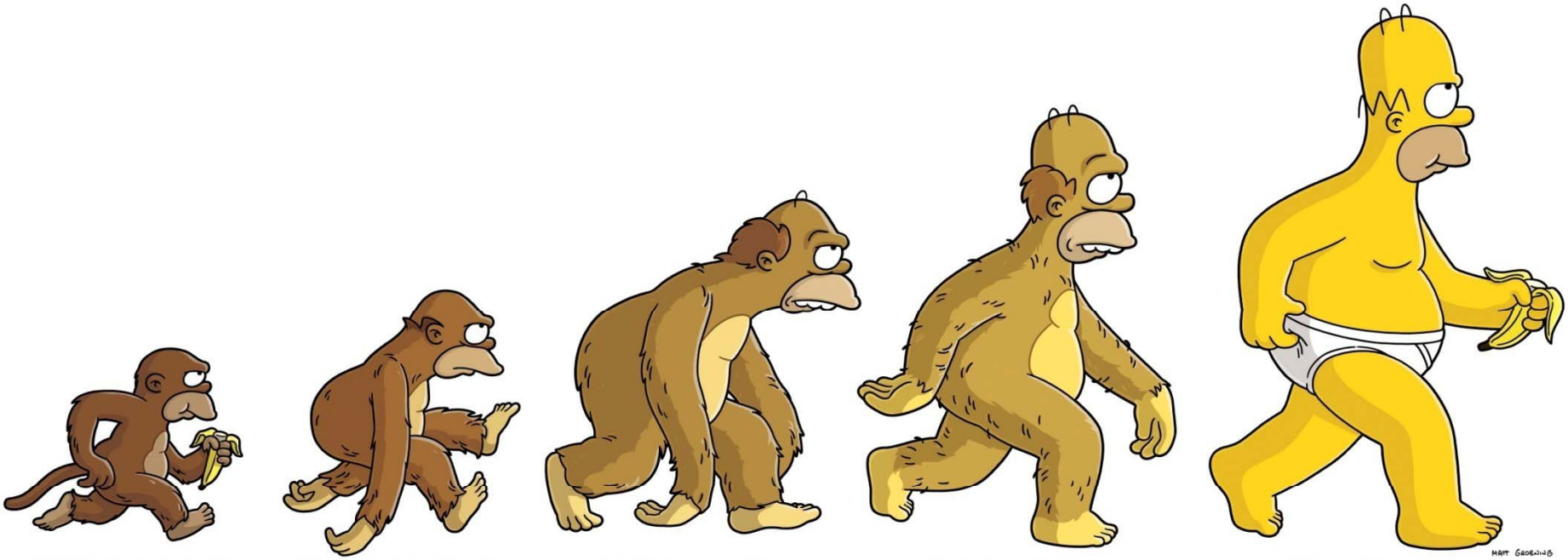
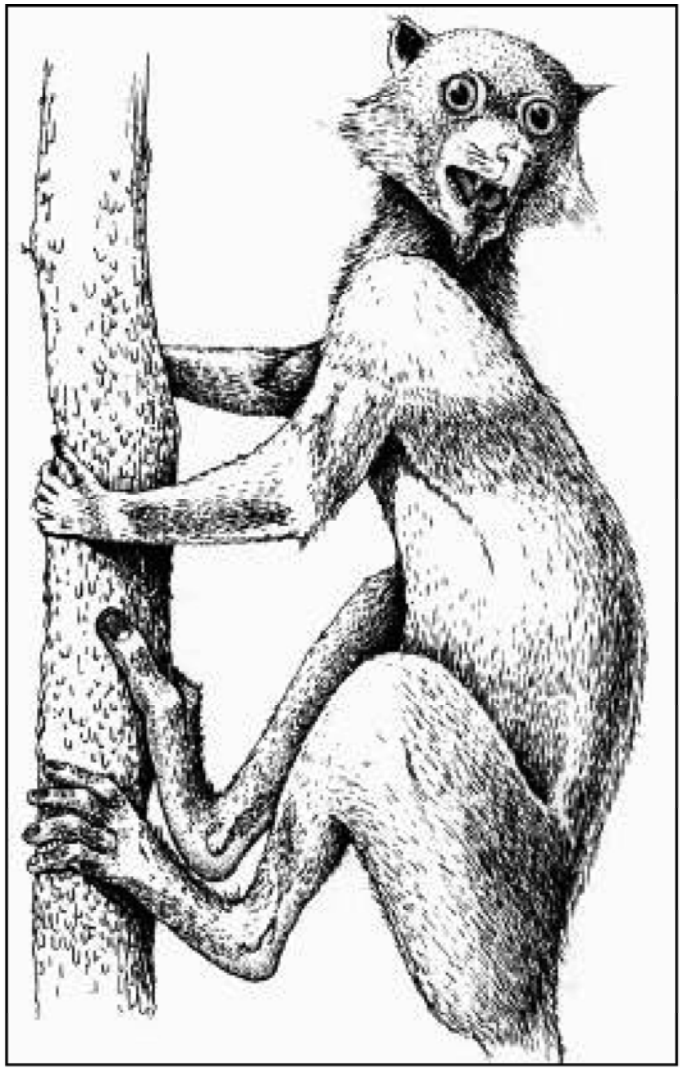
Human Evolution



HOMERSAPIEN

Cantius, ca 55 mya



Cantius was an early Eocene primate. Note the flat nails and forward facing eyes.

The continent-hopping habits of early primates have long puzzled scientists, and several scenarios have been proposed to explain how the first true members of the group appeared virtually simultaneously on Asia, Europe and North America some 55 million years ago.

Paleocene-Eocene thermal maximum (PETM), one of the most rapid and extreme global warming events recorded in geologic history.

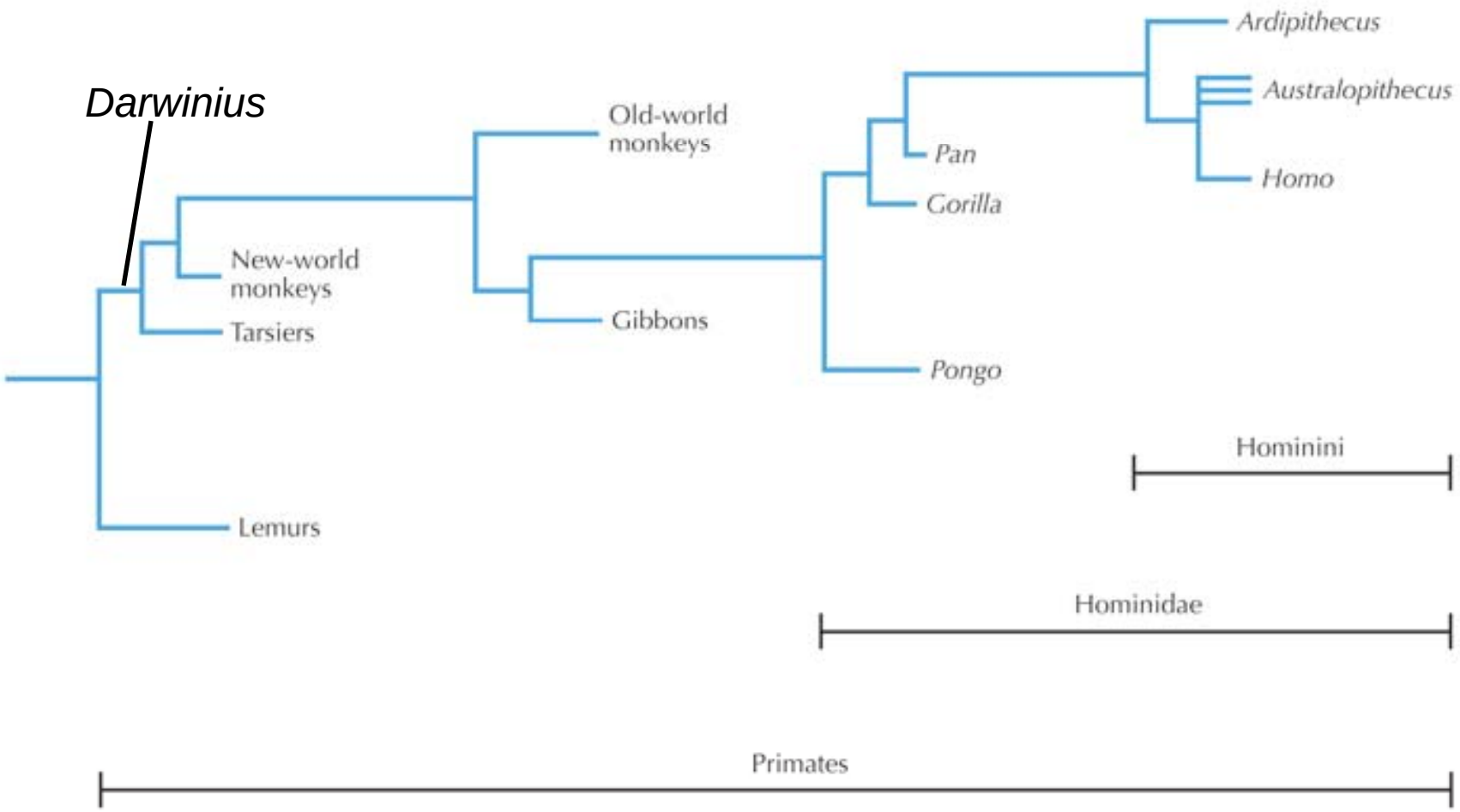
- Originated in Africa and spread across Europe and Greenland to reach North America.
- Originated in North America and traveled across a temporary land bridge connecting Siberia and Alaska.
- Originated in Asia and fanned out eastward to North America and westward to Europe.

Darwinius masillae

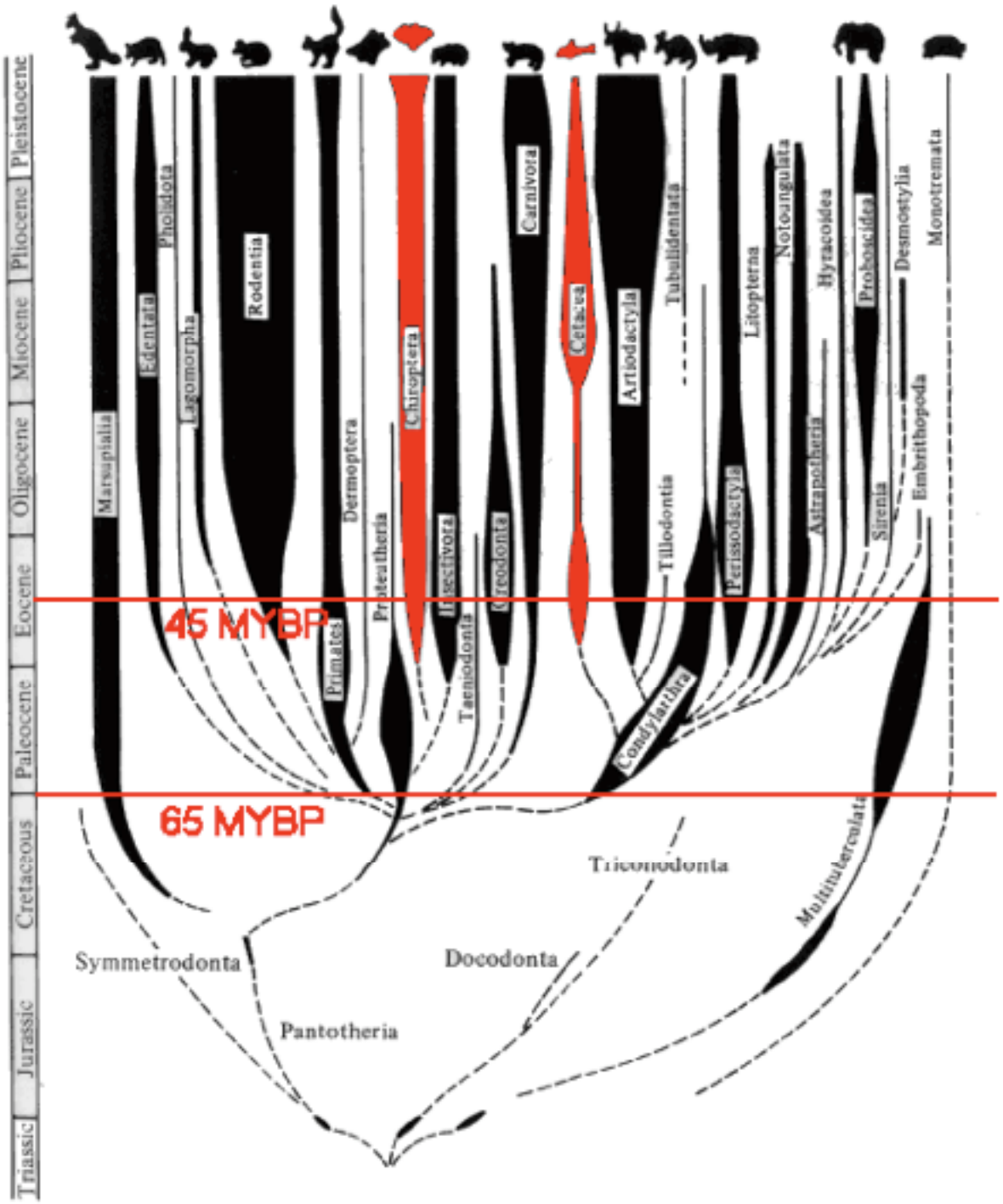
- Ida
- Primate fossil from Messel pit in Germany
- Ca.47 M years old

Franzen et al., PloS One 2009

Placement of *Darwinius* among the primates



- Primate phylogeny (Rem: Our species)



Primates

- Distinct group within the mammals

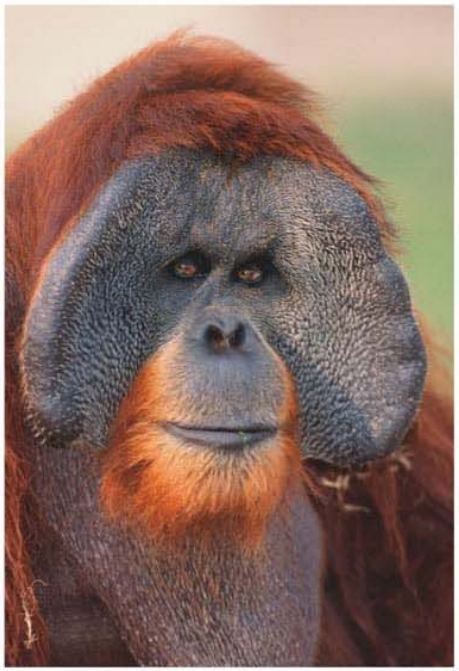
PETM

K/T

Which are our closest relatives?

(A) Gibbon

(B) Orangutan

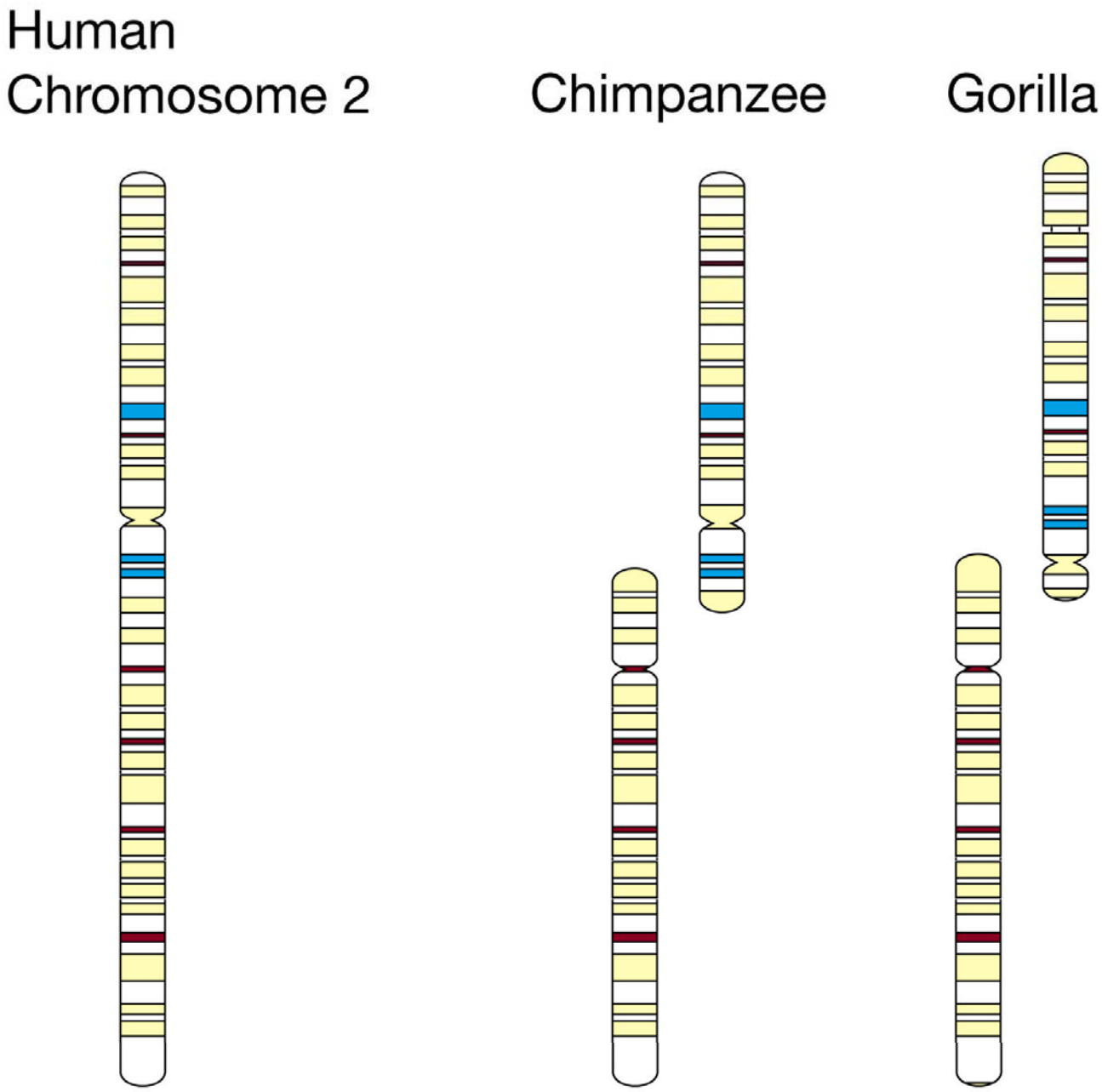


(C) Gorilla

(D) Chimpanzee

Hominoidea Superfamily

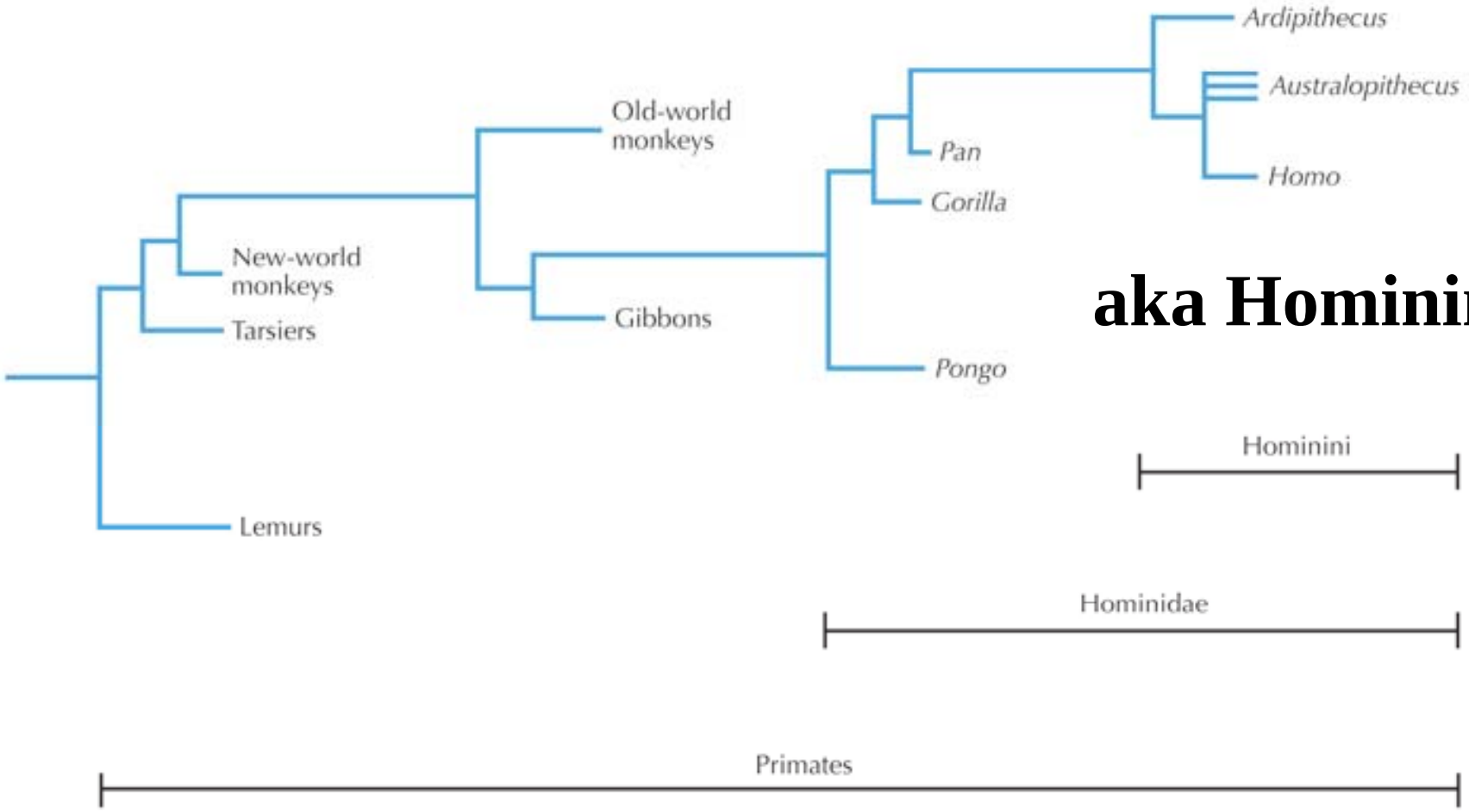
aka Hominids



- About 1 % of bp differ between chimps and humans
- Proteins are extremely similar, but differences exist
- Is it all in the regulatory sequence?

Hominids have a very similar genomic organization!

Evolution of hominins

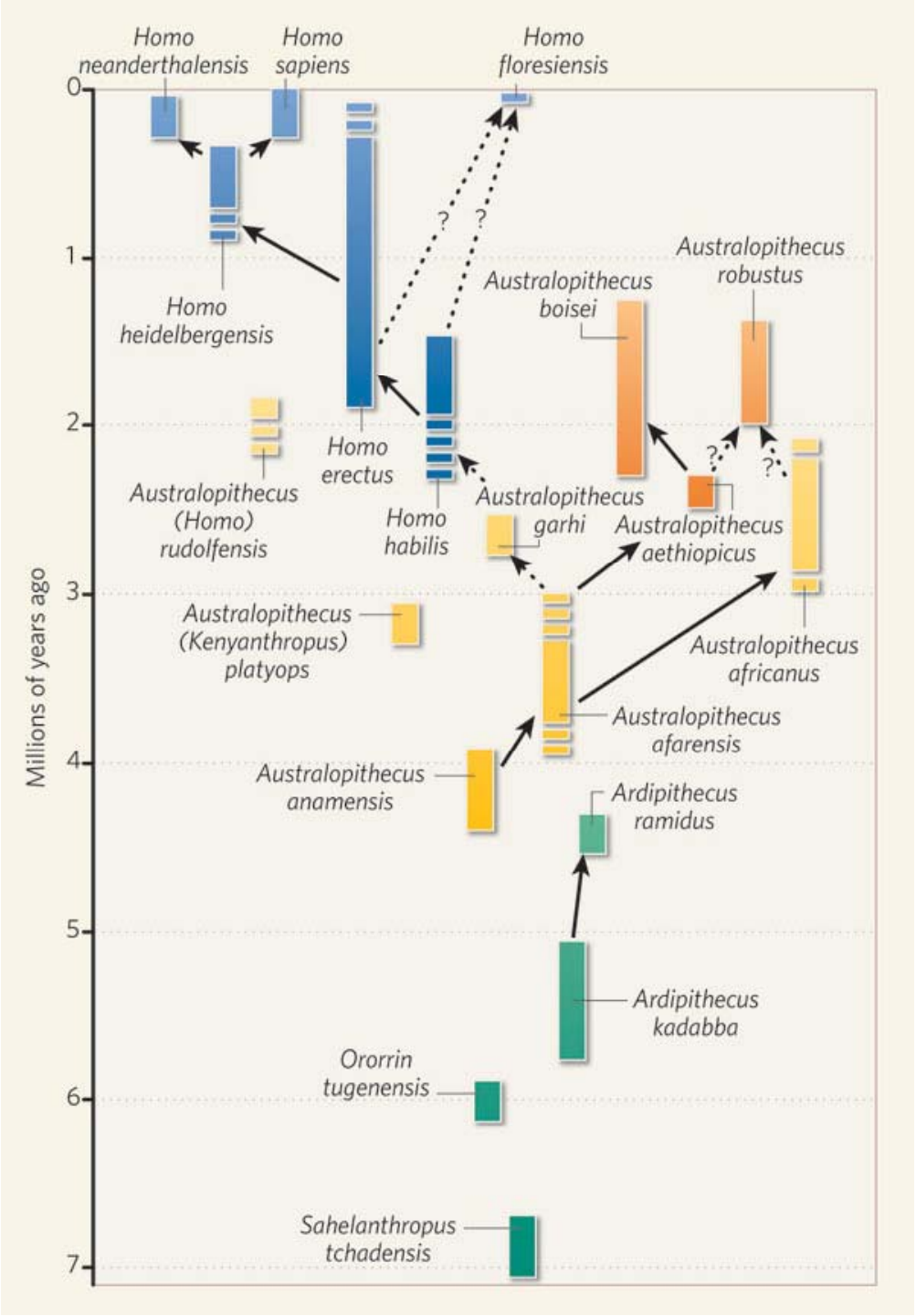


aka Hominins

Species uncertainty within the hominins

- Drawing species limits between fossils is very tricky

Lucy (*Australopithecus afarensis*)

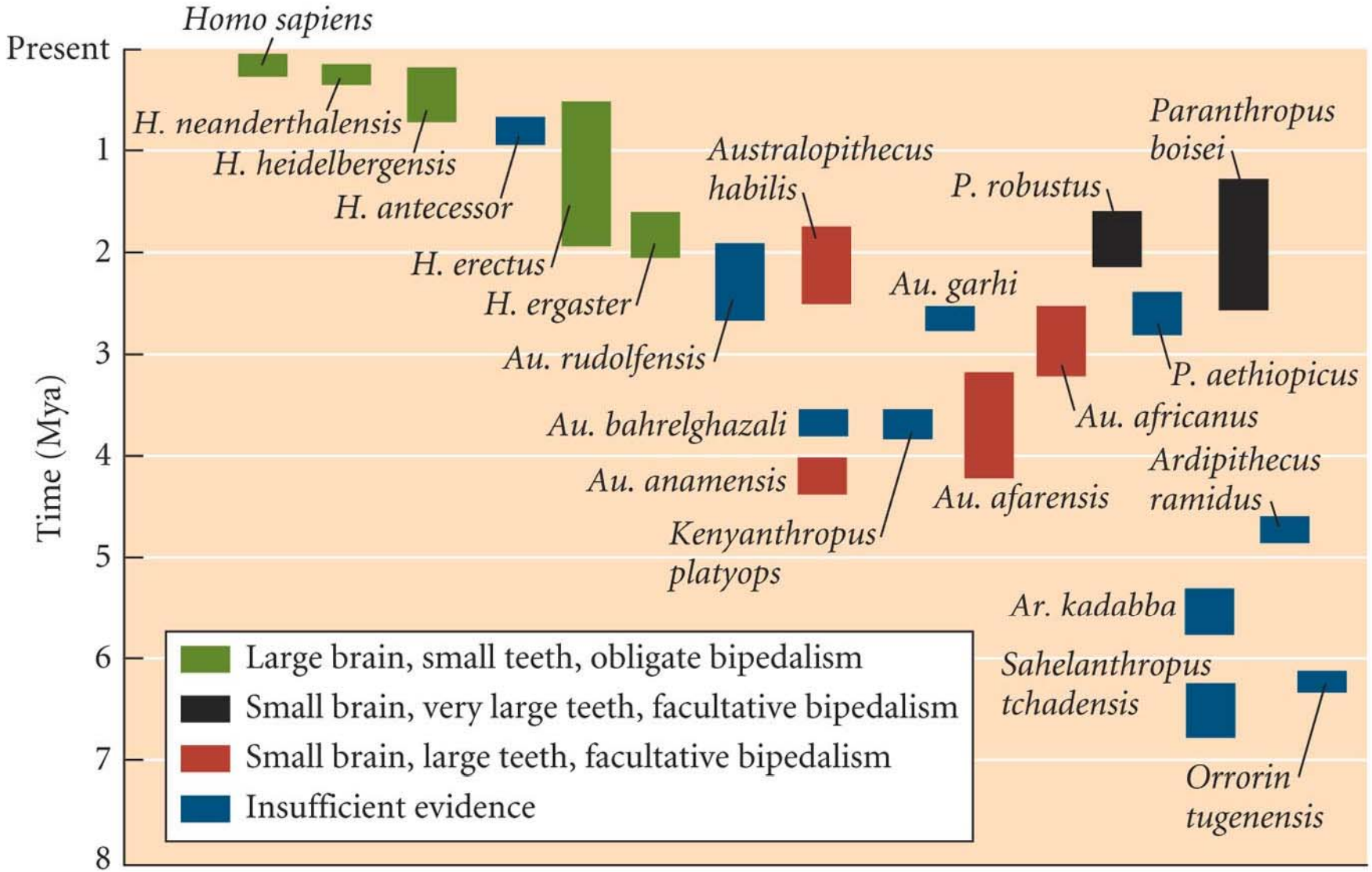


Hominin radiation

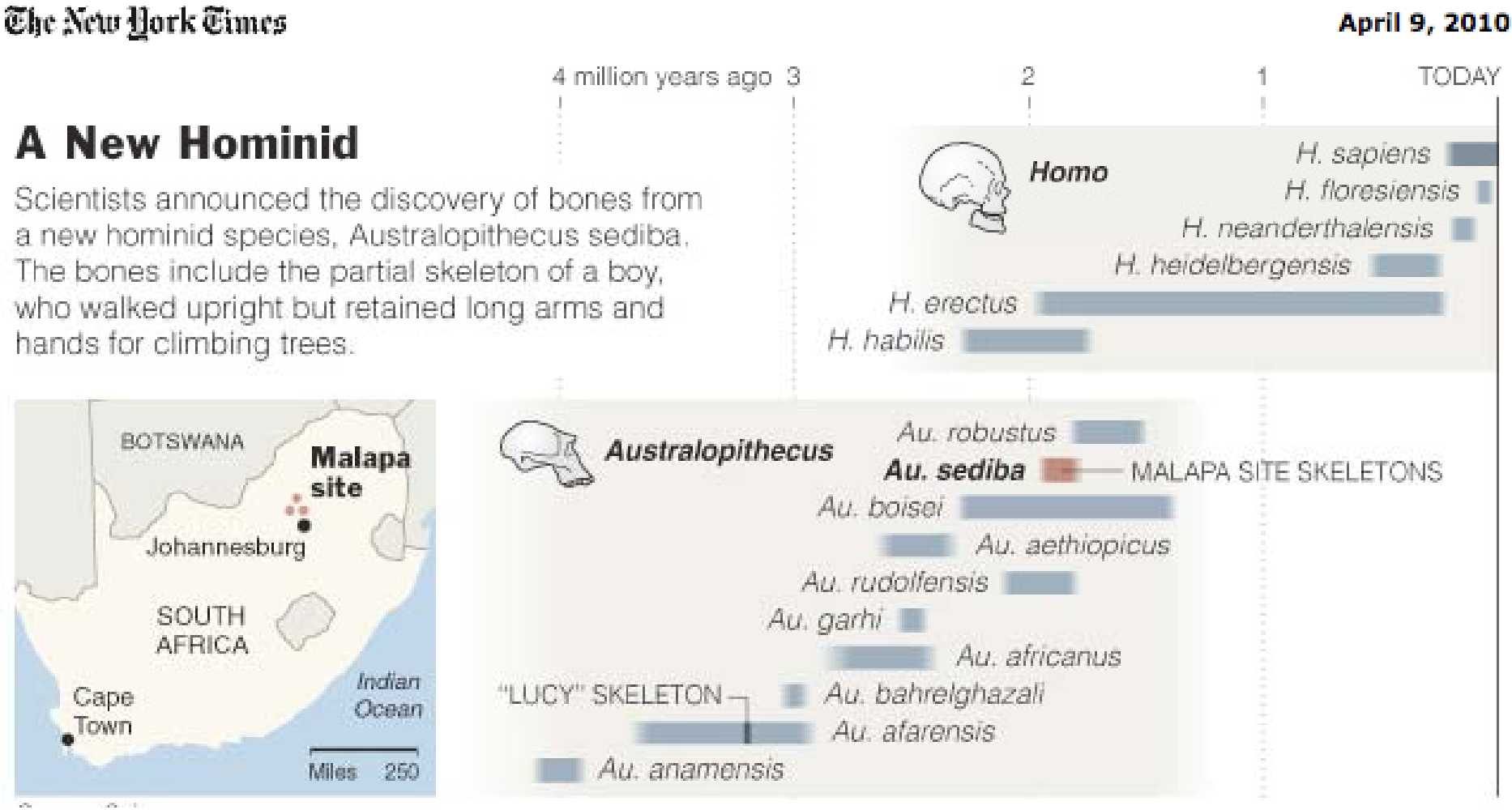
~5 species @ 2 Mya

Height of our diversity? (in Africa)

The approximate temporal extent of named hominin taxa in the fossil record

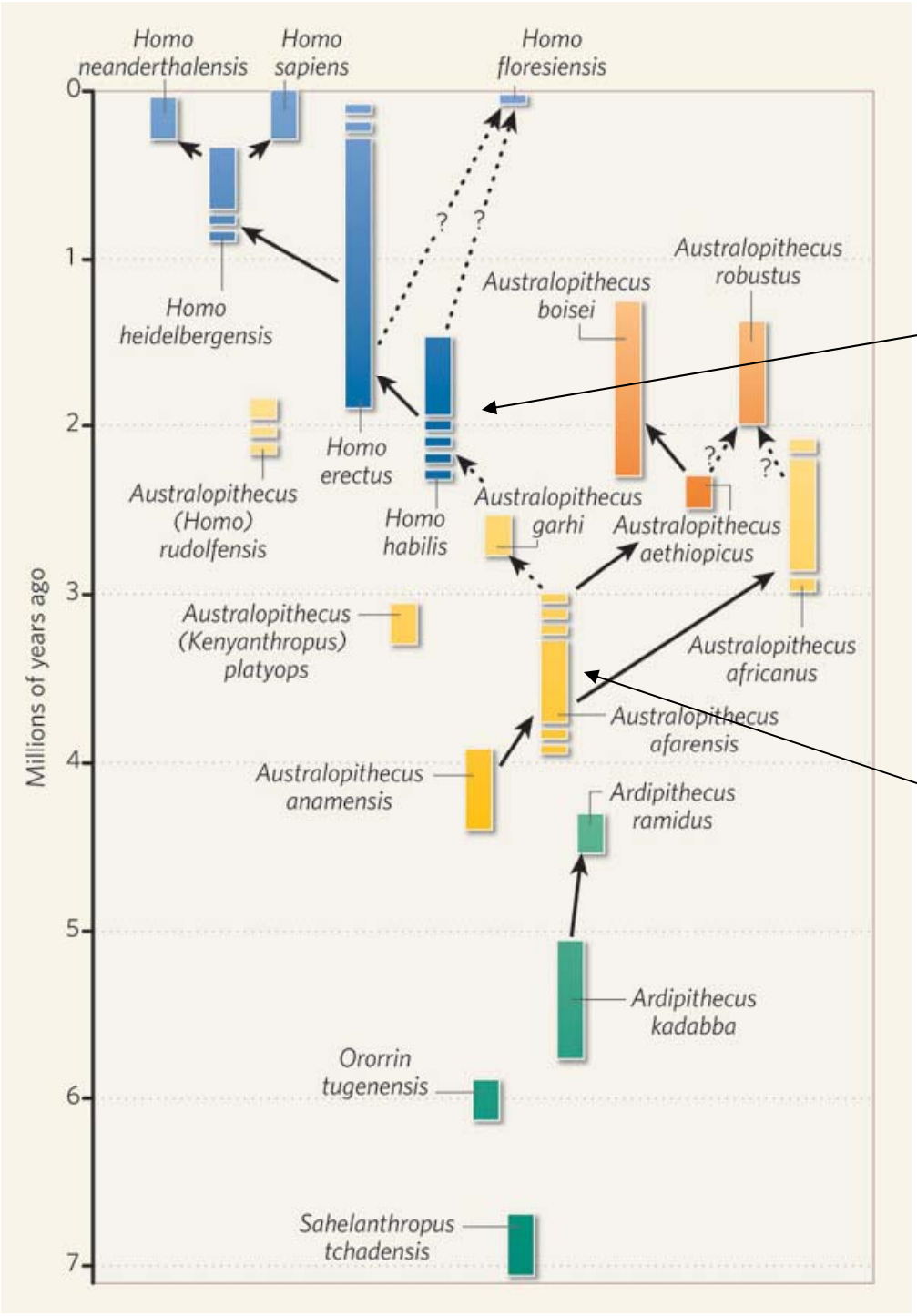


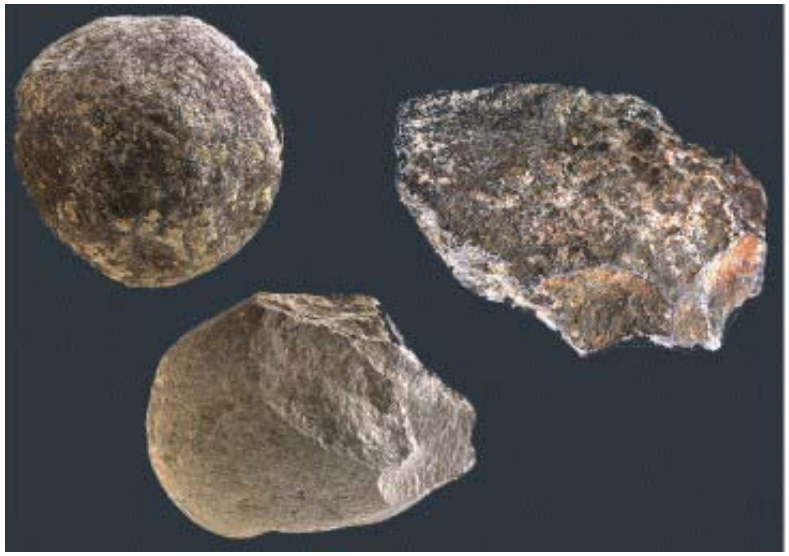
Australopithecus sediba - the dawn of Homo?



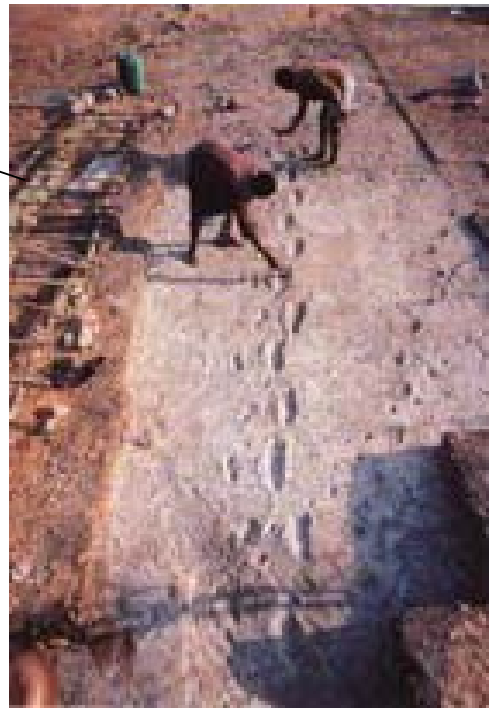
Additional fossils were described in 5 papers in September 9, 2011 issue of Science

For most of the last 4 Mya, hominid species have co-occurred.
E.g., *Australopithecus boisei* (left) and *Homo ergaster* (right)
<u>both</u> lived ~2.0 Mya at Koobi Fora, Kenya.





First manufactured stone tools



Upright walking

Sahelanthropus tchadensis *H. sapiens sapiens*

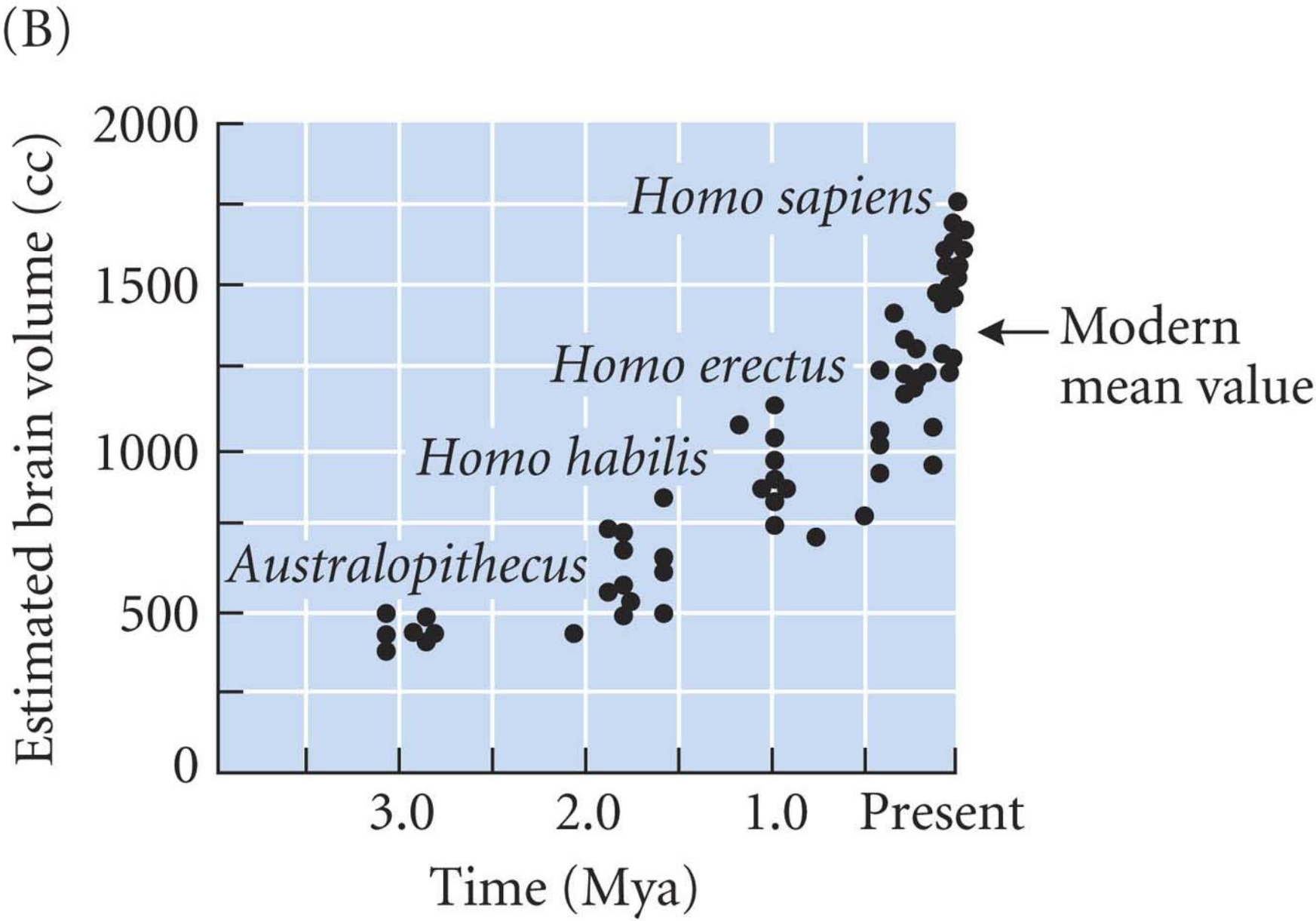
6-7 Mya

Not clear if it was bipedal

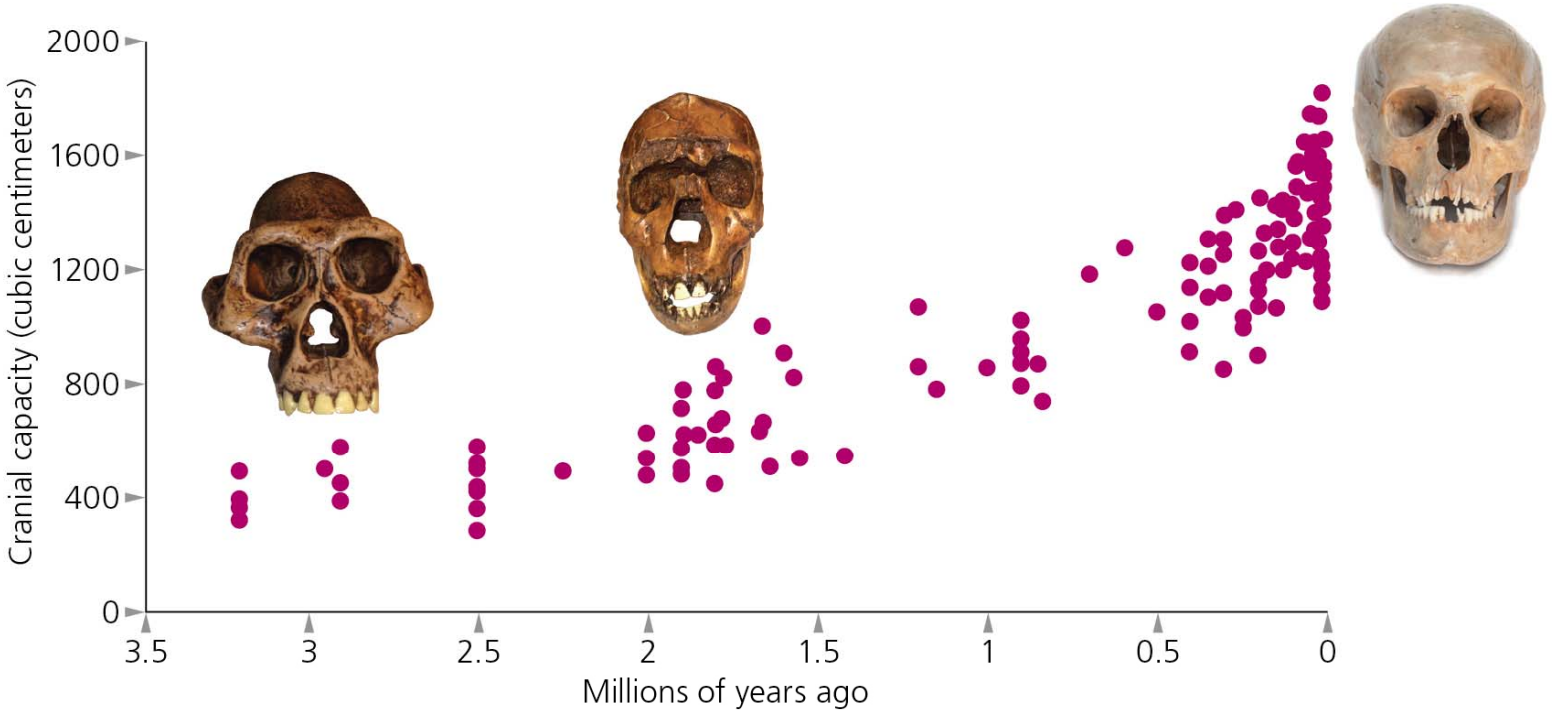
Some suggest this was ancestral to chimps

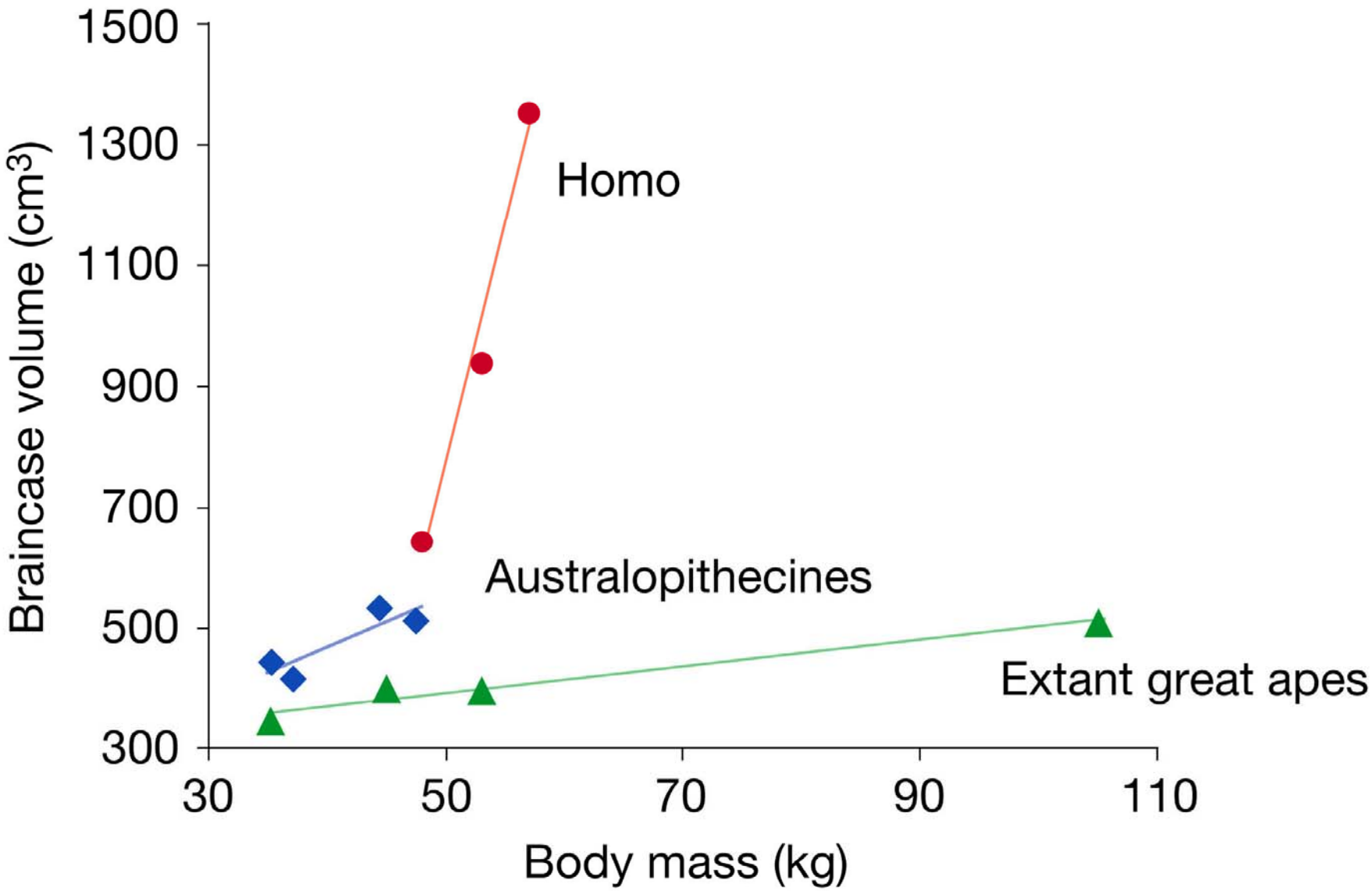
A: Chimpanzee, modern
B: *A. africanus*, 2.6 My
C: *A. africanus*, 2.5 My
D: *Homo habilis*, 1.9 My
E: *H. habilis*, 1.8 My
F: *H. rodolfensis*, 1.8 My
G: *H. erectus*, 1.75 My

H. *H. ergaster*, 1.75 My
I: *H. heidelbergensis*, 125K-300K
J: *H. s. neanderthalensis*, 70K
K: *H. s. neanderthalensis*, 60K
L: *H. s. neanderthalensis*, 45K
M. *H. s. sapiens* (Cro-Magnon), 30K
N. *H. s. sapiens*, modern


(B)
Estimated brain volume (cc)
2000
1500
1000
500
0
Homo sapiens
Homo erectus
Homo habilis
Australopithecus
← Modern mean value
3.0
2.0
1.0
Present
Time (Mya)

Social evolution may have driven increased brain size

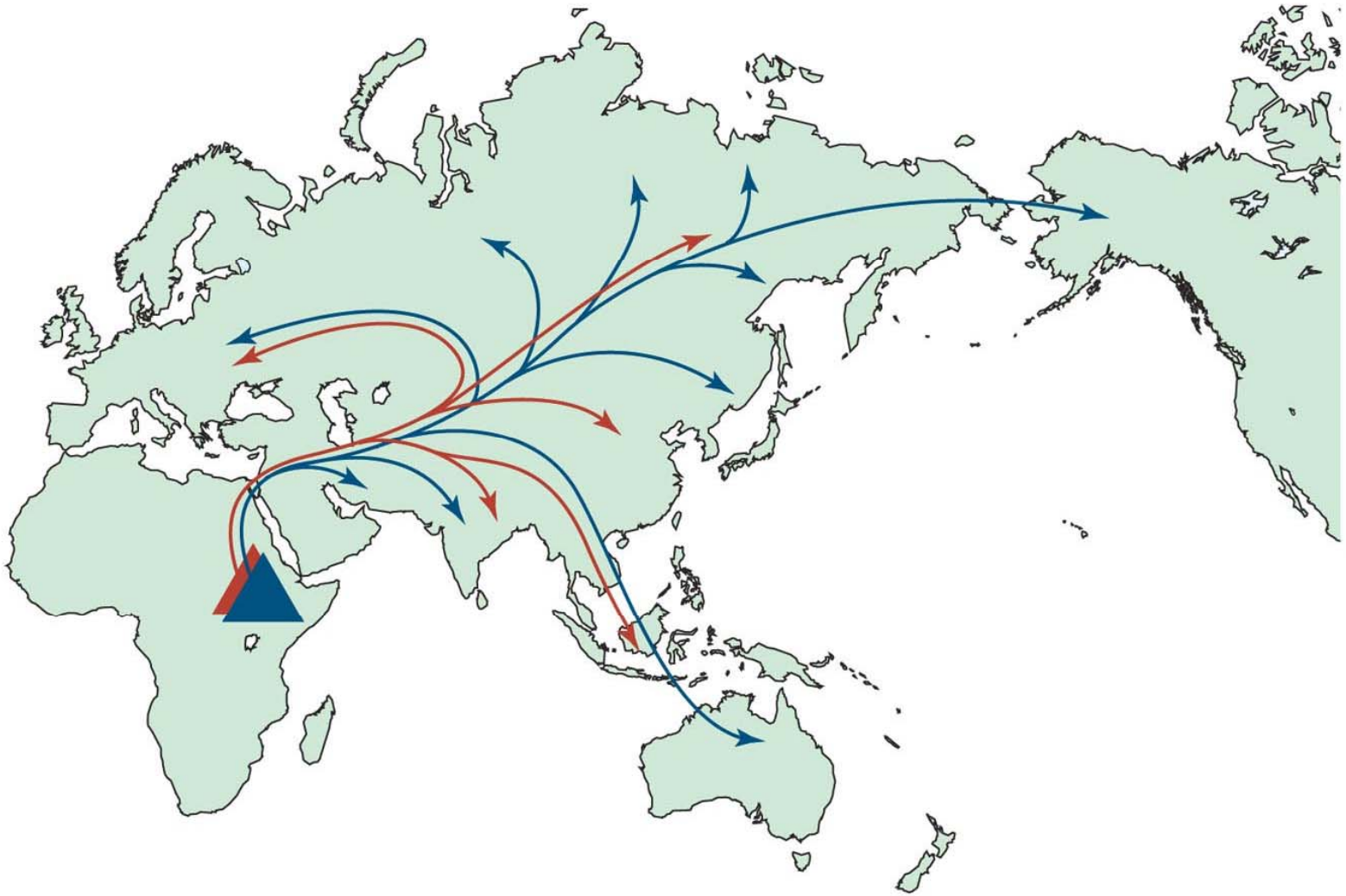



1500
1300
1100
900
700
500
300
Braincase volume (cm³)
Homo
Australopithecines
Extant great apes
30
50
70
90
110
Body mass (kg)

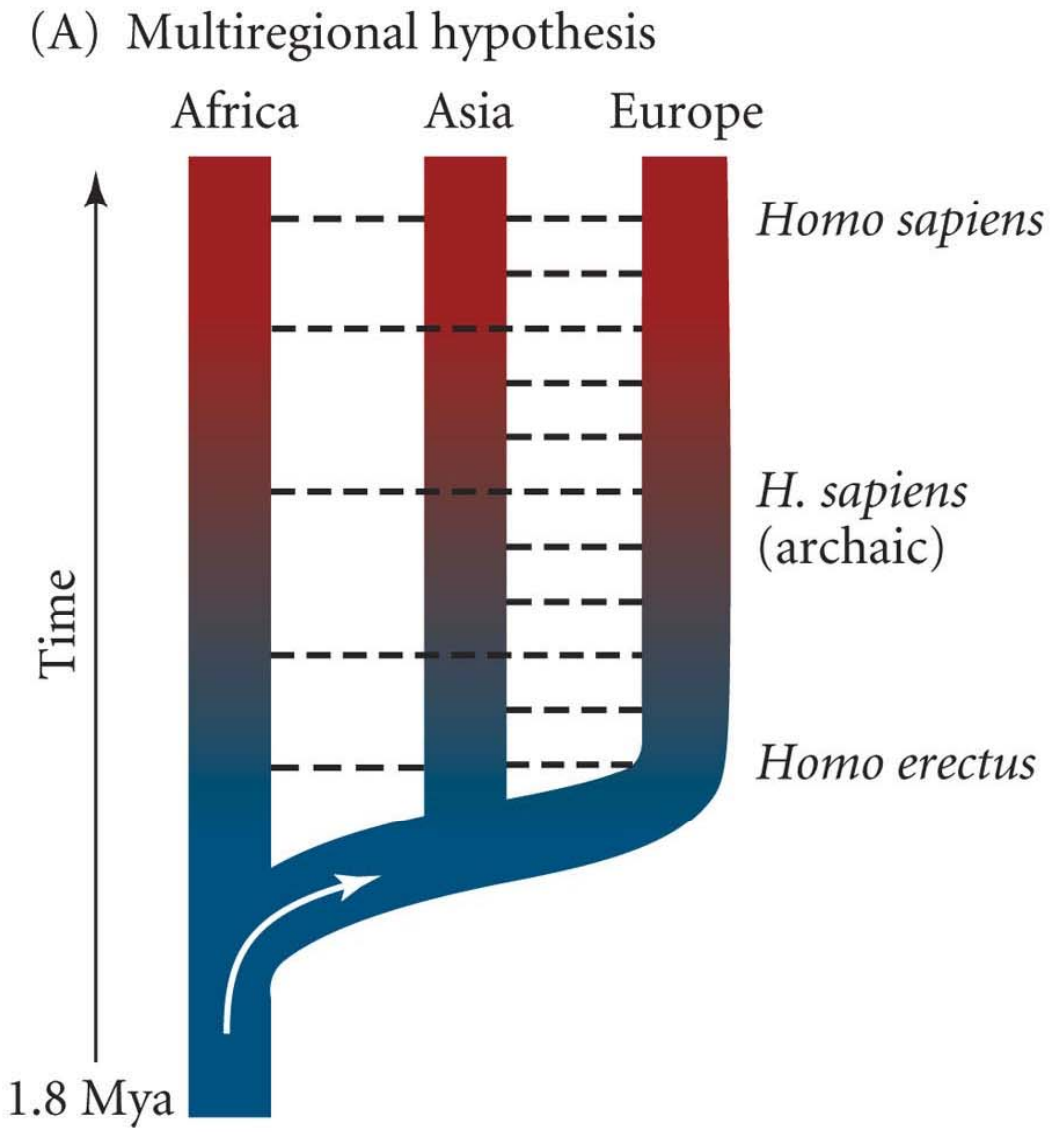
How did we people Earth?

When?

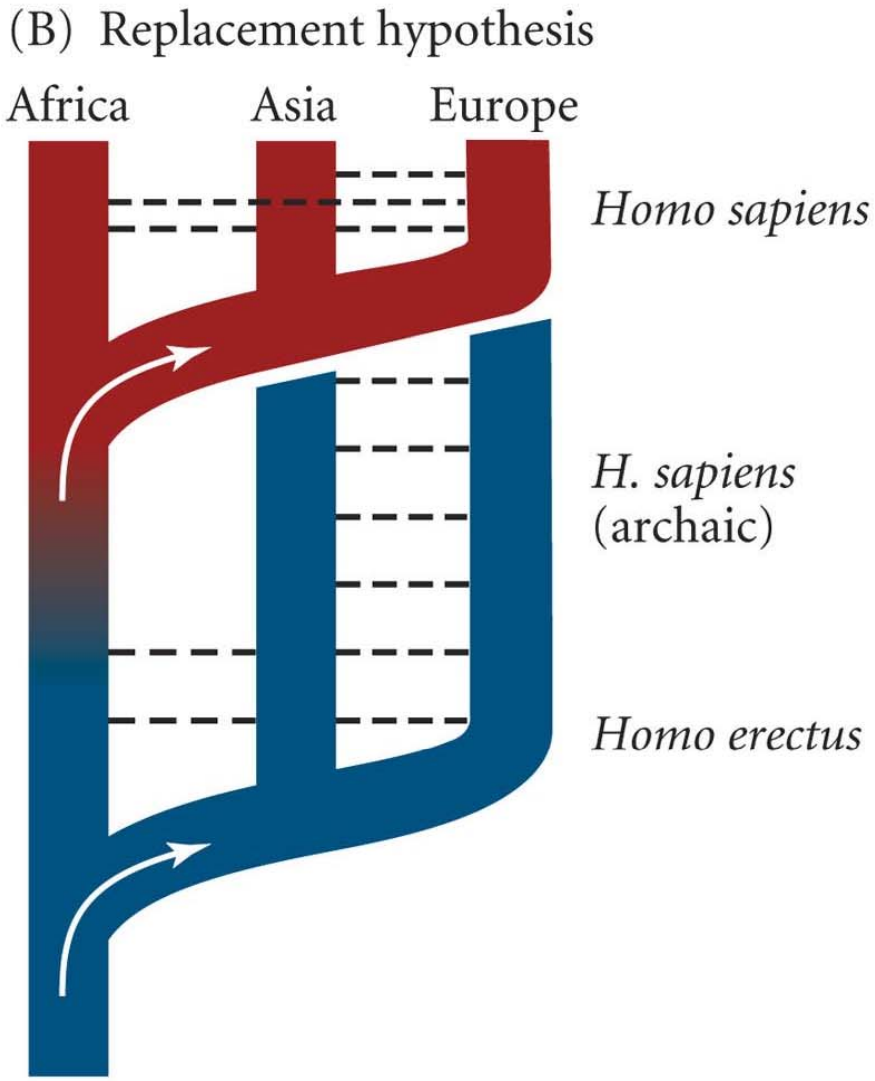
Homo erectus spread (~1.8 Mya) from Africa to Europe and Asia (the first wave) in Red



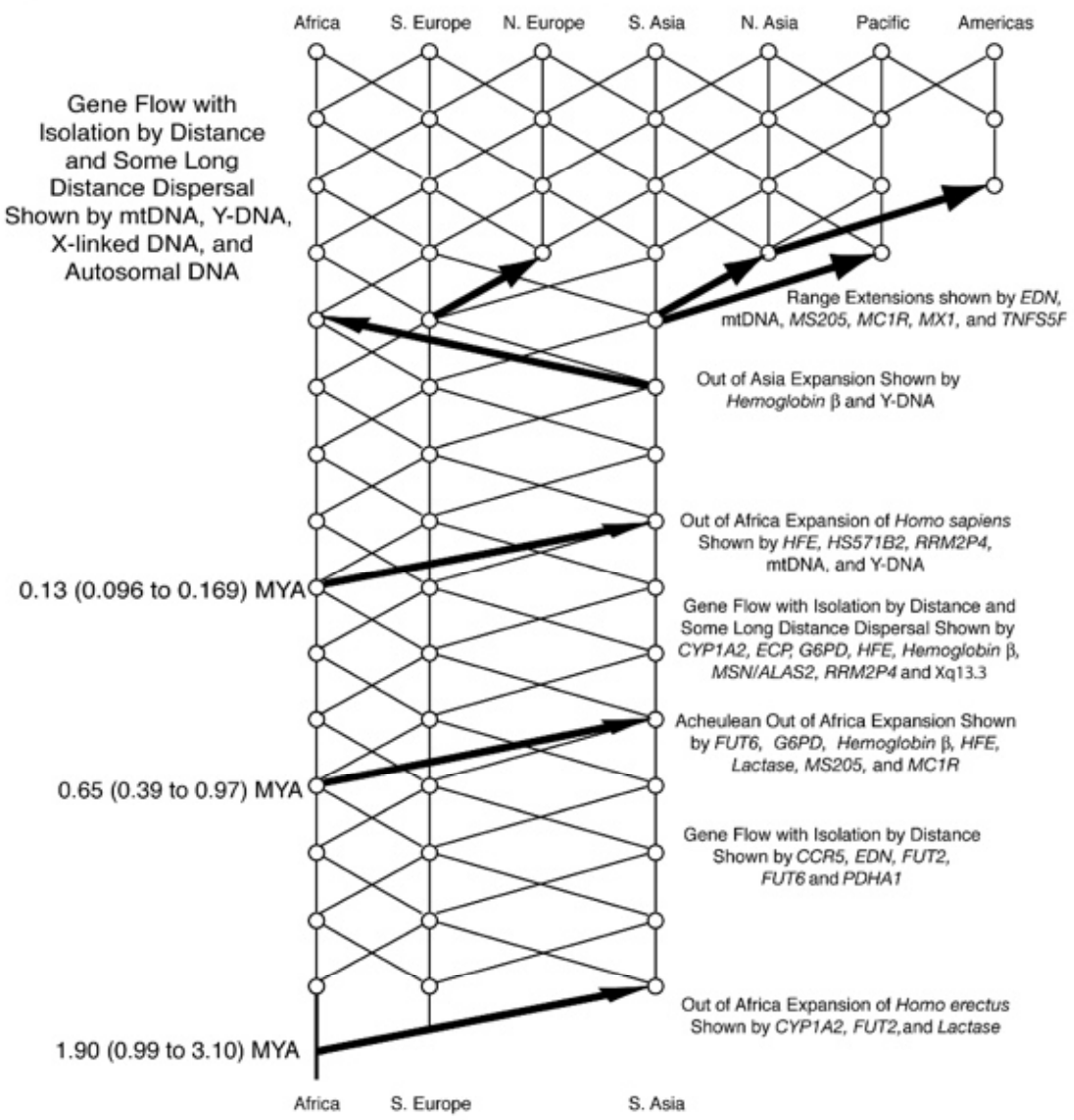
Two hypotheses on the origin of modern humans:



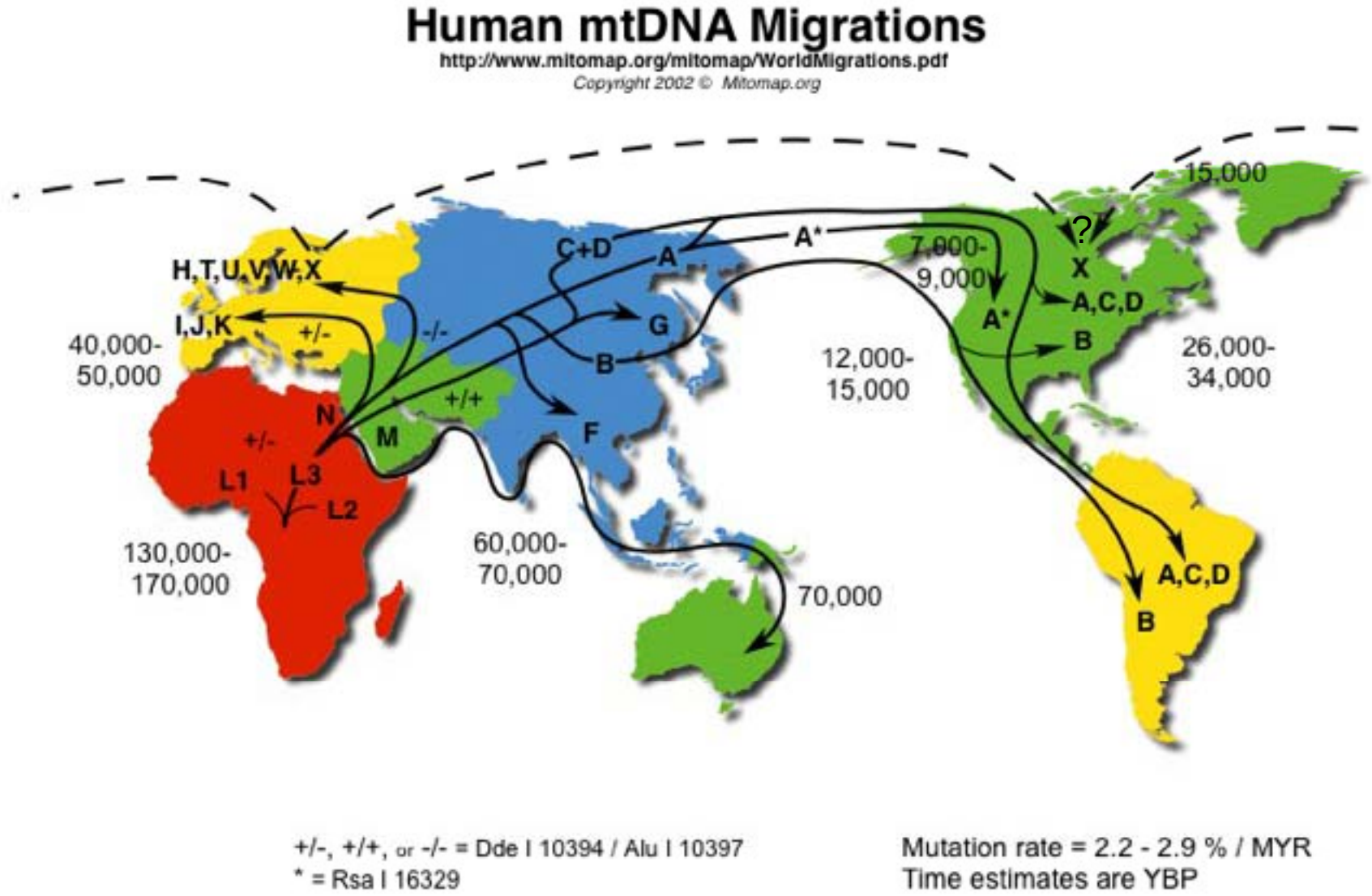
Two hypotheses on the origin of modern humans:



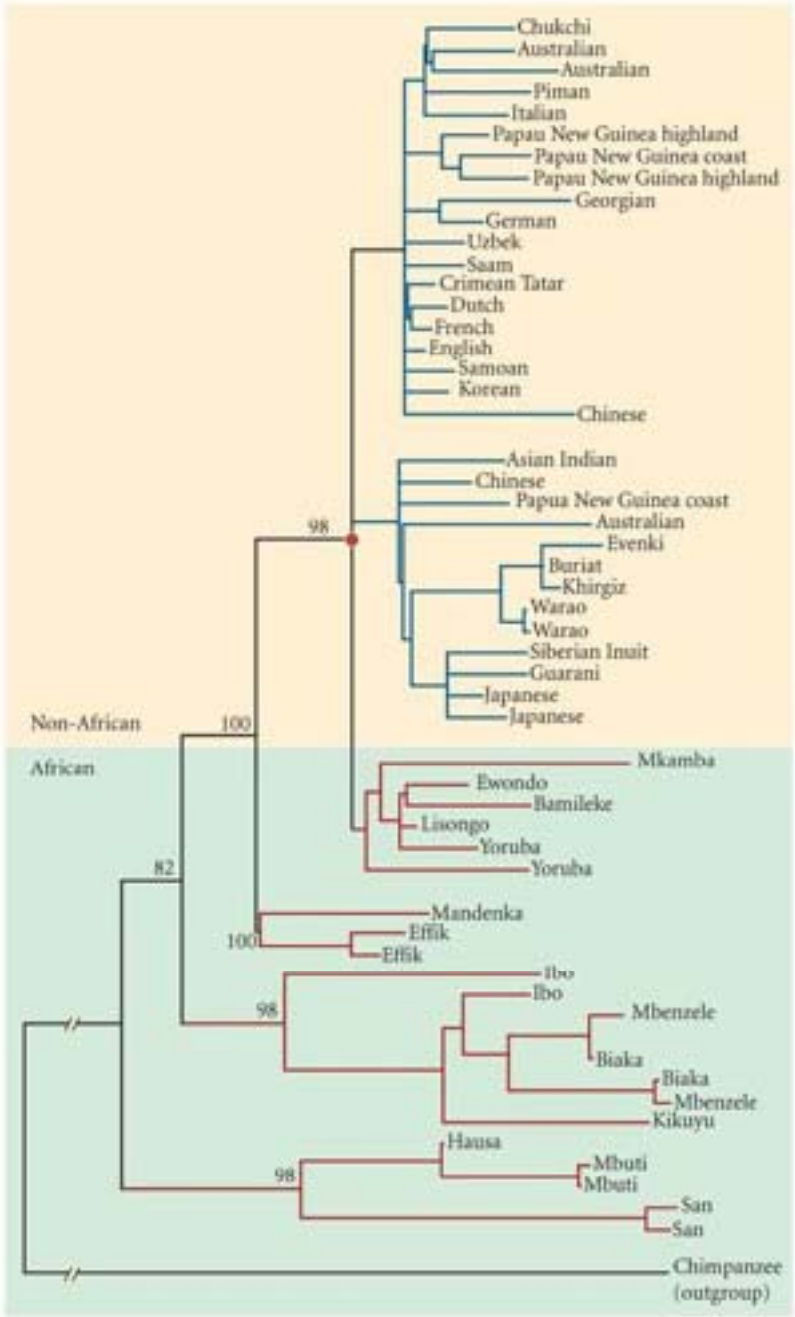
The Mostly-Out-of-Africa Hypothesis



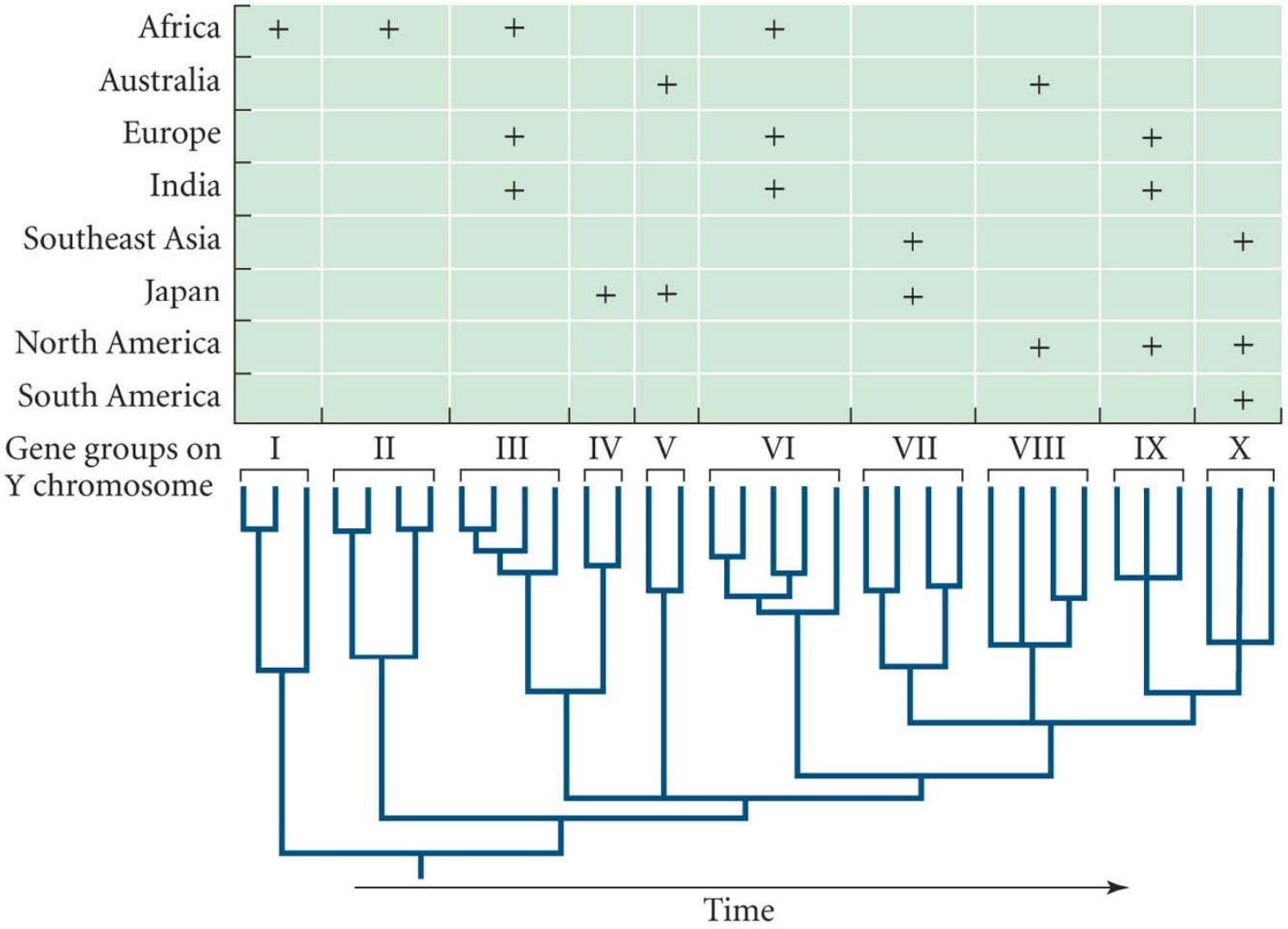
Biogeography of *Homo sapiens*



Tree based on mtDNA

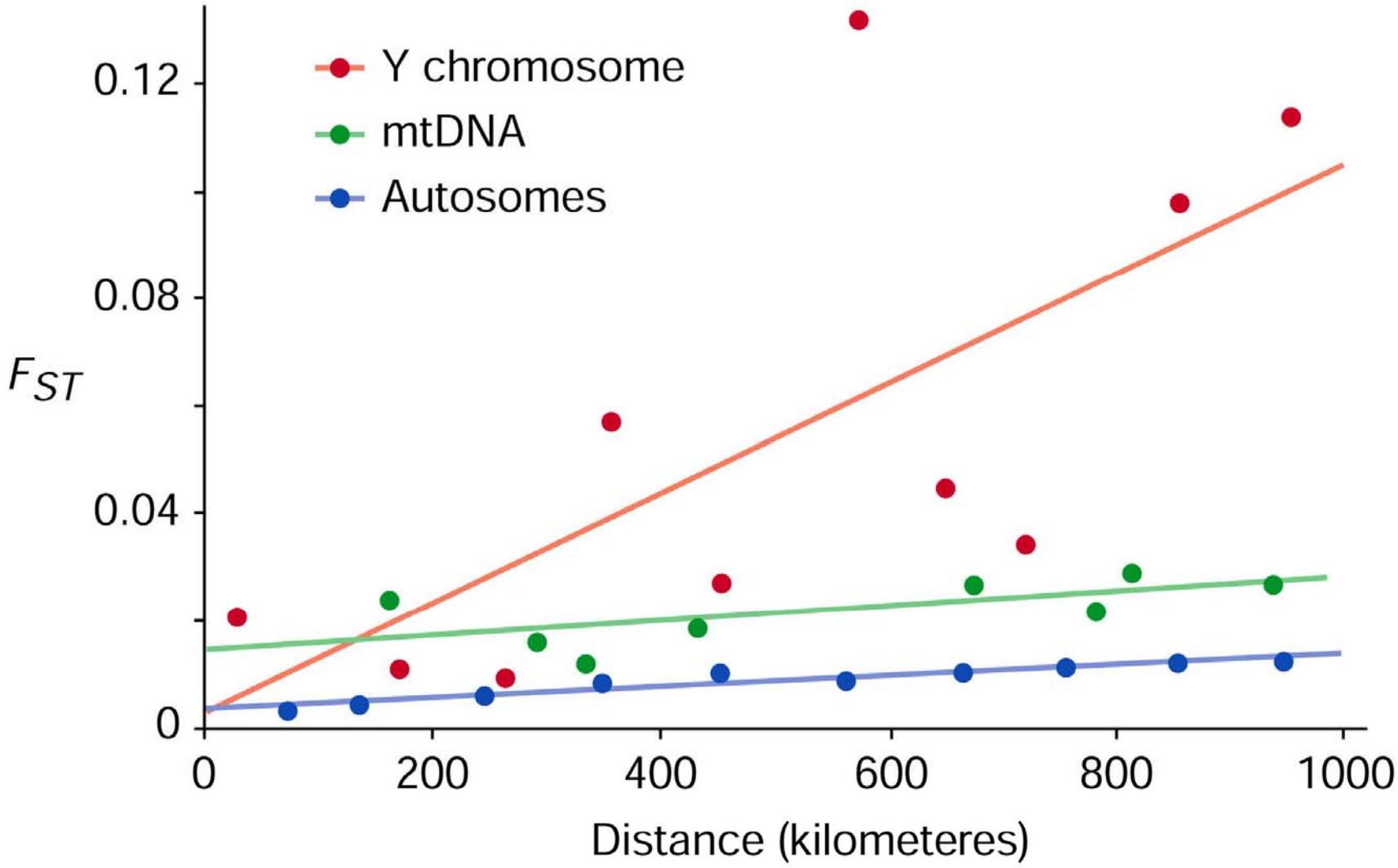


The movement of human populations from about 50,000 to 10,000 years ago



Tree based on Y-chromosome

Higher Female Migration Rate



Genetic Evidence of Geographical Groups among Neanderthals – based on mitochondrial evidence.

Fabre et al., 2009 PloS One

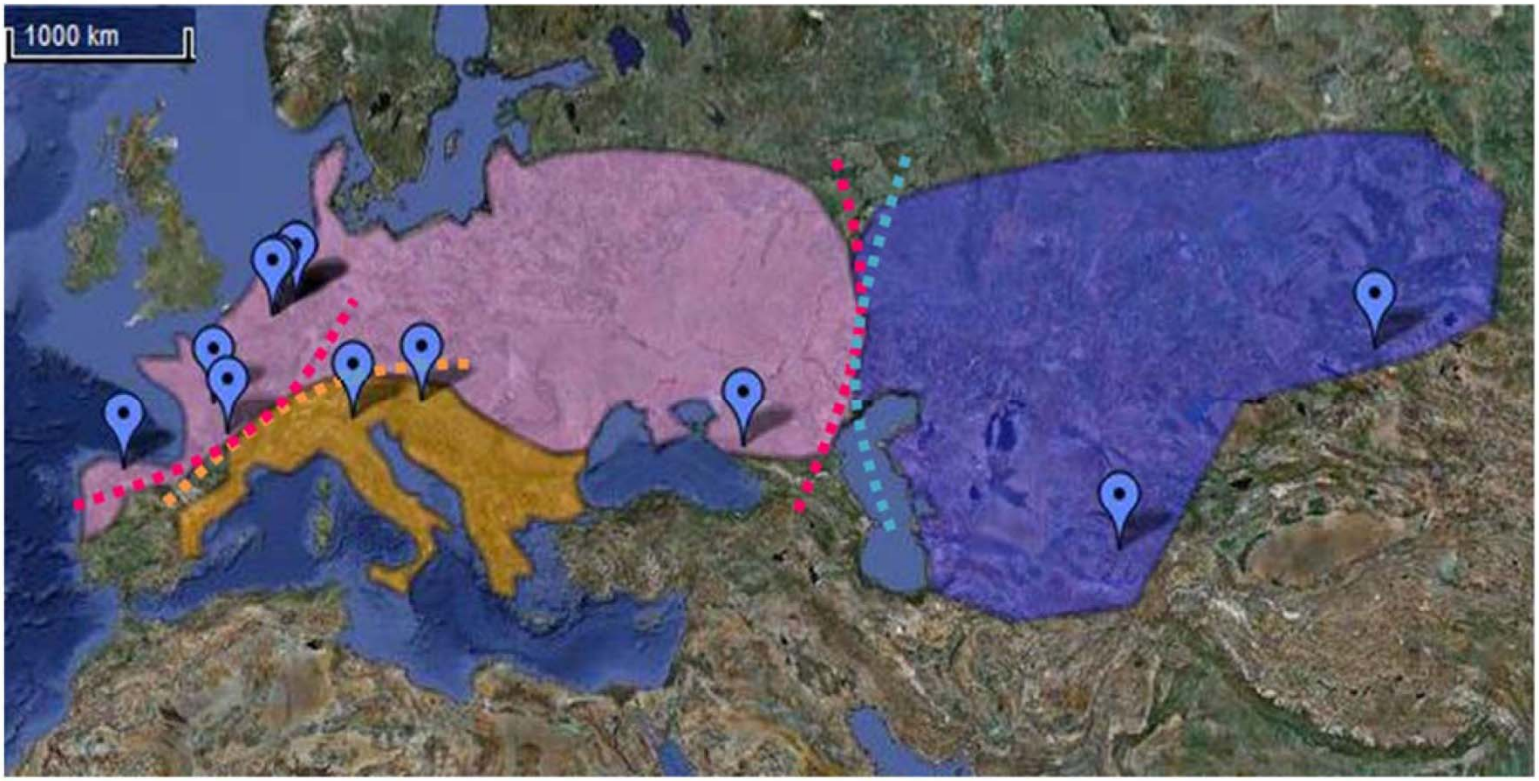
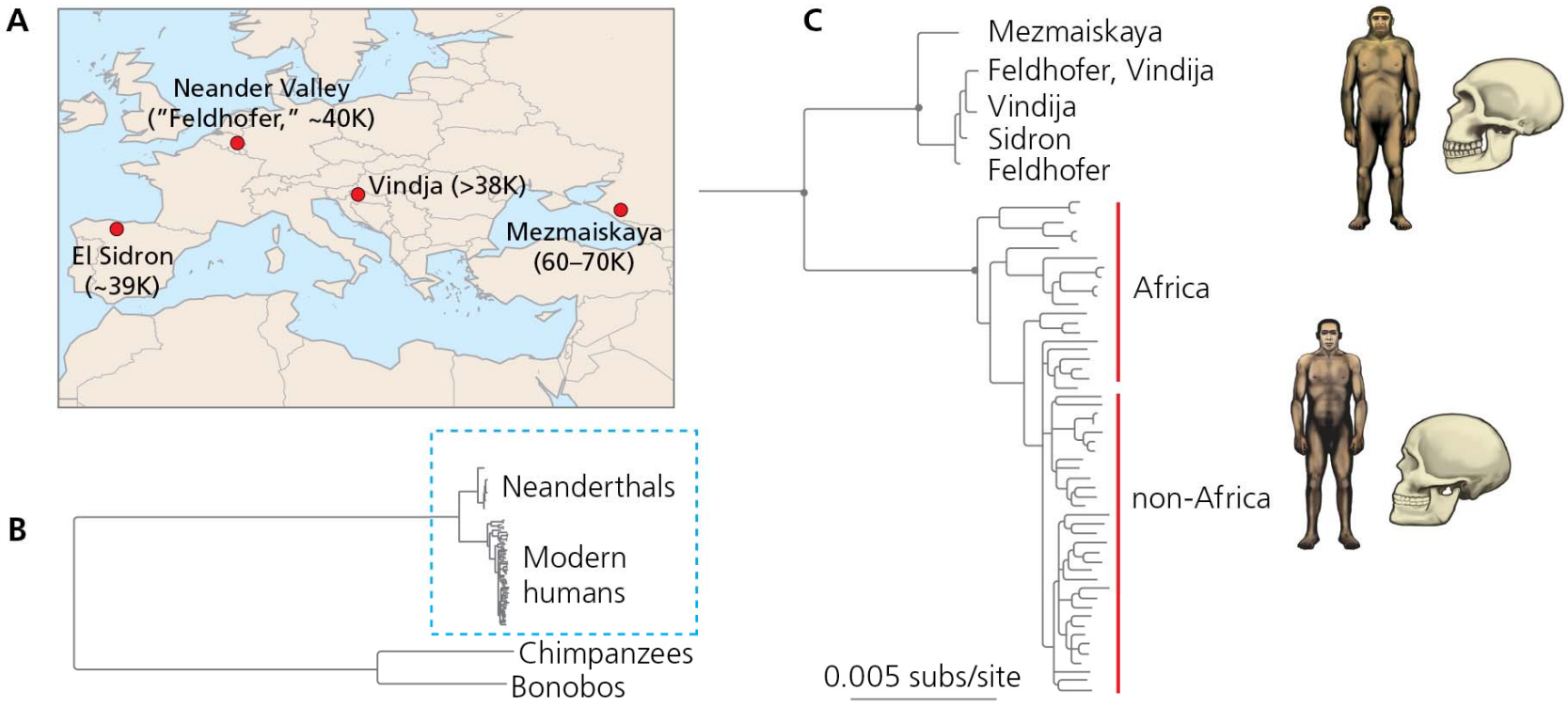
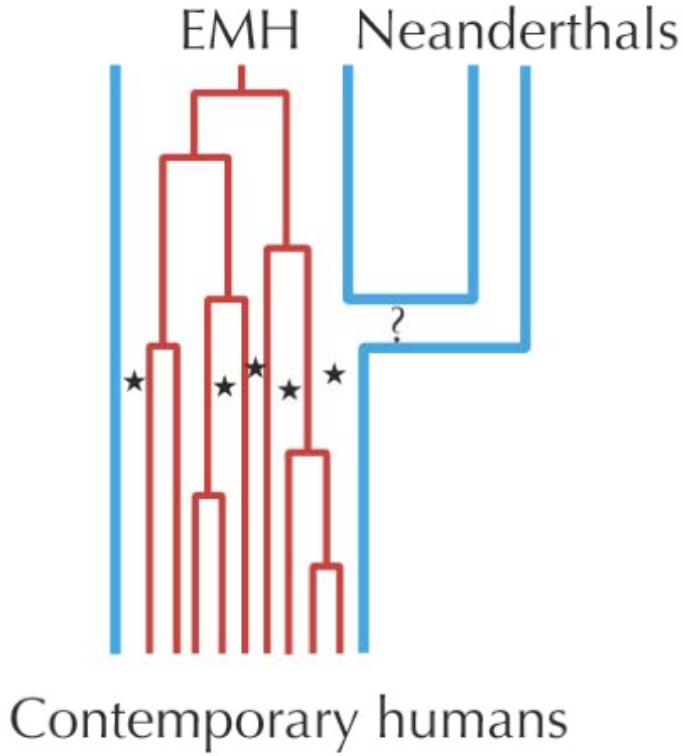


Figure 2. Map representing Neanderthal geographical distribution in groups.
doi:10.1371/journal.pone.0005151.g002

Neanderthals and modern humans form separate monophyletic groups



Can we really exclude *sapiens-neanderthalensis* interbreeding?



Serre et al., 2004 PLoS Biology

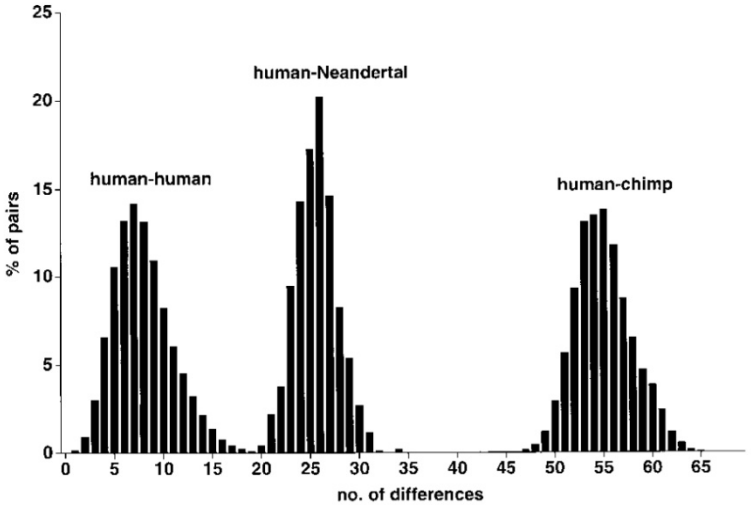


Figure 6. Distributions of Pairwise Sequence Differences among Humans, the Neandertal, and Chimpanzees

X axis, the number of sequence differences; Y axis, the percent of pairwise comparisons.

Krings et al., 1997 Cell

No Evidence of Neandertal mtDNA Contribution to Early Modern Humans

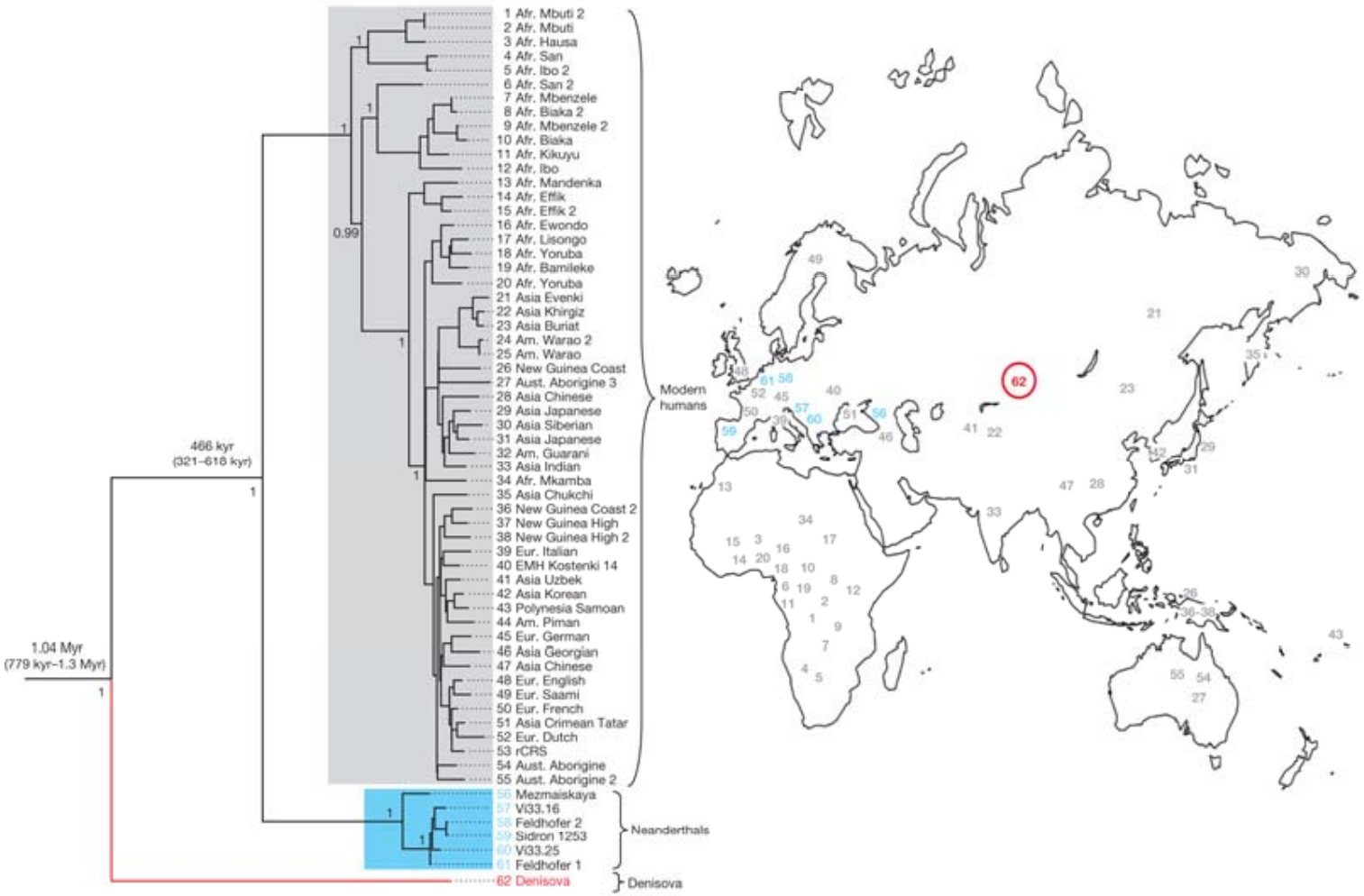
No we cannot after all!

A Draft Sequence of the Neandertal Genome

Neandertals, the closest evolutionary relatives of present-day humans, lived in large parts of Europe and western Asia before disappearing 30,000 years ago. We present a draft sequence of the Neandertal genome composed of more than 4 billion nucleotides from three individuals. Comparisons of the Neandertal genome to the genomes of five present-day humans from different parts of the world identify a number of genomic regions that may have been affected by positive selection in ancestral modern humans, including genes involved in metabolism and in cognitive and skeletal development. We show that Neandertals shared more genetic variants with present-day humans in Eurasia than with present-day humans in sub-Saharan Africa, suggesting that gene flow from Neandertals into the ancestors of non-Africans occurred before the divergence of Eurasian groups from each other.

Green et al., 2010 Science

Could four (or even five) species of homo co-existed until 40-50KYA?



- Reich et al., Nature 2010

Denisovans are a sister group to Neanderthals

ARTICLE

doi:10.1038/nature09710

Genetic history of an archaic hominin group from Denisova Cave in Siberia

David Reich[1,2]*, Richard E. Green[3,4]*, Martin Kircher[3]*, Johannes Krause[3,5]*, Nick Patterson[2]*, Eric Y. Durand[6]*, Bence Viola[3,7]*, Adrian W. Briggs[1,3], Udo Stenzel[3], Philip L. F. Johnson[8], Tomislav Maricic[3], Jeffrey M. Good[9], Tomas Marques-Bonet[10,11], Can Alkan[10], Qiaomei Fu[3,12], Swapan Mallick[1,2], Heng Li[2], Matthias Meyer[3], Evan E. Eichler[10], Mark Stoneking[3], Michael Richards[7,13], Sahra Talamo[7], Michael V. Shunkov[14], Anatoli P. Derevianko[14], Jean-Jacques Hublin[7], Janet Kelso[3], Montgomery Slatkin[6] & Svante Pääbo[3]

Genome sequence of finger bone

Phylogeny using multiple autosomal genes

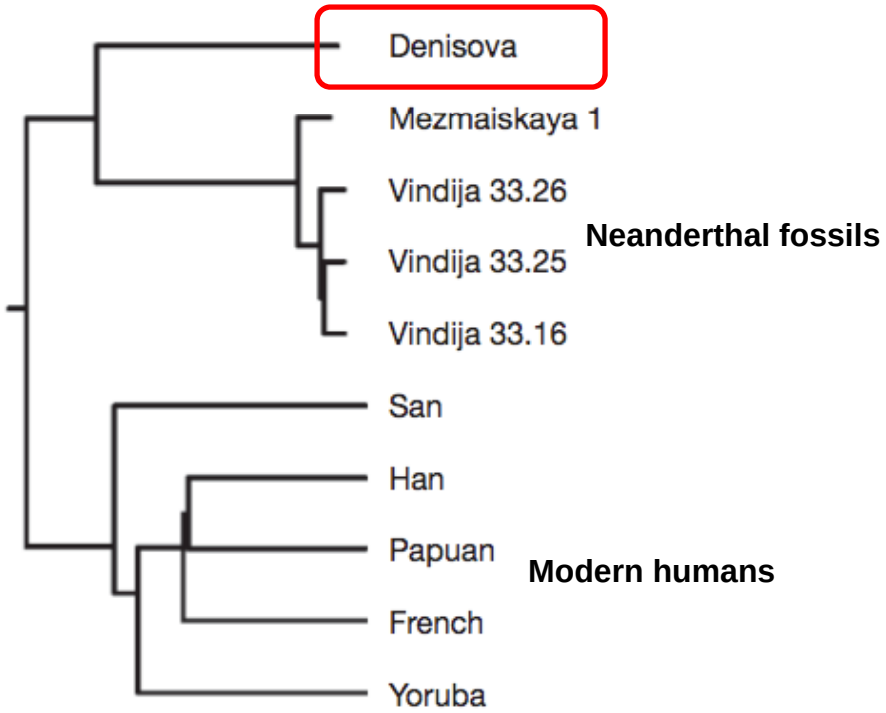
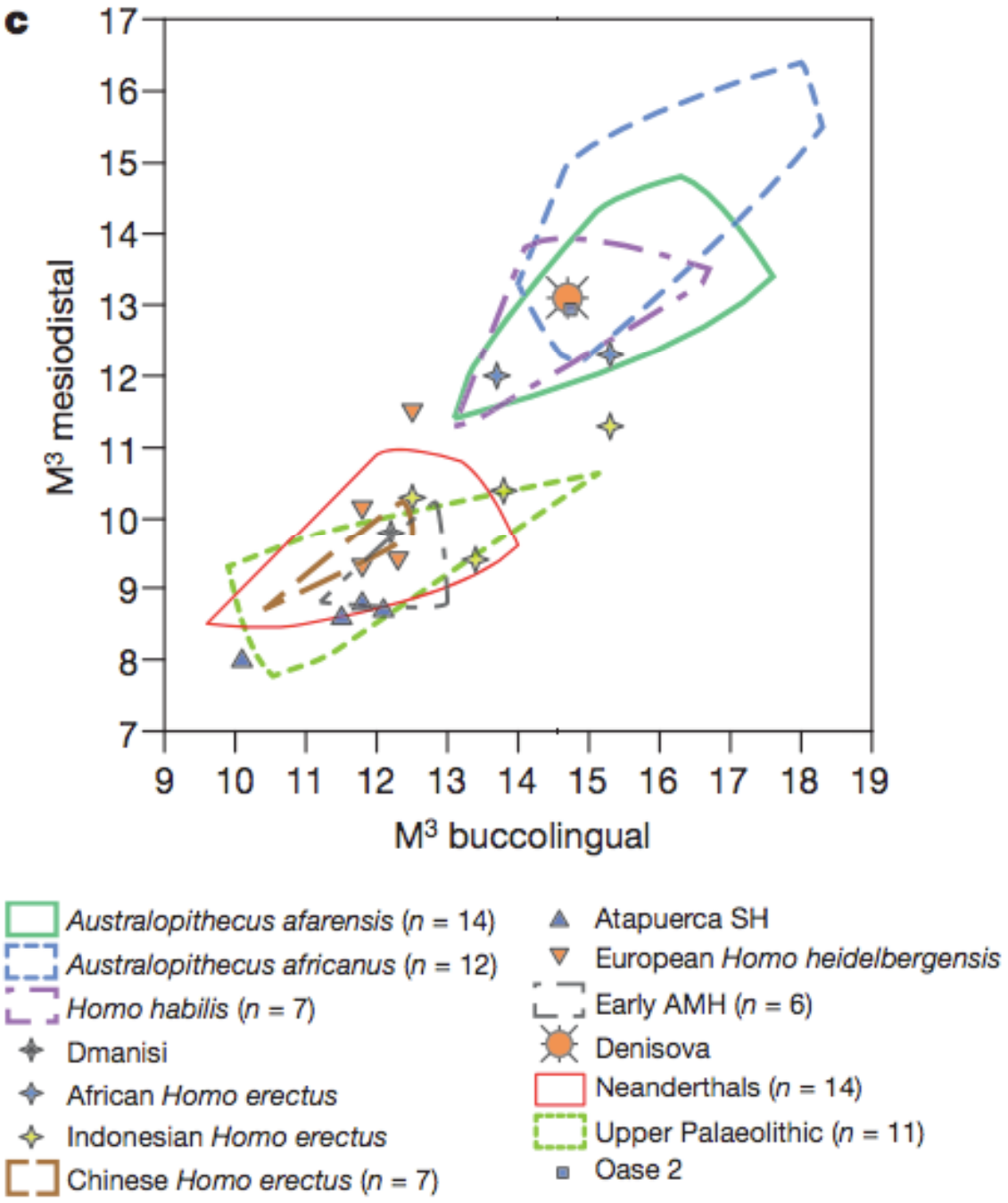


Figure 1 | A neighbour-joining tree based on pairwise autosomal DNA sequence divergences for five ancient and five present-day hominins. Vindija 33.16, Vindija 33.25 and Vindija 33.26 refer to the catalogue numbers of the Neanderthal bones.

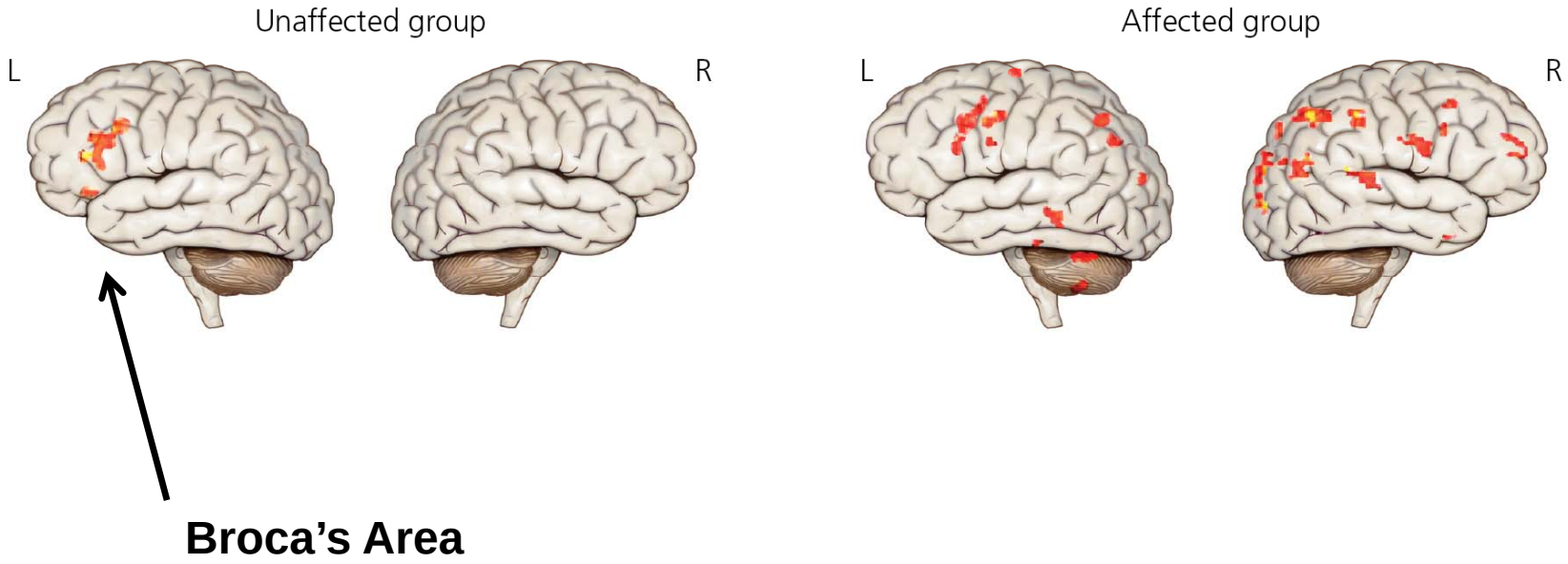
- How can we explain the discrepancy?

Are the Denisovans separate from the Neanderthals?

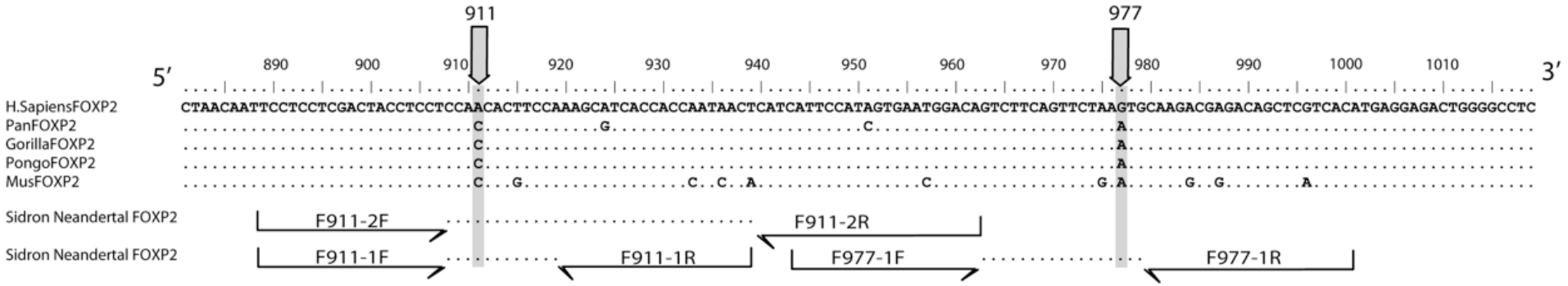
- Population history
- Tooth morphology



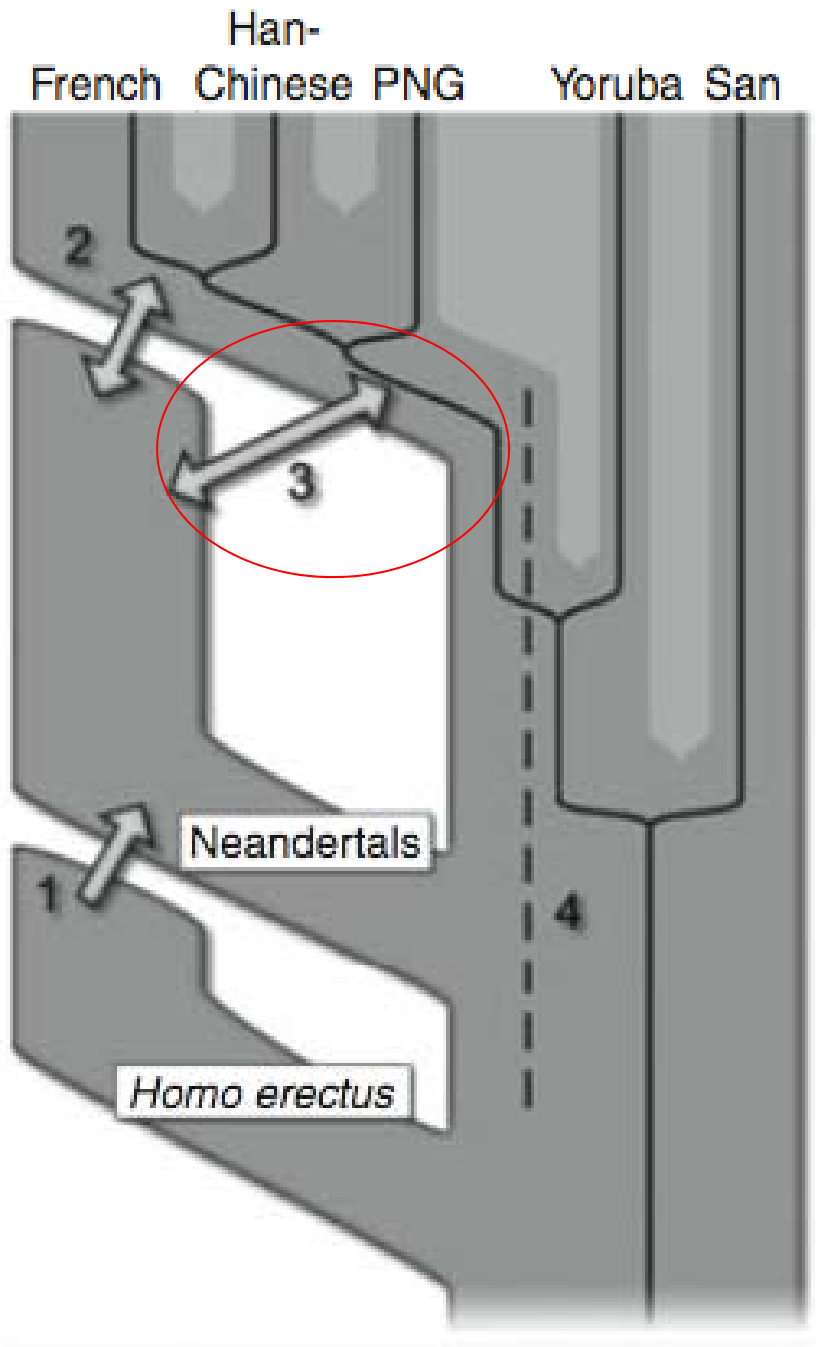
FOXP2 implicated in capacity for language



Homo neanderthalensis and speech

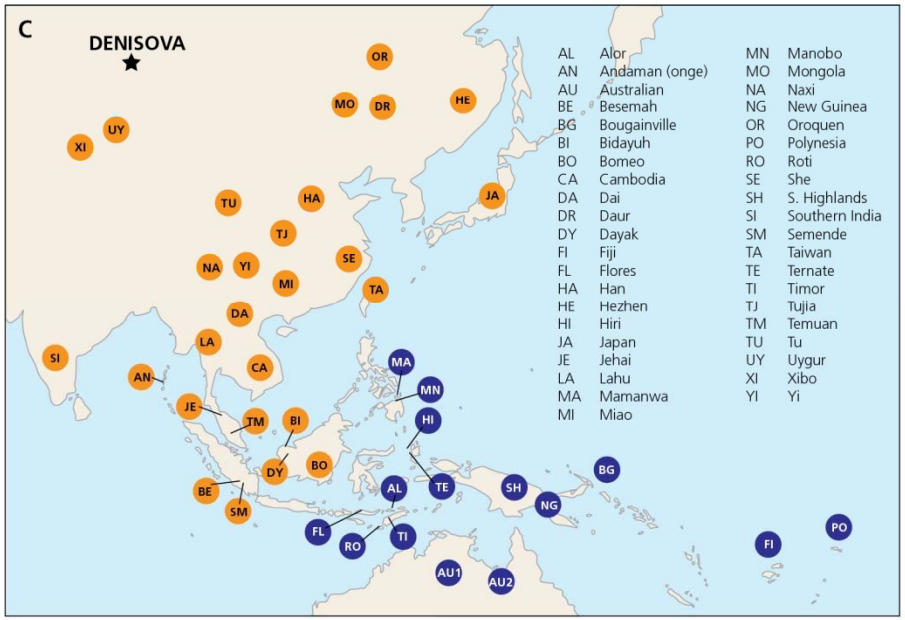


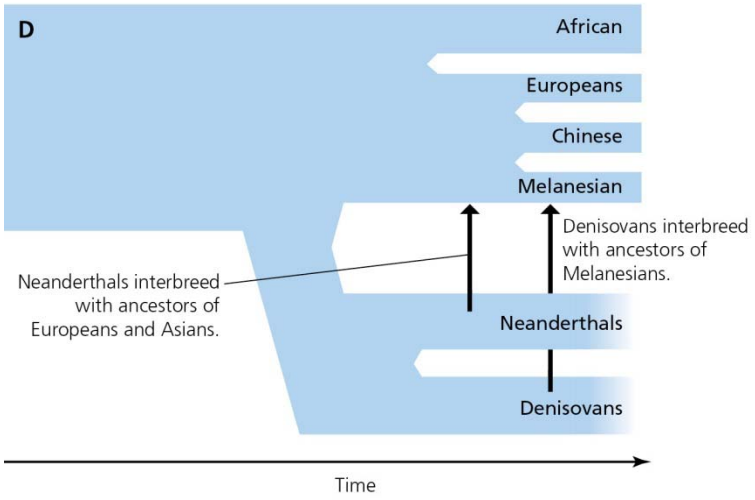
- FOXP2 is the only gene that is known (to date) to be implicated in human speech
  - Inactive copy leads to difficulties in speech (Broca's aphasia)
- *Neanderthals* share unique human nonsynonymous mutations in this gene



Gene flow with *neanderthalensis*

- Only “out of Africa” humans show Neanderthal alleles!
- ~3% Neanderthal introgression
- Gene flow after split and not ancient polymorphism

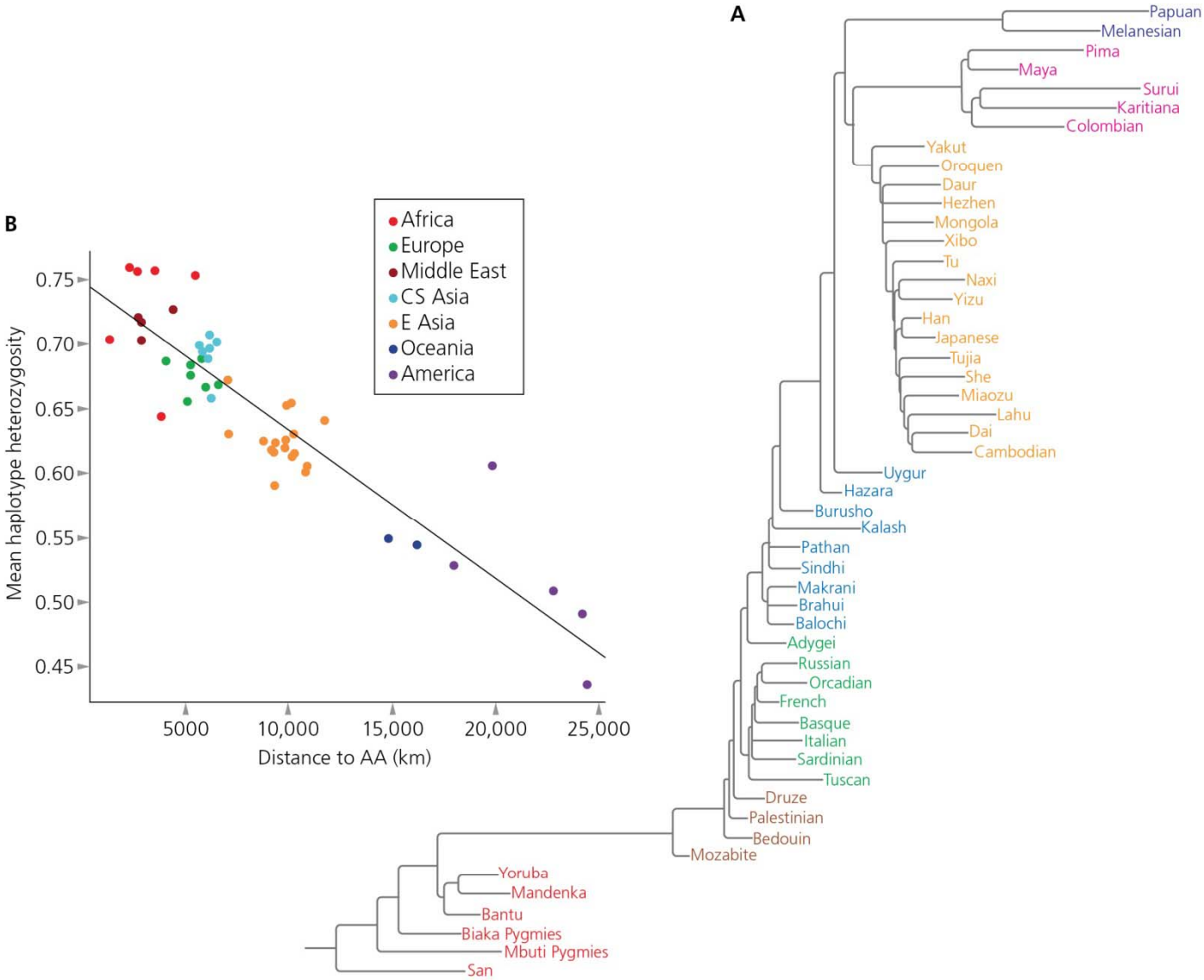




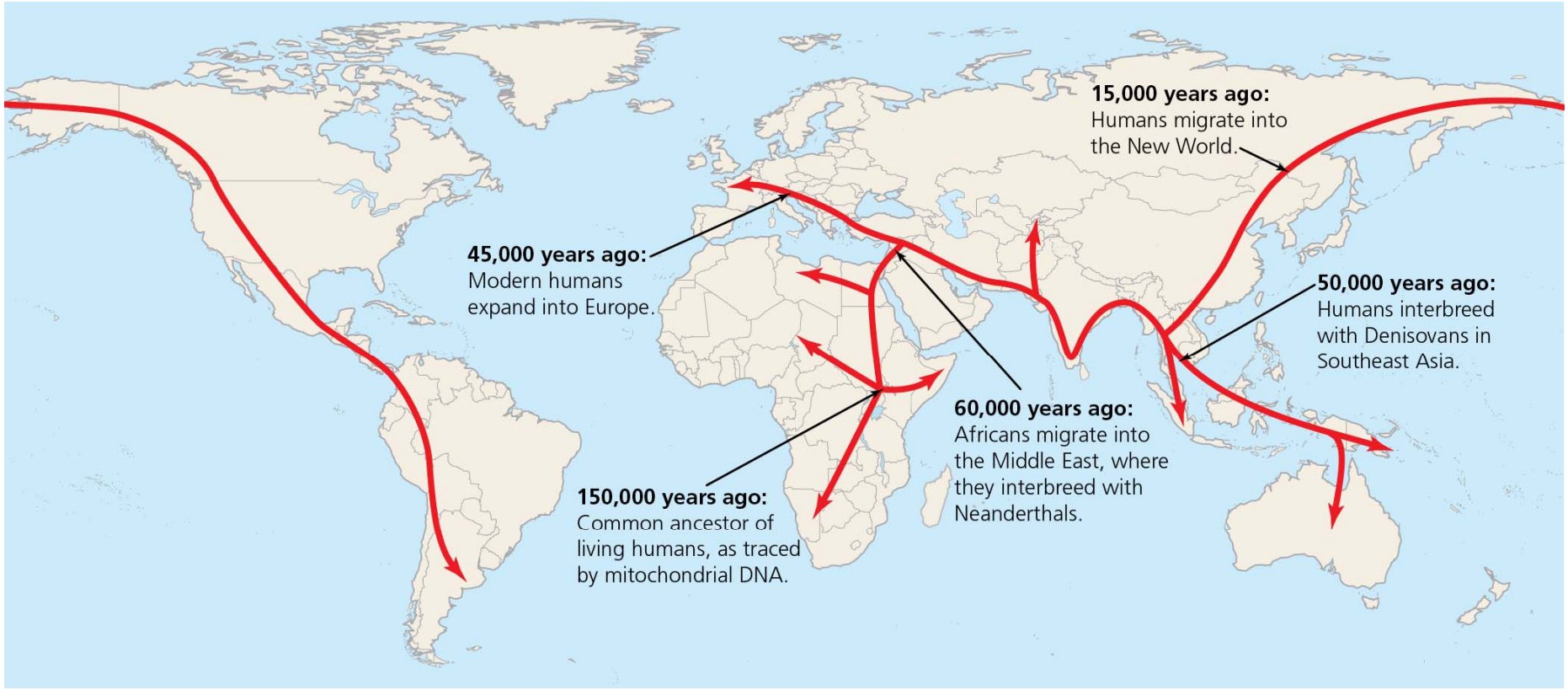
What about gene flow from Denisovans?

- ~ 4% of Melanesian genome shows evidence of Denisovan introgression!
- How do we explain this biogeographically?

Bottlenecks in human history

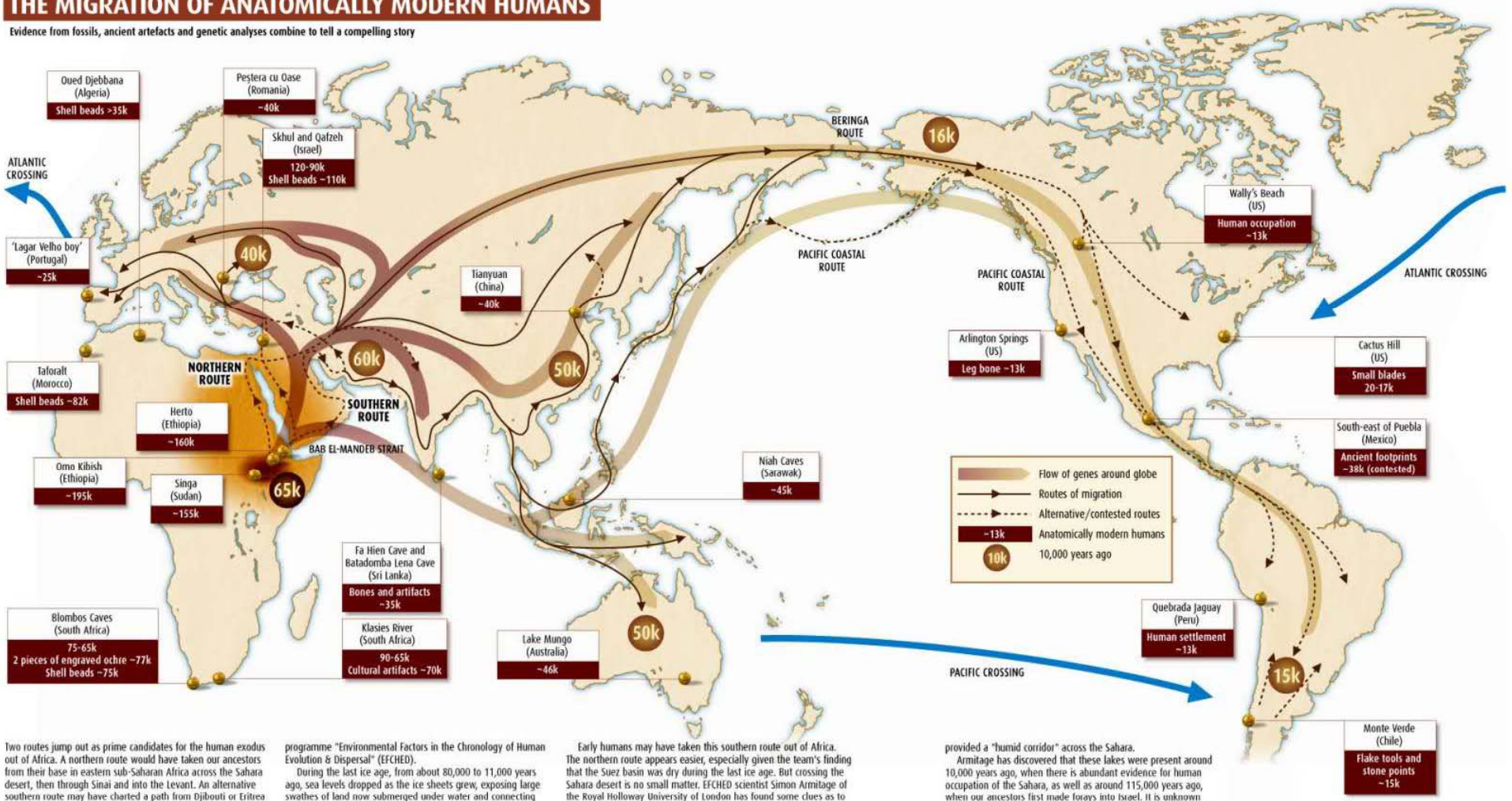


Current hypothesis for expansion mostly out of Africa



THE MIGRATION OF ANATOMICALLY MODERN HUMANS

Evidence from fossils, ancient artefacts and genetic analyses combine to tell a compelling story

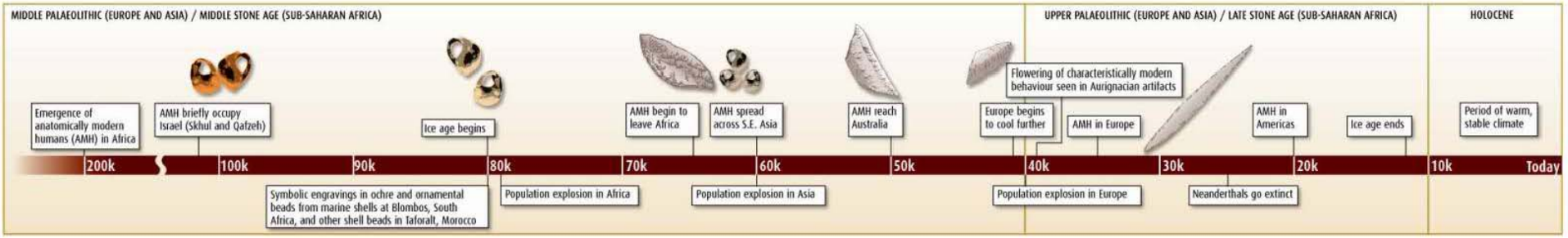


Two routes jump out as prime candidates for the human exodus out of Africa. A northern route would have taken our ancestors from their base in eastern sub-Saharan Africa across the Sahara desert, then through Sinai and into the Levant. An alternative southern route may have charted a path from Djibouti or Eritrea in the Horn of Africa across the Bab el-Mandeb strait and into Yemen and around the Arabian peninsula. The plausibility of these two routes as gateways out of Africa has been studied as part of the UK's Natural Environment Research Council's programme "Environmental Factors in the Chronology of Human Evolution & Dispersal" (EFCHED).

During the last ice age, from about 80,000 to 11,000 years ago, sea levels dropped as the ice sheets grew, exposing large swathes of land now submerged under water and connecting regions now separated by the sea. By reconstructing ancient shorelines, the EFCHED team found that the Bab el-Mandeb strait, now around 30 kilometres wide and one of the world's busiest shipping lanes, was then a narrow, shallow channel.

Early humans may have taken this southern route out of Africa. The northern route appears easier, especially given the team's finding that the Suez basin was dry during the last ice age. But crossing the Sahara desert is no small matter. EFCHED scientist Simon Armitage of the Royal Holloway University of London has found some clues as to how this might have been possible. During the past 150,000 years, North Africa has experienced abrupt switches between dry, arid conditions and a humid climate. During the longer wetter periods huge lakes existed in both Chad and Libya, which would have provided a "humid corridor" across the Sahara.

Armitage has discovered that these lakes were present around 10,000 years ago, when there is abundant evidence for human occupation of the Sahara, as well as around 115,000 years ago, when our ancestors first made forays into Israel. It is unknown whether another humid corridor appeared between about 65,000 and 50,000 years ago, the most likely time frame for the human exodus. Moreover, accumulating evidence is pointing to the southern route as the most likely jumping-off point.



Recent Ancestry of Humans

- Hominid - chimp split occurred ~5 Mya
- Gracile australopithecines ~4.4 to 2.4 Mya
- Robust australopithecines ~2.5 to 1.5 Mya
- Genus Homo ~1.8-2.0 Mya
- Modern Humans ~180-200 Kya to present
- Bottleneck of ~14K pop size @ ~40Kya
- *Homo sapiens are the lone survivors of a an otherwise extinct radiation of bipedal African hominins*

Take Home Message

- Mitochondria good from tracking phylogeography.
- Genomics necessary to catch a glimpse of gene flow.
- More diversity (of late) that we thought possible. Now = Mostly out of Africa!
- Many human fossils are now submerged (last ice age; ~80K to 11K ago).