12 November
2019

INTELLIGENCE & GENUS *HOMO* CONQUERS THE WORLD

Homework #7 on WeBWorK due Wednesday (11/20)

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Venus of W *es Museum Wien) and the Lion Man of the Hohlenstein Stadel, c.*

Intelligence & Genus *Homo* conquers the world

The evolution of intelligence on Earth, aided by happenstance of geology

Meet the hominins

Brains, diet, and toolmaking: going where natural selection fears to tread

Intelligence and f_i

Evolution of genus *Homo* in Africa

Out of Africa

Victory of *sapiens*, and the consolation prize of *neanderthalensis* and the Denisovans

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Darwin's view of natural selection is often described as "survival of the fittest" – see the cover of *Origin*. Is this an accurate summary of natural selection?

Question!

A. Yes, as there is always competition for resources.
B. Maybe: introduction of species from harsh environments to hospitable environments usually results in predominance of those species.
C. No. Natural selection works the same no matter what the abundance of resources, as better-suited species would still reproduce more copiously than poorer-suited ones.

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Development of brains & intelligence

Recall that a multi-cell organism cannot reliably modify its DNA in a prescribed fashion in response to neural impulses within every cell.

Therefore, the evolution of neural capacity still has to be facilitated by

- Mutation or sexual reproduction
- The largest gene pool possible
- Natural selection

…and will therefore take a very long time to produce much in the way of capacity for **thinking**.

Fortunately, hundreds of Myrs were available.

Furthermore, the resources from which intelligence could develop were arranged in a rather lucky fashion as a result of plate tectonics.

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Plate tectonics

Even after Earth had cooled enough to permit a continuous solid crust, the mantle has remained either fluid or plastic.

This has permitted long **rifts** to form where the outer part of the mantle is warmest. From these rifts emerges molten rocky material, pushing the edges of the cracks apart at a rate of 1-10 cm per year.

In turn, this creates other cracks: the **plates** of crust material which propagate away from the rifts can break from the rest of the crust.

The far side of the plate from the rifts slides either over or under the neighboring plates.

Plates topped by lower-density rock, being more buoyant, float a bit higher above the mantle; these are **continents**.

The plates made from the rifts are higher-density rock which floats lower; today, these are the **ocean floors**.

Supercontinents

When one plate slides underneath (**subducts** beneath) another, its material melts and returns to the mantle.

There is friction in subduction, so the growing ocean plates push the other plates across the surface of the mantle (**tectonic** motion).

At several points in the geological record, particularly vigorous rifts have pushed all the continents into a single mass, called a **supercontinent**.

The first four supercontinents existed 3.1-2.8 Gyr, 2.7-2.5 Gyr, 1.9-1.4 Gyr, and 1.1-0.75 Gyr ago. All of these were barren: no land life had yet evolved.

Question!

Should all terrestrial planets exhibit tectonic plate activity?

A. No. If they are too small ($\ll 1M_\oplus$), their interiors should cool off too fast to have the right sort of mantle.

B. Maybe. Radioactive heating could keep the mantles plastic forever.

C. Yes, which is why there is abundant evidence of volcanism and plate boundaries on Mars, Mercury, and the Moon ($M = 0.1 - 0.01M_\oplus$).

Concentration of the gene pool on land

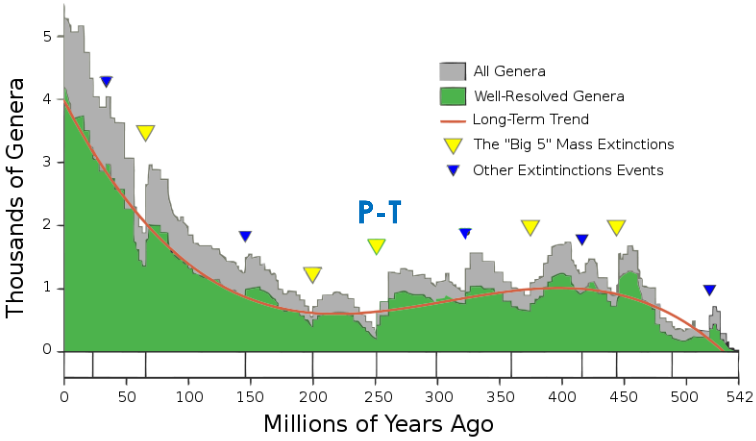
The fifth supercontinent, which geologists call **Pangaea**, conveniently appeared about 300 Myr ago during the **Permian era**. This was about 100 Myr after land plants and insects appeared, and around the time that reptiles first appeared.

Unlike its immediate predecessors, it stretched nearly from pole to pole, most of it having tropical and temperate climates.

Therefore, all land life – the entire land gene pool – was connected 250 Myr ago.

Concentration of the gene pool on land

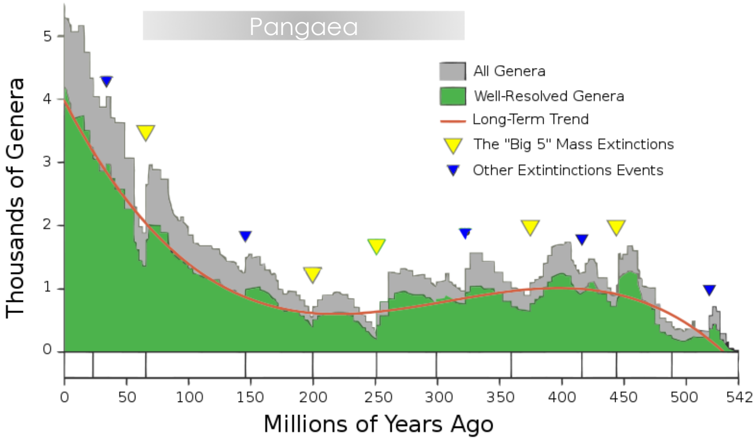
Then disaster struck – the **Permian-Triassic extinction** (252 Myr ago), during which close to 90% of all living beings died: 60% of all families, 80% of all genera, 96% of all marine species. (We will discuss possible causes for this later in the semester.)



Concentration of the gene pool on land

But Pangaea was still connected and remained *largely* so for a long time: all of the land was accessible to all of the species, and the entire gene pool was involved in the recovery.

This promoted genetic diversity, and in particular the evolution of intelligence, much more rapidly than disconnected continents would have, despite two more mass extinctions 200 Myr and 65 Myr ago.

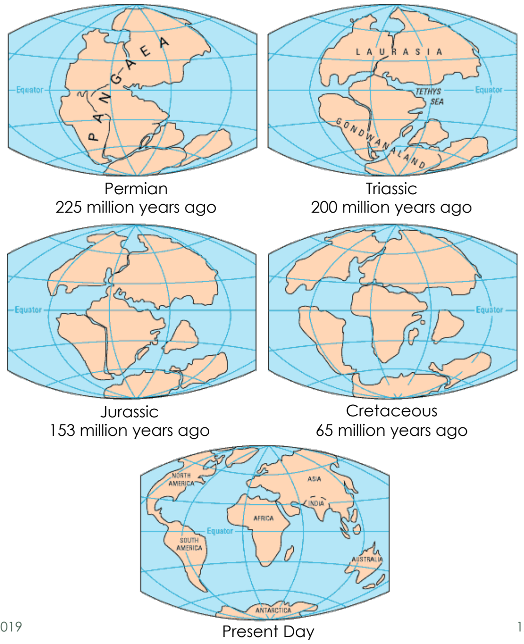


Intelligence

Consider mammals, which first appeared 225 Myr ago. By about 175 Myr ago, the most successful species were marsupials, which overspread Pangaea.

The edges of Pangaea began to break off about 160 Myr ago.

The first to go was a plate containing Antarctica, Australia, and India. The former two remain isolated and sparsely populated compared to the rest, and today, marsupials remain the most advanced native animals.



Permian
225 million years ago

Triassic
200 million years ago

Jurassic
153 million years ago

Cretaceous
65 million years ago

Present Day

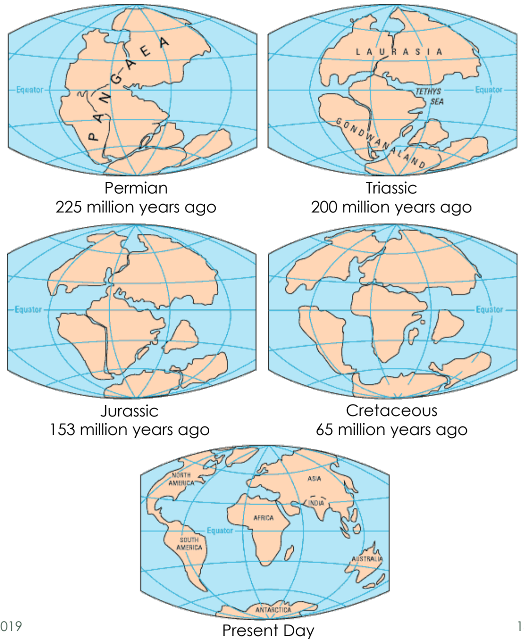
Intelligence

Over the next 50 Myr, placental mammals evolved from the still-large gene pool in the forested areas of Pangaea. The most advanced beings at this time were of the **primate** order: the **prosimian** family, led by the lemur.

Madagascar broke off 110 Myr ago, taking the lemurs along. Lemurs remain the most advanced animals there.

Next to go was South America, about 90 Myr ago.

By then, the lemurs had vanished from Pangaea proper and true **monkeys** existed, which in South America have subsequently evolved into marmosets and spider monkeys.



Permian
225 million years ago

Triassic
200 million years ago

Jurassic
153 million years ago

Cretaceous
65 million years ago

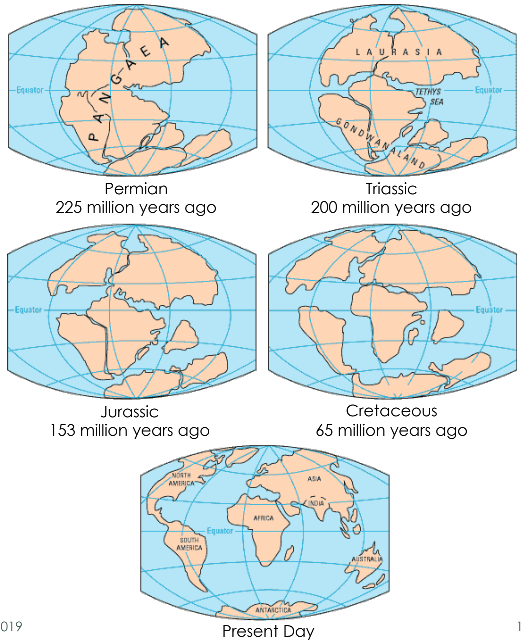
Present Day

Intelligence

A much larger gene pool remained in Africa-Eurasia-North America.

By far, the densest collection of animals of all sorts – the bulk of the gene pool – was the forested, low-altitude parts of the remains of Pangaea, which in turn means Africa.

By about 50 Myr ago, the connections between Africa and the rest became flimsy, due to further rift formation and to periodic desertification of the northern part.



Permian
225 million years ago

Triassic
200 million years ago

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Cretaceous
65 million years ago

Present Day

Question!

Why did the lemurs vanish in the remains of Pangaea after Madagascar broke off?

A. The population which includes lemurs gradually evolved into monkeys, as beneficial mutations were selected.
B. Monkeys evolved and either ate the lemurs or the resources the lemurs needed to survive.
C. We need to know how long they took to vanish before coming up with an explanation.

Intelligence

A few million years ago, the next set of rifts began to develop, splitting Arabia from Africa.

This crack, called the Great Rift, proceeds southwards from the Red Sea into the continent.

It splits around Lake Victoria; the rift itself is occupied by long, very deep lakes like Turkana, Tanganyika, and Nyasa.

Intelligence

The rift process also raised the land on either side of the crack to great heights. For example, the Ruwenzori range reaches 5100 m (16,800 ft).

This had a decisive influence on the climate east of the rift.

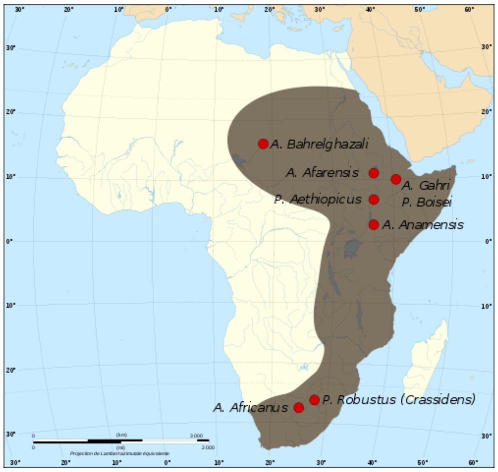
- Weather comes from the west in this part of the world.
- The new mountains caused most of the rain to fall to the west of their crest, leaving a rain shadow to their east.

Intelligence

By this time, the most advanced animals – large brains, fingered limbs, opposable thumbs – were the **simian-family** tree dwellers of the extensive forests. These were the first of the **hominid** family.

Climate change took place on a time scale faster than the usual migration times, leaving a population of tree-dwellers with very few trees.

To go from tree to tree, it was necessary to cross grassland. The ones who survived were the ones who crossed the fastest, walking on two feet.



Hominid fossil finds

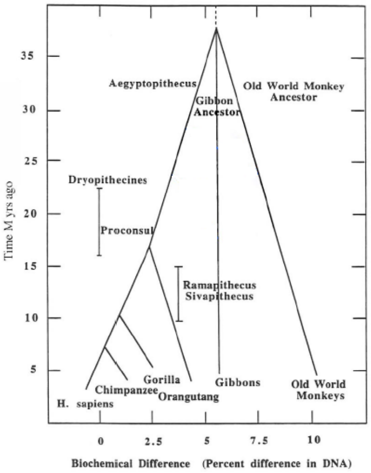
From monkeys to hominins

This left the hands free. Having larger brains, they soon developed other uses for hands.

This selection produced a new subfamily called **hominins**.

Once bipedal hominids (hominins) began to appear in newly-drier East Africa, many mutations were naturally selected which accelerated the differences between them and the apes.

- Distinct process from steady rate of increased difference in junk DNA.
- Most evident in parts of genes called **human accelerated regions** (HARs), of which 49 have been noted.

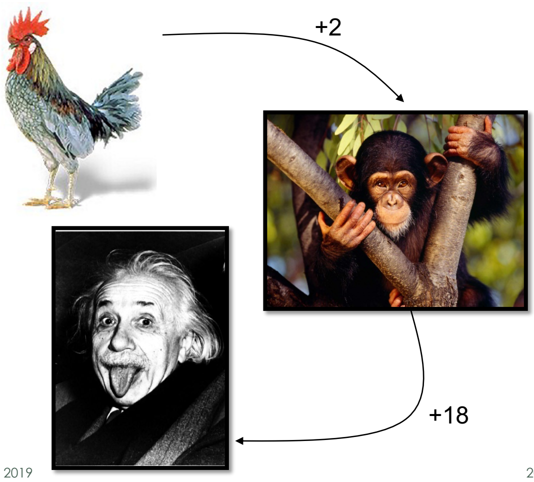


From monkeys to hominins

HARs were discovered in 2006 by Katie Pollard (UCSF) as one of the first huge achievements of the new science of **genomics**.

HAR1, chromosome 20 (non-junk!), for example:

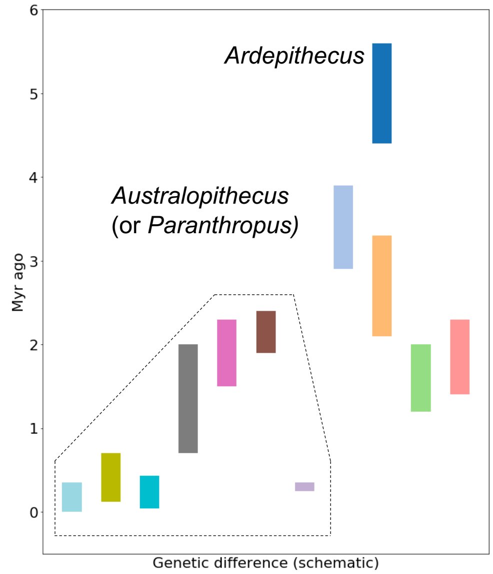
- Present in reptiles onward
- Base-pair difference between chimpanzees and chickens: 2
- Base-pair difference between chimpanzees and humans: 18

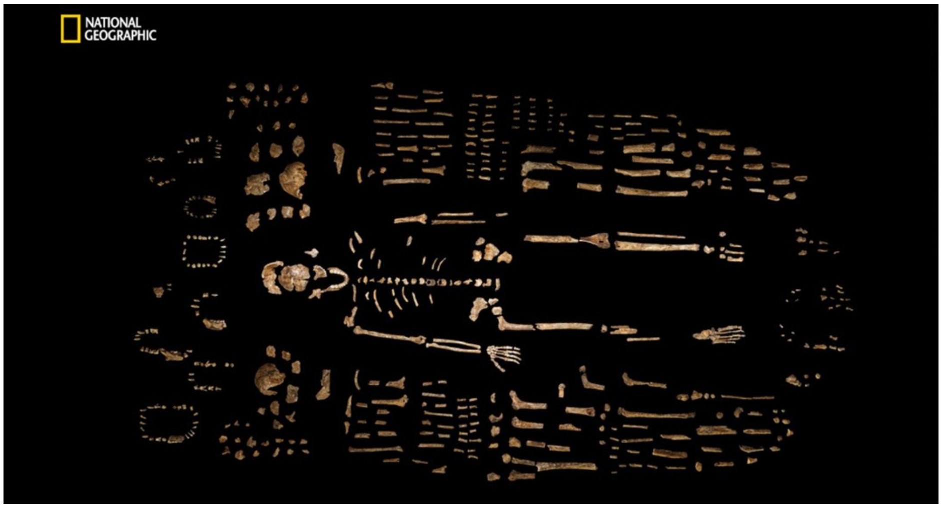


Africa's hominins

All bipedal and tailless

- *Ardepithecus*: several species known mostly by femurs
- *Australopithecus afarensis* (e.g. Lucy), *africanus*, *robustus*, *bosei*. Evolved toward bigger teeth.
- *Homo naledi*, *rudolfensis*, *habilis*, *ergaster/erectus*, *rhodesiensis/heidelbergensis*, *neanderthalensis*, *sapiens*. Evolved toward bigger brains.





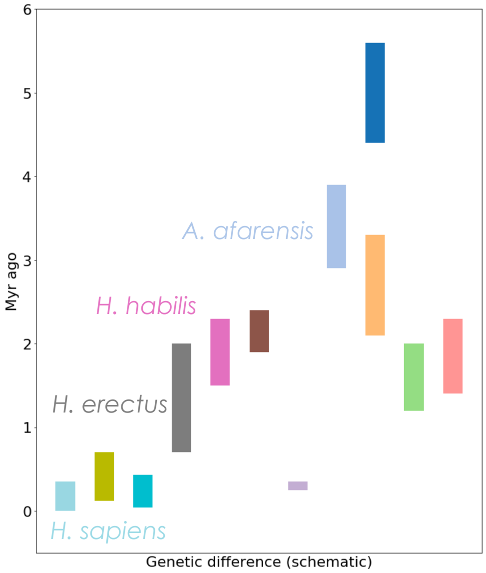
First of genus *Homo*?

Composite skeleton of *Homo naledi*, and related fossil remains from 15 *H. naledi* individuals found in the Rising Star cave system, Gauteng, South Africa, provisionally dated to 2.5-2.8 Myr ago (Berger et al. 2015, National Geographic).

Evolution of diet

As they walked from tree to tree, hominins gradually were selected for eating more than fruit and leaves.

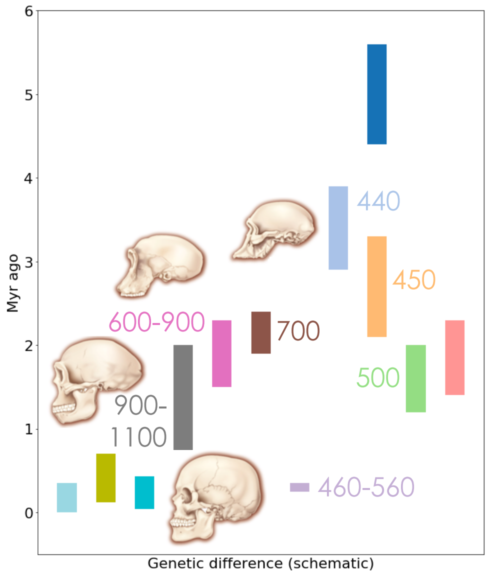
- *A. afarensis*: grasses and meat as well (e.g. Sponheimer & Lee-Thorp 1999)
- *H. habilis*: even more meat
- *H. erectus*: wider variety of meat
- *H. sapiens*: as much meat as they could get



Evolution of brains

Cranial capacity increases dramatically along the *Homo* branch of the hominids.

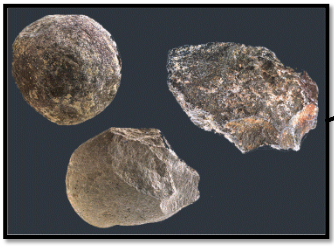
- *A. afarensis*, at an average of 440 cc, would fit comfortably in the chimpanzee range (300–500 cc).
- Capacity about the same for all post-*erectus* species (except *H. naledi*)

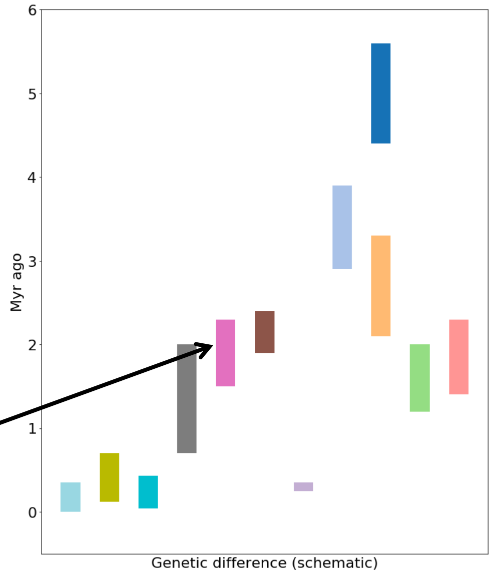


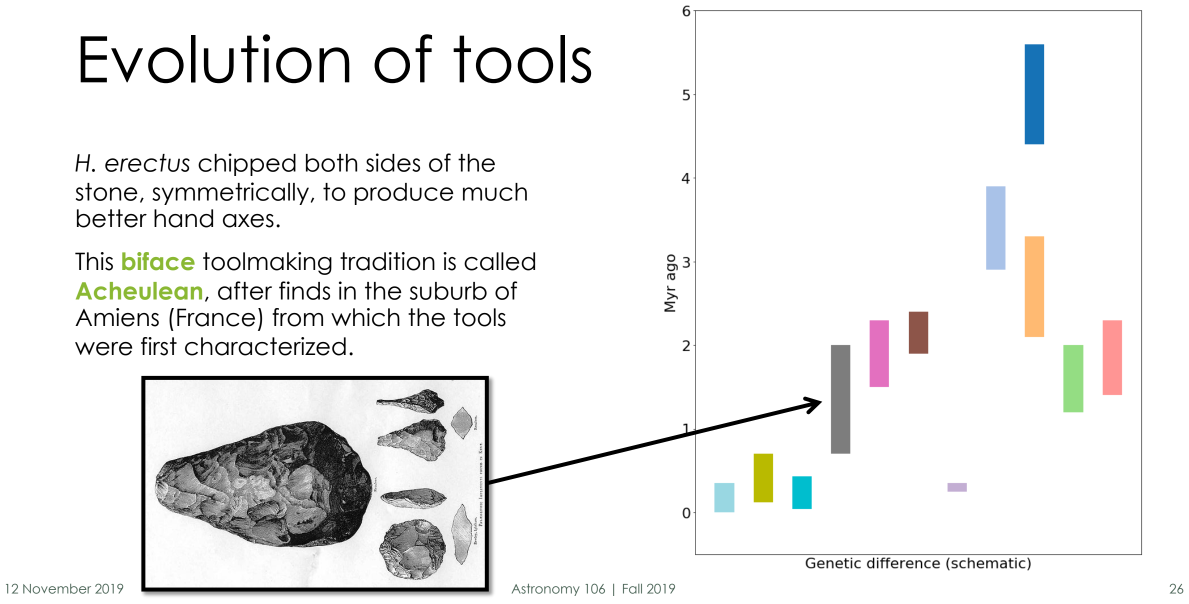
Evolution of tools

The ability to develop tools is the hallmark of intelligence.

H. habilis ("handy man") was the **first hominin to make tools**: stone hand-axes and scrapers that go with scraped animal femurs, both found with *habilis* remains.







Evolution of tools

H. erectus chipped both sides of the stone, symmetrically, to produce much better hand axes.

This **biface** toolmaking tradition is called **Acheulean**, after finds in the suburb of Amiens (France) from which the tools were first characterized.

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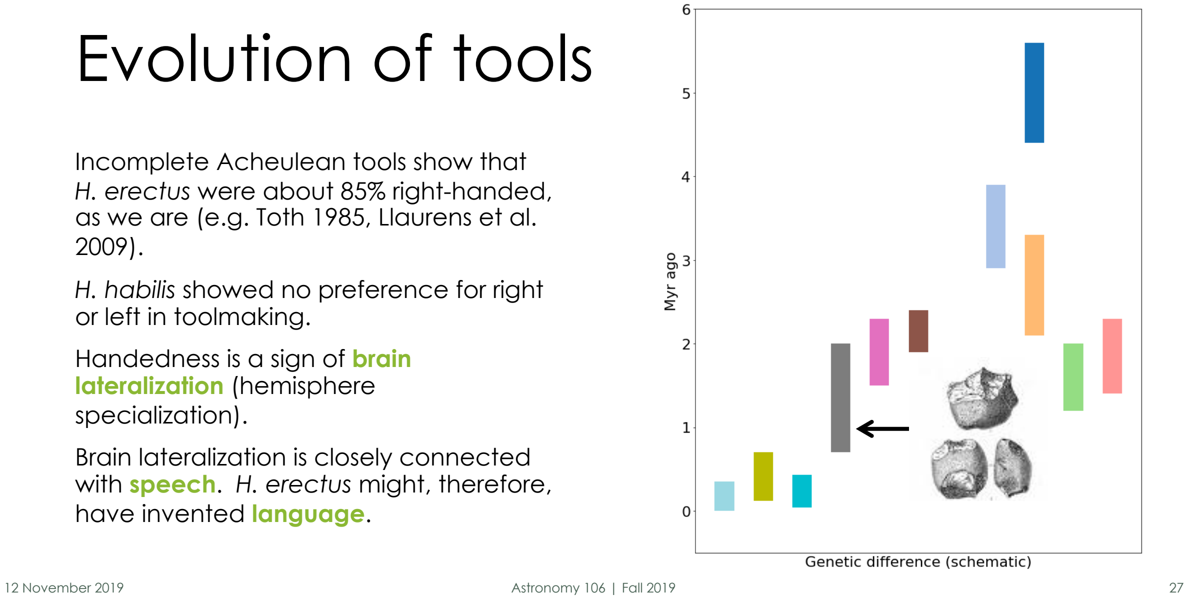

Evolution of tools

Incomplete Acheulean tools show that *H. erectus* were about 85% right-handed, as we are (e.g. Toth 1985, Llaurens et al. 2009).

H. habilis showed no preference for right or left in toolmaking.

Handedness is a sign of **brain lateralization** (hemisphere specialization).

Brain lateralization is closely connected with **speech**. *H. erectus* might, therefore, have invented **language**.

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The end of natural selection for genus *Homo*

There are, of course, indications in non-human animals that non-genetic knowledge is exchanged.

- Some young predators like wolves and lions learn to hunt while belonging to their pack and do not learn how to hunt (while young) if they are raised in captivity.

With the invention of tools and language by *Homo* we have

- A definitive detection of the emergence of intelligence from the natural-selection evolutionary processes
- With the **possibility of passing traits to members of the community whether genetically linked or not**: a change in the rules for subsequent evolution

Next: f_i

Intelligence & f_i

We are going to stray dangerously close to Making Stuff Up. Drake's original wild guess was $f_i = 0.01$; though much has happened in evolutionary biology since the 1960s, little of it has helped to constrain f_i.

Direct estimate: Count up the number of independent emergences of intelligence and divide by the number of independent tries to get f_i.

- This obviously includes a potentially misleading Earth bias.

What counts as a **robust** emergence of intelligence? This is arguable, but we can probably do no better than to use the criteria we found in our discussion of the evolution of genus *Homo*:

- Independent creation and use of tools
- Independent development of language that involves who-what-where-when concepts at minimum.

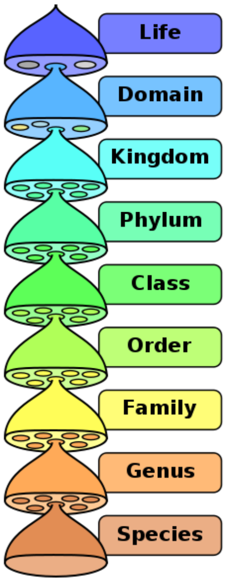
Intelligence & f_i

There are other criteria we could use, such as the ability to solve puzzles, run through mazes, or work cooperatively with other animals. But,

- Not many have been widely applied to many kinds of animals
- Some of them are too qualitative, e.g. "cooperation"
- Some are vulnerable to the Clever Hans effect of observer-expectancy: animals achieving results only because the experimenter subtly and inadvertently gives them clues
- In animal-language studies, it is usually difficult to decode utterances into who-what-where-when concepts

Therefore, we will select candidate intelligence detections based on observations of animal interactions rather than human interaction. Also, we discount some wild claims on behalf of deep-sea invertebrates.

Intelligence & f_i



What counts as an independent try? A "body plan" distinct and different from others at the same phylogenic rank.

- If all identified intelligences share an ancestor at a given rank – say, phylum or class – we will count this as one robust emergence of intelligence.
- All the others among that rank (including extinct ones) count as independent tries.

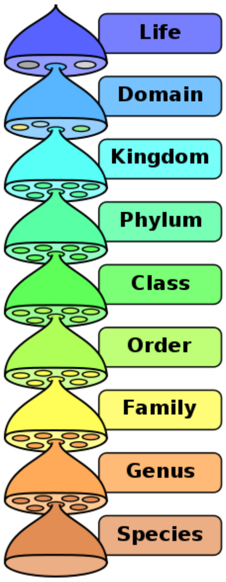
The number of categories at each rank increases by about a factor of ten with every step down.

- There have been 5-8 kingdoms, 110 phyla, $\sim 10^3$ classes, 10^4 orders,… 10^7 species.

Intelligence genera?

Kingdom	Phylum	Class	Order	Family	Genus	Common name	Language?	Uses tools?	Makes tools?
Animalia	*Chordata*	*Aves*	*Passeriformes*	*Corvidae*	***Corvus***	Crow	?	Y	Y
Animalia	*Chordata*	*Mammalia*	*Proboscidea*	*Elephantidae*	***Elphas***	Indian elephant	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Carnivora*	*Mustelidae*	***Enhydra***	Sea otter	N	Y	N
Animalia	*Chordata*	*Mammalia*	*Primatae*	*Hominidae*	***Gorilla***	Gorilla	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Primatae*	*Hominidae*	***Homo***	Human	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Proboscidea*	*Elephantidae*	***Loxodonta***	African elephant	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Cetacea*	*Delphinidae*	***Orcinus***	Orca	Y	?	?
Animalia	*Chordata*	*Mammalia*	*Primatae*	*Hominidae*	***Pan***	Chimpanzee	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Cetacea*	*Physeteridae*	***Physeter***	Sperm whale	Y	N	N
Animalia	*Chordata*	*Mammalia*	*Primatae*	*Hominidae*	***Pongo***	Orangutan	Y	Y	Y
Animalia	*Chordata*	*Mammalia*	*Cetacea*	*Delphinidae*	***Tursiops***	Bottlenose dolphin	Y	Y	Y

Intelligence & f_i



The seven definite emergences of intelligence belong to four different families and four different orders, but only one class (Mammalia).

- There have been about 1000 classes. This suggests that $f_i = 0.001$.

If crows really do have a language in which individuals exchange who-what-where-when information – or if there are other birds that do and also share the crow's accomplishments in toolmaking – then the intelligence-emergences belong to two classes and only one phylum (Chordata).

- There have been about 100 phyla. This suggests $f_i = 0.01$.

Intelligence & f_i

We are left with some fuzzy constraints:

- f_i seems unlikely to be a hefty fraction of 1.
- Similarly, it seems unlikely to be close to the lower bound of about 10^{-9} (Earth/number of earthlike planets).
- Any value between and far from these can be defended.
- We shall then split the difference (logarithmically) between our two estimates above and take

$$\boxed{f_i = 0.003}$$

- It could be ten times larger; it could be 100-10000 times smaller; no result would really be a surprise.

Question!

What do you think is the value of f_i?

A. 0.1
B. 0.01
C. 0.001
D. 0.0001
E. 0.00001

Genetic diversity of Africa

From *H. erectus* and onward, the adaptability and organizational skills permitted by larger brain size – especially tool- and and speech-making capabilities – allowed ancient humans to spread past the bounds of their East African homeland.

They had to, for dietary reasons.

- Big herbivores like gorillas and chimps can live (in forests) at population densities of about 1 per km^2.
- The genus *Homo* line, who preferred meat, could no longer digest leaves and grasses and were not so efficient at hunting yet, could only live at densities **no greater than about 0.1 per km^2.**

Competition among the hominids led to

- The more advanced ones forced the less advanced ones to inhospitable places, or
- The more advanced ones either killed or ate the less advanced ones.

They spread throughout the temperate Africa south of the Sahara and the **Sudd**, a huge swamp along the Nile.

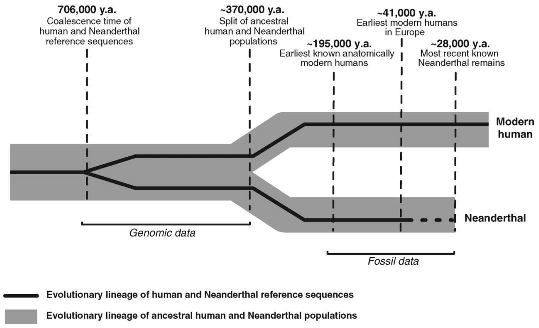
Genetic diversity of Africa

From the viewpoint of the fossil record and relative to the "out of Africa" humans, this "survival of the fittest" addition to ordinary natural selection ensured

- A relatively rapid evolutionary progress toward even more dangerous members of genus Homo
- A rapid replacement of previous models

About 370 kyr ago, this evolution appears to have produced two surviving branches of our genus:

- Archaic Homo, represented in the African fossil record by *H. rhodesiensis*, and elsewhere by *H. heidelbergensis*, the "Denisovans," and most numerously by the Neanderthals, *H. neanderthalensis*.
- Modern Homo: *H. sapiens*, the species to which we belong.



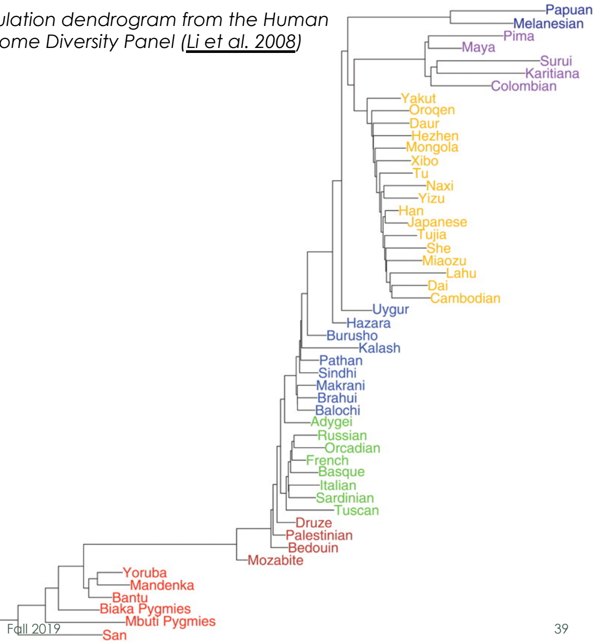
Noonan et al. (2006)

Genetic diversity of Africa

By roughly 100,000 years ago, *H. sapiens* had occupied all of sub-Saharan Africa and eliminated its competition, leaving the apes and monkeys to their trees.

Still dominating the human gene pool and having 0.4 Myr of differentiation, this process led to a notable diversity of **races** among African *H. sapiens* that remains the greatest, even now that the species is worldwide.

Population dendrogram from the Human Genome Diversity Panel (Li et al. 2008)

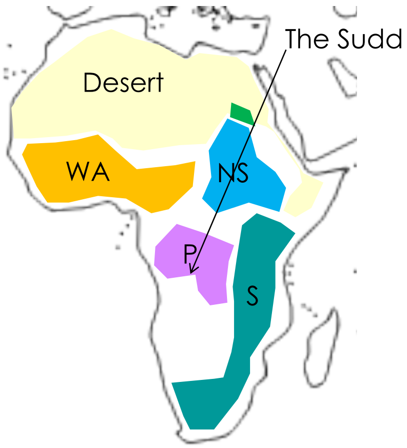


Genetic diversity of Africa

The four main branches of African *H. sapiens* are shown to the right, the differences among which are as great as the rest of the world.

- **West Africans** (Niger-Congolese language group)
- **Nilo-Saharans**
- **Pygmys**
- **San** (a.k.a. Khoisan)

All were originally also language groups, though the Pygmys now speak West African (specifically, Bantu) languages.



Out of Africa

There was some leakage from the African gene pool as humans explored for better food sources.

Presumably, the best exit has always been to endure the passage of the Sudd and follow the Nile; this is consistent with the ages of archaic human fossils, which tend to be closer to the Isthmus of Suez the older they are.

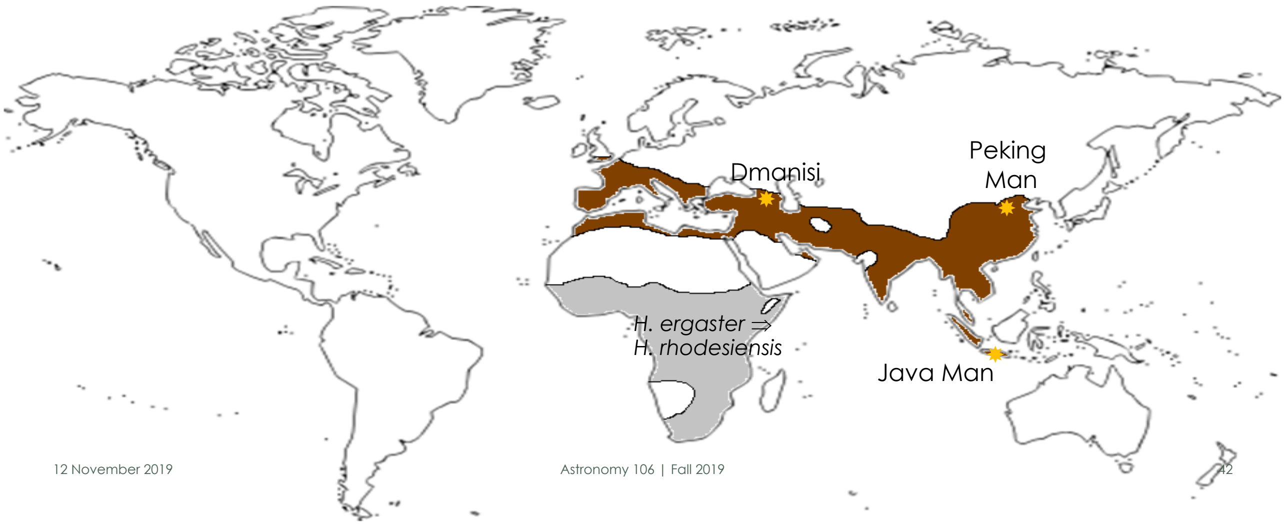
There have been at least three escapes: by *H. erectus*, by *H. heidelbergensis*, and by *H. sapiens*. (Probably the Denisovans, too.)

H. erectus escaped sub-Saharan African somewhere around 1 Myr ago, rather early in the life of the species. They rapidly spread throughout the temperature regions of North Africa, Europe, and Asia, bringing the Acheulean toolkit along: the exemplars of the **lower Paleolithic age**.

- Thus "Java man" and "Peking man"

Range of *H. erectus*

Ice-age drops in sea level enabled *H. erectus* to walk to Java and Britain.



Out of Africa

About 130,000 years ago, near the beginning of the most recent ice age (Wisconsin-Weichsel-Wurm), a small band of *H. heidelbergensis* left Africa.

- They seem to have quickly displaced *H. erectus* in Europe, the Near East, and central Asia.
- They flourished by hunting ice-age megafauna, such as mastodons and mammoths, on the treeless tundra south of the ice sheets.
- The natural selection to which their new, cold environment subjected them led to the emergence of a new species, ***H. neanderthalensis***, which spread further and supplanted *H. heidelbergensis*.
- Neanderthal remains and the products of their **Mousterian** tool industry comprise the **oldest finds of the Middle Paleolithic Age** in Europe and the Near East.

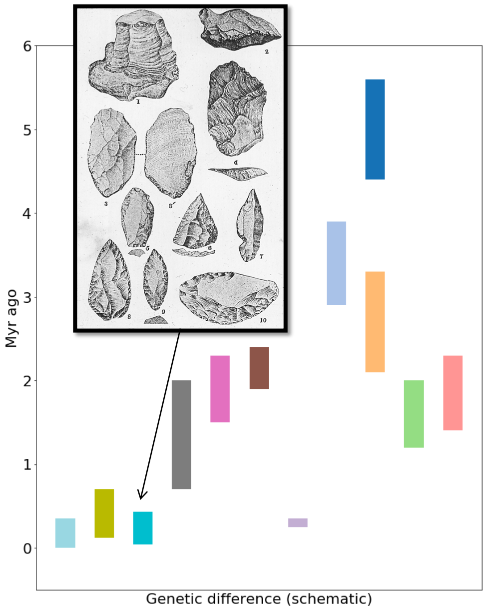
Neanderthal skills

Mousterian tools: made by flaking and included points

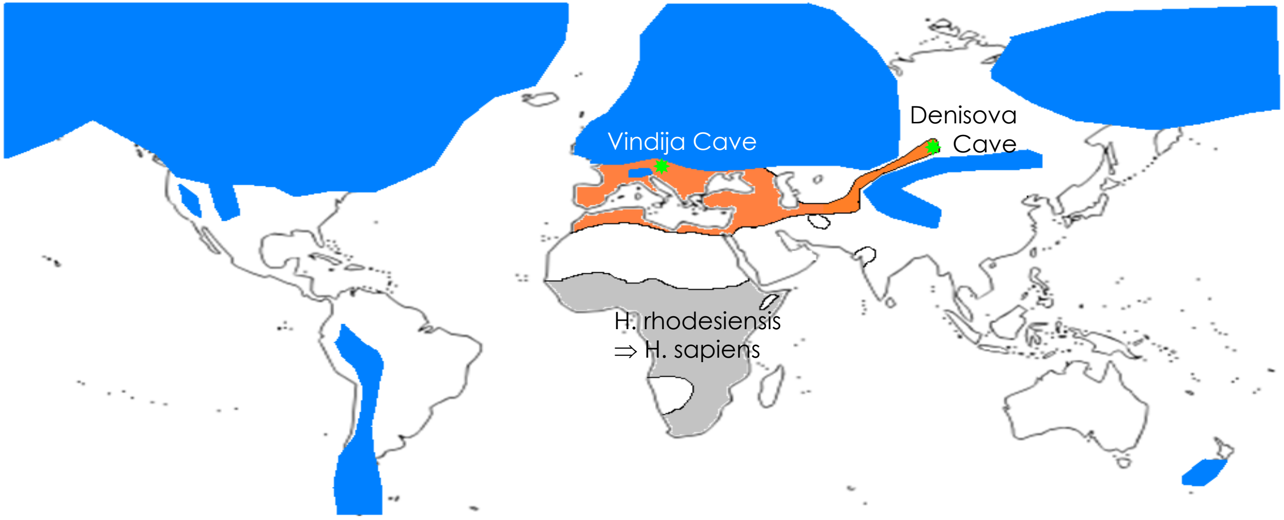
Fire, and probably some cooking skills

Clothing, as they could live in cold climates

They also often dug holes in their cave floors which led to *much* confusion due to the mixture of different-age artifacts.



Range of *H. neanderthalensis* and (W) ice sheets



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Out of Africa

About 80,000 years ago, with the W ice age still in progress, a small group of *H. sapiens* left Africa via the Nile valley. Similar to its predecessors, they began to reproduce, flourish, and expand all over the world.

Also like its predecessors, this group represented a tiny selection of the African gene pool and reproduced very rapidly as it soon took over all the habitats.

Since its numbers grew large so much faster than the time over which *H. sapiens* had evolved, the Out of Africa portion of the species is genetically very homogeneous.

- Norwegians, Chinese, and Australian Aborigines are genetically very similar.
- All are genetically different from all of the remaining African races.

By c. 18 kyr ago, *H. sapiens* had completely replaced their predecessors.

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Out of Africa

Though the idea that this takeover took place by violent conquest has been popular (along with suggestions of cannibalism), it has been suggested many times throughout the years that *H. erectus* and *H. neanderthalensis* interbred with *H. sapiens*, and that this replacement was at least partly an assimilation of smaller communities by a larger one.

- *H. sapiens*, with its better tool set and organization, would plausibly have multiplied much faster than the other out-of-Africa communities. It would not have taken long for them to outnumber all others.
- Certainly *H. sapiens* and *H. neanderthalensis* lived side-by-side in Europe and the Middle East for at least 40 kyr.

Out of Africa

The odds would seem to be against this as a means of replacement of *H. erectus*:

- Mitochondrial DNA studies indicate that the maternal lineage of living humans goes back only to about 190-200 kyr ago, thus identifying the epoch of **mitochondrial Eve**.
- Similarly, Y-chromosome studies take the paternal lineage back to the range 60-140 kyr ago: somewhere in there is the epoch of **Y-chromosomal Adam**.
- Neither of these time frames overlaps with *H. erectus*, who was long gone from Africa by this time and might have gone from Eurasia by the time *H. sapiens* left Africa.

Genetics of the *H. sapiens* takeover

But recently, paleogeneticists led by Svante Pääbo retrieved complete genomes for Neanderthal remains found in Vindija Cave, Croatia, and in southern Siberia. These indicate that

- Their gene sequence is distinctively different from all current races of *H. sapiens*.
- **Current Eurasian *H. sapiens* share 1-4% of their coding (non-junk) DNA with the Vindija Neanderthals through maternal or paternal descent.**
- **Current African *H. sapiens* do not share any.**

This is very strong evidence that Neanderthals and modern humans interbred after the latter left Africa.

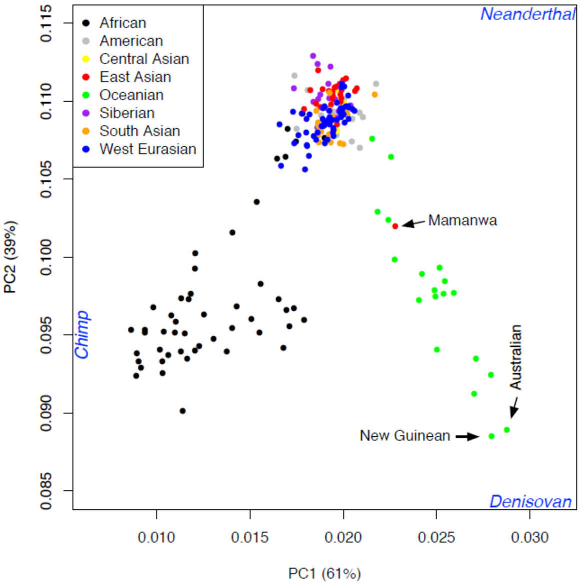
Pääbo and an old friend

Genetics of the *H. sapiens* takeover

And then there are the Denisovans.

- Closely related to "classical" Neanderthals, though genetically distinctive. Maybe a separate thread of African emigration; very thin fossil record, though.
- Fossils from 4 distinct Denisovan individuals have been found in the Denisovan cave.

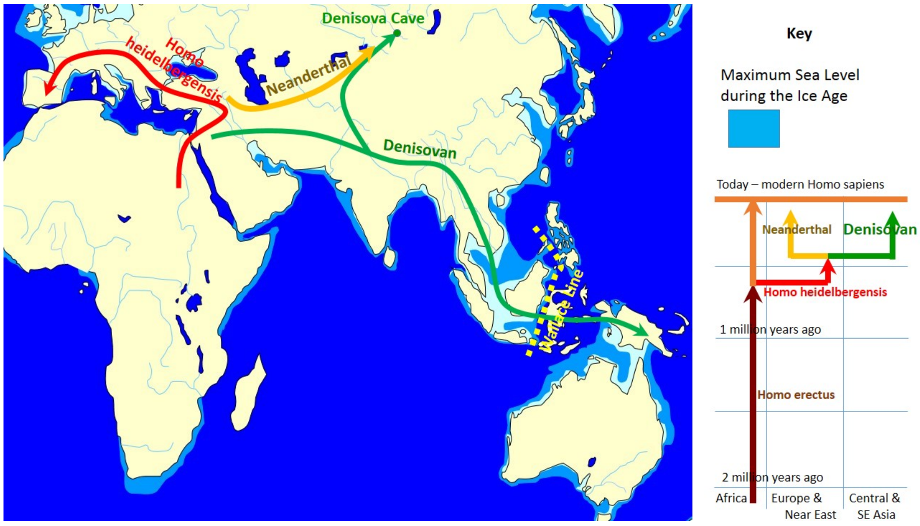
Denisovan cave, *location of "X Woman."*



Densiovans

4% of the non-junk DNA of **most** present-day Melanesians is descended from Denisovans, evidence of more inbreeding.

Principle component analysis of current populations v. Neanderthals, Denisovans, and chimpanzees (Qin & Stoneking, 2015)



Out of Africa, pre-*H. sapiens*

Denisovans and Neanderthals split from *H. sapiens* between 600,000 and 740,000 years ago; they diverged from each other about 200,000 years later.