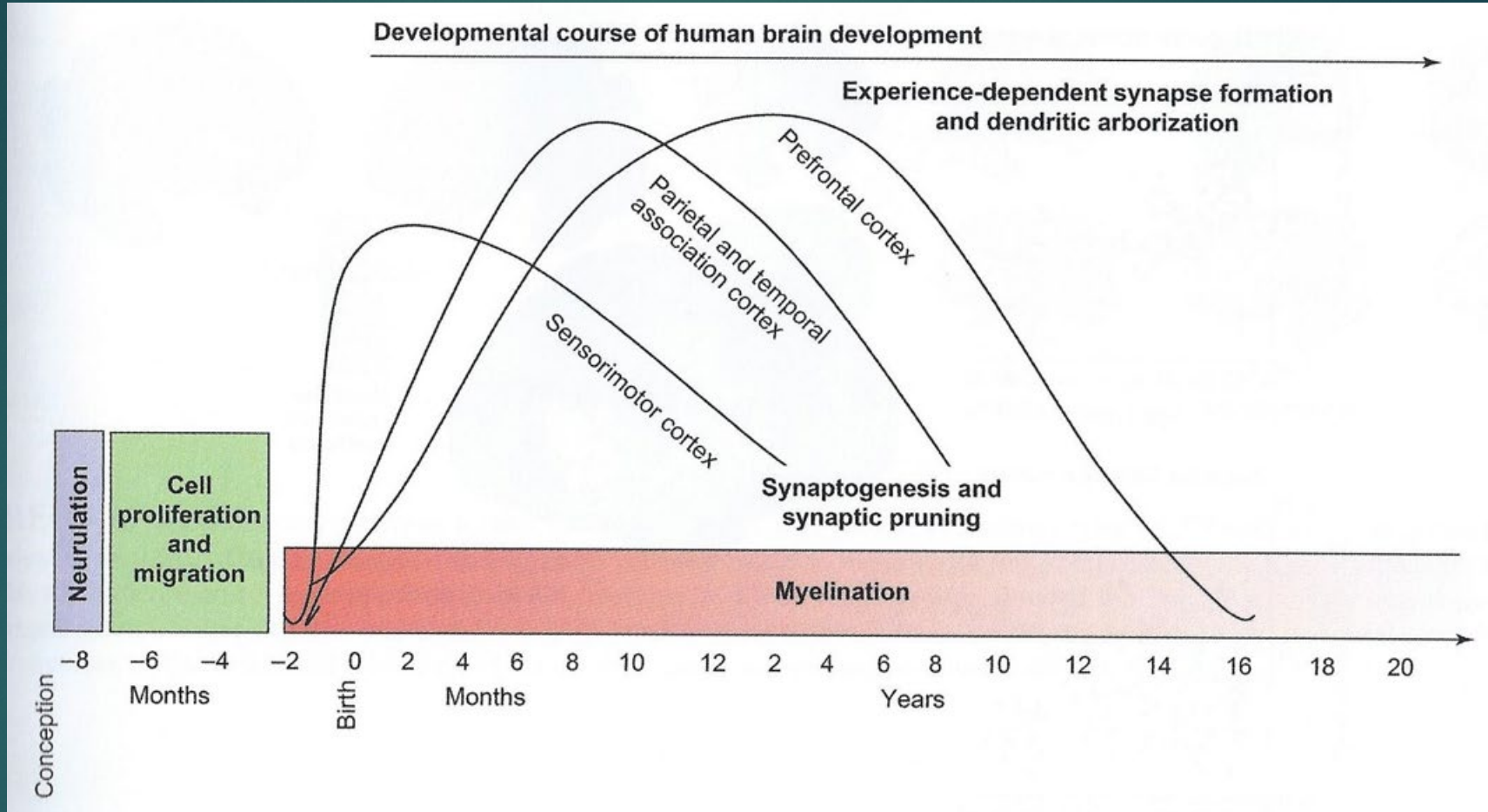
- ▶ Complement system enhances (complements) the ability of antibodies and phagocytic cells to clear microbes and damaged cells from an organism
- ▶ The C4 gene is part of “the complement cascade,” a process by which the immune system marks tumors, viruses, or dying human cells for elimination and removal.
- ▶ Role in brain development: the system helps to “prune” unneeded or unused synaptic connections, sculpting the brain into a more efficient structure.
- ▶ Complement molecules serve as an “eat me” signal, summoning microglia to converge on unused synapses and prune them away.



# Complement System

- ▶ Complement pruning has been found in
  - ▶ Normal adolescent brain maturation
  - ▶ In schizophrenia,
    - ▶ excessive activity of the complement system results in inappropriate pruning length –
    - ▶ more C4 present, the higher the risk of developing schizophrenia:
    - ▶ excessive levels of the protein could lead to over pruning and to the thinning out of brain tissue that appears to coincide with the worsening of schizophrenia symptoms
- ▶ In memory disorders: Pathogens induce complement activation and result in in presynaptic terminal loss in hippocampus resulting in memory loss:
  - ▶ Amyloid plaques in Alzheimer's
  - ▶ HIV
  - ▶ West Nile virus infections

# The Great Pruning: A leaner brain is a better brain



Not enough pruning: Intellectually challenged & autistics have significantly more synaptic connections than gifted do; Too much pruning: schizophrenia, ADHD

# Newfound 'brain signature' linked to multiple psychiatric disorders

- ▶ Young adults with multiple mental illnesses may share a common neurological "signature".
- ▶ Identified patterns of brain wiring that seem to be linked to a person's risk of having multiple psychiatric disorders. Identified specific patterns of brain connectivity tied to symptoms of psychiatric disorders.
- ▶ N = 1,300 14-year-olds followed to age 19, yearly fMRIs. Patterns of functional connectivity — a measure of the strength of connections between different brain regions — in the teens' brains.

# Risk of multiple psychiatric conditions

- ▶ They then looked at how these patterns were associated with behavioral symptoms linked to eight different mental disorders. Produced a neuropsychopathological (NP) factor score.
- ▶ Four of the disorders were "externalizing," or disorders where the associated behaviors tend to be related to interactions with others, including autism spectrum disorder, attention-deficit/hyperactivity disorder (ADHD), conduct disorder, and oppositional defiant disorder.
- ▶ The other four were internalizing disorders, whose effects tend to be directed inward, toward oneself. These included generalized anxiety disorder, depression, eating disorders and specific phobias.

# Pruning disorder produces dysfunctional more hyper-connected brain

- ▶ This finding hints that high NP factors could reflect a developmental issue affecting the synapses.
- ▶ Participants with high NP factors did not show the typical patterns of synaptic "pruning" during adolescence, in which the brain reduces the number of synapses so that its information processing can become more efficient.
- ▶ Instead, these teens had a hyperconnected brain circuit centered in the prefrontal cortex, a trait sometimes associated with deficits in executive function, or a person's ability to plan and accomplish everyday tasks and goals. (Similar hyperconnectivity has been linked to autism)

# High NP factor

- ▶ "Brain signature" could be used to predict whether a person was at high risk for both sets of behaviors. The team established the NP factor at age 14 and then validated their work by checking whether this pattern was predictive of participants' behaviors at age 19.
- ▶ Participants with high NP factors showed increased connectivity in several areas of the prefrontal cortex
- ▶ Found that having a high NP factor was linked to carrying a gene variant associated with both ADHD and major depressive disorder

# Lack of neuron 'pruning' may be behind many brain-related conditions

- ▶ Brain scans show that **adolescents with more symptoms of certain mental health conditions, autism or ADHD have undergone less pruning than usual** of synaptic connections between neurons
- ▶ Many disparate conditions, such as depression, phobias and attention deficit hyperactivity disorder (ADHD), may have the same underlying cause: a delay in "pruning", a process in which unneeded connections between brain cells disappear.

# Lack of prefrontal pruning

- ▶ People who had the highest scores for these psych. conditions, indicating stronger symptoms, were more likely to have greater density of synaptic tissue in the prefrontal cortex.
- ▶ This, say the researchers, indicates a lack of, or delay in, pruning in their brains.



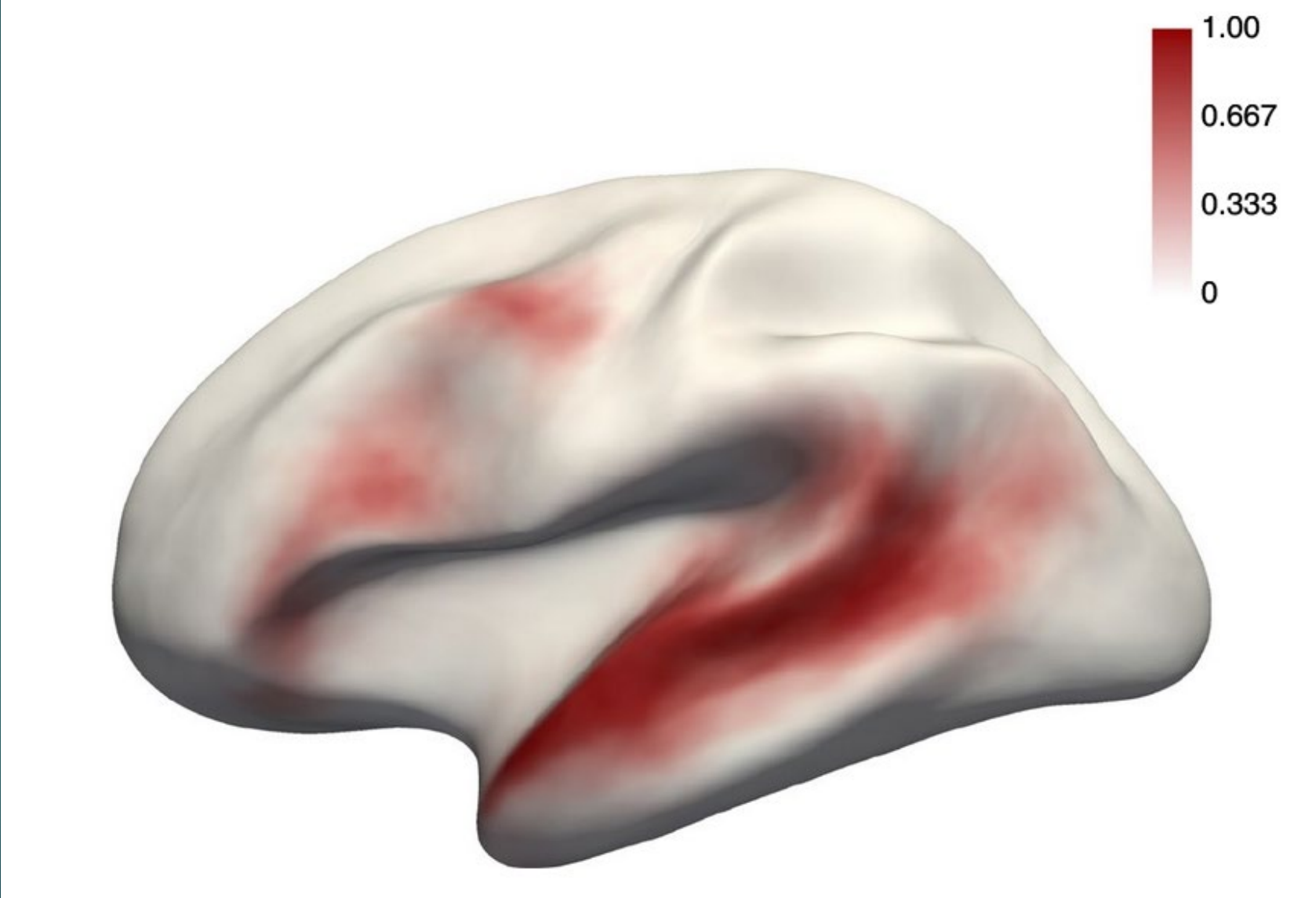
# Same neurobiological root

- ▶ Same network of brain connections that underly six psychiatric disorders — schizophrenia, bipolar disorder, depression, addiction, OCD and anxiety
- ▶ Study of regions where gray matter had atrophied, or shrunk, in the context of psychiatric disorders. Anterior cingulate and insula showed up often.
- ▶ All of the atrophied regions hooked up to a common brain network.

# Brain's language network

- ▶ Japanese, Italian, Ukrainian, Swahili, Tagalog and dozens of other spoken languages cause the **same "universal language network" to light up in the brains of native speakers.**
- ▶ This hub of language processing has been studied extensively in English speakers, but now neuroscientists have confirmed that the exact same network is activated in speakers of 45 different languages representing 12 distinct language families.
- ▶ In native English speakers, the brain areas that activate during language processing appear mostly in the left hemisphere of the brain, primarily in the frontal lobe and in the temporal lobe.
- ▶ These same brain areas activated regardless of the language being heard.

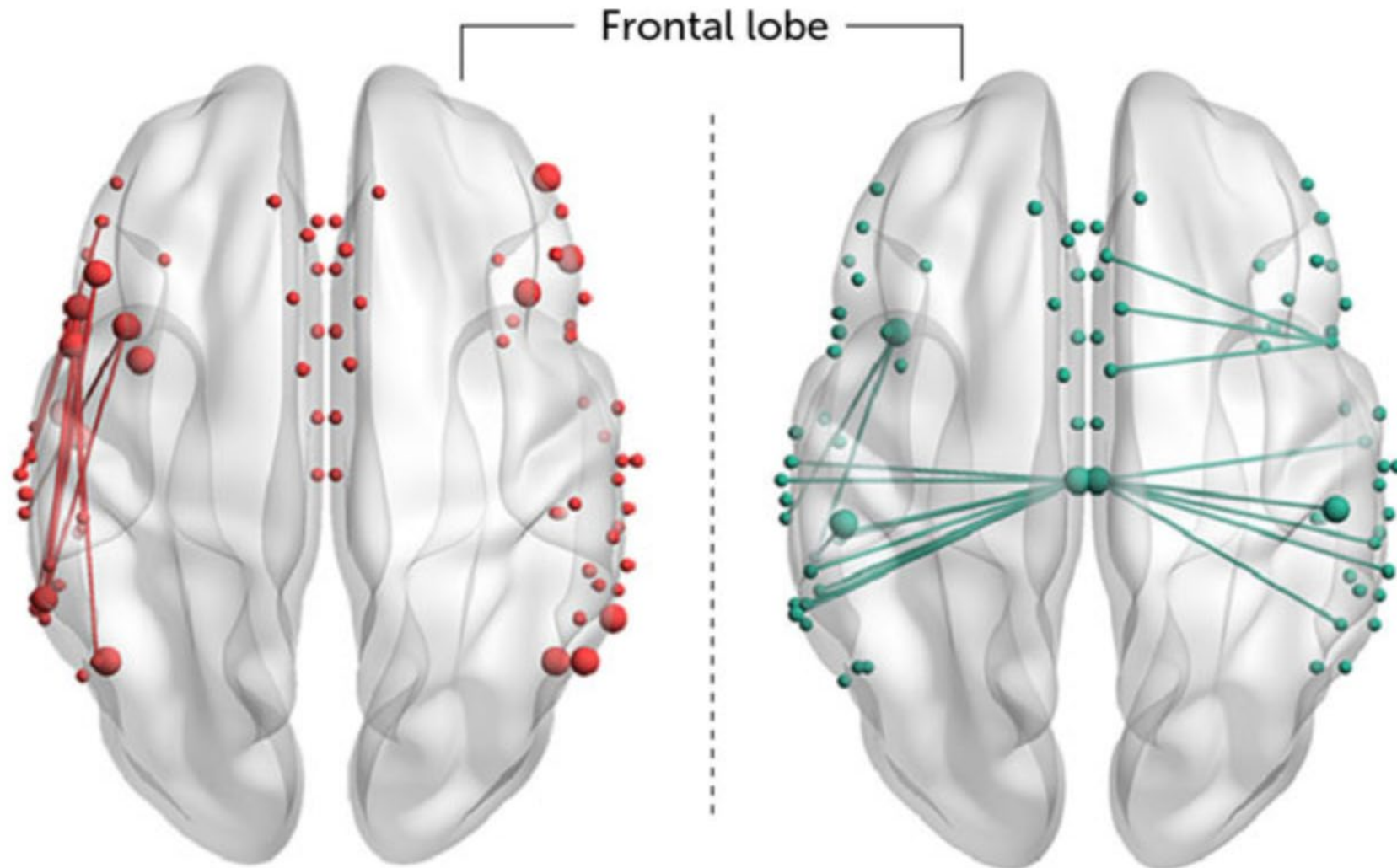
# Language areas



# Languages have different wiring routes in the brain

- ▶ German and Arabic native speakers have different connection strengths in specific parts of the brain's language circuit
- ▶ The cognitive demands of our native languages physically shape the brain
- ▶ Our brains process language in a constellation of **brain regions connected by white matter**. This tissue routes long, cablelike nerve cells from one part of the brain to another and speeds up communication between them. Wiring brain regions together this way is part of how we learn: The more often we use a connection, the more robust it becomes.
- ▶ **Arabs tended to have stronger white matter connections across their left and right hemispheres**, the scans revealed, whereas the **German speakers had a denser network of connections within the left hemisphere**.

## Differences in language circuit connectivity in German and Arabic speakers



The brains of German native speakers (left) had stronger white matter networks (red lines) within the left hemisphere. The brains of Arabic native speakers (right) had denser networks (cyan lines) bridging the two hemispheres. Each sphere represents a different part of the language circuit, with its size showing how central it is

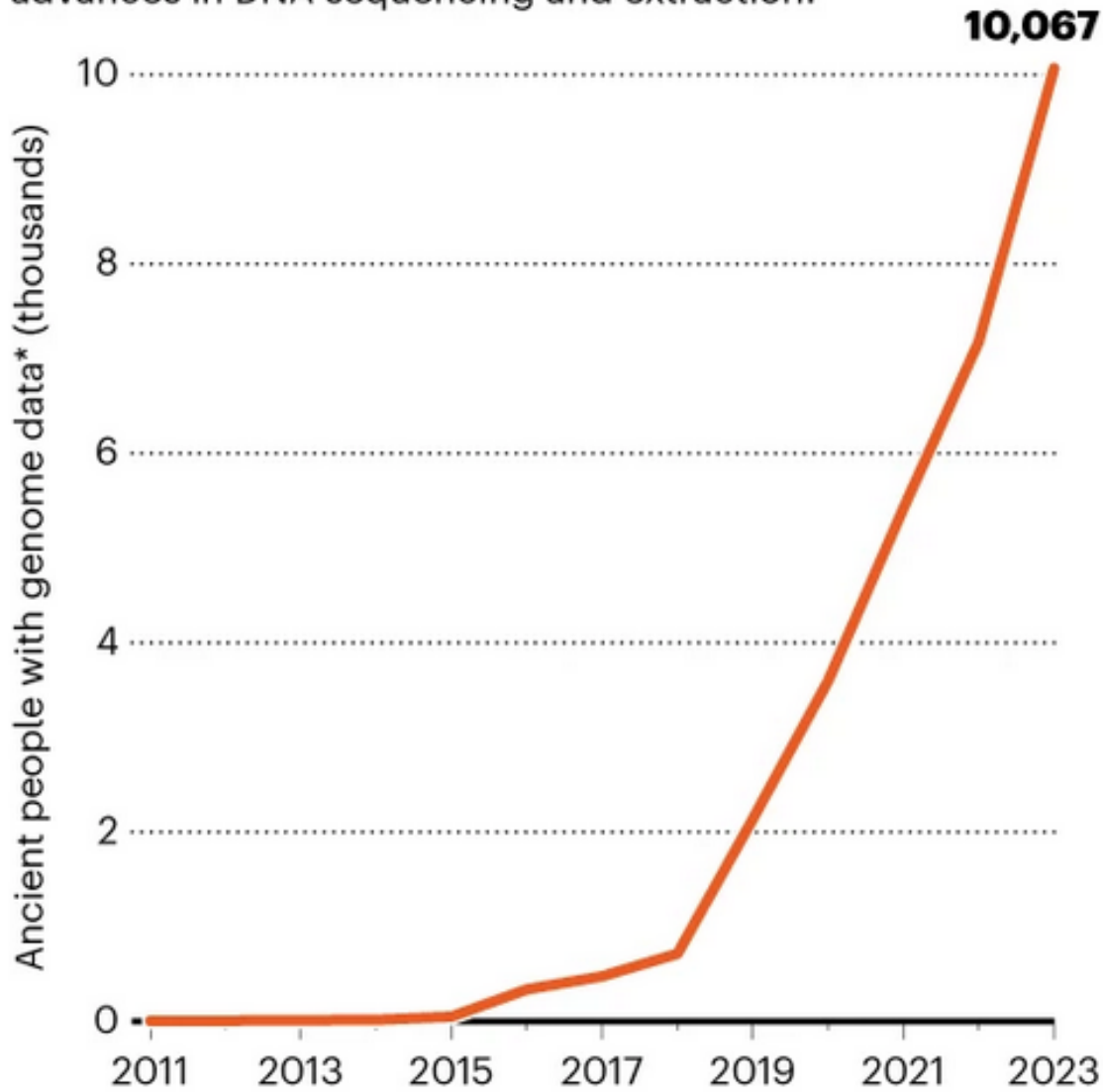
# 'Truly gobsmacked':

## Ancient-human genome count surpasses 10,000

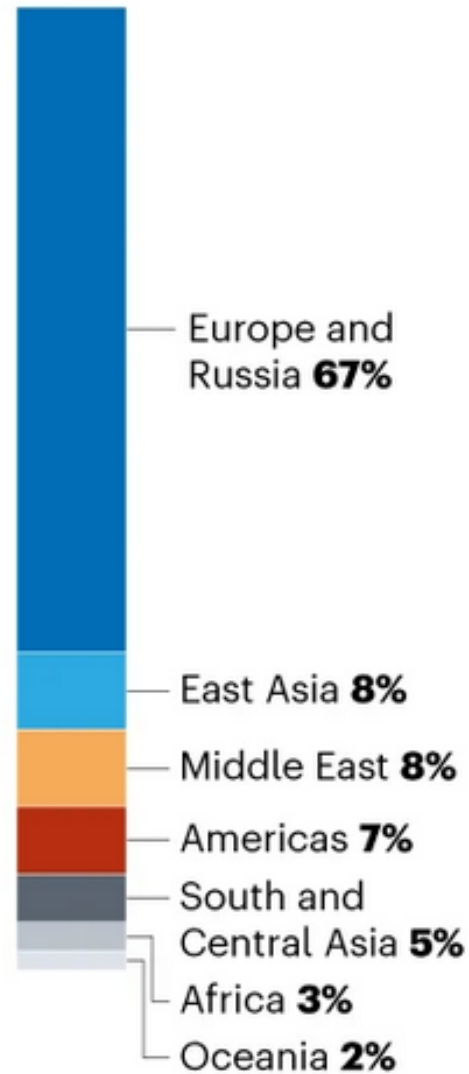
- ▶ The majority of sequences come from people who lived in Western Eurasia, but samples from other regions are on the rise.
- ▶ In 2010, researchers published the first genome sequence from an ancient human, using tufts of hair from a man who lived around 4,000 years ago in Greenland.
- ▶ In the 13 years since, scientists have generated genome data from more than 10,000 ancient people — and there's no sign of a slowdown.
- ▶ Reich: Harvard - maintains a database of published ancient-human genome data, called the **Allen Ancient DNA Resource**

# ANCIENT-DNA GOLDRUSH

The quantity of genome data from ancient-human remains has grown rapidly since 2018, owing to advances in DNA sequencing and extraction.



## Geographical distribution

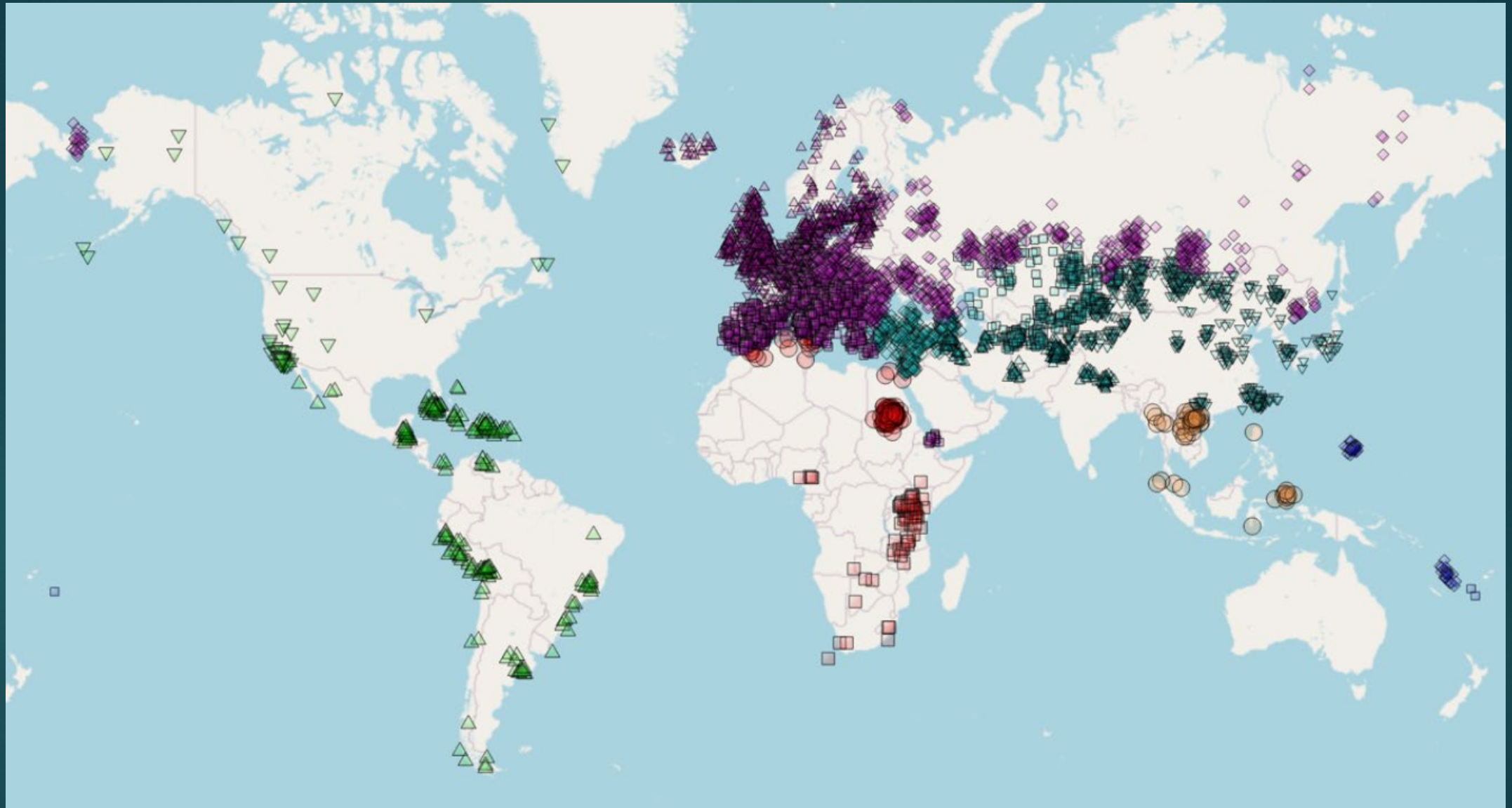


Researchers sequence a set of one million DNA bases that tend to vary between people, instead of an entire genome, which is much costlier.

# New Genomes

- ▶ Propelled by **a focus on more recent samples from the 12,000 years since the last ice age ended**, which are more abundant and tend to have higher-quality DNA than older human remains.
- ▶ The **vast majority of ancient-human genomes come from people who lived in Western Eurasia**, an area encompassing Europe, Russia and the Middle East.
- ▶ Sampling from other regions, particularly East Asia, Oceania and Africa, is becoming more frequent. Africa's centrality to the human story means that it is especially important for its proportion to grow





Where the genomes come from

## 3 labs = 80% of aDNA

- ▶ Nearly 80% of ancient-human genome sequences in the database come from just three institutions:
  - ▶ 1 - Reich at his Harvard lab: 50% of the total
  - ▶ 2 - Eske Willerslev - University of Copenhagen, Denmark
  - ▶ 3 - Svante Pääbo - two Max Planck Institutes, Germany.
- 
- ▶ More than **two hundred papers** have reported genome-wide data from ancient humans.

# Evolution of cortical geometry and its link to function, behavior and ecology

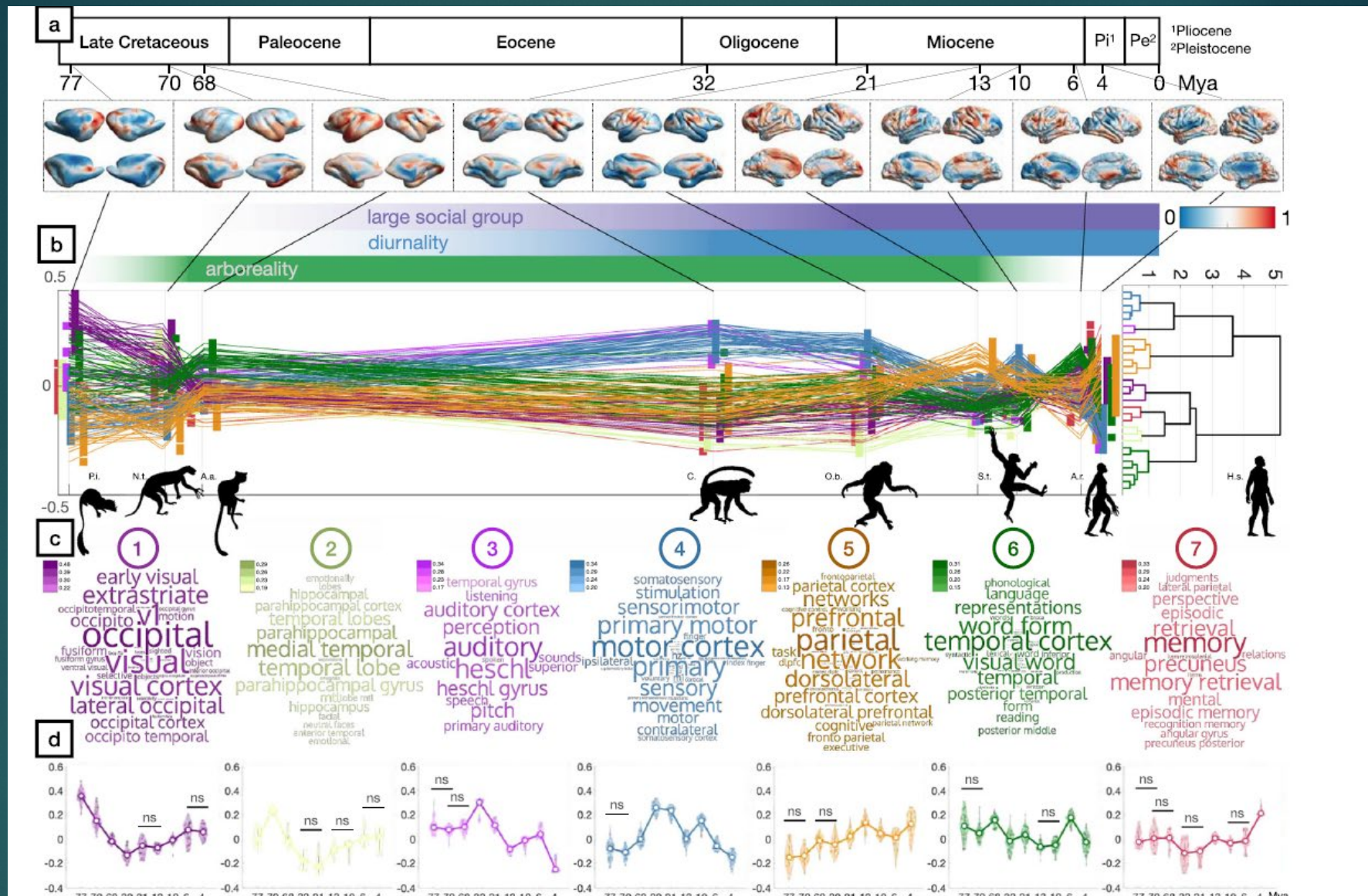
- ▶ Study the relationship between the shape of the cerebral cortex and the topography of its function.
- ▶ Established a joint geometric representation of the cerebral cortices of ninety species of extant Euarchontoglires (rodents, primates)
- ▶ Show that variability in surface geometry relates to species' ecology and behavior, independent of overall brain size.

# Ecological and behavioral factors

- ▶ Analysis of habitats ordered from arboreal to terrestrial to fossorial species that revealed a sequential decrease in relative cortical expansion in visual, motor, frontal parietal as well as default mode related areas
- ▶ Morphology of the cerebral cortex reflects ecological and behavioral factors that pose specific cognitive demands to individual species
- ▶ Evolutionary adaptation to specific environmental niches and neuroplasticity of the cerebral cortex cause individual cortical areas to become more attuned to specific types of sensory processing.
- ▶ In extant species, this adaptation was successful and resulted in increases in overall body and brain size. The combination of these effects leads to an expansion of cross-modal processing regions and a segregation of sensory processing regions.

# Localized evolutionary cortical expansion in Homo

- ▶ 7 distinct evolutionary components of the morphological evolution of the human cerebrum.
- ▶ Starting with the
  - ▶ expansion of visual areas,
  - ▶ followed by parahippocampal regions in the late Cretaceous,
  - ▶ auditory and sensorymotor areas in the early Oligocene until the mid-Miocene and
  - ▶ finally expansion of association areas in the late Miocene and Pliocene up until the present day.



Abbreviations: P.I. Ptilocercus iowii. N.t. Notharctus tenebrosus. A.a Archicebus achilles, C. Cercopithecoidea, O.b. Oreopithecus bambolii, S.t. Sahelanthropus tchadensis, A.r. Ardipithecus ramidus, H.s. Homo sapiens.

# Arboreality vs sociality

- ▶ Cortical surfaces locate the time point of maximum correlation between cortical expansion and large group size (ACC, cingulate, cingulate cortex) at the divergence between Homininae and Ponginae, some 12 Ma.
- ▶ Compared to other great apes, orangutans (Pongo) are more arboreal and less social. These results are indicative of an indirect influence of decreasing arboreality in African apes on brain evolution.
- ▶ Possible explanations for this relationship lie in evolutionary advantages in predator avoidance posed by congregating in larger groups in a more terrestrial habitat.
- ▶ While more arboreal apes can rely on the safety of their habitat, more terrestrial species have to more actively secure their environment by forming large social groups.

# Conflict, violence, and warfare among early farmers in Northwestern Europe

- ▶ Bioarchaeological evidence of interpersonal violence and early warfare presents important insights into conflict in past societies.
- ▶ Compiling data from various sources, it becomes apparent that **violence was endemic in Neolithic Europe, sometimes reaching levels of intergroup hostilities that ended in the utter destruction of entire communities.**
- ▶ Patterns emerge that see conflict likely fostered by increasing competition between settled and growing communities, e.g., for access to arable land for food production.



# Neolithic violence

- ▶ The study of 2,363 individuals from 180 sites in the United Kingdom, Denmark, France, Germany, northern Spain and Sweden, dated between 8-4 ka ago, shows that more than 10% had wounds caused by weapons, indicating a high degree of Violence and conflict in the Neolithic period of northwestern Europe
- ▶ Determines that for Northwestern Europe at least, the conception of the “**peaceful Neolithic**” is dead.. In recent times, Stephen Pinker’s widely read and frequently cited but also criticized work took the position that aggregate levels of violence have been in decline for centuries. The predominantly historical sources on which Pinker’s thesis was based become progressively less distinct with increasing distance from the present, and his study virtually omits the Neolithic skeletal record in his assertions.
- ▶ The current study and other recent publications regarding the Neolithic present a strong case for this period possibly representing a high watermark of human violence.

\*\*\* Ancient DNA and multimethod dating confirm the late arrival of AMHs in southern China at 50 Ka, not 120 Ka

- ▶ Some paleoanthropologists have argued that Chinese MH fossil discoveries from Huanglong, Zhiren, Luna, and Fuyan caves in southern China indicate one or more prior dispersals, perhaps as early as ca. 120 ka.
- ▶ We investigated the age of the human remains from three of these localities and two additional early AMH sites. Although U–Th dating of capping flowstones suggested they lie within the range ca. 168 to 70 ka, analyses of aDNA and direct AMS <sup>14</sup>C dating on human teeth from Fuyan and Yangjiapo caves showed they derive from the Holocene (11.7 K).
- ▶ OSL dating of sediments and AMS <sup>14</sup>C analysis of mammal teeth and charcoal also demonstrated major discrepancies from the flowstone ages.

## AMH in southern China: 50 Ka not 120 Ka

- ▶ In this instance, the use of U–Th dating on cave flowstone to infer the arrival time of AMHs in southern China has produced erroneously old ages and resulted in a false conflict between fossil and genetic data. While some paleoanthropologists believe that AMHs settled this region during the interval ca. 120 to 70 ka, our research shows otherwise.
- ▶ Our work highlights the surprisingly complex depositional history recorded at these subtropical caves which involved one or more episodes of erosion and redeposition or intrusion as recently as the late Holocene. In light of our findings, the first appearance datum for AMHs in southern China should probably lie within the timeframe set by molecular data of ca. 50 to 45 ka.

Early presence of *Homo sapiens* by 86-68 Ka in Southeast Asia at Tam Pà Ling cave, Northern Laos.

- ▶ Previous discoveries from Tam Pà Ling cave (Laos) identified *H. sapiens* in Southeast Asia by 46 Ka.
- ▶ Analysis reveals a depositional sequence spanning ~ 86 Ka.
- ▶ New frontal bone fossil TPL 6 confirms the presence of *H. sapiens* by  $70 \pm 3$  kyr, and TPL 7 extends this range to  $77 \pm 9$  kyr, supporting an early dispersal of *H. sapiens* into Southeast Asia.

- ▶ The TPL 6 frontal, described here for the first time, provides direct evidence of an early, possibly unsuccessful, dispersal from Africa or the Near East towards Southeast Asia by 70 Ka.
- ▶ TPL 6 is remarkably gracile implying that it descended from a gracile immigrant population and not the outcome of local evolution from, or admixture with, *H. erectus* or Denisovans.
- ▶ Together with the recent local discovery of a Denisovan molar in northern Laos, as well as fossils attributed to *H. erectus*, *H. floresiensis* and *H. luzonensis*, Southeast Asia is proving to be a region that was rich in Homo diversity in the Middle to Late Pleistocene.

## Early African exits: pre 60 Ka

- ▶ Fossil and archaeological evidence for early range expansions include the famous sites of Skhul and Qafzeh in Israel and more recent finds in the eastern Mediterranean, Arabian Peninsula, East and Southeast Asia, and Australia.
- ▶ Fossils from Apidima Cave in Greece and Misliya Cave in Israel., dated to around 210 kyr and 180 Ka respectively, have been described as the earliest *H. sapiens* outside of Africa predating the Skhul and Qafzeh fossils by at least 60,000 years, and in Saudi Arabia a phalanx from Al Wusta is dated to ca. 90 Ka.
- ▶ Further East, fossils predating 50 Ka are mainly teeth from the Chinese sites of Fuyan Cave (120 – 80 kyr) Huanglongdong (100 – 80 kyr), Lunadong (127 – 70 kyr), and Zhirendong (116 – 106 kyr) = dates are all being reassessed

## Early African pre 60 Ka exits – some with questionable dating

- ▶ A recent attempt to verify the dating of several of these sites by Sun et al. presented a number of issues including inaccurate radiocarbon estimations, misattribution to Homo of a sampled tooth, potential contamination in genetic analyses and incorrect provenience.
- ▶ Similarly, the modern looking cranium from Liujiang has been dated within the range of ca. 139 to 68 kyr, however its provenience is uncertain.
- ▶ Other Late Pleistocene sites where modern humans were found include Lida Ajer in Sumatra, dated to 73 – 63 kyr, which yielded two teeth attributed to H. sapiens, and Tam Pà Ling in northern Laos, where a handful of cranio-mandibular and more fragmentary postcranial remains span the period of 70 – 46 kyr.

## Early African pre 60 Ka exits

- ▶ Finally, **Madjedbebe**, the oldest archaeological site in Australia is dated to 65 Ka.
- ▶ Taken together these findings suggest a more complex pattern of dispersal that is hard to reconcile with current genetic evidence unless these early dispersals represent unsuccessful colonization's.



# N hearing ability at Sima de los Huesos imply they spoke

- ▶ The Sima de los Huesos cochleae fossils show a very primitive morphology, indicating that Homo sapiens and Neanderthal cochleae evolved separately, from originally different anatomies, to similar morphology.
- ▶ This evidence indicates that the hearing of our species and that of Neanderthals evolved separately to end up hearing in the same way.
- ▶ That is, the external and middle ear of our species is indistinguishable from that of Neanderthals, while the external and middle ears of the Sima people were more primitive, although already clearly different from that of the oldest hominins (such as australopithecines). .

# N hearing

- ▶ The result of this evolution is that Neanderthals and we have great acoustic sensitivity to the same sounds.
- ▶ What could those sounds be so important that the ears of both species adapted to hearing them with great sensitivity?
- ▶ All available evidence indicates that these sounds were the same sounds we use today to communicate verbally: vowels and consonants. The consequence is immediate: Neanderthals used the same sounds as us to communicate; that is, they spoke.

# DNA Confirms Oral History of Swahili People

- ▶ DNA shows 'Persian Princes' helped found medieval African trading culture.
- ▶ One seemingly fanciful account dates from the 1500s, when Arab chroniclers recorded the stories Swahili people told about their origins. According to one version, known as the Kilwa Chronicle, seven Persian princes fleeing persecution set sail from the trading hub of Shiraz. After washing up on the coast of Africa, they founded a dynasty that ruled the Swahili coast for centuries.
- ▶ A genetic analysis of dozens of ancient skeletons from East Africa helps pin down the origins of coastal Swahili society.  
A long history of mercantile trade along the eastern shores of Africa left its mark on the DNA of ancient Swahili people.

# Swahili People

- ▶ A new analysis of centuries-old bones and teeth collected from **six burial sites across coastal Kenya and Tanzania** has found that, around 1,000 years ago, local African women began having children with Persian traders — and that the **descendants of these unions gained power and status in the highest levels of pre-colonial Swahili society.**
- ▶ Suggest that long-told origin stories, passed down through generations of Swahili families, may be more truthful than many outsiders have presumed.
- ▶ The **genetics corroborate the Swahili people's own history that they tell about themselves, not what others were saying about them.**

# Persian princes

- ▶ The urban peoples of the Swahili coast traded across eastern Africa and the Indian Ocean and were among the first practitioners of Islam among sub-Saharan people
- ▶ Report ancient DNA data for 80 individuals from 6 medieval and early modern (ad 1250–1800) coastal towns and an inland town after ad 1650.
- ▶ More than half of the DNA of many of the individuals from coastal towns originates from primarily female ancestors from Africa, with a large proportion—and occasionally more than half—of the DNA coming from Asian ancestors.

# Persian princes

- ▶ The Asian ancestry includes components associated with Persia and India, with 80–90% of the Asian DNA originating from Persian men.
- ▶ Peoples of African and Asian origins began to mix by about ad 1000, coinciding with the large-scale adoption of Islam. Before about ad 1500, the Southwest Asian ancestry was mainly Persian-related, consistent with the narrative of the Kilwa Chronicle, the oldest history told by people of the Swahili coast<sup>3</sup>. After this time, the sources of DNA became increasingly Arabian, consistent with evidence of growing interactions with southern Arabia.

# Persian princes

- ▶ Evidence of predominantly male Southwest Asian ancestors mixing with predominantly female African and, to a much lesser extent, female Indian ancestors in the lineages of medieval people on the Swahili coast.
- ▶ Many towns grew immensely wealthy thanks to a vibrant trading network with merchants who sailed across the Indian Ocean on the monsoon winds. Middle Eastern pottery, Asian cloths and other luxury goods came in. African gold, ivory and timber went out — along with a steady flow of enslaved people, who were shipped off and sold across the Arabian Peninsula and Persian Gulf.
- ▶ The Kiswahili language, which is Bantu in origin but borrows heavily from Indian and Middle Eastern tongues.

## mtDNA = African; Y chromosome = Persian

- ▶ They **generally preferred their own origin story**, one in which princes from present-day Iran (then known as Persia) sailed across the Indian Ocean, married local women and enmeshed themselves into East African society. Depending on the narrative source, that story dates to around 850 or 1000 — the same period during which genetic mixing was underway, according to the DNA analysis.
- ▶ **mtDNA gene sequences were overwhelmingly African in origin.**
- ▶ **Y chromosome was Asian DNA that the researchers found was common in modern-day Iran. So, a large fraction of Swahili ancestry presumably came from Persian men.**



# Cultural absorption

- ▶ The picture that emerges is one of Persian men mixing with African women at multiple locations along the Swahili Coast around the turn of the first millennium, with each group contributing about half of the genes that are found in Swahili people today.
- ▶ In East Africa, Persian customs never came to dominate. Instead, most foreign influences — language, architecture, fashion, arts — were incorporated into a way of life that remained predominantly African in character, but with social strictures, kinship systems and agricultural practices that reflected Indigenous traditions.
- ▶ One major caveat to the study: Nearly all the bones and teeth came from ornamental tombs that were located near grand mosques, sites where only the upper class would have been laid to rest.

# Current Swahili

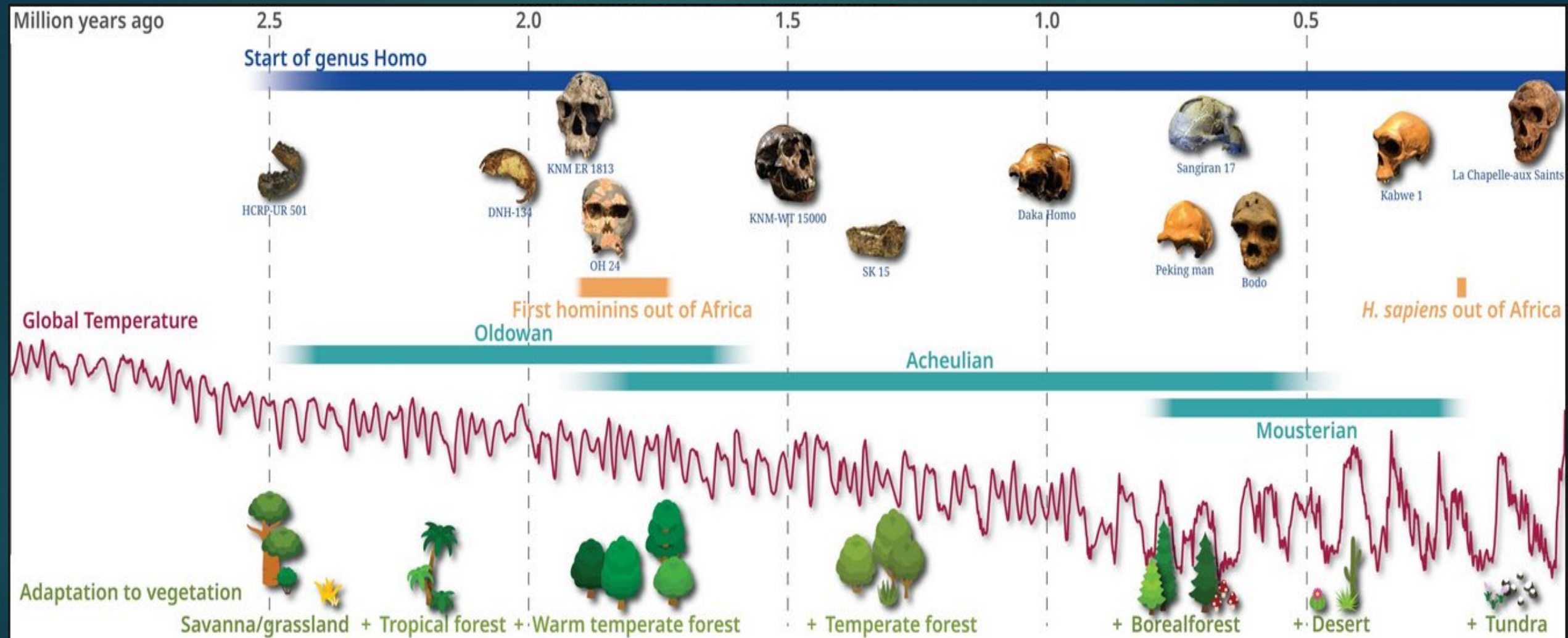
- ▶ Today, many Swahili people have little genetic relationship with the medieval individuals in the study. Samples from almost 200 modern people who identified as Swahili showed that **only those with ancestral ties to coastal towns retained large amounts of Persian ancestry.**
- ▶ “These results highlight an important lesson,” says David Reich. **“While we can learn about the past with genetics, it does not define identity.”**

# Human ancestors preferred mosaic landscapes and high ecosystem diversity

- ▶ Early human species adapted to mosaic landscapes and diverse food resources, which would have increased our ancestor's resilience to past shifts in climate.
- ▶ A compilation of more than 3232 well-dated human fossil specimens and archaeological sites, representing six different human species, in combination with realistic climate and vegetation model simulations, covering the past 3 million years.

## Mosaic landscapes and high ecosystem diversity

- ▶ Focused their analysis on biomes—geographic regions which are characterized by similar climates, plants, and animal communities (e.g., savannah, rainforest, or tundra).
- ▶ Revealed **which biomes were favored by the extinct hominin species *H. ergaster*, *H. habilis*, *H. erectus*, *H. heidelbergensis*, *H. neanderthalensis* and *H. sapiens***



Timeline of hominin evolution and adaptation to various vegetation types.  
Biome adaptation played a key role in the geographic expansion of our genus Homo

# Mosaic landscapes and high ecosystem diversity

- ▶ Earlier African groups preferred to live in open environments, such as grassland and dry shrubland.
- ▶ Migrating into Eurasia around 1.8 million years ago, hominins, such as *H. erectus* and later *H. heidelbergensis* and *H. neanderthalensis* developed higher tolerances to other biomes over time, including temperate and boreal forests.
- ▶ To **survive as forest-dwellers**, these groups developed more advanced stone tools and likely also social skills
- ▶ Eventually, *H. sapiens* emerged around 200,000 years ago in Africa, quickly becoming the master of all trades. Mobile, flexible, and competitive, our direct ancestors, unlike any other species before, survived in harsh environments such as deserts and tundra.

**Ecosystem diversity** played a key role in human evolution.

- ▶ Our ancestors actively selected for spatially diverse environments.
- ▶ Found a significant clustering of early human occupation sites in regions with increased biome diversity. Our human ancestors had a liking for mosaic landscapes, with a great variety of plant and animal resources in close proximity
- ▶ New Diversity Selection Hypothesis: Homo species, and *H. sapiens*, in particular, were uniquely equipped to exploit heterogeneous biomes.
- ▶ Crucial importance of landscape and plant diversity as a selective element for humans

# Favored habitats

- ▶ Habitats of both *H. habilis* and *H. ergaster* were predominately located in savanna and grassland areas.
- ▶ In contrast with the earlier African species, *H. erectus*— who left Africa no later than 1.8 Ma—selected for a much more diverse suite of habitats, with 58% of the sites associated with temperate or tropical forest and 38% with grassland and savanna regions
- ▶ More recent species such as *H. heidelbergensis* and *H. neanderthalensis* were able to adapt to colder habitats, with 8 and 11% of their occurrences falling in the boreal forest biome, respectively. This adaptation to cold environments is associated with the northward expansion of these species.



# Habitats

- ▶ *H. sapiens* managed to settle in extreme environments, including previously less occupied biome types such as tundra and desert, revealing *H. sapiens* as a “generalist specialist”.
- ▶ This ability to occupy even extreme habitats suggests the acquisition of advanced, unparalleled cognitive abilities, which is consistent with reported changes in brain shape, more sophisticated technologies, and the transition from Middle to Upper Paleolithic toolmaking traditions around 0.05 to 0.03 Ma.

# Neandertals

- ▶ Early African hominins and Neanderthals appear to have preferred either open or closed habitats, whereas other species favored mixed conditions.
- ▶ Our analysis suggests that *H. habilis* and *H. ergaster* mostly lived in savanna/dry-woodland and grassland/dry-shrubland.
- ▶ *H. neanderthalensis* became a temperate forest dweller, preferring closed environments. Neanderthals exhibited only limited capability to adapt to cold-climate open biomes such as tundra.
- ▶ This finding, along with the simulated Late Pleistocene biome variability, also suggests that Neanderthals went through a massive contraction of their habitat during glacial maxima, forcing them to settle in the warmer and more forested Mediterranean region.

# Ecological plasticity of *H. sapiens*

- ▶ Our data suggest that in contrast to early African Homo and *H. neanderthalensis*, *H. erectus* and *H. heidelbergensis* were able to settle in both open and closed biomes.
- ▶ Diversifying their habitats translated into their much wider expansion across Eurasia.
- ▶ Subsampling of *H. sapiens* data by matching the number of observations of older species continues to show the **wide range of occupied biomes**.

# Different biomes

- ▶ The mean biome types across Europe (59% temperate and 14% boreal forest) are quite distinct from those in Africa (49% of the land area = savanna/dry woodland or grassland/dry shrubland),
- ▶ From 1.8 Ma onward, a gradual trend in biome preferences from open grassland to temperate forests occurred.
- ▶ After 600 ka, the fraction of European temperate and warm-temperate forest dwellers correlates with regional temperatures, suggesting that hominins migrated in response to the climate and vegetation changes they experienced

# Humans as diversity seekers

- ▶ Hominins did not choose their whereabouts at random.
- ▶ Hominins lived in areas with multiple biome types in close proximity, suggesting that **hominins preferred landscape mosaics** rather than uniform environments.
- ▶ Human species were actively seeking out more abundant and diverse food resources in regions with higher ecosystem diversity
- ▶ Propose that diverse landscapes may have also sustained larger hominin populations, serving as hotspots for cultural innovation and playing an important role in genetic diversification

# Habitat diversity and diverse food resources.

- ▶ The derived inclination of humans toward landscape mosaics and their ability to adapt to regionally diverse vegetation conditions has not been shown before at continental scales, leading us to propose the diversity selection hypothesis:
- ▶ Homo species, and H. sapiens in particular, were specially equipped to exploit heterogeneous habitat conditions. Such heterogeneity, which correlates to high plant and vertebrate richness in current ecosystems, may have conferred hominin resilience to environmental perturbations by providing a wider and more stable resource base.
- ▶ Behavioral and cultural plasticity may have allowed humans to exploit habitat diversity and diverse food resources.

# Modern humans

- ▶ According to our analysis, our genus Homo has adapted over the Pleistocene and migrated to areas with higher landscape diversity.
- ▶ Utilizing resources from various biomes provided a resilient and successful strategy over hundreds of millennia. However, during the Anthropocene, our species has caused a massive decline in global ecosystem diversity due to land use practices, gradually shifting away from integrated agricultural practices and toward monocultures.

# Hunter-gatherer genes helped early European farmers survive disease

- ▶ 20% of the ancestry of descendant late Stone Age people could be traced to the local European hunter-gatherers. They analyzed genome-wide DNA from 677 individuals spanning Mesolithic and Neolithic Europe.
- ▶ When early Stone Age farmers first moved into Europe from the Near East about 8,000 years ago, they met and began mixing with the existing hunter-gatherer populations. More hunter-gatherer ancestry in adaptive-immunity genes in the mixed population than would be expected by chance.
- ▶ The researchers also detected more farmer ancestry in a gene called SLC24A5, which is involved in skin pigmentation.



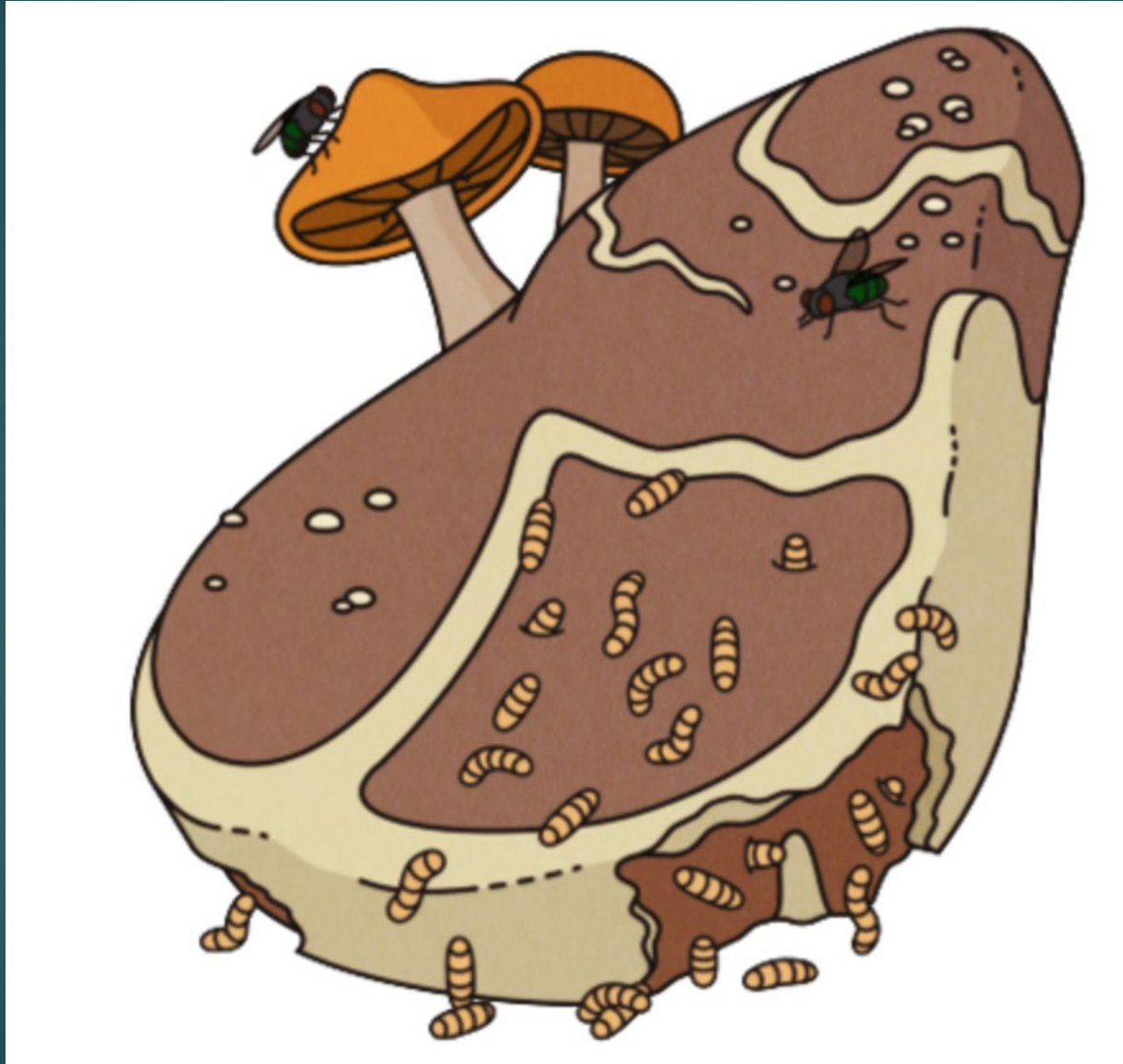
# Hunter-gatherer genes

- ▶ Their analysis found that a pigmentation-associated gene was the most overrepresented from the Neolithic local ancestry.
- ▶ In contrast, the mixed group retained more genes from the important MHC immunity locus from the hunter-gatherers.
- ▶ The immunity alleles from the hunter-gatherers might have been positively selected for because they facilitated greater survival and adaptation to pathogens in the Neolithic group.
- ▶ Findings highlight immune function as a prime target of natural selection in late-Stone-Age populations.

# HG Immunity genes in farmers

- ▶ When farming groups expanded from the Near East into Europe and mixed with local hunter-gatherers, the natural prediction would be that the farmers' immunity genes would be best adapted to the farming lifestyle and thus selected for.
- ▶ However, we see the opposite, that hunter-gatherer ancestry is enriched at the MHC immunity locus in farmers. This could, for example, be because the hunter-gatherers were already adapted to pathogens found in Europe, or it could be the result of natural selection favoring diversity in immunity genes.
- ▶ One hypothesis is that lighter skin pigmentation allowed farmers to synthesize more vitamin D from ultraviolet radiation, while hunter-gatherers were able to obtain sufficient vitamin D from their diet

# The Real Putrid Paleo Diet



J. Speth and E. Morin,  
2022

# The real Paleo diet

- ▶ Hunter-gatherers and small-scale farmers everywhere commonly ate putrid meat, fish and fatty parts of a wide range of animals. Native populations consumed rotten remains, either raw, fermented or cooked just enough to singe off fur and create a more chewable texture. Many groups treated maggots as a meaty bonus.
- ▶ Some Indigenous communities feasted on huge decomposing beasts, including hippos that had been trapped in dug-out pits in Africa and beached whales on Australia's coast.
- ▶ Hunters in those groups typically smeared themselves with the fat of the animal before gorging on greasy innards. After slicing open animals' midsections, both adults and children climbed into massive, rotting body cavities to remove meat and fat.

# Real Paleo diet

- ▶ Or consider that Native Americans in Missouri in the late 1800s made a prized soup from the greenish, decaying flesh of dead bison. Animal bodies were buried whole in winter and unearthed in spring after ripening enough to achieve peak tastiness.
- ▶ Intriguingly, no reports of botulism and other potentially fatal reactions to microorganisms festering in rotting meat appear in writings about Indigenous groups before the early 1900s. Instead, **decayed flesh and fat represented valued and tasty parts of a healthy diet**.
- ▶ The **revulsion Westerners feel toward putrid meat and maggots is not hardwired in our genome but is instead culturally learned**,

# Paleo diet

- ▶ This dietary revelation also challenges an influential scientific idea that cooking originated among our ancient relatives as a way to make meat more digestible, thus providing a rich calorie source for brain growth in the *Homo* genus.
- ▶ Present-day hunter-gatherers in polar regions: North American Inuit, Siberians and other far-north populations still **regularly eat fermented or rotten meat and fish**.
- ▶ **Fermented fish heads**, also known as “stinkhead,” are one popular munchy among northern groups. Chukchi herders in the Russian Far East, for instance, bury whole fish in the ground in early fall and let the bodies naturally ferment during periods of freezing and thawing. Fish heads the consistency of hard ice cream are then unearthed and eaten whole.

# Putrid food

- ▶ Putrid walrus, seals, caribou, reindeer, musk oxen, polar bears, moose, arctic hares and ptarmigans have all been fair game.
- ▶ Indigenous peoples encountered a variety of microorganisms from infancy on, unlike people today who grow up in sanitized settings. Early exposures to pathogens may have prompted the development of an array of gut microbes and immune responses that protected against potential harms of ingesting putrid meat.
- ▶ Putrefaction predigests meat and fish, softening the flesh and chemically breaking down proteins and fats so they are more easily absorbed and converted to energy by the body.

# Scavengers

- ▶ Given the ethnohistorical evidence, hominids living 3 million years ago or more could have scavenged meat from decomposing carcasses, even without stone tools for hunting or butchery, and eaten their raw haul safely long before fire was used for cooking
- ▶ Thompson and colleagues suggested in *Current Anthropology* in 2019 that **before about 2 million years ago, hominids were primarily scavengers who used rocks to smash open animal bones and eat nutritious, fat-rich marrow and brains.**
- ▶ That conclusion, stemming from a review of fossil and archaeological evidence, **challenged a common assumption that early hominids — whether as hunters or scavengers — primarily ate meat off the bone.**



# Speculative

- ▶ Butchered animal bones at sites dating to nearly 2 million years ago indicate that hominids ate most parts of carcasses, including brains and internal organs.
- ▶ **Problem:** Argument about eating putrid carcasses is very speculative and untestable,
- ▶ Untangling whether ancient hominids truly had a taste for rot will require research that spans many fields, including microbiology, genetics and food science, Speth says.

# Edible plants

- ▶ Suggests that ancient cooks were not turning out meat dishes. Instead, Speth speculates, cooking's primary value at first lay in making starchy and oily plants softer, more chewable and easily digestible.
- ▶ Edible plants contain carbohydrates, sugar molecules that can be converted to energy in the body. **Heating over a fire converts starch in tubers and other plants to glucose**, a vital energy source for the body and brain. Crushing or grinding of plants might have yielded at least some of those energy benefits to hungry hominids who lacked the ability to light fires.

# Ns = high level carnivores

- ▶ Exceptionally high  $\delta^{15}\text{N}$  (nitrogen) values in collagen single amino acids confirm Neandertals as high-trophic level carnivores
- ▶ Elevated levels of a diet-related form of nitrogen in Neandertal bones and teeth hint that they were committed carnivores, eating large amounts of protein-rich lean meat
- ▶ Meat from wild, hoofed animals and smaller creatures such as rabbits contains almost no fat, or marbling. Evidence indicates that people can safely consume between about 25 and 35 percent of daily calories as protein.
- ▶ Above that threshold, several investigations have indicated that the liver becomes unable to break down chemical wastes from ingested proteins, which then accumulate in the blood and contribute to rabbit starvation.

# Need for fat

- ▶ Limits to the amount of daily protein that can be safely consumed meant that ancient hunting groups, like those today, needed animal fats and carbohydrates from plants to fulfill daily calorie and other nutritional needs.
- ▶ Accounts describe Inuit people eating much larger amounts of fatty body parts than lean meat.
- ▶ Over the last few centuries, they have favored tongue, fat deposits, brisket, ribs, fatty tissue around intestines and internal organs, and marrow.
- ▶ Internal organs, especially adrenal glands, have provided vitamin C — nearly absent in lean muscle — that prevented anemia and other symptoms of scurvy.

# Chyme

- ▶ Western explorers noted that the Inuit also ate **chyme**, the stomach contents of reindeer and other plant-eating animals. Chyme provided at least a side course of plant carbohydrates.
- ▶ Likewise, Neandertals in Ice Age Europe probably subsisted on a fat- and chyme-supplemented diet
- ▶ Like arctic hunters did a few hundred years ago, Neandertals may have eaten putrid meat and fish studded with maggots. That would explain elevated nitrogen levels in Neandertal fossils.

# Neandertals probably carb-loaded

- ▶ Better evidence of Neandertals' plant preferences comes from sites in warm Mediterranean and Middle Eastern settings.
- ▶ Neandertals in a range of environments must have consumed lots of starchy plants. Even Stone Age northern European and Asian regions included plants with starch-rich appendages that grew underground, such as tubers.
- ▶ Neandertals could also have obtained starchy carbs from the edible, inner bark of many trees and from seaweed along coastlines.

# Neandertals

- ▶ There is direct evidence that Neandertals munched on plants.  
Microscopic remnants of edible and medicinal plants have been found in the tartar on Neandertal teeth
- ▶ Plants represented a more predictable, readily available food source than hunted or scavenged meat and fat
- ▶ In at least some places, Stone Age people apparently cooked to experience pleasing tastes and not just to fill their stomachs.

# N spices

- ▶ **Charred plant food fragments** from Shanidar Cave in Iraqi Kurdistan and Franchthi Cave in Greece **consisted of crushed pulse seeds, possibly from starchy pea species, combined with wild plants that would have provided a pungent, somewhat bitter taste,** microscopic analyses show.
- ▶ Added ingredients included wild mustard, wild almonds, wild pistachio and fruits such as hackberry. **Wild pulses in food from both caves display microscopic signs of having been soaked, a way to dilute poisons in seeds and moderate their bitterness.**



# Neandertals were the first hominids to turn forest into grassland 125,000 years ago

- ▶ Neandertals' campfires and other activities had transformed the local landscape from forested to largely open around 125,000 years ago.
- ▶ Analyses of pollen, charcoal, animal fossils and other material previously unearthed at **two ancient lake basins in Germany** provide the oldest known evidence of hominids reshaping their environments.
- ▶ At Neumark-Nord: over a span of about 2,000 years, included setting campfires, butchering game, collecting wood, making tools and constructing shelters
- ▶ Stone tools and bone fragments displaying signs of heating, burned wood, charred seeds and dense patches of charcoal particles suggested that Neandertals had frequently set fires near the Neumark-Nord lakes.

# Molecular clocks

- ▶ **Molecular clocks** are based on two key biological processes that are the source of all heritable variation: mutation and recombination.
- ▶ In a single human genome, there are about 70 nucleotide changes per generation – minuscule in a genome made up of six billion letters.
- ▶ Scientists **can use mutations to estimate the timing of branches in our evolutionary tree**. First they compare the DNA sequences of two individuals or species, counting the neutral differences that don't alter one's chances of survival and reproduction. Then, knowing the rate of these changes, they can calculate the time needed to accumulate that many differences. This tells them how long it's been since the individuals shared ancestors.
- ▶ The historical generation interval in humans is 26–30 y

# Dating of N-MH introgression

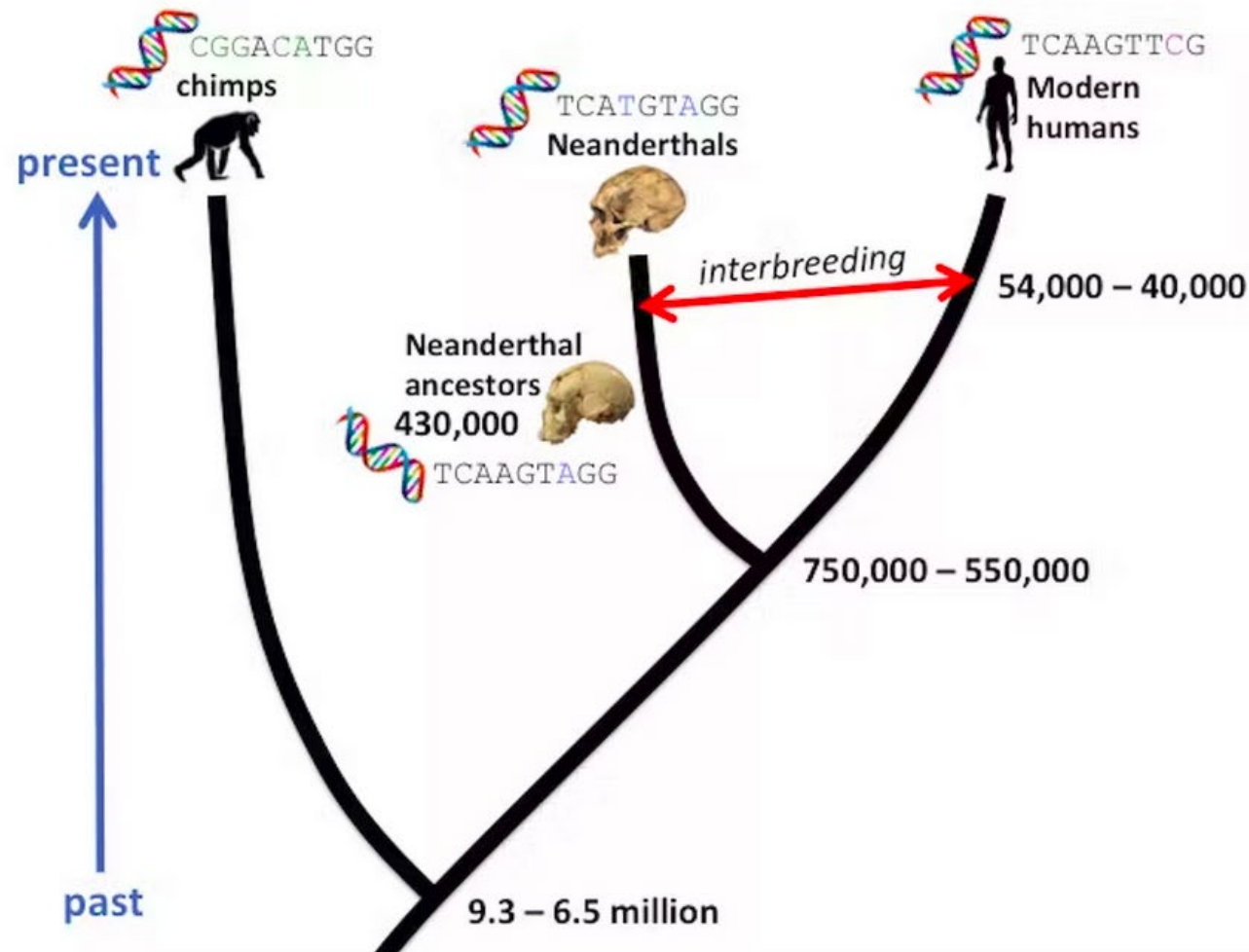
- ▶ Summary: Gene flow between ancestors of modern humans and Neanderthals
- ↑ All non-Africans have ~1-2% of Neanderthal ancestry
- ↑ We can use DNA clocks to Infer when Neanderthal mixture occurred by estimating the length of Neanderthal blocks In our genomes
- ↑ Using ancient DNA of early modern humans, we Infer the timing of the mixture ~40,000 - 55,000 years ago.
- ↑ Fossil evidence of same layer with both MH and N in this time range

# Recombination clocks

- ▶ Recombination, also known as crossing-over, is the other main way DNA accumulates changes over time. It leads to shuffling of the two copies of the genome (one from each parent), which are bundled into chromosomes.
- ▶ In humans, about 36 recombination events occur per generation, one or two per chromosome. As this happens every generation, segments inherited from a particular individual get broken into smaller and smaller chunks. Based on the size of these chunks and frequency of crossovers, geneticists can estimate how long ago that individual was your ancestor.
- ▶ Because mutations accumulate so slowly, this clock works better for very ancient events, like evolutionary splits between species. The recombination clock, on the other hand, ticks at a rate appropriate for dates within the last 100,000 years.

# Case of Ns

- ▶ The case of Neanderthals illustrates how the mutation and recombination clocks can be used together to help us untangle complicated ancestral relationships. Geneticists estimate that there are **1.5-2 million mutational differences between Neanderthals and modern humans.** Applying the mutation clock to this count suggests the groups initially split between **765,000 to 550,000 years ago.**
- ▶ Applying the recombination clock to Neanderthal DNA retained in present-day humans, researchers estimate that the **groups interbred between 54,000 and 40,000 years ago.** When scientists analyzed a *Homo sapiens* fossil, known as **Oase 1**, who lived around 40,000 years ago, they found large regions of Neanderthal ancestry embedded in the Oase genome, suggesting that **Oase had a Neanderthal ancestor just four to six generations ago.** In other words, **Oase's great-great-grandparent was a Neanderthal.**



An evolutionary tree displays the divergence and interbreeding dates that researchers estimated with molecular clock methods for these groups. Bridget Alex, CC BY-ND

# Mal'ta 1

- ▶ The Mal'ta1 individual dated as 23,891–24,423 calBP old was sampled in south-central Siberia and was sequenced to an average coverage of 1.0×.
- ▶ We applied the single-sample statistic and estimated that the Neanderthal gene flow occurred  $22,301 \pm 2,169$  y before he lived. In turn, this difference translates into an estimated age of  $24,935 \pm 4,851$  y, which is consistent with its radiocarbon date.
- ▶ Method only applicable to genomes with N ancestry

# Oase 1

150

- ▶ The age of the Oase1 genome from Romania has been estimated to be  $\sim 37,000\text{--}42,000$  calBP by radiocarbon dating
- ▶ We estimated that the Neanderthal gene flow in Oase1 occurred  $227 \pm 22$  y before he lived. Provided an **estimated age of  $42,467 \pm 3,767$  y**, consistent with the radiocarbon date of this specimen. Oase1,
- ▶ By explicitly fitting a model of two Neanderthal gene flow events, we estimated that the admixture occurred  $2,012 \pm 385$  y and  $164 \pm 14$  y before he lived, translating to **age estimates of  $40,682 \pm 3,787$  and  $42,530 \pm 3,767$  y, respectively**



# History of Hominin Use of Fire



# Use of Fire/Cooking

- ▶ We can get some clues about the earliest hominins' relationship with fire by looking at modern ape behavior.
- ▶ A study published in April showed that **savannah-dwelling chimpanzees often prefer to travel in regions that have recently been burned, and that they find more food in those places.** It's not hard to imagine hominins shifting from this passive use of fire to something more active. But when they did so remains wildly uncertain.
- ▶ Many of the “smoking guns” for prehistoric fire use – charred bone fragments or chunks of charcoal – do not necessarily imply that early humans could **control fire.** Our opportunistic ancestors may simply have exploited the occasional wild fires triggered by lightning, for example.

# Fire and bigger brains

- ▶ For over 20 years, Harvard biologist Richard Wrangham has been promoting the hypothesis that hominins started cooking around 2 million years ago.
- ▶ That's not long after our genus, *Homo*, evolved.
- ▶ Crucially, it is when brains evolved to be much bigger. Wrangham argues that cooked food, which is more nutritious and easier to chew, enabled the evolution of large brains.

# Use of fire

- ▶ Classic site: a 780,000-year-old settlement in Gesher Benot Ya'aqov in Israel's northern Jordan river valley. No human remains have been found there, but based on its age and the stone tools at the site, the inhabitants are most likely to have been *Homo erectus*.
- ▶ Evidence that hominins were cooking carp fish in an earthen oven around 780,000 years ago in what is now Israel.

# Use of fire

- ▶ Previously, the **oldest unambiguous evidence of cooking was from 170,000 years ago in South Africa**: Wadley *et al.* report the identification of whole, charred rhizomes of plants of the genus *Hypoxis* from Border Cave, South Africa, dated up to 170,000 years ago.
- ▶ These archaeobotanical remains represent the **earliest direct evidence for the cooking of underground storage organs**.
- ▶ **1.5 Ma evidence of hominins roasting meat at a site in Kenya's Koobi Fora region**: unusual patches of reddened dirt. They were argued to indicate where ancient controlled fires had thermally altered the ground beneath. And stone artefacts and burned bone; stone tool fragments have a distinct curved appearance; this unusual curving occurs only when a stone tool is being made near a fire

# Cooking

- ▶ Researchers **must discern fires started and controlled by humans from ordinary forest fires.**
- ▶ In 2011, a systematic review found that **controlled fire use could be traced back 400,000 years.**
- ▶ That's before the origin of our species, so Neanderthals (and possibly other hominins) could control fire. Humans may have been much later to master fire than we thought.
- ▶ A review of supposed archaeological hearths in Europe suggests that the oldest date to just 400,000 years ago. The finding suggests that humans expanded into cold northern climates without the warmth of fire – and that cooking was not the evolutionary trigger that boosted our brain size.

# Fire debate

- ▶ The **earliest European hearths date back between 300 and 400,000 years**, the researchers conclude – much later than existing theories suggest.
- ▶ **Some archaeologists think that controlled fire use dates back 1.6 million years.** Richard Wrangham of Harvard University has even suggested that hominins began using fire 1.9 million years ago, leading to a cooking tradition that made digestion easier and freed up the extra energy our ancestors needed to grow bigger brains.
- ▶ Another recent study, which described pulses that had been pounded and charred at caves in Greece and the Kurdistan region of Iraq. These sites are more recent, within the past 100,000 years, but **Neanderthals are still the most plausible candidates for the cooks**

## Mitogenome evidence shows two radiation events and dispersals of matrilineal ancestry from northern coastal China to the Americas and Japan

- ▶ Used mtDNA to trace a mtDNA lineage from northern coastal China to the Americas.
- ▶ A 10-year hunt for the mtDNA D4h3a haplotype, combing through 100,000 modern and 15,000 ancient DNA samples across Eurasia, eventually landing on 216 contemporary and 39 ancient individuals who came from the ancient lineage.
- ▶ Ancestors of Native Americans primarily came from Siberia and northern coastal China also served as a genetic reservoir contributing to the Native American gene pool
- ▶ During the second migration, the same lineage of people settled in Japan, which could help explain similarities in prehistoric arrowheads and spears found in the Americas, China and Japan.



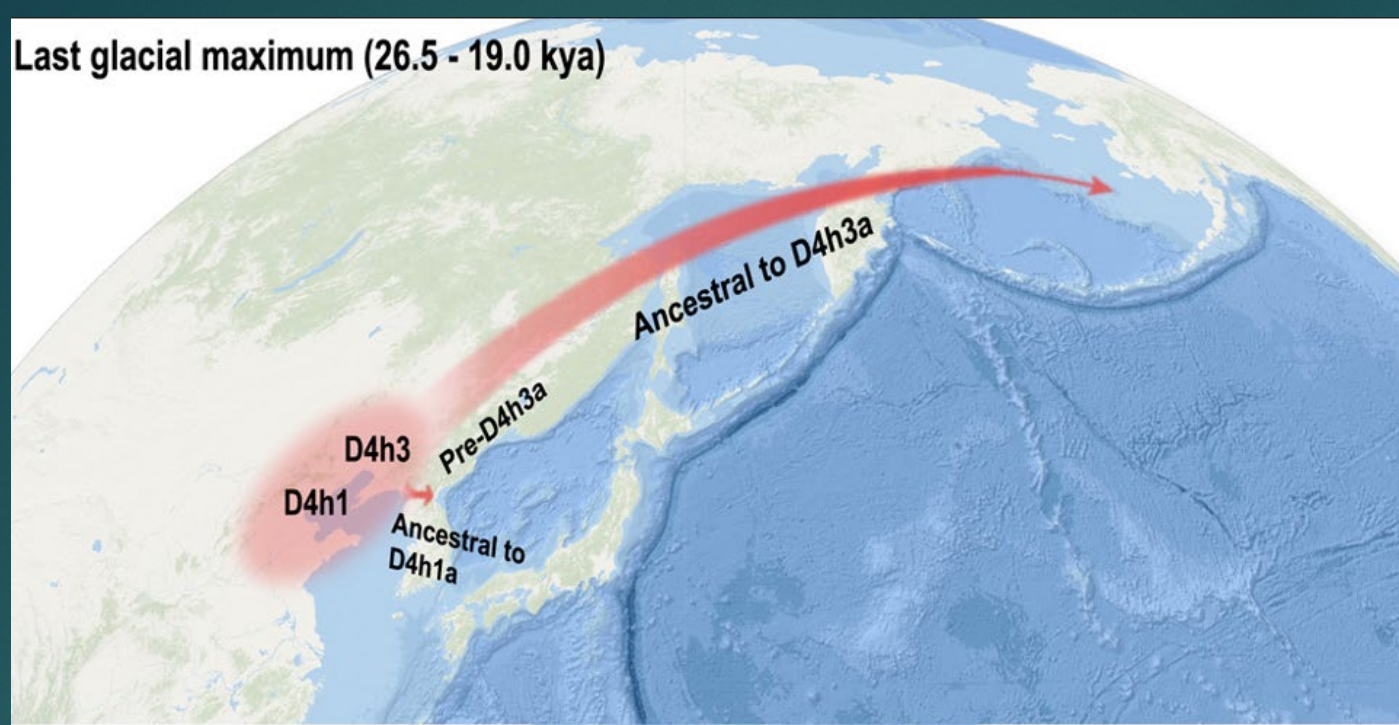


During the **second migration**, the same lineage of people **settled in Japan**, which could help explain similarities in prehistoric arrowheads and spears found in the **Americas** (pictured), **China** and **Japan**.

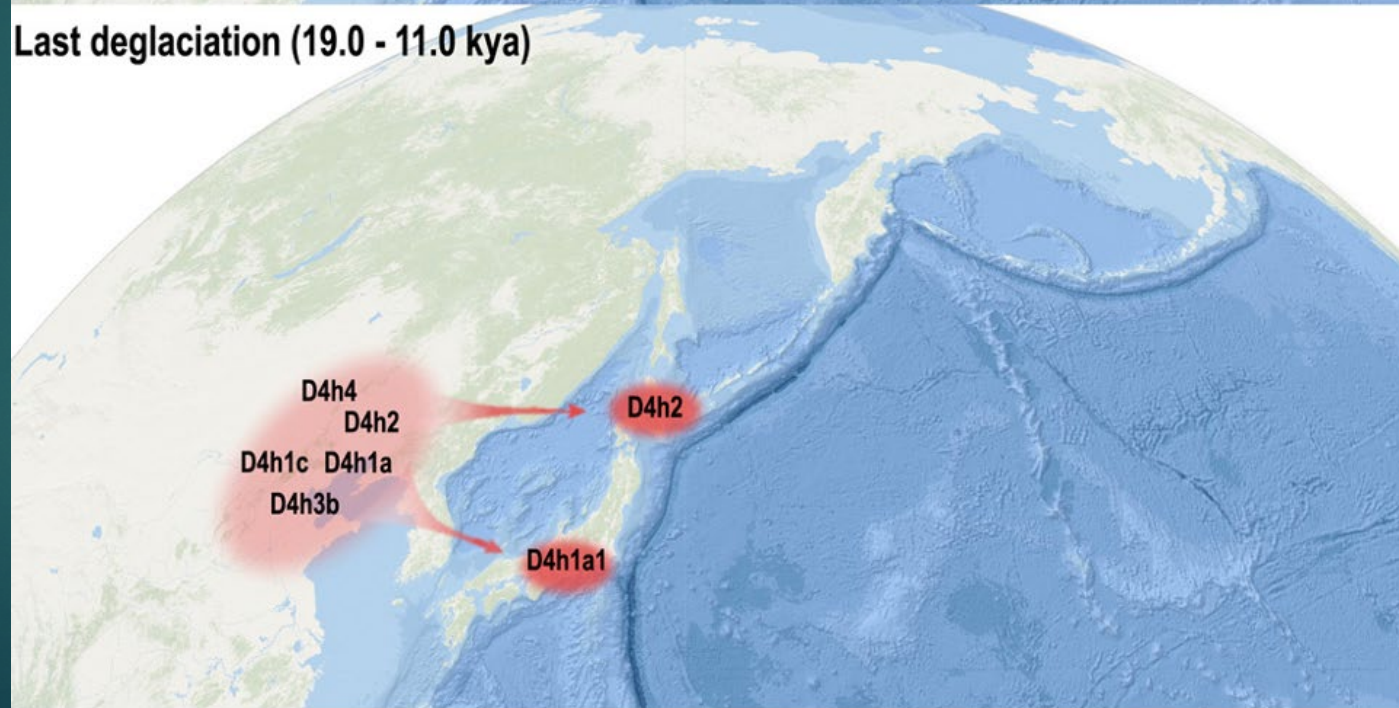
# Genetic link of NAs and Japanese Ainu

- ▶ The results revealed **two migration events**. The **first** was between **19,500 and 26,000 years ago during the Last Glacial Maximum**, when ice sheet coverage was at its greatest and climate conditions in northern China were probably inhospitable.
- ▶ The **second** occurred during the melting period, between **19,000 and 11,500 years ago**. Increasing human populations during this period might have triggered migrations.
- ▶ Discovered **genetic link between Native Americans and Japanese people, particularly the indigenous Ainu**. In the melting period, a subgroup branched out from northern coastal China to Japan, contributing to the Japanese people, a finding that chimes with **archeological similarities between ancient people in the Americas, China and Japan**.

Last glacial maximum (26.5 - 19.0 kya)



Last deglaciation (19.0 - 11.0 kya)



# Chinese mtDNA and Native Americans

- ▶ Link between mtDNA lineage D4h3a (typical of NAs) and D4h3b (found so far only in East China and Thailand)
- ▶ Complementary evidence from Y chromosomal DNA (C2-M217) showing that male ancestors of Native Americans lived in northern China at the same time as female ancestors
- ▶ Coastal radiations of D4h support the Pacific coastal route of early Native Americans

# Japan

- ▶ During the deglaciation period, another group branched out from northern coastal China and traveled to Japan. Related to Ainu.
- ▶ The three regions share similarities in how they crafted stemmed projectile points for arrowheads and spears.
- ▶ This evidence strongly supports the existence of an old ancestry source, arising between 40 and 23 kya, that contributed to populations including East Asians, Jomons, Eastern Siberians, and Nas.

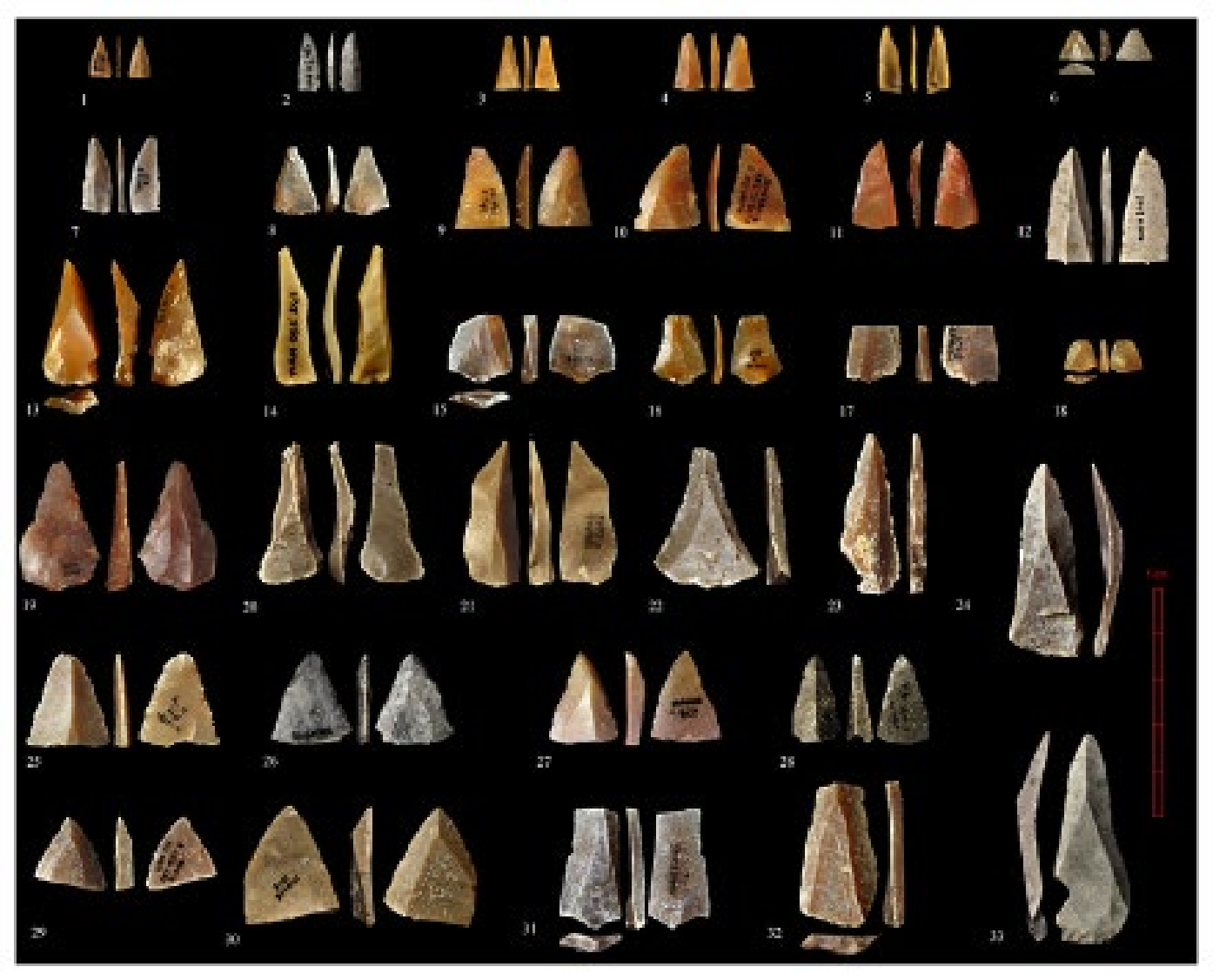
# The three waves: Rethinking the structure of the first Upper Paleolithic in Western Eurasia – L. Slimak, 2023

- ▶ The **Neronian** is a lithic tradition recognized in the Middle Rhône Valley of Mediterranean France now directly linked to *Homo sapiens* and securely dated to **54 Ka**, pushing back the arrival of modern humans in Europe by 10 ka.
- ▶ This incursion of modern humans into Neandertal territory and the relationships evoked between the Neronian and the Levantine Initial Upper Paleolithic (IUP) question the validity of concepts that define the first *H. sapiens* migrations and the very nature of the first Upper Paleolithic in western Eurasia.

# Three waves

- ▶ Direct comparative analyses between lithic technology from Grotte Mandrin and East Mediterranean archeological sequences, especially Ksar Akil, suggest that the three key phases of the earliest Levantine Upper Paleolithic have very precise technical and chronological counterparts in Western Europe, recognized from the Rhône Valley to Franco-Cantabria.

# Neronian industry





# Mandrin, France: Rethinking of the origin of the upper paleolithic: A Mediterranean odyssey

- ▶ These trans-Mediterranean technical connections **suggest three distinct waves of *H. sapiens* expansion into Europe between 55–42 ka**. These elements support an original thesis on the origin, structure, and evolution of the first moments of the Upper Paleolithic in Europe tracing parallel archaeological changes in the East Mediterranean region and Europe.
- ▶ **The recent attribution of the Neronian industry to *Homo sapiens* at around the 54<sup>th</sup> millennium (56.8–51.7 ka) at Grotte Mandrin in France not only indicates a 10,000-year push back of the arrival modern humans in Europe, but also concrete evidence of interactions between Neanderthals and modern populations are demonstrated in a specific territory.**

# Mandrin, France

- ▶ **Evidence:** E level of the sequence that has a tooth and prong technology and micropoints called Neronian, dated at 56.8-51.7 ka, between Mousterian levels that preceded and succeeded it.
- ▶ **Slimak, 2023 study:** concludes that they indicate the existence of three different waves of modern humans inside Europe, based on lithic similarities of Ksar Akil and Mandrin..

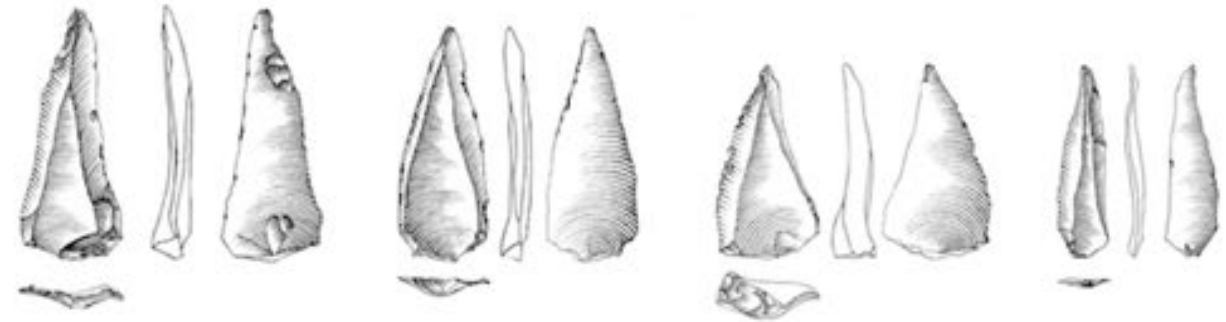
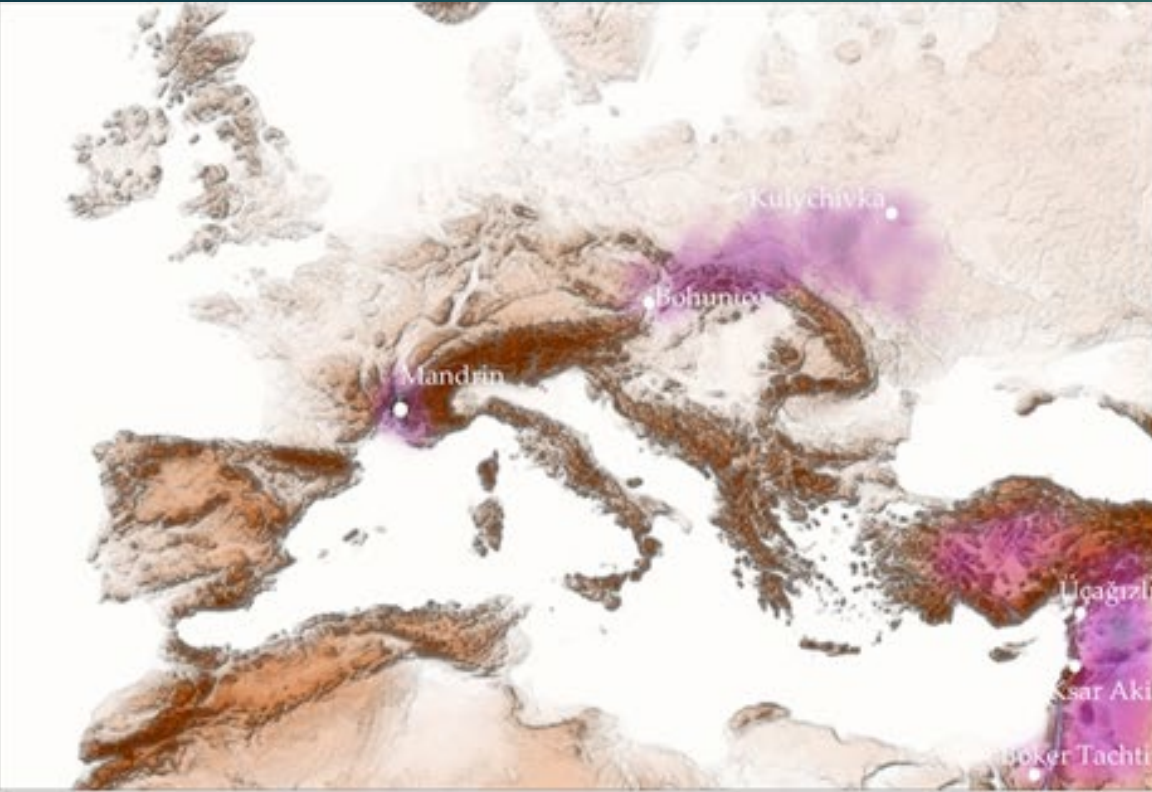
# Three different waves of modern humans inside Europe

- ▶ **Ksar Akil sequence in Lebanon, MP to UP:** unity between the European Protoaurignacian and the Levantine Early Ahmarian
- ▶ The **sequence of Ksar Akil** allows us to document the precise **technical emergence of industries identical to the Protoaurignacian of Europe (SEA)**, a development that can be broken down **into three successive technical stages** resulting from a progressive evolution of the technical systems of the first Levantine UP; IUP/ NEA/ SEA.

# Ksar Akil = Mandrin

- ▶ These successions in the stratigraphy have remarkable parallels with the western end of Europe with the Neronian/Châtelperronian/Protoaurignacian triptych.
- ▶ Three phases of the first Levantine Upper Paleolithic find a strict corollary across Europe
- ▶ From the Ksar Akil sequence, three phases of the first Levantine Upper Paleolithic are proposed that are analogous to the three industries associated with such waves in Western Europe:

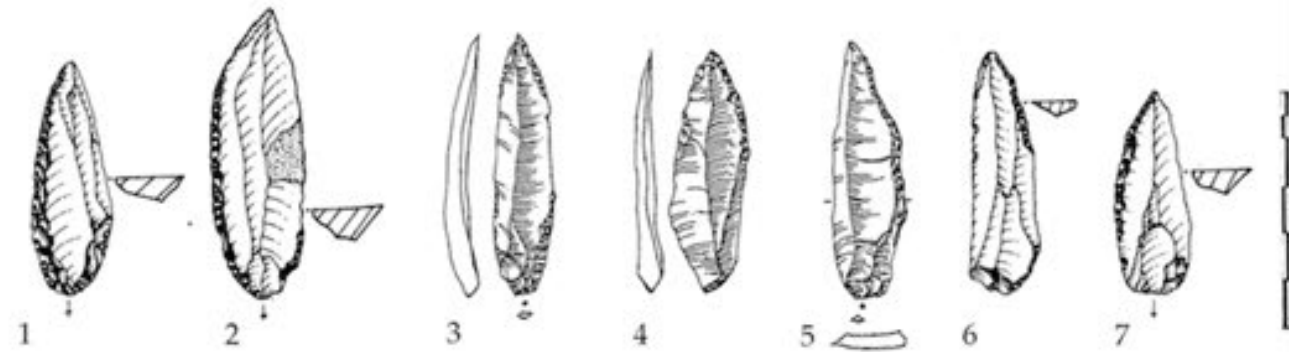
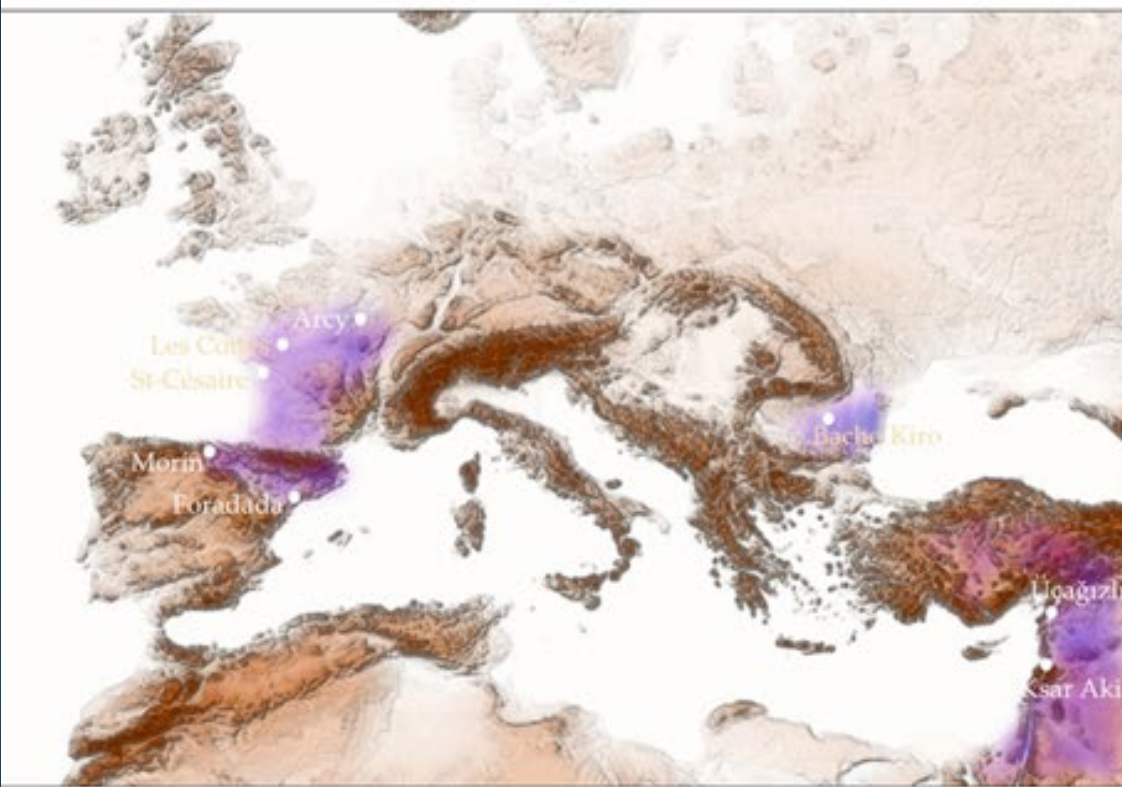
# 1<sup>st</sup> wave: Initial Upper Paleolithic



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

1 - The first phase (**Initial Upper Paleolithic**, IUP) occurred in the **50 to 60 ka range**. It would be equivalent to the aforementioned sapiens populations that settled for a brief period of time in "Neanderthal territory", and left the Mandrin cave Neronian (points and micropoints) and very little other evidence.

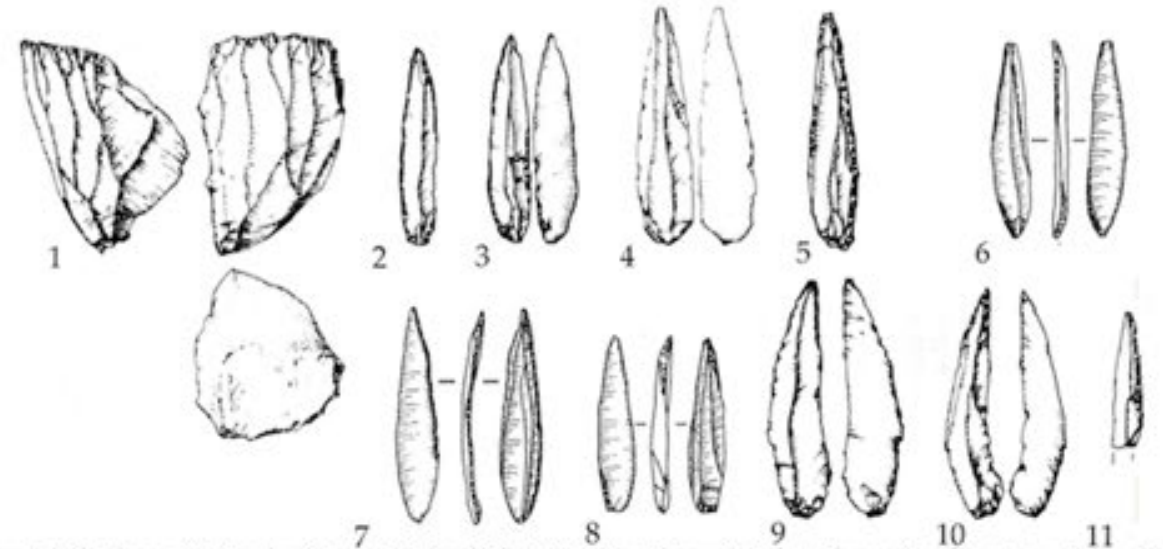
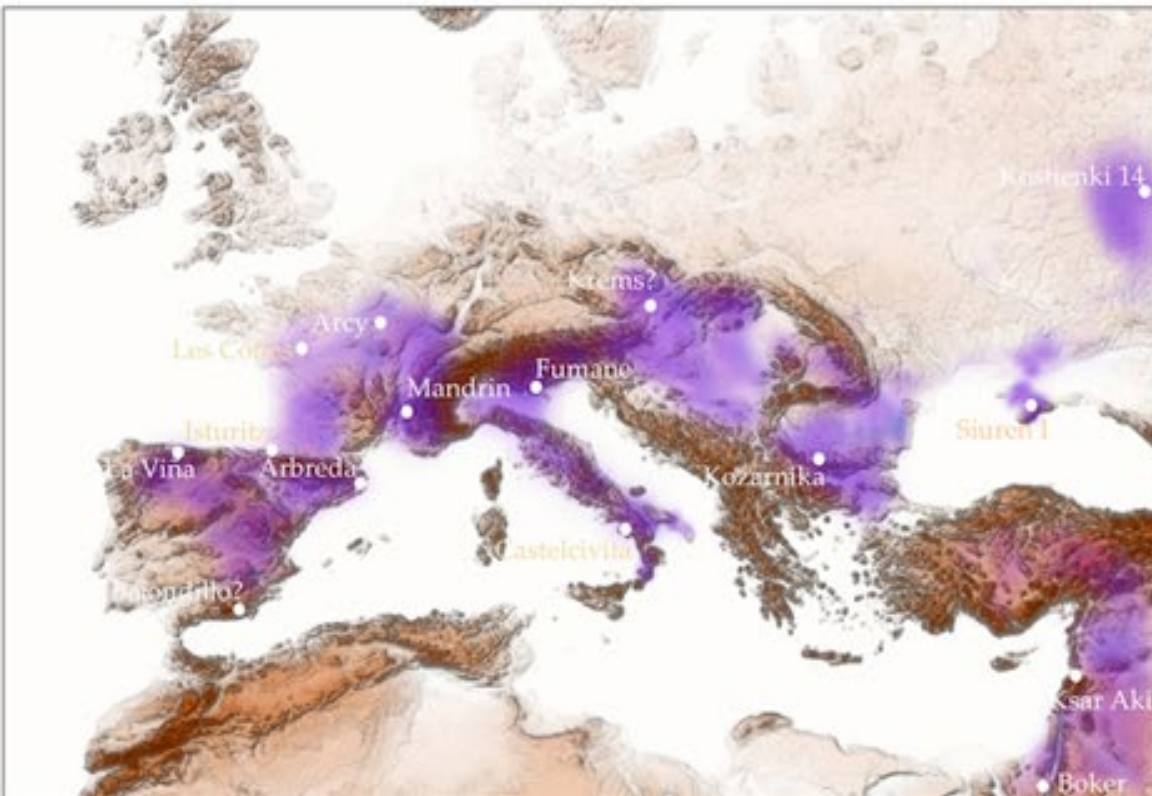
## 2<sup>nd</sup> wave: Early Upper Paleolithic I, EUP I, or Northern Early Ahmariense, NEA



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

2 - The second phase (Early Upper Paleolithic I, EUP I, or Northern Early Ahmariense, NEA) would correspond to the Châtelperronian culture developed around 45 ka on the Atlantic coast of France and, on the Iberian Peninsula, the Cantabrian coast and the north of the Mediterranean area. But it is not observed in the Rhone Valley.

# 3<sup>rd</sup> wave: Early Upper Paleolithic II, EUP II, or Southern Early Ahmariense, SEA



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

3 - The **third phase (Early Upper Paleolithic II, EUP II, or Southern Early Ahmariense, SEA)** would correspond in Europe to the **proto-Aurignacian industry of about 42 ka**. This is a **much more marked and recognizable expansion throughout western Europe to the Levant**, leading to further cultural unification of the various sapiens populations across western Eurasia.

# From colonization to relations with the Neandertals

- ▶ **Three phases** from the beginning of the Upper Paleolithic can be interpreted **as three distinct migratory waves of biologically modern populations that systematically had their origin within the Mediterranean Levant.**
- ▶ Lithics are archaeological signature of three distinct migratory phases, all likely stemming from the same Levantine cultural substrate.



# Neronian sapiens

- ▶ Possible links between these waves with the gradual replacement of the last Neanderthals are proposed:
- The **Neronian sapiens** showed a mastery of both banks of the Rhône river and knowledge of all siliceous resources in a relatively large area, suggesting close relationships with Neanderthal aboriginal groups or isolated individuals of this species who would have prior knowledge of the territory. Rhône was one of the main migratory arteries of Western Europe
- In the **second phase**, there seems to be a rejection or resistance from the Neanderthals that occupied the Rhone Valley to the sapiens that spread through Atlantic, continental and Mediterranean territories.
- The **Proto-Aurignacian** marks the complete replacement of Neanderthals by sapiens, throughout a gradual process that would last up to 12 ka in areas such as the Rhône Valley.

## N-MH overlap in Eurasia: 1400 to 2900 years

- ▶ Optimal linear estimation models predict 1400–2900 years of overlap between *Homo sapiens* and Neandertals prior to their disappearance from France and northern Spain -- Igor Djakovic, et al., 2022
- ▶ Neanderthals and modern humans coexisted in a period of 1,400 to 2,900 years in the region corresponding to present-day France and northern Spain. This conclusion has been reached using statistical models of the probability of crosses from the dating of 56 objects attributed to both species, from 17 sites, and 10 Neanderthal specimens from that region

# N-MH overlap and Mandrin Cave

- ▶ Archaeologically, the **first part of this period**—the Middle to Upper Palaeolithic transition—is characterized by so-called ‘Initial Upper Palaeolithic’ assemblages (e.g. Bacho Kiro) which are increasingly interpreted as representing an initial, possibly unsuccessful migration of AMH into Europe occurring around 47–44 kya cal BP.
- ▶ The term ‘unsuccessful’ has been used as these initial groups appear to **have left no visible genetic contributions to present-day populations in Europe**. Recently published evidence from **Grotte Mandrin**, south-eastern France, may however **extend this initial migration to as far back as ~ 54,000 years ago**. At this site, a **deciduous molar attributed to Homo sapiens** was recovered from an archaeological layer bearing a **distinctive IUP-type stone tool industry and dating to somewhere between 58 and 51,000 years ago**.

# Early MHs in Europe

- ▶ If confirmed with additional evidence, this would constitute a significant shift in perspective—placing AMHs in far western Europe upwards of 12,000 years earlier than previously thought.
- ▶ Interestingly, there is no evidence of AMH occupation in any region of France for upwards of 12–14,000 years following the disappearance of the Neronian industry—which in fact seems to represent a brief, geographically restricted technological entity.

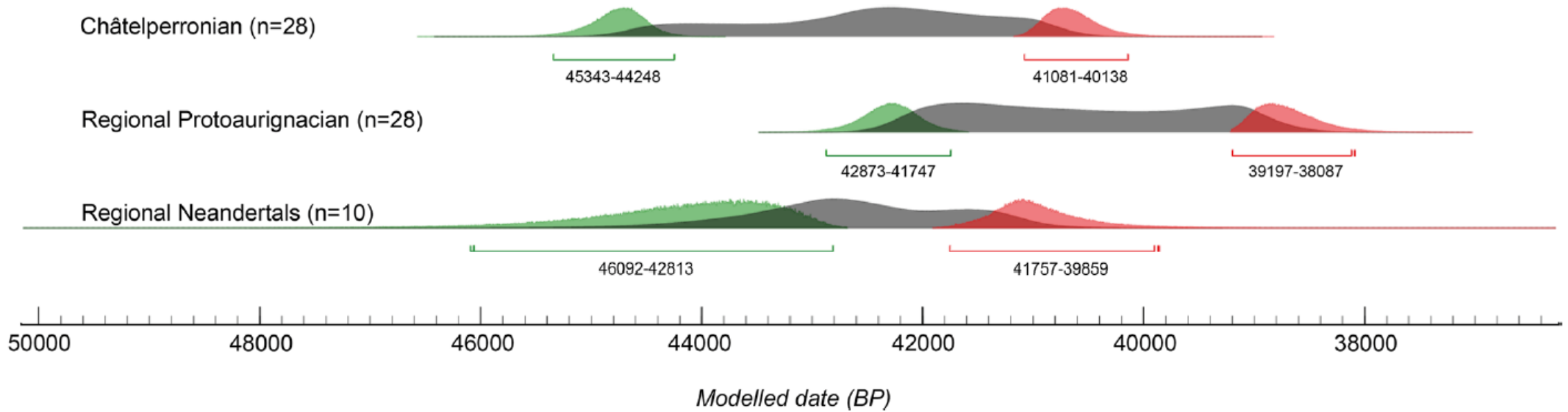
- ▶ Instead, until ~ 42,000 years ago, the archaeological record of France appears to be characterized exclusively by Neandertal remains and cultural material. The evidence from Grotte Mandrin may in fact lend strength to the idea that this initial period of AMH presence in Europe consisted primarily of small scale, unsuccessful migrations—without persistent co-existence between incoming AMHs and Neandertals.
- ▶ The onset of the Aurignacian complex (sensu lato) across Europe at around 42 kya cal BP is widely accepted as reflecting a second, more successful migration of AMH groups into Europe's western extensions, and may signal the first major and persistent phase of European colonization by our species.

# Transitional stratigraphy

- ▶ In many regions, Protoaurignacian and Early Aurignacian assemblages appear to rapidly replace so-called 'transitional' stone tool industries (e.g. Uluzzian, Châtelperronian, Lincombian-Ranisian-Jerzmanowician), some of which are considered to be products of Neandertals
- ▶ At present, the Châtelperronian industry of France and northern Spain shows the strongest association between one of Europe's 'transitional' industries and Neandertal fossil remains. Neandertal remains have been recovered from stratigraphic layers containing Châtelperronian artefacts at the two key French sites of Saint-Cesaire and Grotte du Renne.

# The great debate

- ▶ However, the **validity of these associations is heavily debated**, and **consensus regarding both the makers of this industry and the reliability of the Neandertal associations is not unanimous**.
- ▶ Nonetheless, despite ongoing discussion, **a Neandertal authorship for this industry remains the most parsimonious and well-accepted model**. The principle reason for this is that, debates aside, the **only human remains to as of yet be recovered from stratigraphic layers containing Châtelperronian artefacts are those of Neandertals**.
- ▶ Bayesian modelling of radiocarbon ages for Protoaurignacian and Châtelperronian assemblages in this region has already indicated that these occupations may have co-existed for upwards of 1600 years

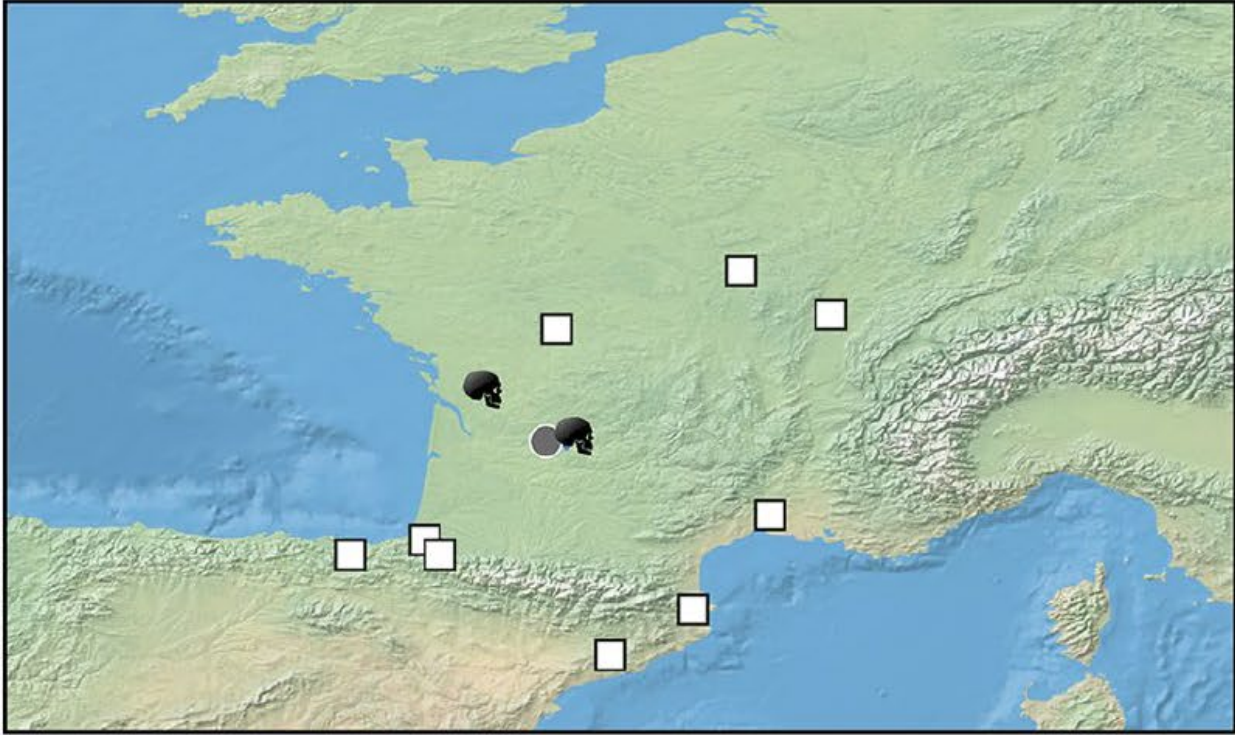


**Figure 2.** Kernel Density Estimation plots and Bayesian start/end date probabilities summarising the distribution of the aggregated calibrated radiocarbon ages for (a) the Châtelperronian assemblages (n = 28), (b) the Protoaurignacian assemblages (n = 28), and (c) the directly-dated late Neandertals (n = 10) included in this

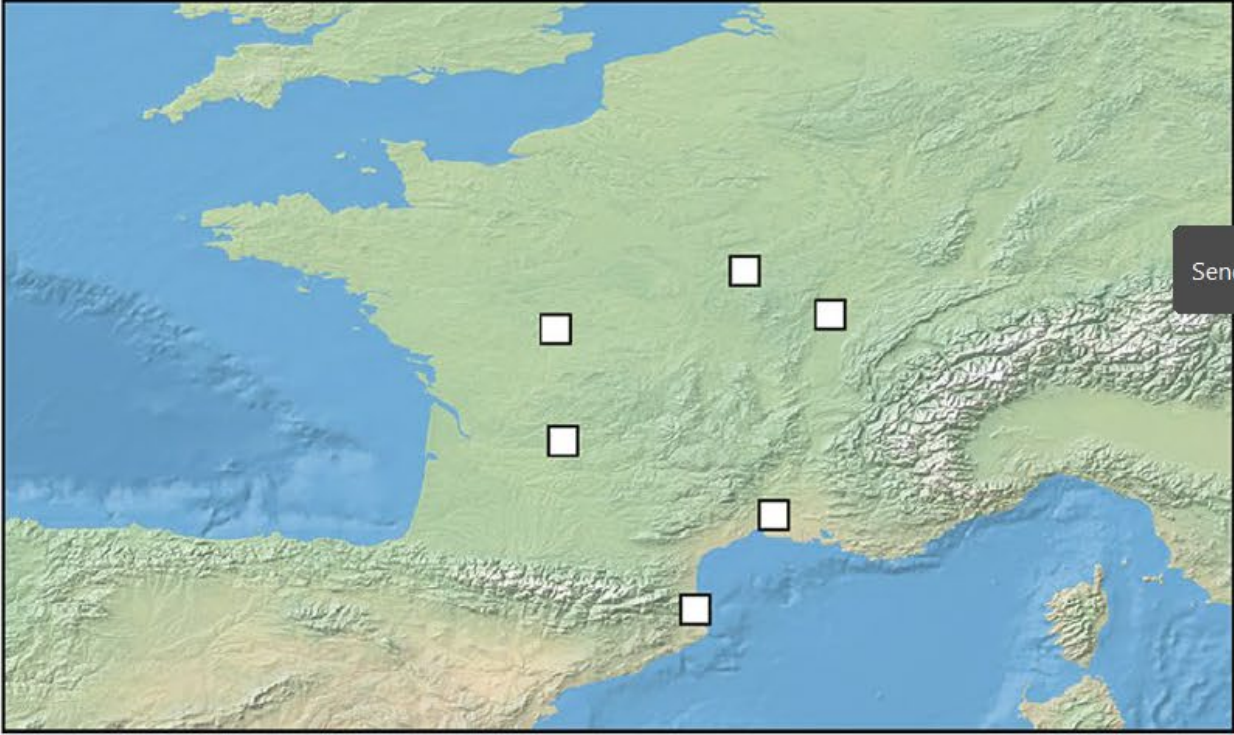


Geographic appearance of dated occurrences for the Châtelperronian (grey circles), Protoaurignacian (white squares), and directly-dated Neandertals (black skulls) in the study region between 43,400 (a) and 39,400 (f) years cal BP

(e) 40400 - 40000 kya cal



(f) 39800 - 39400 kya cal BP



# Modeling

- ▶ Combined, modelling suggests the Protoaurignacian to have emerged around 1399–2196 and 2375–2855 years before Neandertals and the Châtelperronian industry (respectively) disappeared from the region.
- ▶ Based on OLE modelling of their respective ‘origination’ and ‘extinction’ dates, the Protoaurignacian potentially appeared around 1400–2900 years before Neandertals and the Châtelperronian industry disappeared from France and northern Spain.
- ▶ This is largely consistent with previous estimates, and reaffirms the duration of co-existence between these groups during the early western European Upper Palaeolithic

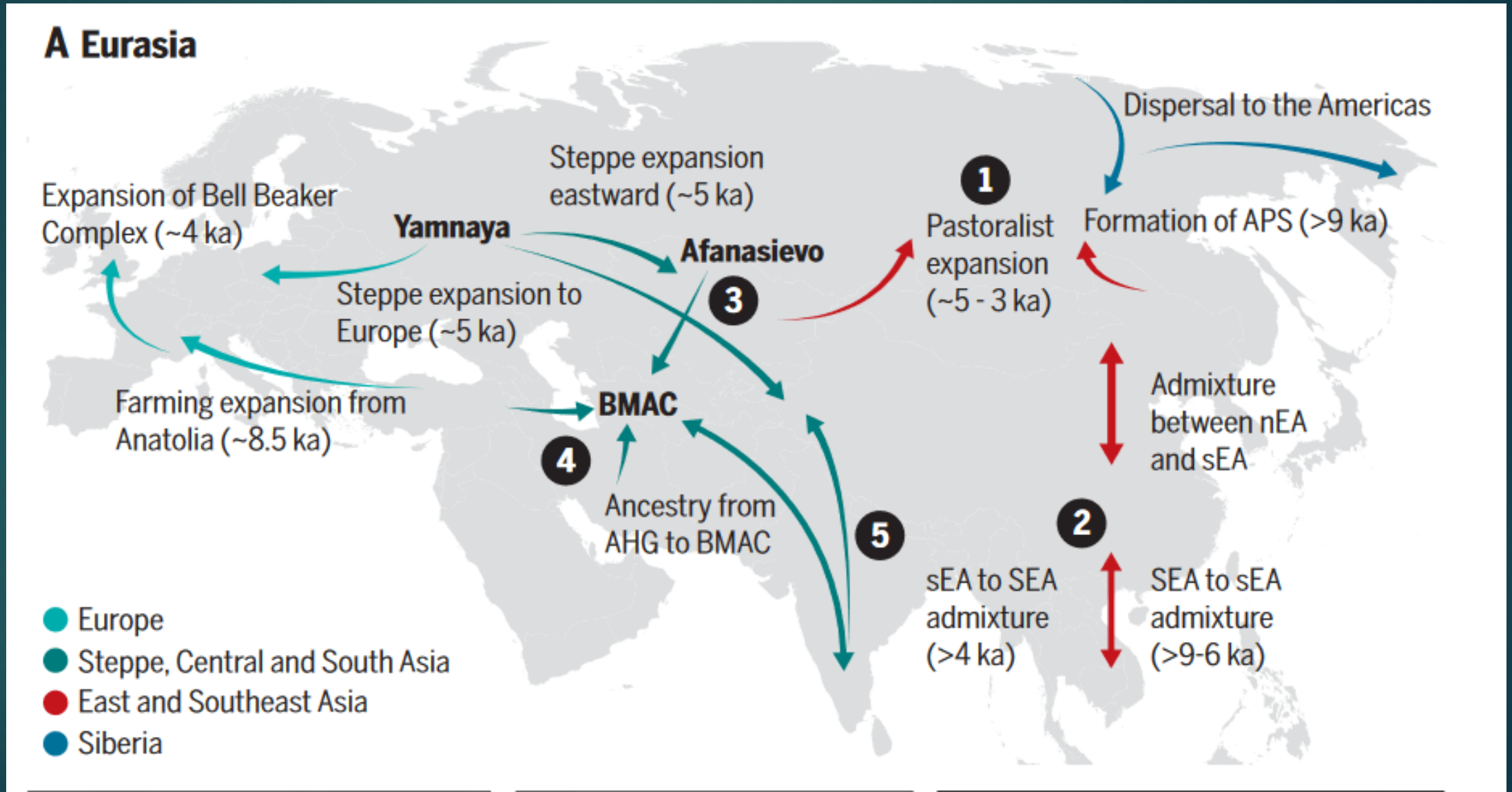
# MH-N co-existence

- ▶ Modelling predicts the appearance of *Homo sapiens* and the Protoaurignacian in France and northern Spain at 42.3 to 42.7 Ka, and the 'extinction' of the Châtelperronian and regional Neandertals at 40 and 40.9 Ka respectively—suggesting a possible overlap of around 1400 to 2800 years between these human groups in the region.
- ▶ Additionally, this chronological overlap appears to be geographically structured, with the Protoaurignacian following a south to north pattern of appearance.
- ▶ Taken together, these observations strengthen the proposition that the initial Upper Paleolithic in this region likely involved a period of co-existence between Neandertals and *Homo sapiens*. The precise nature of this co-existence, however, remains to be resolved

Paleogenetics, Pt. 16  
East Asia and Pacific

May 2023

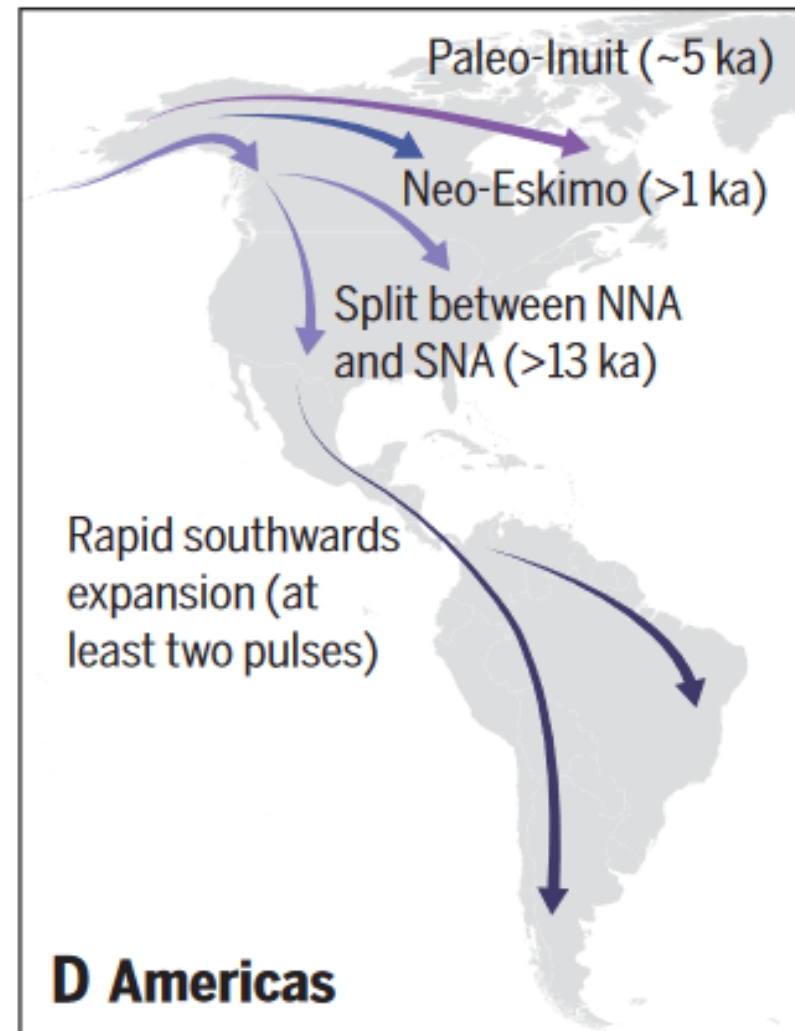
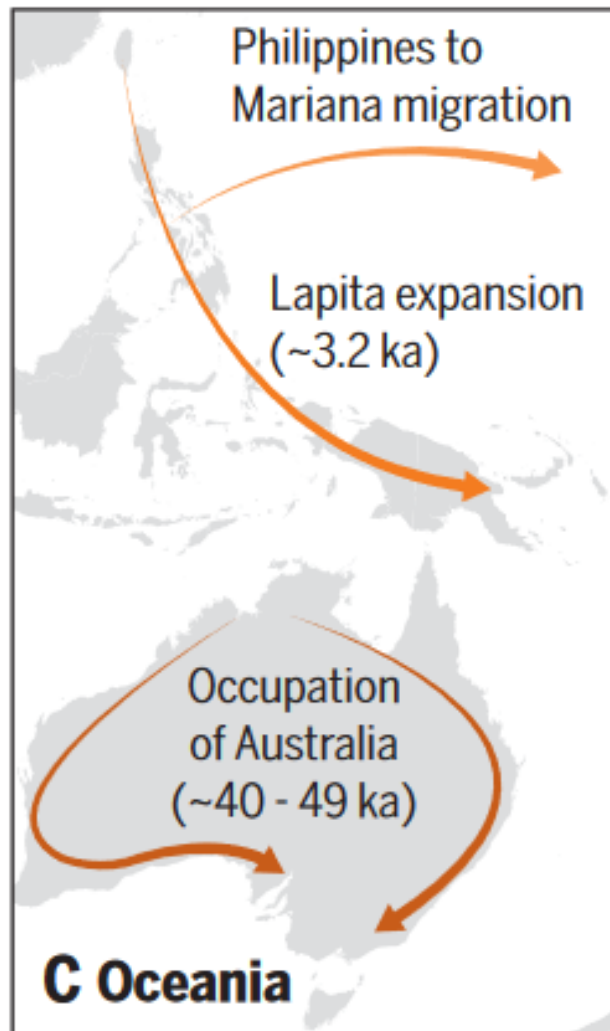
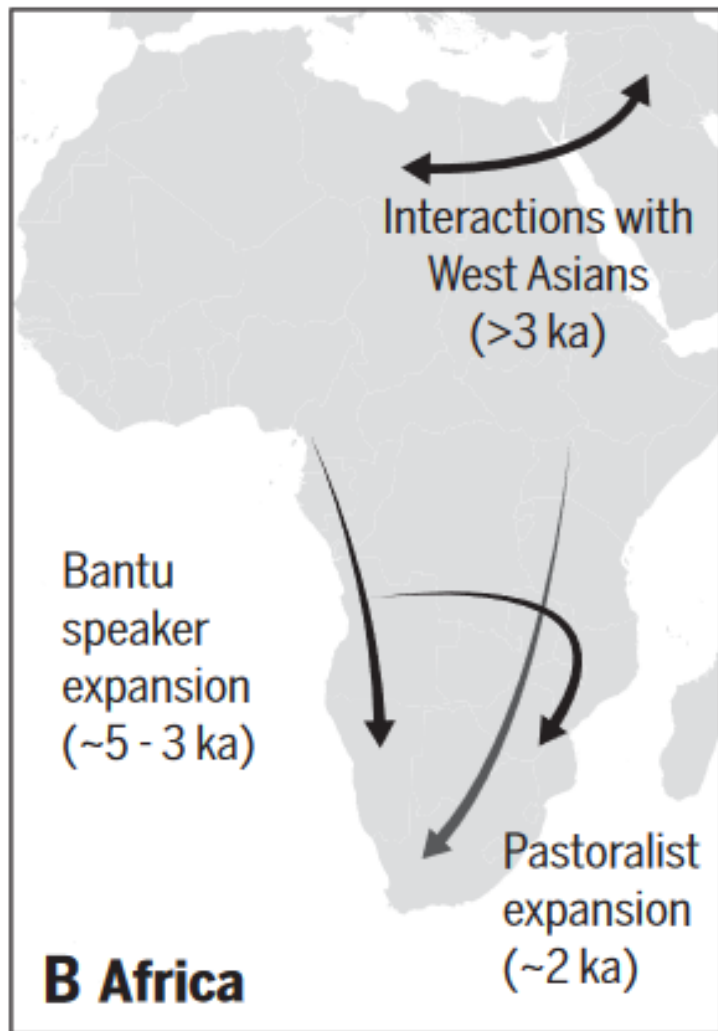
# Major Population Dynamics across the globe after the LGM



# Major population dynamics across the globe after the LGM

(A) **Eurasia**. In Siberia (blue arrows), APS were formed from the admixture between ancient East Asians and ANE. In East Asia and Southeast Asia (red arrows),

- ▶ (1) **Steppe ancestry** was introduced through multiple waves of pastoralist expansion ~5 to 3 ka in Mongolia.
- ▶ (2) Gene flow was detected between **northern East Asians (nEA)** and **southern East Asians (sEA)** as well as sEA and Southeast Asians (SEA) in Steppe, Central and South Asia (dark green arrows).
- ▶ (3) **Steppe expansion to South Asia** ~4 ka.
- ▶ (4) **The formation of BMAC (Bactria-Margiana Archaeological Complex)**–related populations consisted of ancestries from Iranian farmers (60 to 65%) and Anatolian farmers (20 to 25%), with minor contributions from West Siberian hunter-gatherers (~10%) and Andamanese hunter-gatherers (AHG) (2 to 5%).
- ▶ (5) The **mixture of ANI and ASI** led to the main genetic cline in South Asia. In Europe (light blue arrows), farming expanded from Anatolia, and steppe ancestry expanded from Pontic-Caspian-Ural steppe region, with a subsequent expansion of Bell Beaker Complex to the British Isles.



# Major population dynamics across the globe after the LGM

- ▶ (C) **Oceania**. Two major expansion routes included the Lapita expansion and a Philippines to Mariana islands migration. Australia has been occupied by modern humans for ~65 kyr, and neither mitochondrial genomes nor Y chromosomes suggest recent geneflow into Australia.
- ▶ (D) **Americas**. Major events during the peopling of the Americas.
- ▶ (
- ▶ B) **Africa**. Bantu speaker expansion spread agriculture and West African–related ancestry across Africa, and pastoralists expanded from eastern to southern Africa. Africans also showed connections with West Asians.

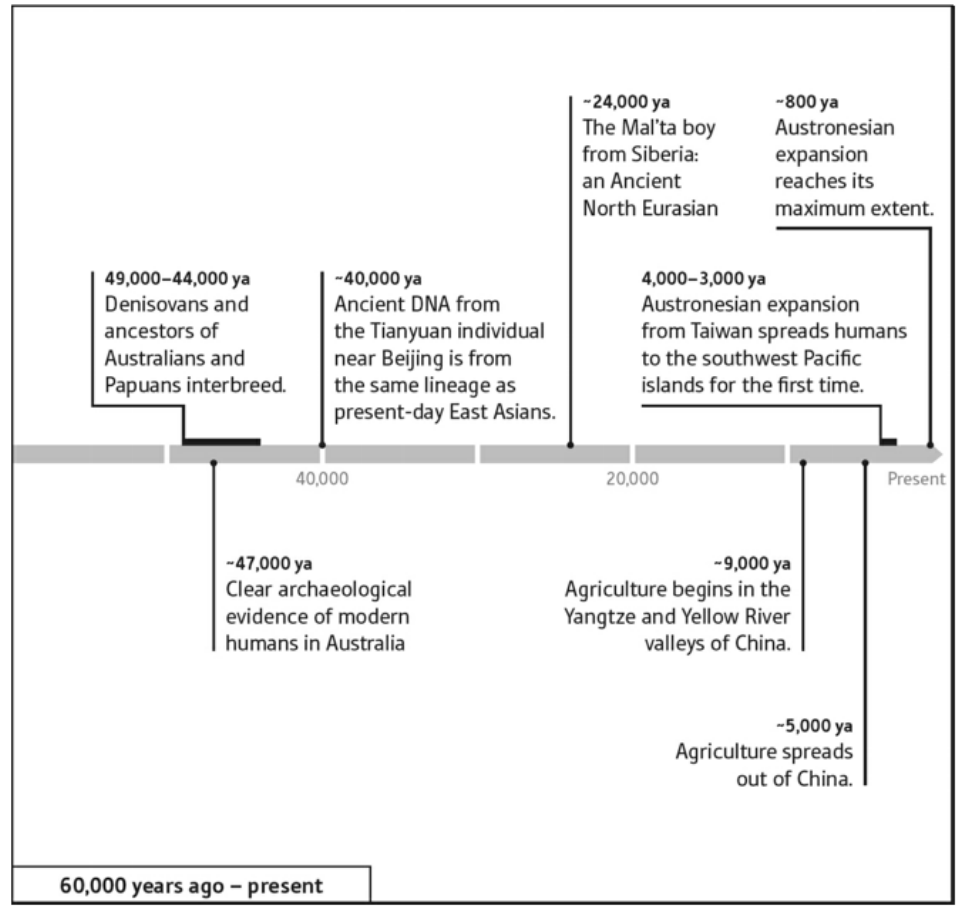
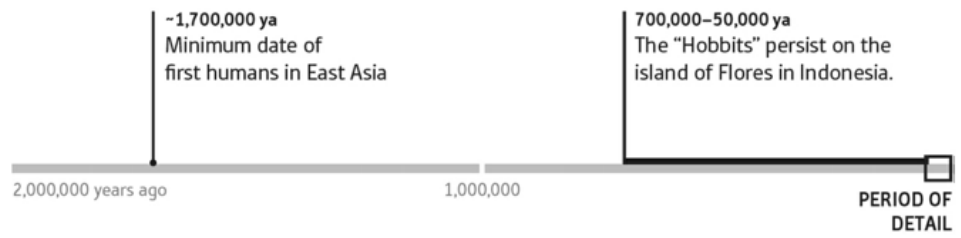


# *Who We Are and How We Got Here*

## Chapter 8, “The Genomic Origins of East Asians,”

- describes how much of East Asian ancestry derives from major expansions of populations from the Chinese agricultural heartland.
- See **Bergström, 2021**

# East Asia and the Pacific



# East Asia and the Pacific

- ▶ -1,700,000 ya Minimum date of first humans (*H. erectus*) in East Asia
- ▶ 700,000-50,000 ya The "Hobbits" persist on the island of Flores in Indonesia.
- ▶ 49,000-44,000 ya Denisovans and ancestors of Australians and Papuans interbreed
- ▶ -47,000 ya (now 65,000 ya) Clear archaeological evidence of modern humans in Australia
- ▶ -40,000 ya Ancient DNA from the Tianyuan individual near Beijing is from the same lineage as present-day East Asians.

# East Asia and the Pacific: 60,000 ya to Present

- ▶ -24,000 ya The Mal'ta boy from Siberia: an Ancient North Eurasian
- ▶ -9,000 ya Agriculture begins in the Yangtze and Yellow River valleys of China.
- ▶ -5,000 ya Agriculture spreads out of China.
- ▶ 4,000-3,000 ya Austronesian expansion from Taiwan spreads humans into the southwest Pacific islands for the first time.
- ▶ -800 ya Austronesian expansion into the Pacific reaches its maximum extent.

# East Asia

- ▶ East Asia—the vast region encompassing China, Japan, and Southeast Asia—is one of the great theaters of human evolution.
- ▶ Has 30% of the world's population and 30% of its language diversity.
- ▶ Pottery was first invented there at least 19 Ka.
- ▶ It was the jumping-off point for the peopling of the Americas before 15 Ka.

# East Asia

- ▶ East Asia witnessed an independent and early invention of agriculture around 9000 years ago.
- ▶ East Asia has been home to the human family for at least around 2.1 million years, the date of the oldest known *Homo erectus* skeleton found in China.
- ▶ *Homo sapiens* after 60 Ka; have lived in East Asia continuously since those times. For example, genetic evidence shows that **the Denisovans** mixed with ancestors of present-day Australians and New Guineans shortly after 50 Ka.

# East Asia

- ▶ One-meter-tall “Hobbits” also persisted until around this same time on Flores island in Indonesia.
- ▶ There has been intense debate about the extent to which the archaic humans of East Asia (i.e. *H. erectus*) contributed genetically to people living today (except as ghost population in Denisovan DNA or as dwarfed Hobbits).
- ▶ Chinese and Western geneticists nearly all agree that present-day humans outside of Africa descend from a dispersal after around 50-60 Ka ago, which largely displaced previously established human groups.

# East Asia

- ▶ Some Chinese anthropologists and archaeologists, on the other hand, have documented similarities in skeletal features and stone tool styles in people who lived in East Asia before and after this time, raising the question of whether there has been some degree of continuity.
- ▶ Our knowledge of East Asian population history is relatively limited: less than 5 percent of published ancient DNA data comes from East Asia.
- ▶ Nearly impossible for researchers to export samples from China and Japan because of government restrictions or a preference that studies be led by local scientists.



## East Asia: no UP tools

- ▶ This has meant that these regions have missed out on the first few years of the ancient DNA revolution In the west, the grand narrative is that sometime after around 50 Ka ago, modern humans began making sophisticated Upper Paleolithic stone tools, which are characterized by narrow stone blades struck in a new way from preprepared cores
- ▶ The Near East is the earliest known site of Upper Paleolithic stone tools and this technology spread rapidly to Europe and northern Eurasia. It would be natural to expect that this UP know-how would have overspread East Asia too. But that is not what happened.

# East Asia

- ▶ The archaeological stone tool pattern in the east does not conform to that in the west.
- ▶ Around 40 Ka ago and across a vast tract of land in China and east of India there is indeed archaeological evidence of the arrival of modern humans.
- ▶ **In Australia**, archaeological evidence of human campsites makes it clear that **modern humans arrived there at least by about 47 Ka (now 65 Ka)**, which is about as old as the earliest evidence for modern humans in Europe.

# MHs arrive in East Asia

- ▶ So it is absolutely clear that modern humans arrived in East Asia and Australia around the same time as they came to Europe.
- ▶ But, puzzlingly, the first modern humans in central and southern East Asia, and those in Australia, did not use Upper Paleolithic stone tools. Instead, they used earlier stone technologies
- ▶ Prompted by these observations, the archaeologists Marta Mirazon Lahr and Robert Foley argued that the first humans in Australia might derive from a migration of modern humans out of Africa and the Near East prior to the development of Upper Paleolithic technology in the west.

# Southern Route hypothesis

- ▶ According to this “Southern Route” hypothesis, the migrants left Africa well before fifty thousand years ago and skirted along the coast of the Indian Ocean, leaving descendants today among the indigenous people of Australia, New Guinea, the Philippines, Malaysia, and the Andaman Islands.
- ▶ **Katerina Harvati** et al. documented skeletal similarities between Australian Aborigines and Africans that, they argued, provide evidence for this model.
- ▶ Southern Route hypothesis was far more than a claim that there were modern humans outside of Africa well before fifty thousand years ago

# Southern Route hypothesis: earlier African exits

- ▶ Evidence of early modern humans outside of Africa well before 50 Ka ago includes the morphologically modern skeletons in Skhul and Qafzeh in present-day Israel that date to between around 130 to 100 Ka ago.
- ▶ Stone tools found at the site of Jebel Faya (Arabia) from around 130 Ka ago are similar to ones found in northeast Africa from around the same time, suggesting that modern humans made an early crossing of the Red Sea into Arabia.

# Southern Route

- ▶ Almost all scholars now agree that there were early dispersals of modern humans into Asia that preceded the widely accepted dispersals after 50 Ka ago
- ▶ The outstanding question raised by the Southern Route hypothesis is not whether such expansions occurred, but whether they had an important long-term impact on humans living today.
- ▶ In 2011, Eske Willerslev led a study that seemed to show that the early expansions indeed left an impact. Europeans share more mutations with East Asians than with Aboriginal Australians, as would be expected from a Southern Route contribution to the lineage of Australia

# Failure of Southern Route theory

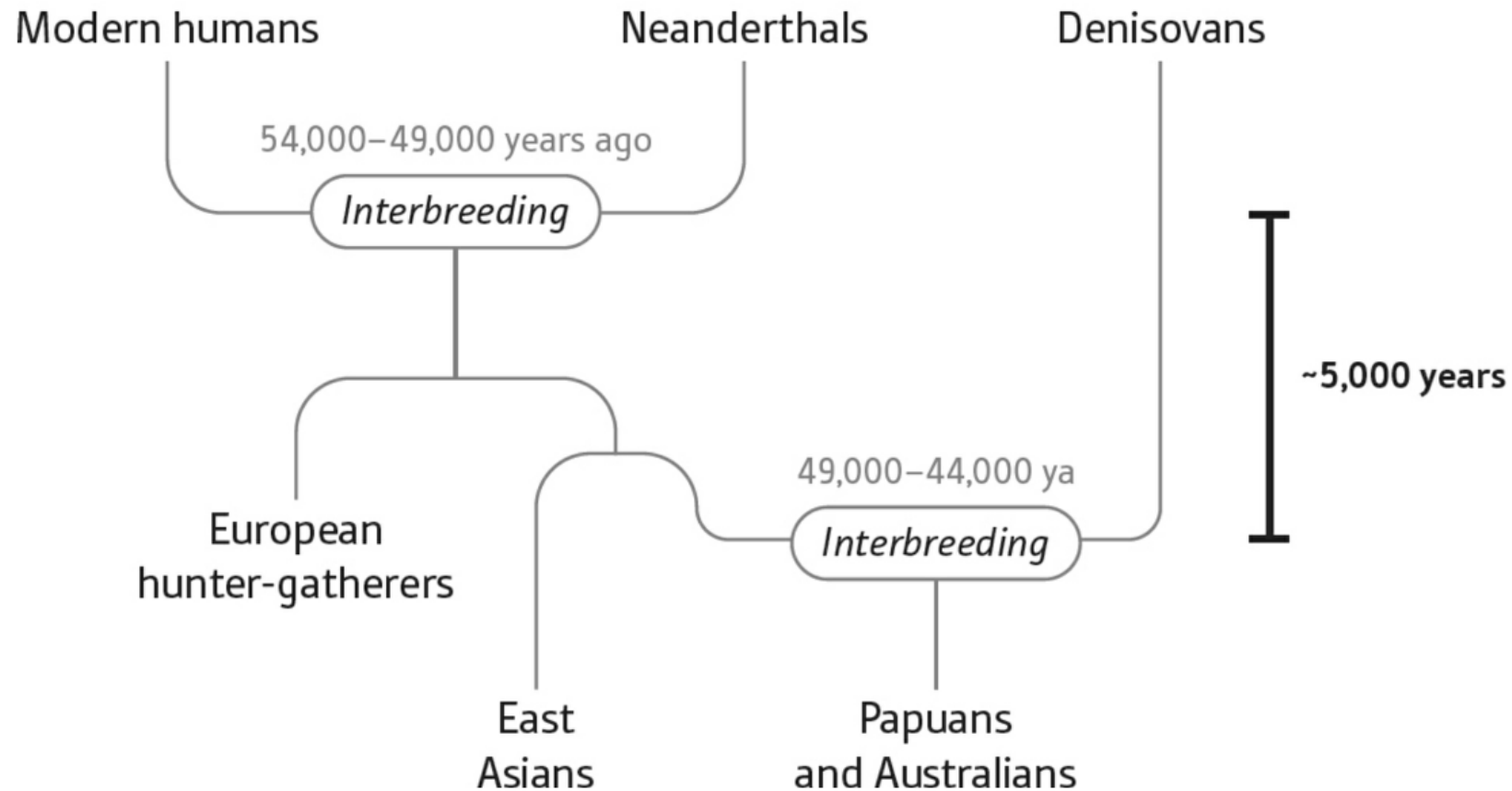
- ▶ Applying a Southern Route migration model to the genomic data, they estimated that Australian Aborigines harbor ancestry from a modern human population that split from present-day Europeans at twice the time depth that East Asian ancestors split from Europeans (75 to 62 Ka ago versus 38 to 25 Ka ago).
- ▶ There was a problem, though, which is that the analysis did not account for the 3 to 6 percent of ancestry that Australians inherited from archaic Denisovans.
- ▶ Because Denisovans were so divergent from modern humans, mixture from them could cause Europeans to share more mutations with Chinese than with Australian Aborigines. Indeed, this explained the findings.

# Denisovan DNA

- ▶ After accounting for Denisovan mixture, Europeans do not share more mutations with Chinese than with Australians, and so Chinese and Australians derive almost all their ancestry from a homogeneous population whose ancestors separated earlier from the ancestors of Europeans.
- ▶ This revealed that a series of major population splits in the history of non-Africans occurred in an exceptionally short time span—beginning with the separation of the lineages leading to West Eurasians and East Eurasians, and ending with the split of the ancestors of Australian Aborigines from the ancestors of many mainland East Eurasians.
- ▶ These population splits all occurred after the time when Neanderthals interbred with the ancestors of non-Africans 54-49 Ka, and before the time when Denisovans and the ancestors of Australians mixed, genetically estimated to be at 49-44 Ka.



## Two Major Population Splits Within About 5,000 Years



Two major splits were sandwiched in an approximately five-thousand-year period between the Neanderthal and Denisovan interbreeding events.

# Failure of Southern Route MHs

- ▶ Even if early modern humans expanded into East Asia via a Southern Route, they were likely also replaced by later waves of human migrants and can be ruled out as having contributed more than a very small percentage of the ancestry of present-day people.
- ▶ The old African *H. sapiens* populations of Eurasia collapsed, and in their place came new groups that swiftly inhabited the landscape. There is no genetic evidence of any substantial ancestry from these earlier populations in present East Asians.

# Why no UP technology: it had not been developed at time of migration

- ▶ What explains how Southeast Asians and Australians missed out on the Upper Paleolithic technology that is so tightly linked with the spread of modern human populations into the Near East and Europe?
- ▶ The first UP long-bladed stone tools in the archaeological record date to between 50 and 46 Ka ago.
- ▶ But genetically, the split of the lineages leading to West Eurasians and East Asians may have been more ancient
- ▶ So the main split of West Eurasian and East Asian ancestors could have occurred before the development of Upper Paleolithic technology, and the geographic distribution of this technology could just reflect the spread of the population that invented it.

# UP tech developed later

- ▶ There is a piece of corroborating evidence for the theory that Upper Paleolithic technology developed after the split of the main lineages leading to West Eurasians and East Asians.
- ▶ The Ancient North Eurasians, known earliest from the approximately 24 Ka remains of the boy from the Mal'ta site in eastern Siberia, are on the lineage leading to West Eurasians, which has always been puzzling for geneticists because the Ancient North Eurasians lived geographically closer to East Asia.
- ▶ But it makes sense in light of the geographic distribution of Upper Paleolithic stone tools, which are associated not just with West Eurasians but also North Eurasians and Northeast Asians. Both the distributions of stone tool technology and of genetic ancestry are as expected if Upper Paleolithic technology came into full flower in a population that lived prior to the separation of the lineages leading to Ancient North Eurasians and West Eurasians, but after the separation of the lineage leading to East Asians.

# MH inventiveness

- ▶ Whatever the reason for the fact that Upper Paleolithic technology never spread to southern East Asia, Upper Paleolithic technology itself was not essential to the successful spread of modern humans into Eurasia after around 50 Ka ago.
- ▶ It was something more profound than Upper Paleolithic stone tool technology—an inventiveness and adaptability that allowed these expanding modern humans to prevail everywhere, including in the east.

# The Beginnings of Modern East Asia

- ▶ The first genomic survey of modern East Asian populations was published in 2009, and reported data on ~2000 individuals from almost seventy-five populations.
- ▶
- ▶ Human diversity is greater in Southeast Asia than in Northeast Asia.
- ▶ They interpreted this evidence of a single wave of modern humans reaching Southeast Asia and then spreading from there northward into China and beyond, following a model in which the genetic diversity of present-day populations can be accounted for by a single population moving out of Africa and spreading in all directions, losing genetic diversity as each small pioneer group budded off.

# Not a south to north migration

- ▶ This model is likely to be of limited use. In Europe there have been multiple population replacements and deep mixtures, and we now know from ancient DNA that present-day patterns of diversity in West Eurasia provide a distorted picture of the first modern human migrations into the region.
- ▶ The model of a south-to-north migration, losing diversity along the way, is profoundly wrong for East Asia.
- ▶ In 2015 Chuanchao Wang: genome wide data from about four hundred present-day individuals from about forty diverse Chinese populations. China had been sparsely sampled in DNA studies because of regulations limiting the export of biological material. Wang and his colleagues therefore did the genetic work in China, and he brought the data to Reich lab electronically.

## 3 clusters in East Asians

- ▶ Found that the ancestry of the great majority of East Asians living today can be described by three clusters.
- ▶ The first cluster is centered on people currently living in the Amur River basin on the boundary between northeastern China and Russia. For more than 8000 years.
- ▶ The second cluster is located on the Tibetan Plateau
- ▶ The third cluster is centered in Southeast Asia = Indigenous populations living on the islands of Hainan and Taiwan off the coast of mainland China.



# East Asians from 2 ancient lineages

- ▶ Our analysis supported a model of population history in which the modern human ancestry of the great majority of mainland East Asians living today derives largely from mixtures—in different proportions—of two lineages that separated very anciently.
- ▶ Members of these two lineages spread in all directions, and their mixture with each other and with some of the populations they encountered transformed the human landscape of East Asia.

# The Ghost Populations of the Yangtze and Yellow Rivers

- ▶ One of the handful of places in the world where farming independently began was China.
- ▶ Starting around 9000 Ka, farmers started tilling the sediments near the Yellow River in northern China, growing millet and other crops.
- ▶ Around the same time, in the south near the Yangtze River, a different group of farmers began growing other crops, including rice.
- ▶ Yangtze River agriculture expanded along two routes—a land route that reached Vietnam and Thailand beginning around 5000 Ka, and a maritime route that reached the island of Taiwan around the same time.

# The Ghost Populations of the Yangtze and Yellow Rivers

- ▶ In India and in central Asia, Chinese agriculture collided for the first time with the expansion of agriculture from the Near East.
- ▶ Today the languages of mainland East Asia comprise at least eleven major families: Sino-Tibetan, Tai-Kadai, Austronesian, Austroasiatic, Hmong- Mien, Japonic, Indo-European, Mongolie, Turkic, Tungusic, and Koreanic.
- ▶ Peter Bellwood has argued that the first six correspond to expansions of East Asian agriculturalists disseminating their languages as they moved.

## Yangtze River Ghost Population,

- ▶ In Southeast Asia and Taiwan, there are many populations that derive most or all of their ancestry from a homogeneous ancestral population.
- ▶ Since the locations of these populations strongly overlap with the regions where rice farming expanded from the Yangtze River valley, it is tempting to hypothesize that they descend from the people who developed rice agriculture.
- ▶ Do not yet have ancient DNA from the first farmers of the Yangtze River valley, but Reich thinks that they will match this reconstructed “Yangtze River Ghost Population,” the name given the population that contributed the overwhelming majority of ancestry to present-day Southeast Asians.

## Yangtze River Ghost Population,

- ▶ Found that Han Chinese (1.2 billion)—is not consistent with descending directly from the Yangtze River Ghost population.
- ▶ Han also have a large proportion of ancestry from another deeply divergent East Asian lineage, found in northern Han.
- ▶ The Han harbor subtle differences along a north-to-south gradient. This pattern is as expected from a history in which the **ancestors of the Han** radiated out from the north and mixed with locals as they spread south.

## Yellow River Ghost Population

- ▶ What could the other ancestry type be?
- ▶ The Han, who unified China in 202 BCE, are believed to have emerged from the earlier Huaxia tribes who themselves emanated from earlier groups in the Yellow River Valley of northern China.
- ▶ This was one of the two Chinese regions where farming originated, and it is also the place from which farming spread to the eastern Tibetan Plateau beginning around 36 Ka.

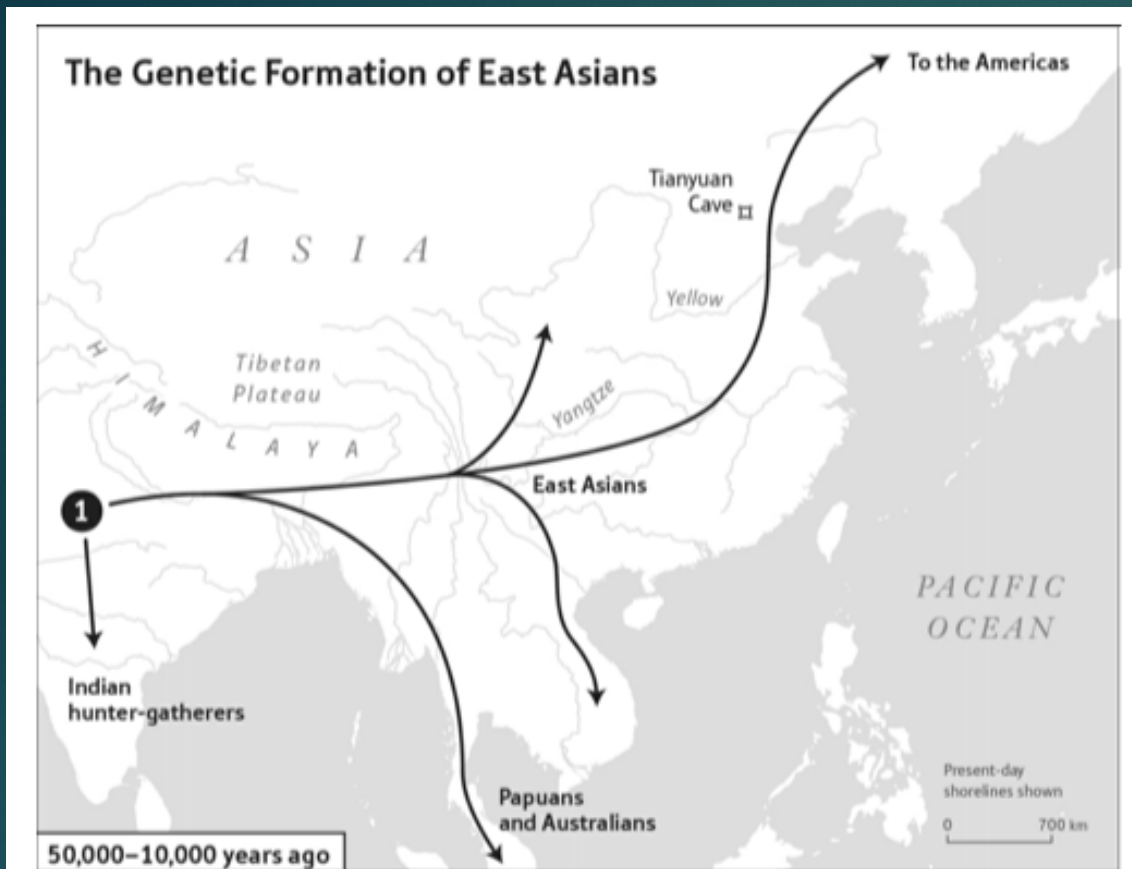
# Yellow River Ghost Population

- ▶ Wang built a model of deep East Asian population history: he found that the Han and Tibetans both harbored large proportions of their ancestry from a population that no longer exists in unmixed form and that we could exclude as having contributed ancestry to many Southeast Asian populations.
- ▶ Called this the “Yellow River Ghost Population,” hypothesizing that it developed agriculture in the north while spreading Sino-Tibetan languages.
- ▶ Ancient DNA from the first farmers of the Yellow River Valley will reveal whether this conjecture is correct.

# The Great Admixtures At the East Asian Periphery

- ▶ The peoples of the Tibetan Plateau—who harbor a mixture of about two-thirds of their ancestry from the same Yellow River ghost population that contributed to the Han—are one example of this expansion.
- ▶ They likely brought farming for the first time to the region, as well as about one-third of their ancestry from an early branch of East Asians that plausibly corresponds to Tibet's indigenous hunter-gatherers.
- ▶ Another example is the Japanese. For many tens of thousands of years, the Japanese archipelago was dominated by hunter-gatherers, but after around 2300, mainland-derived agriculture began to be practiced and was associated with an archaeological culture with clear similarities to contemporary cultures on the Korean peninsula.





Between 50 and 10 Ka, hunter-gatherer groups diversified and spread northeast toward the Americas and southeast toward Australia.

By 9 Ka, two very divergent populations from this initial radiation—one centered on the northern Yellow River and one on the Yangtze River—independently developed agriculture, and then by 5 Ka spread in all directions. In China, their collision created the gradient of northern and southern ancestry seen in the Han today.

# Japan: 2 ancestries

- ▶ The genetic data confirm that the spread of farming to the islands was mediated by migration.
- ▶ Modeling present-day Japanese as a mixture of two anciently divergent populations of entirely East Asian origin—one related to present-day Koreans and one related to the Ainu who today are restricted to the northernmost Japanese island and whose DNA is similar to that of pre-farming hunter-gatherers.
- ▶ Present-day Japanese have about 80 percent farmer and 20 percent hunter-gatherer ancestry.
- ▶ The average date of mixture to be around 1600 years ago

# Deep history of humans in mainland Southeast Asia

- ▶ This date is far later than the first arrival of farmers to the region and suggests that after their arrival, it may have taken hundreds of years for social segregation between hunter-gatherers and farmers to break down.
- ▶ The date corresponds to the Kofun period, the first time when many Japanese islands were united under a single rule, perhaps marking the beginnings of the homogeneity that characterizes much of Japan today.

# Southeast Asia: language spread thru migration

- ▶ In ancient Vietnam, all the samples were a mixture of an early splitting lineage of East Eurasians and the Yangtze River Ghost Population, with the proportion of the Yangtze River Ghost Population higher in some of the Man Bac farmers than in others.
- ▶ The main group of Man Bac farmers also had proportions of ancestry from these two lineages that were similar to those seen in present-day speakers of isolated Austroasiatic languages.
- ▶ These findings are consistent with the theory that Austroasiatic languages were spread by a movement of rice farmers from southern China who interbred with local hunter-gatherers

# Vietnam

- ▶ Even today, large Austroasiatic-speaking populations in Cambodia and Vietnam harbor substantial albeit smaller proportions of this hunter-gatherer ancestry.
- ▶ In another study, Lipson showed that in western Indonesia where Austronesian languages are predominant, a substantial share of the ancestry comes from a population that derives from the same lineages as some Austroasiatic speakers on the mainland.
- ▶ Lipson's discovery suggested that Austroasiatic speakers may have come first to western Indonesia, followed by Austronesian speakers with very different ancestry.

# Austronesian expansion

- ▶ The most impressive example of the movements of farmers from the East Asian heartland to the periphery is the Austronesian expansion.
- ▶ Today, Austronesian languages are spread across a vast region including hundreds of remote Pacific islands.

# Into the Pacific

50 slides

## #6: Austronesian Origins?



- Austronesian migration: Tonga and Samoa 8000 years ago, 5000 ago to Taiwan, 4000 ago to Philippines and New Guinea
- 1300 years ago: Indonesia to Madagascar by boat



# Oceania: Pacific – Lapita culture

- ▶ The pivotal moment in Pacific archaeological history happened in 1952, when a team of researchers found a cache of dentate-stamped pots at a place called Lapita in New Caledonia, a French collectivity to the southwest of Vanuatu.
- ▶ More than 200 sites eventually turned up nearly duplicate versions of this innovation across an enormous span of the region. The pots were often found with particular varieties of preserved plants and nuts, as well as stone adzes.
- ▶ 2003 discovery of skeletons at Teouman, Island nation of Vanuatu: first ancient DNA in the Pacific

# The Ghosts of Teouma

- ▶ **Vanuatu** is a volcanic archipelago of more than 80 islands littered in an extended slingshot shape across an 800-mile arc of South Pacific
- ▶ By some measures, **Vanuatu is per capita the most linguistically diverse country on the planet**: Its quarter-million citizens, predominantly the native ni-Vanuatu, speak as many as 140 different indigenous languages and maintain an astonishing variety of cultural practices.
- ▶ Eventually reached by people in outriggers.
- ▶ Archaeologists came to identify these first voyagers with a set of jars and tools unique to the region, the “Lapita cultural complex,” and determined that they crossed the boundary into Remote Oceania some 3,000 years ago.

# Lapita Culture Pottery: dentate stamped pattern



The pivotal moment in Pacific archaeological history happened in 1952, when a team of researchers found a cache of dentate-stamped pots at a place called Lapita in **New Caledonia**, an island to the southwest of Vanuatu. More than 200 sites eventually turned up nearly duplicate versions of this innovation across an enormous span of the region.

# Lapita culture

- ▶ **Lapita culture of the Western Pacific** is primarily the easterly expansion of the Island SE Asian Neolithic, that **originates in Taiwan perhaps 5500 years ago as pottery using farmers**.
- ▶ It then spreads through the Philippines and Eastern Indonesia shortly after 4000 years ago, and just over **3000 years ago appears in the Western Pacific as the Lapita culture**.
- ▶ This spreads from the islands off New Guinea's eastern end through Solomons, Vanuatu, New Caledonia, Fiji and on to Tonga and Samoa.
- ▶ There is then a major pause until just over 1000 years ago in Western Polynesia before descendant groups spread to places such as Hawaii, Easter Island and finally to New Zealand about 700 years ago.

# Lapita Culture

- ▶ Whoever made those pots some 3,000 years ago had traveled across more than 2,000 miles of ocean — from near Papua New Guinea to Tonga and Samoa — in perhaps as little as 10 generations.
- ▶ Where had this “Lapita” culture come from, and who were the people associated with it?

# Out of Taiwan

- ▶ A population of early farmers departed from Taiwan about 5,000 years ago, with the help of the newly developed outrigger canoe.
- ▶ They moved down through the Philippines and the Spice Islands, along the northern coasts of New Guinea and eventually out to the Bismarck Archipelago, more or less the limit of Near Oceania; the “tracer dye” for their path was the language family they left behind, one known as Austronesian
- ▶ Along the way, they encountered populations of “Papuan” — a generic shorthand for highly distinct groups of people who had been in the Papua New Guinea region for 40,000 years.

# Oceania

- ▶ The interactions between the incoming “Austronesians,” another shorthand for whoever was presumably spreading those languages, and the indigenous Papuans created the constellation of practices that would become known as Lapita.
- ▶ Finally, the people now associated with Lapita sailed into the open ocean for the first time, crossing the Remote Oceania divide to Vanuatu and, from there, outward to the farthest reaches of the Pacific.

# Spread in the Pacific: 1<sup>st</sup> Taiwanese, then Papuans

- ▶ **Austronesian languages & islands:**
- ▶ Indonesians, Madagascar via people movements
- ▶ Deepest genetics in Taiwan; expanse thru Philippines; then open Pacific, then Polynesia
- ▶ All have Taiwanese genetic background
- ▶ Solomon Islands by 50 Ka, New Caledonia by 3000 y ago;
- ▶ All are originally east Asian, Taiwanese; but then New Guianan/Papuan genetics takes over;
- ▶ 1<sup>st</sup> Taiwanese, then Papuans



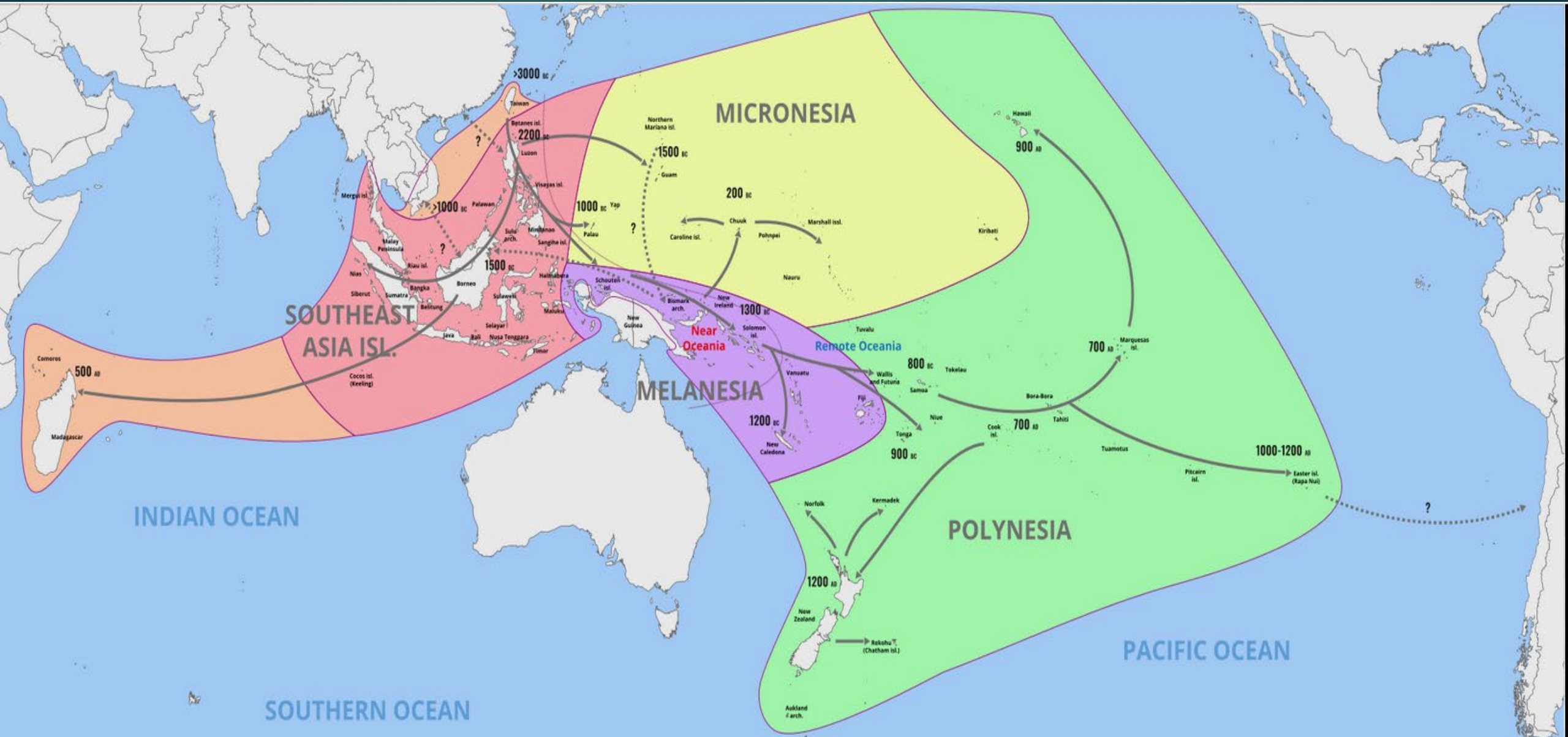
# Vanuatu

- ▶ The people of contemporary Vanuatu are black, like the Papuan people of New Guinea, but they speak Austronesian languages that can ultimately be traced to Asia.
- ▶ Reich believed that the existing consensus was the perfect sort of hypothesis to put to the ancient-DNA test. The Austronesians and the Papuans had been separated by at least 40,000 years of genetic differentiation,

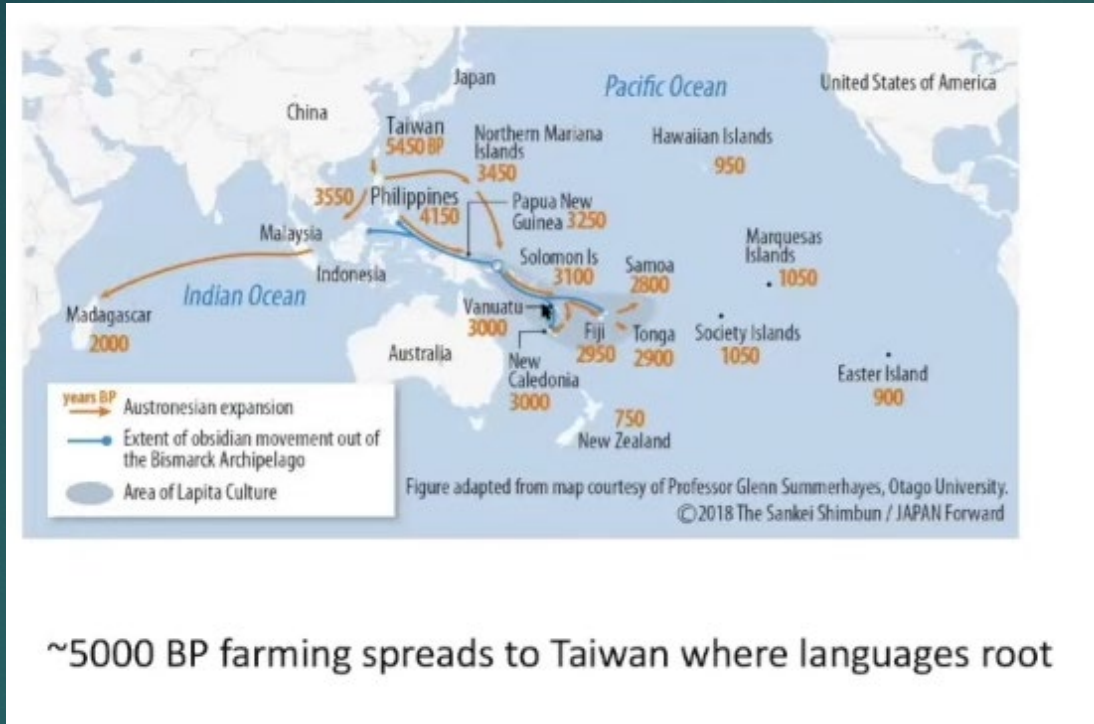
# SW Pacific: First Remote Oceanians

- ▶ Would the samples taken from the skulls at Teouma show a closer relationship to the people of nearby Papua or the people of distant Asia?
- ▶ In October 2016, the Skoglund paper, was published in Nature as “Genomic Insights Into the Peopling of the Southwest Pacific.”
- ▶ The analysis of ancient DNA from three 3,000-year-old skulls from Teouma, along with one skull dated a few hundred years later from Tonga, appeared to provide unambiguous confirmation of Lapita genetic ancestry. The **First Remote Oceanians**, as the paper calls them, were not, after all, a heterogenous group; they were of unmixed Asian descent.

# Surprises in South Pacific



# Archeology and linguistic evidence of expansion into remote Oceania



Early data indicate no people in islands until after 3000 ya

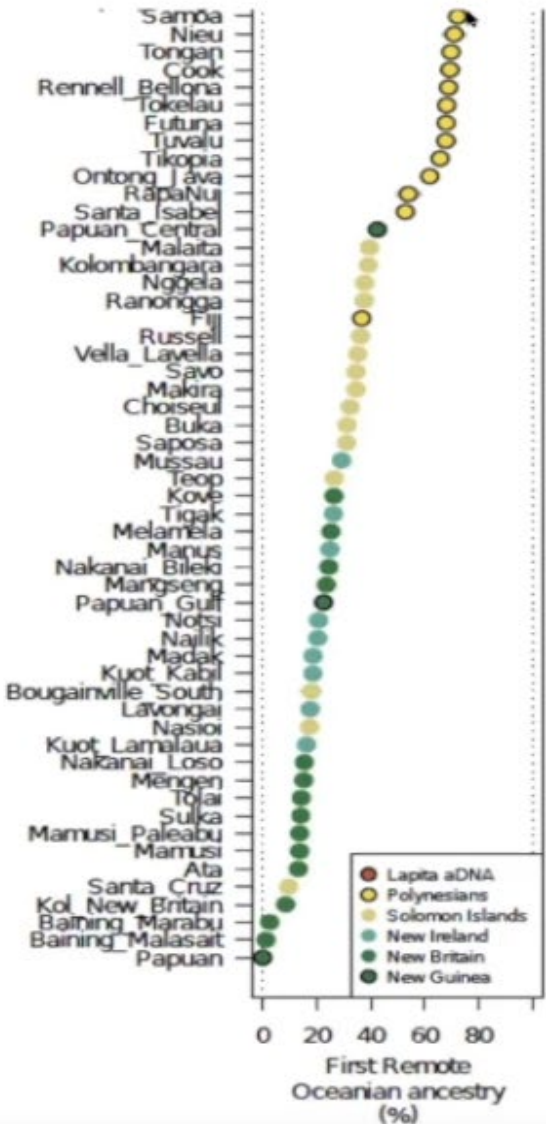
~4000 BP probable invention of outrigger canoe; spread to Philippines and east New Guinea

~3300 BP appearance of the Lapita pottery in New Guinea and first spread of humans beyond Near Oceania

~2000-800 BP expansion of humans east to Hawaii, New Zealand, Easter Island, and west to Madagascar

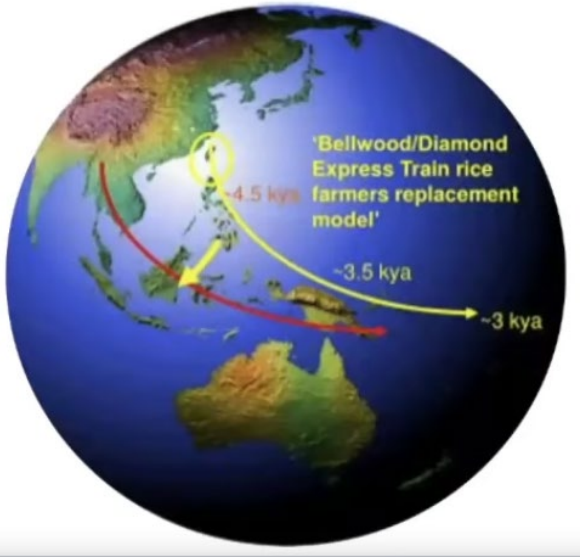


# Today All Near and Remote Oceanians Have Papuan ancestry



## Model 1 predominant in genetics until 2016:

The >25% Papuan ancestry in Pacific people is due to mixture that happened in New Guinea region during the Lapita expansion (Kayser et al. 2010; Matisoo-Smith et al. 2015)



## Model 2: Near complete bypass

# 3000-2500 BP samples from Lapita contexts

Skoglund et al. 2016

3 samples from Vanuatu

1 sample from Tonga

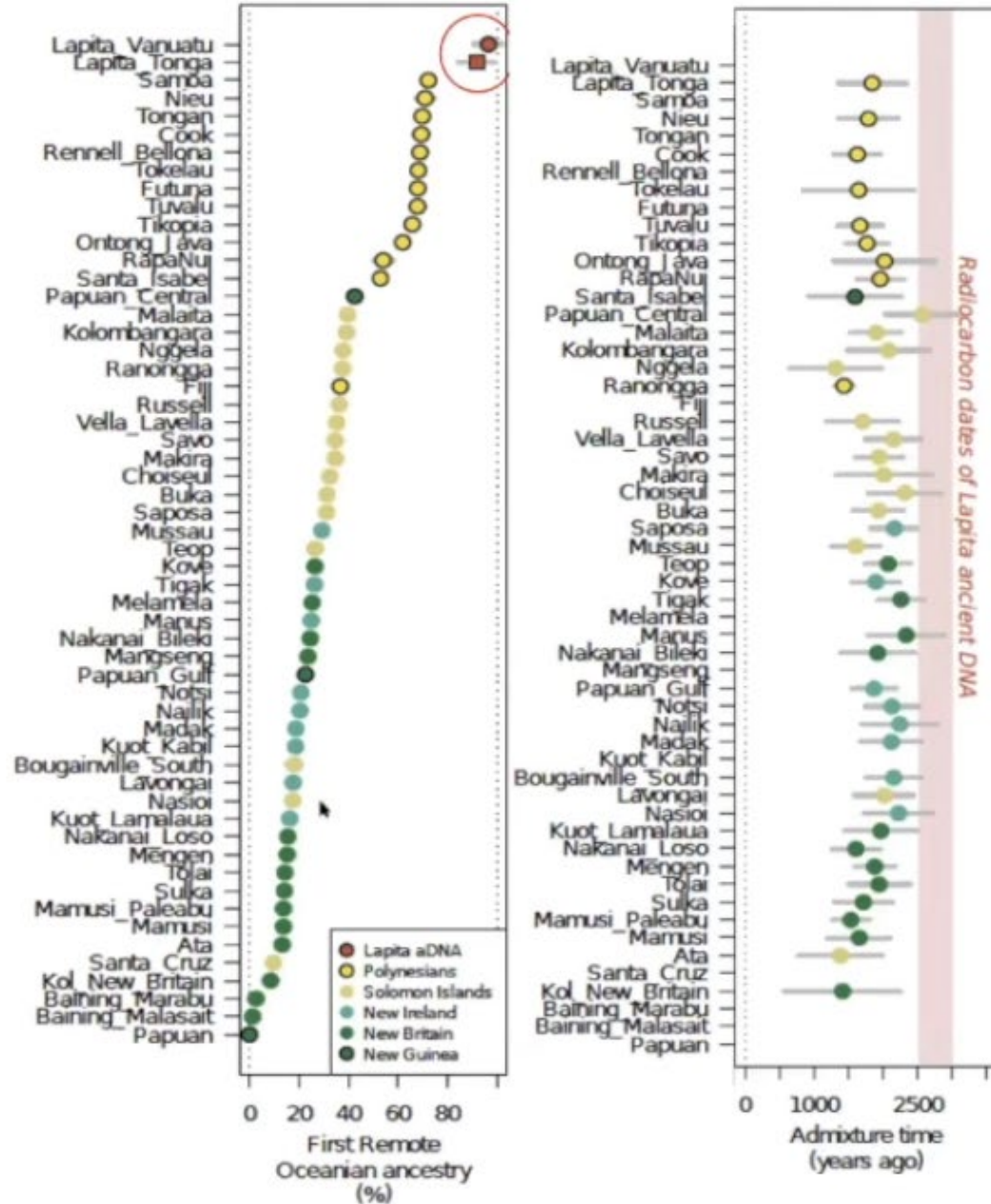
## Model 1 Disproved

Lapita 0-5% Papuan ancestry

Today even Polynesians >25%

Polynesians cannot be simple descendants of first Lapita

Mixture is too late



2500 y  
after Lapita  
spread



# The complex genetic history of peoples in Vanuatu

- ▶ Two major ancient DNA studies were published in 2018 that, together with analyses of genomes from contemporary peoples, gave insights into the genetic history of populations in Vanuatu
  - ▶ Posth et al. "Language continuity despite population replacement in Remote Oceania", and
  - ▶ Lipson et al. "Population Turnover in Remote Oceania Shortly after Initial Settlement"
- ▶ Together they show that the earliest inhabitants of Vanuatu were from the Lapita culture with East Asian genetic ancestry.



# Genetic history of peoples in Vanuatu

- ▶ But beginning around 2,500 years ago Papuans from the Bismark Archipelago began to migrate into the region; their genetic contributions continued up until the present day and have almost completely supplanted the East Asian signal of ancestry.
- ▶ However, many of the languages of contemporary peoples of Vanuatu descend from the Lapita. This finding highlights how genetic heritage cannot necessarily be inferred from cultural/linguistic identity and vice versa:

# Taiwan and the Pacific

- ▶ Archaeological, linguistic, and genetic data taken together have suggested that **around 5000 years ago, mainland East Asian farming spread to Taiwan**, where the deepest branches of the Austronesian language family are found.
- ▶ These farmers spread southward to the Philippines about 4000 years ago, and **farther south around the large island of New Guinea and into the smaller islands to its east.**
- ▶ When they spread from Taiwan, they **probably invented outrigger canoes**, boats with logs propped on the side that increase their stability in rough waters, making it possible to **navigate the open seas.**

# Lapita Culture and Polynesia

- ▶ After 3300 years ago, ancient peoples making pottery in a style called Lapita appeared just to the east of New Guinea and soon afterward started expanding farther into the Pacific, quickly reaching Vanuatu 3000 kilometers from New Guinea.
- ▶ It took only a few hundred more years for them to spread through the western Polynesian islands including Tonga and Samoa, and then, after a long pause lasting until around 1200 years ago, they spread to the last habitable Pacific islands of New Zealand, Hawaii, and Easter Island by 800 years ago
- ▶ Whoever made those pots some 3,000 years ago had traveled across more than 2,000 miles of ocean—in perhaps as little as 10 generations.
- ▶ As Patrick V. Kirch, the dean of American archaeology in the Pacific, once put it, “Without a doubt, the Lapita colonization of Remote Oceania ranks as one of the great sagas of world prehistory.”

# Austronesian expansion from Taiwan

- ▶ The Austronesian expansion to the west was equally impressive, reaching Madagascar off the coast of Africa, and explaining why almost all Indonesians today as well as people from Madagascar speak Austronesian languages.
- ▶ Nearly all Austronesian language speakers harbor at least part of their ancestry from a population that is more closely related to aboriginal Taiwanese than it is to any mainland East Asian population. This supports the theory of an expansion from the region of Taiwan.
- ▶ Some geneticists balked at the suggestion that the first humans who peopled the remote islands of the Southwest Pacific during the Lapita dispersal were unmixed descendants of farmers from Taiwan

# Immigration dilemma

- ▶ How could these migrants have passed over the region of Papua New Guinea, occupied for more than forty thousand years, without mixing with its inhabitants?
- ▶ Today, all Pacific islanders east of Papua New Guinea have at least 25 percent Papuan ancestry. Papuan ancestry was subsequently diluted through admixture but remains at least 80%–90% in most islands.
- ▶ How could this fit with the prevailing hypothesis that the Lapita archaeological culture was forged during a period of intense exchange between people ultimately originating in the farming center of China (via Taiwan) and New Guineans?
- ▶ In 2016, ancient DNA struck again, disproving the view that had prevailed until then in the genetic literature.

# Vanuatu and Tonga

- ▶ Reich: DNA from 4 skulls of the Lapita pottery culture in the Pacific islands of Vanuatu and Tonga who lived from around 3000 to 2500 years ago.
- ▶ Far from having substantial proportions of Papuan ancestry, found that in fact these 3000 yo skulls had little or none.
- ▶ This showed that there must have been a later major migration from the New Guinea region into the remote Pacific.

# Vanuatu

- ▶ The late migration must have begun by at least 2400 years ago, as all the Vanuatu samples we have analyzed from that time and afterward had at least 90 percent Papuan ancestry.
- ▶ How this later wave could have so comprehensively replaced the descendants of the original people who made Lapita pottery and yet retained the languages these people probably spoke remains a mystery.
- ▶ But the genetic data show that this is what happened.

# 3 immigrations

- ▶ Analyzed the Papuan ancestry in Vanuatu, found that it was more closely related to that in groups currently living in the Bismarck Islands near New Guinea than to groups currently living in the Solomon Islands—despite the fact that the Solomon Islands are directly along the ocean sailing path to Vanuatu.
- ▶ Found that the Papuan ancestry present in remote Polynesian islands is not consistent with coming from the same source as that in Vanuatu.
- ▶ Thus there must have been not one, not two, but at least three major migrations into the open Pacific,
  - ▶ with the first migration bringing East Asian ancestry and the Lapita pottery culture,
  - ▶ the later migrations bringing at least two different types of Papuan ancestry.
  - ▶ So instead of a simple story, the spread of humans into the open Pacific was highly complex.



# Multiple Waves of Migration to Oceania







Ancient DNA shows that the first people of the southwest Pacific islands had none of the Papuan ancestry ubiquitous in the region today and that first arrived in New Guinea after 50 Ka (top) (1). The pioneer migrants had almost entirely East Asian ancestry (2). and later streams of migration brought primarily Papuan ancestry (3).



A young Ni-Vanuatu boy.

Majority of the Lapita East Asian ancestry appears to come from female rather than male ancestors.

This suggests the Papuans who arrived on the islands were mainly men who mixed with females from the Lapita culture who were already living there.

Two great gene pools - the Papuan and the Asian First Remote Oceans

Blond hair evolved independently in Melanesia

# Three skulls of Teouma

- ▶ In 2014, **Stuart Bedford** got a call from genetics lab at Harvard.
- ▶ They wanted to know **whether Bedford might facilitate access to the 3 skulls discovered at Teouma**. Bedford agreed. It was the first successful DNA extraction from ancient samples taken from the tropics. The remains date to around 3,110 to 2,710 years old. Over the next four years, the **Harvard team used the DNA they found to present a radical new story about Remote Oceania's first settlers.**
- ▶ **Ancient DNA from Southeast Asia revealed at least three major waves of human migration over the last 50,000 years.**

1 of three 3000-year-old skulls found among 100 skeletons;  
found in a large cemetery on Efate Island in Vanuatu and one  
from the Talasiu site in Tonga.



# Southeast Asia

- ▶ The **large studies of ancient genetic diversity from Southeast Asia** were published in 2018 year by Lipson et al. and McColl et al..
- ▶ Together these studies show that farming populations migrated from China throughout Southeast Asia approximately 5000-4000 years ago, mixing with mainland Hòabìnhians (but not completely replacing them).
- ▶ **Initial Austronesian settlement was followed by several Papuan gene flow events.**
- ▶ This complex history of migrations helps to settle a long-term debate among archaeologists, linguists, and biological anthropologists.

# Oceania

- ▶ Region had racialized archeological theorizing:
  - ▶ Early Europeans fixated on the differences between the Melanesians and the Polynesians,
    - ▶ imagining the Polynesians as a kind of laggard aristocracy, comparable to the ancient Greeks, and
    - ▶ the Melanesians as naturally backward black people.
  - ▶ Natural relationship of incoming enlightenment and indigenous savagery theory:
    - ▶ lighter skinned Polynesians vs darker New Guineans.



# Racialized history

- ▶ When it came to the question of how ancient peoples had populated the Pacific, the most persistent proposals rested on racial typologies.
- ▶ The **Melanesians** obviously came from in and around Papua, which was relatively nearby and inhabited by “savage” black people, whereas the lighter-skinned and more “advanced” **Polynesians** probably sojourned via heroic open-sea navigation from Asia.
- ▶ **Anything “superior”** — technology or social structure — was linked to the migratory intervention of exceptional groups from distant shores.
- ▶ The **European colonial enterprise** was thus justified as part of the natural relationship of incoming enlightenment and indigenous savagery.

# Problematic DNA

- ▶ The 2016 Skoglund paper was accepted over the steadfast objections of two of the three peer reviewers on its anonymous panel. Confidential documents made reveal deep concerns with the paper's methods and its conclusions: 3 skulls did not fit the skeletons.
- ▶ The study's authors, the objecting reviewers insist, had made disproportionate or even wholly unwarranted claims on the basis of both the archaeological and genetic evidence they had provided.
- ▶ Yes, the Teouma skulls came from an important site, and yes, the new data they provided was a fascinating additional piece of evidence.
- ▶ But they still just represented three samples from one site on one island; too small a sample for large conclusions. Paper was originally rejected. Later addition of petrous bone from Tonga; Paper accepted. Reich believes data is solid.

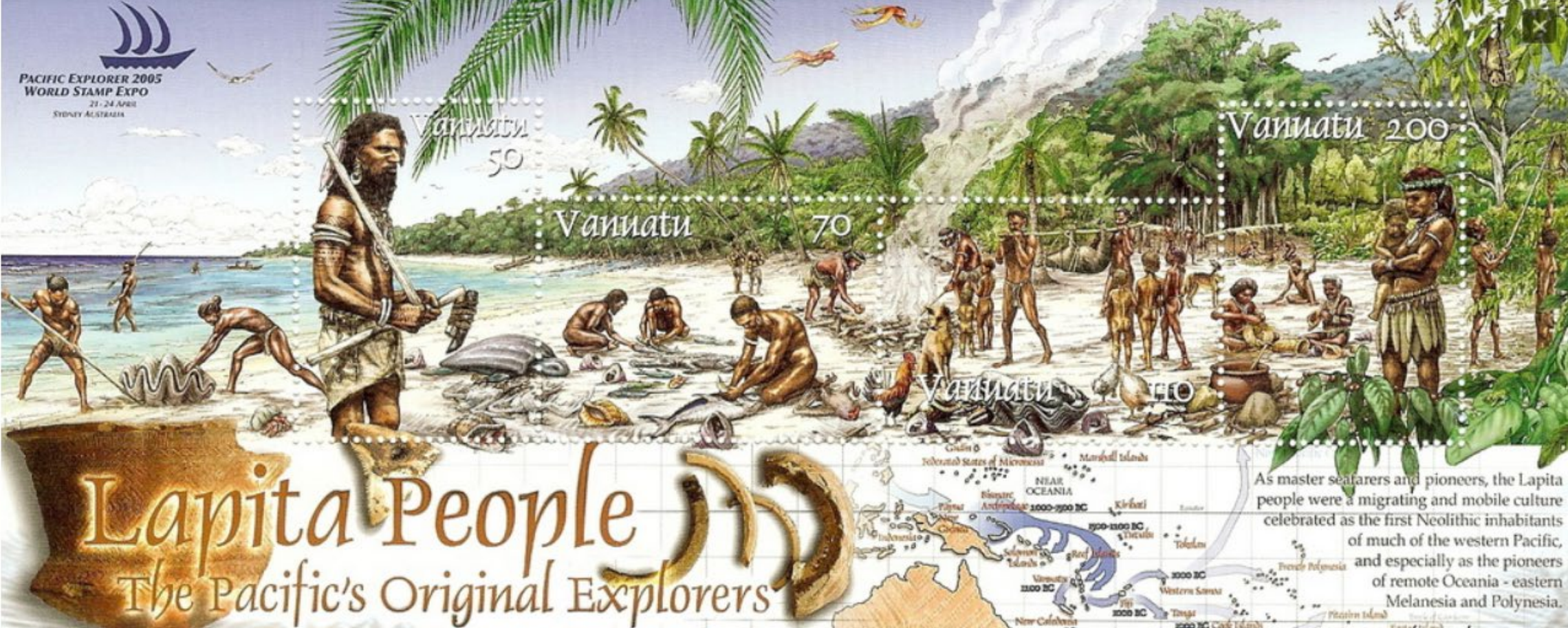
# Fears of the indigenous groups

- ▶ After the publication of 2016 paper, the indigenous Kanaks of “neighboring” New Caledonia declared a three-year moratorium on any genetic research, for fear that their limited sovereignty might be undermined.
- ▶ Paper’s conclusion: current ni-Vanuatu’s ancestors were not Lapita after all, but latecomers to an archipelago first settled by purely Asian expeditions.
- ▶ Native concern that outsiders said that their donated spit held secrets about the past, the ni-Vanuatu might worry that those secrets — if these foreigners said they were “actually” from elsewhere, indeed latecomers to their own nation — could nullify their rights to the land

# Oceania

- ▶ Recent genomic analyses show that the earliest peoples reaching Remote Oceania—associated with Austronesian-speaking Lapita culture—were almost completely East Asian, without detectable Papuan ancestry.
- ▶ However, Papuan-related genetic ancestry is found across present-day Pacific populations, indicating that peoples from Near Oceania have played a significant, but largely unknown, ancestral role

# 2005 Postage Stamp of Vanuatu Lapita People



Note dark skin color of original Lapita founders

# Vanuatu Origin Story

- ▶ For peoples around the world today, **these new theories about origin and migration can have destabilizing implications.**
- ▶ In the South Pacific nation of Vanuatu, a few thousand kilometers northeast of Australia, the **national postal dept. issued stamps that commemorated the first settlers** on their remote shores.
- ▶ In an artist's recreation of the founding scene, the **people were drawn to resemble the country's black modern inhabitants**, an indigenous group called the ni-Vanuatu.
- ▶ Recent aDNA work has suggested that the **original settlers were in fact the distant descendants of a group of light skinned migrants from East Asia** — people who looked nothing like the contemporary ni-Vanuatu.
- ▶ Do they need a new origin story?

# Language continuity despite population replacement in Remote Oceania – C. Posth, et al., 2018

- ▶ The earliest peoples reaching Remote Oceania—associated with Austronesian-speaking Lapita culture—were almost completely East Asian, without detectable Papuan ancestry.
- ▶ However, Papuan-related genetic ancestry is found across present-day Pacific populations.
- ▶ Here, new genome-wide data from 19 ancient South Pacific individuals provide direct evidence of a so-far undescribed Papuan expansion into Remote Oceania starting ~2,500 yr bp,
- ▶ New genome-wide data from 27 contemporary ni-Vanuatu demonstrate a subsequent and almost complete replacement of Lapita-Austronesian by Near Oceanian ancestry.

# Language continuity

- ▶ Despite this massive demographic change, incoming Papuan languages did not replace Austronesian languages.
- ▶ Population replacement with language continuity is extremely rare—if not unprecedented—in human history.
- ▶ The process was incremental and complex, with repeated migrations and sex-biased admixture with peoples from the Bismarck Archipelago.



# Papuan expansion

- ▶ This 2018 study: direct evidence of a so-far undescribed Papuan expansion into Remote Oceania starting ~2.5 Ka.
- ▶ Demonstrates a subsequent and almost complete replacement of Lapita-Austronesian by Papuan Near Oceanian ancestry
- ▶ Despite this massive demographic change, incoming Papuan languages did not replace Austronesian languages. It was a still a mystery that secondary Papuan migrants had replaced the original settlers but somehow adopted their Austronesian language.

# Papuan expansion

- ▶ While so much of Reich's work has conjured the notion of sweeping, wholesale replacements by one population of another, the 2018 paper proposed instead a much more gradual process.
- ▶ Demonstrated not a single decisive turnover event but at least 500 years of ongoing traffic between Papuans and Austronesians — plenty of time to explain how the former had managed to pick up the latter's languages, for one thing.
- ▶ While the genetic samples showed at least 500 years of Austronesian-Papuan mixture, Reich's follow-up paper argued — on the basis of a single sample from a single island — that the First Remote Oceanians from Taiwan had been replaced by at least one wave of belated Papuans.

# Admixtures

- ▶ Reich had, however, updated his analysis of the original skulls with improved, “higher-resolution” statistical techniques.
- ▶ One new data point, which Reich saw as a refinement, struck some critics as a significant revision: While Reich emphasized that the **first 2016 paper conclusively demonstrated no mixture** between the Austronesians and the people they encountered, the updated analysis showed that Teouma’s “Lapita individuals had a nonzero proportion of Papuan-related ancestry.”
- ▶ It “remains striking,” the new paper remarked, that these **first migrants** were only “minimally admixed” — but **admixed they were.**

# History of Prehistory

- ▶ Conviction reflected in the findings of Reich's papers, which seemed to blithely recapitulate discredited theories of Pacific expansion, making categorical claims not only about three individual skulls but about the shape of human history — “claims that were essentially indistinguishable from the **racialized notions** of the swashbuckling imperial era.”
- ▶ One reviewer of the 2015 **Vanuatu study**; “A small sample is only representative of itself.”

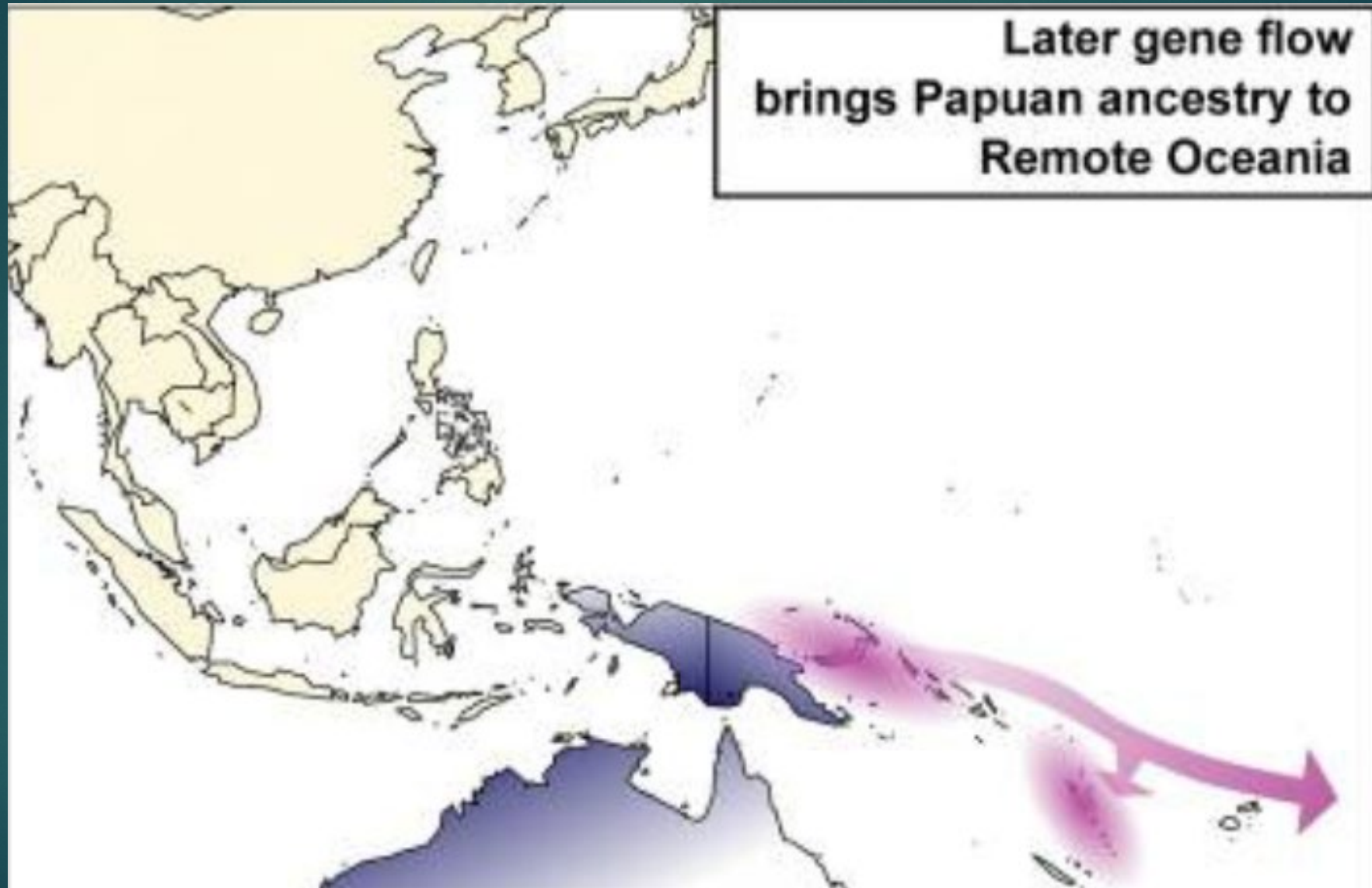
# Two contrasting papers

- ▶ “Both papers,” S. Bedford maintained, “arrive at a similar conclusion,” that **initial Austronesian settlement was followed by a Papuan gene flow**. But as the introduction continued, it became increasingly clear that he could not, in fact, at all believe that both could be right, and he tipped his hand in favor of the second paper, with its emphasis on an “incremental and complex” process that accorded much better with the artifactual record as he had spent his career understanding it.
- ▶ As one contributor to Bedford’s forum observed, **archaeologists had told the ni-Vanuatu for decades that they were the descendants of the Lapita voyagers; now they had to go back and advise them to alter the commemorative postage stamps to feature not black people but Taiwanese aboriginals**. A national self-image was not something to take lightly. “One can only feel,” one forum contributor wrote, “a collective sense of betrayal in all of this.”

# 2016 Skoglund et al.

- ▶ Present genome-wide ancient DNA data from three individuals from Vanuatu (about 3,100–2,700 years before present) and one from Tonga (about 2,700–2,300 years before present), and analyze them with data from 778 present-day East Asians and Oceanians.
- ▶ Today, indigenous people of the South Pacific harbor a mixture of ancestry from Papuans and a population of East Asian origin that no longer exists in unmixed form, but is a match to the ancient individuals.
- ▶ Most prior analyses have interpreted the minimum of twenty-five per cent Papuan ancestry in the region today as evidence that the first humans to reach Remote Oceania, including Polynesia, were derived from population mixtures near New Guinea, before their further expansion into Remote Oceania.
- ▶ Current findings that the ancient individuals had little to no Papuan ancestry implies that later human population movements spread Papuan ancestry through the South Pacific after the first peopling of the islands.

## 4 migration models of Pacific expansion



# Models of population movements

- ▶ **B:** 40,000 years ago - modern humans arrived in the Australia-New Guinea region (blue shading) and mixed with archaic Denisovans (brown shading).
- ▶ **C:** prior 3,000 years ago - in which the First Remote Oceanian population formed by spread of a population of East Asian origin to a region including Vanuatu and Tonga, and experienced little or no mixture with the Papuans they encountered along their journey (red shading). Note that geographic routes are speculative.
- ▶ **D:** Populations of mixed Papuan-First Remote Oceanian ancestry in Near Oceania after 3,000 years ago in a patchwork of islands with different proportions of First Remote Oceanian ancestry (pink shading).
- ▶ **E:** A secondary expansion of admixed populations bringing Papuan ancestry into Remote Oceania, which was still not complete in Tonga by the date of the Talasiu individual at 2680-2340 BP.



# First Remote Oceanians

- ▶ The **2016 Skoglund et al. paper** suggested that the old archaeological consensus — that the Lapita advances reflected the joint contributions of Austronesian and Papuan peoples — could be replaced by a much starker story.
- ▶ Unambiguous confirmation of Lapita heritage. The First Remote Oceanians, as the paper calls them, were not, after all, a heterogenous group; they were of unmixed Asian descent. [This was later revised by Reich]
- ▶ The genetic record can be more “parsimoniously explained,” by at least two separate migrations to Vanuatu:
  - ▶ first, the **Austronesians**, with their East Asian ancestry, and
  - ▶ then, hundreds of years later, **the Papuans.**
  - ▶ This wasn’t a story of “admixture” but one of successive waves of migratory “turnover.”
- ▶ ni-Vanuatu’s ancestors were not Lapita after all, but latecomers to an archipelago first settled by purely Asian expeditions.

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## Contact Info

- ▶ Charles J. Vella, PhD
- ▶ [www.charlesjvellaphd.com](http://www.charlesjvellaphd.com)
- ▶ [charlesvella@comcast.net](mailto:charlesvella@comcast.net)
- ▶ 415-939-6175