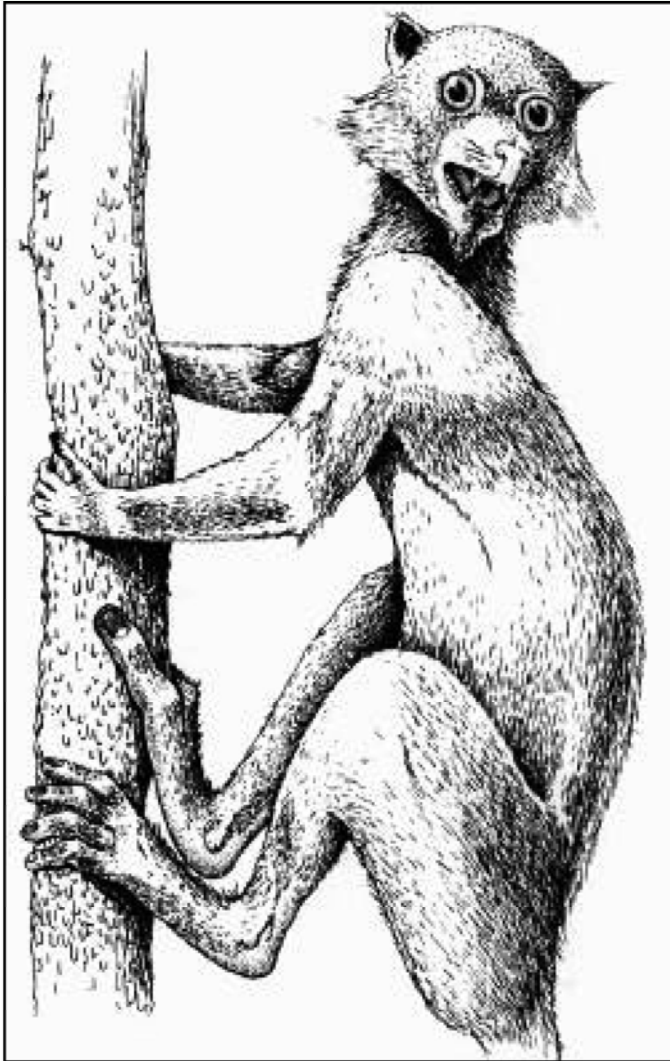


# Human Evolution

## 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.

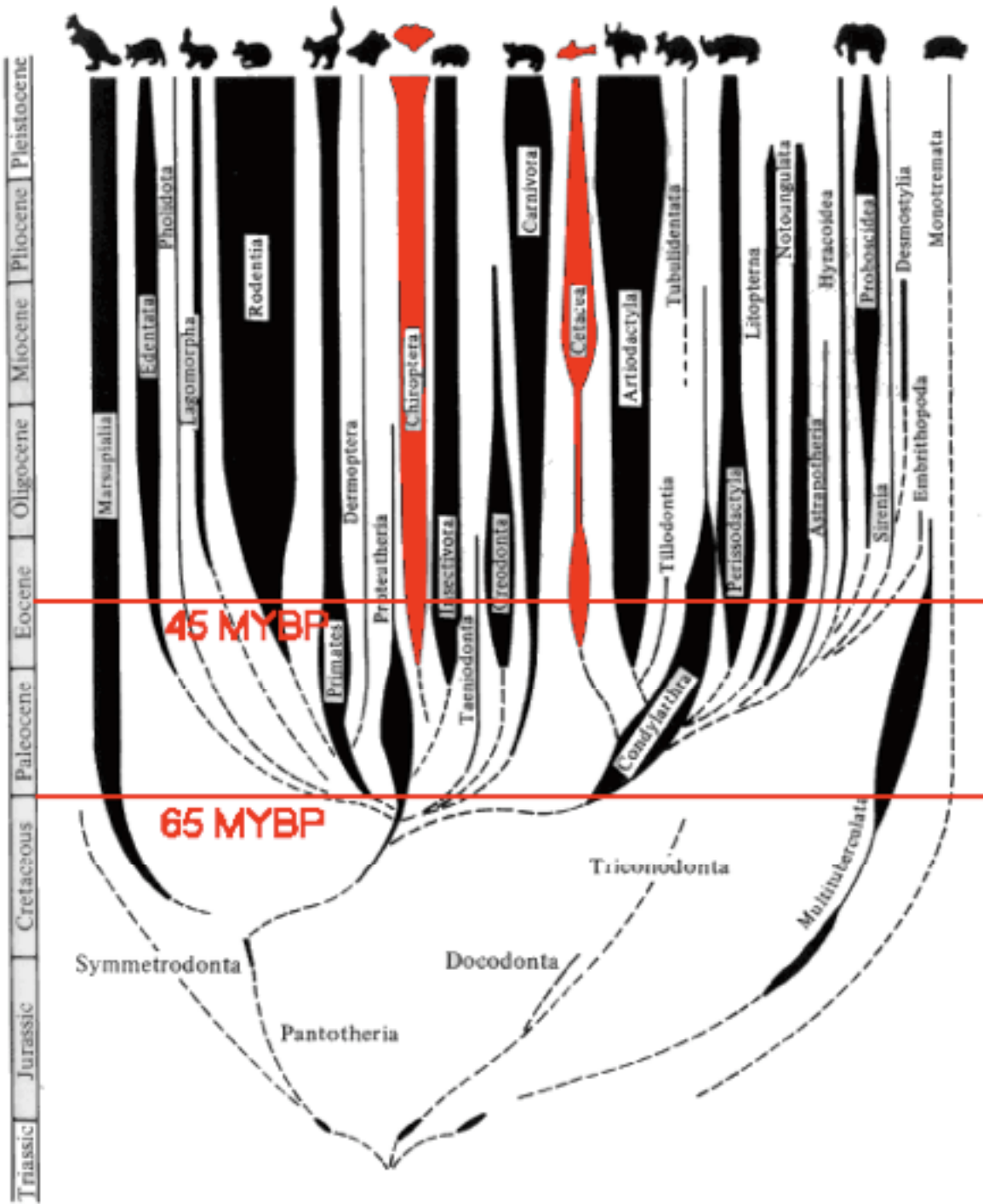


# *Darwinius masillae*



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

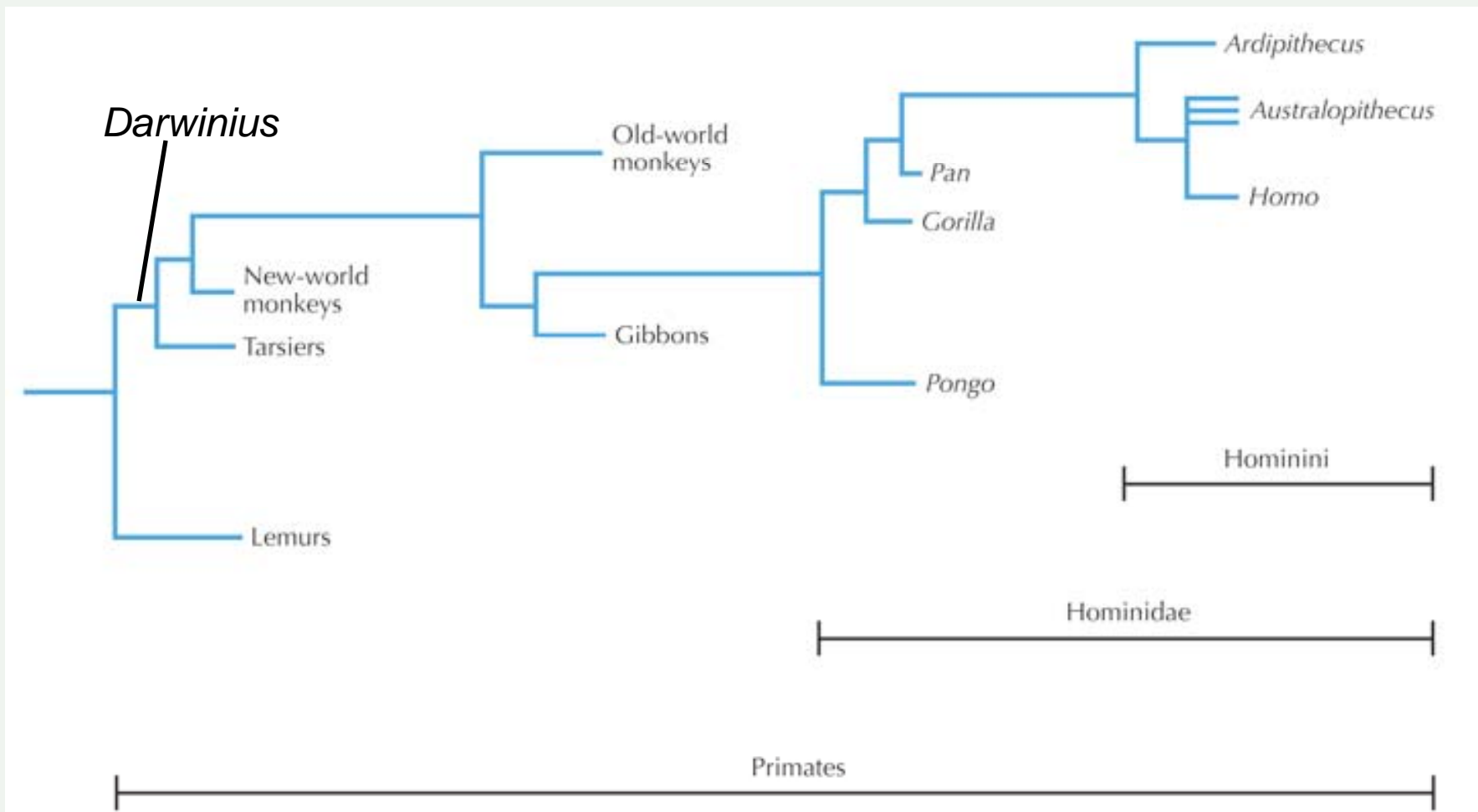
Franzen et al., PloS One 2009



# Primates

- Distinct group within the mammals

# Placement of *Darwinius* among the primates



- Primate phylogeny

# Which are our closest relatives?

(A) Gibbon



(B) Orangutan



(C) Gorilla



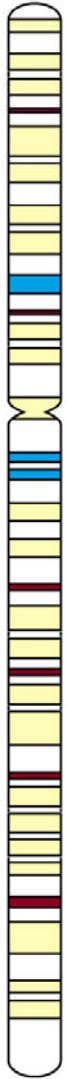
(D) Chimpanzee



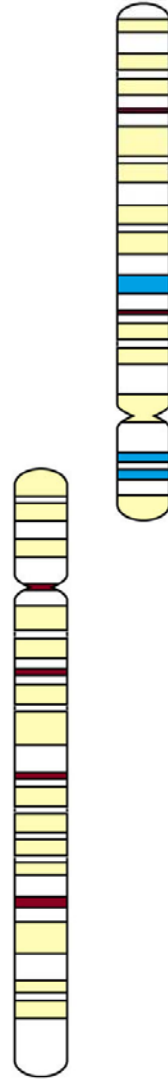
Hominoidea Superfamily

Human

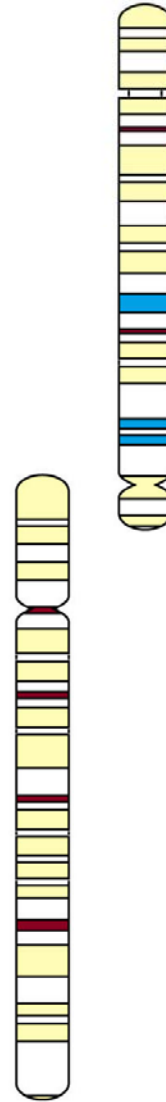
Chromosome 2



Chimpanzee



Gorilla

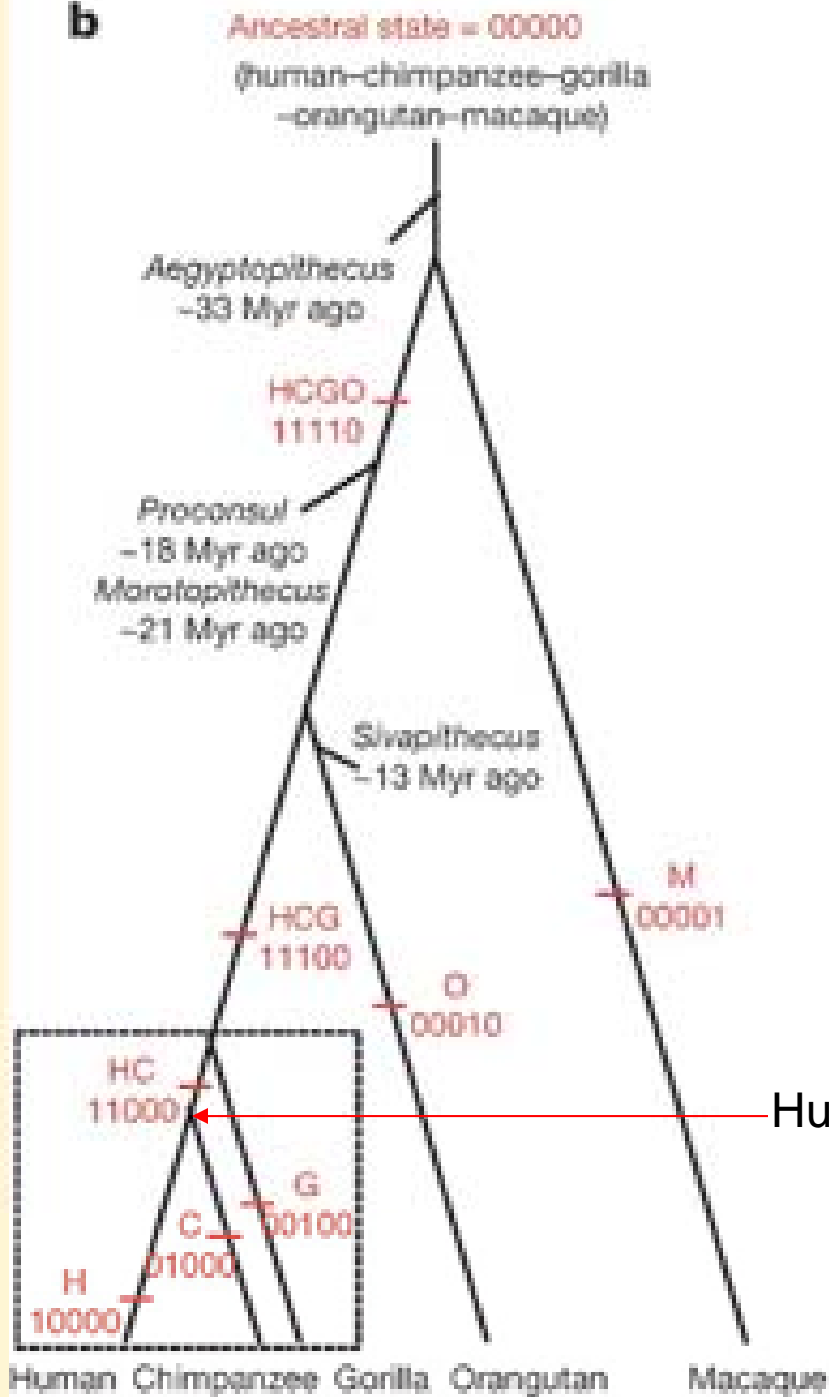


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- About 1 % of bp differ between chimps and humans
- Proteins are extremely similar, but differences exist
- Is it all in the regulatory sequence?

Hominids have a very similar genomic organization!

**b**

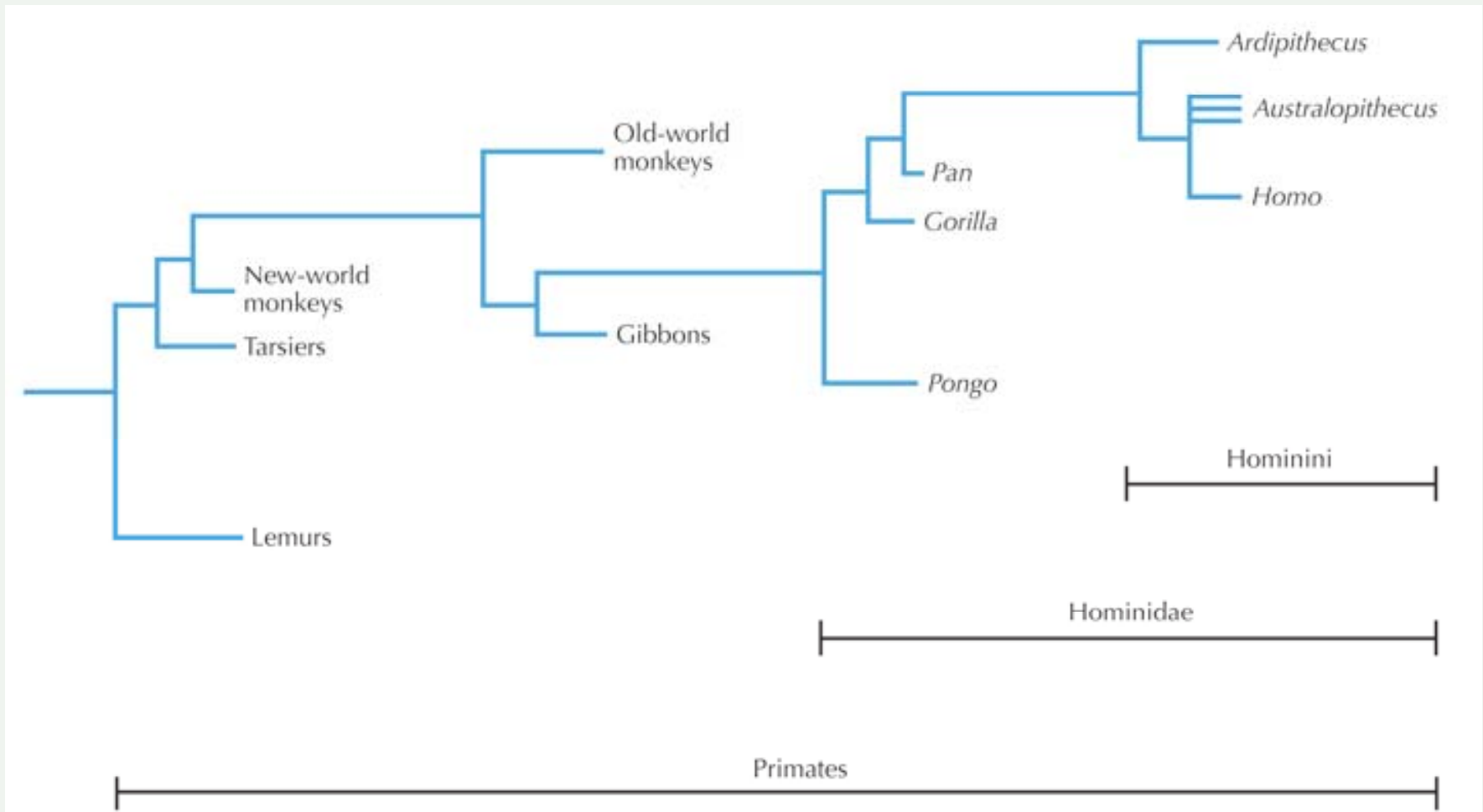


Human/ape split ca 5-8 MYA

Patterson et al., Nature 441, pp1103-1108



# Evolution of hominins



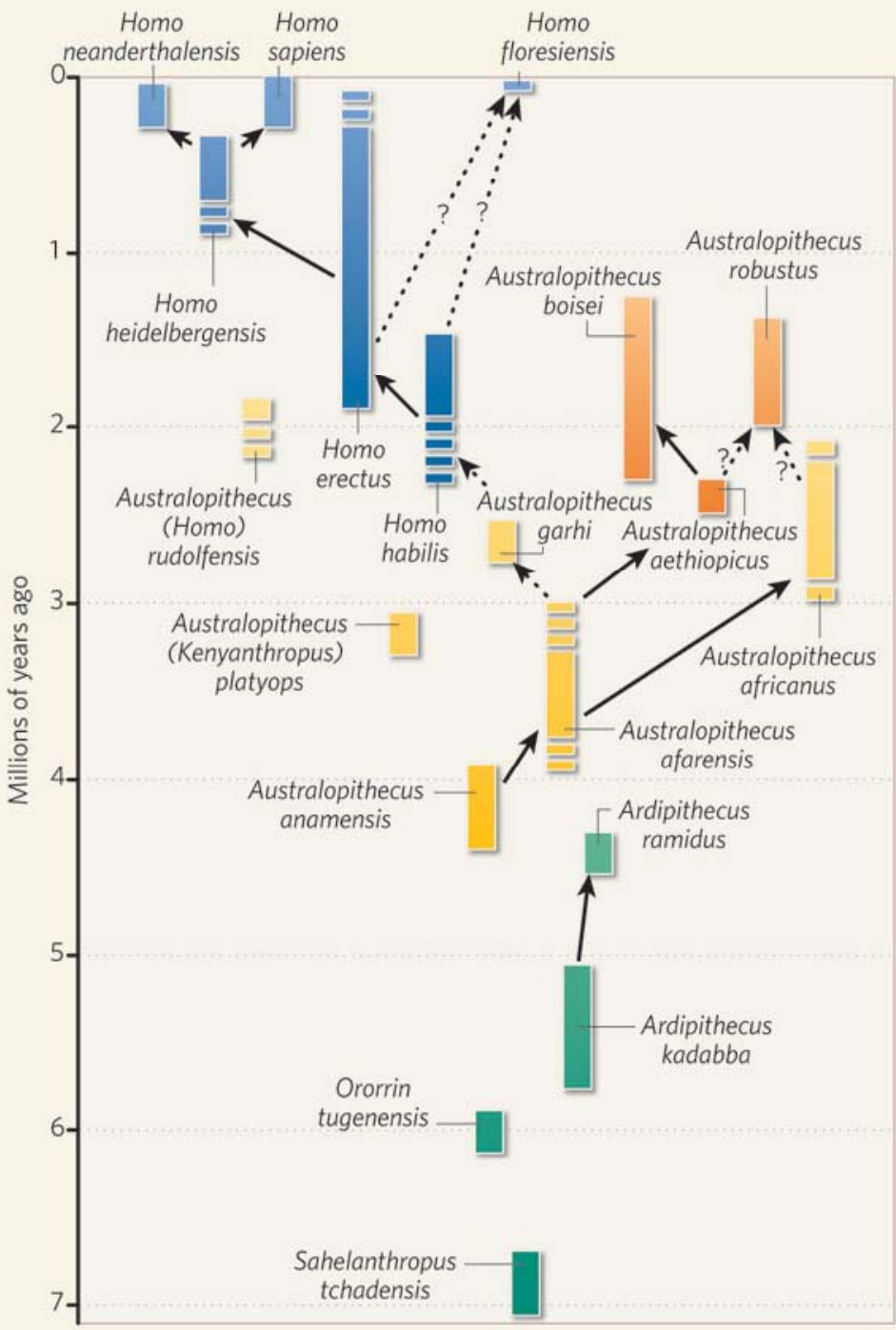
# Species uncertainty within the hominins

- Drawing species limits between fossils is very tricky

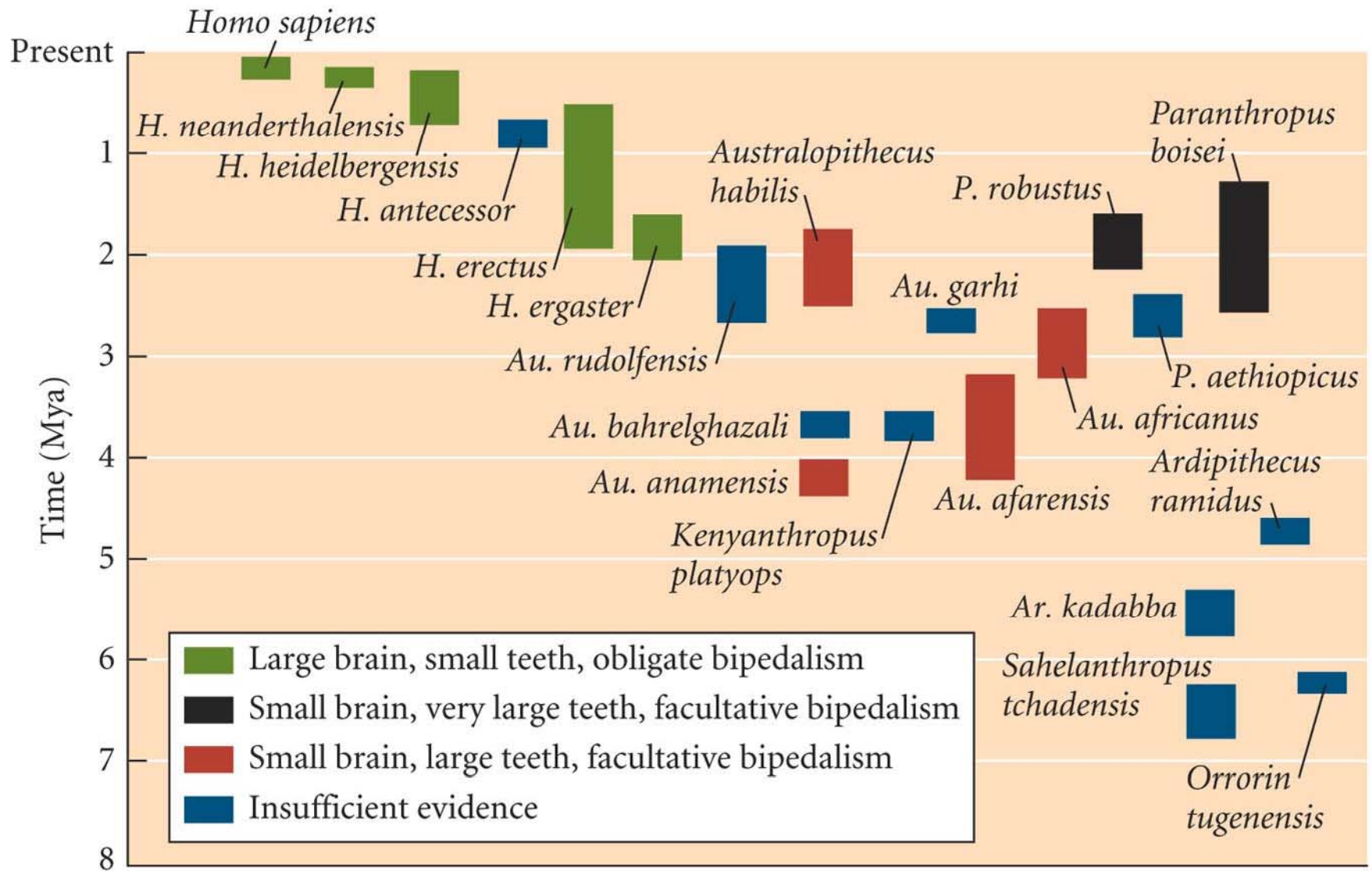


Lucy (*Australopithecus afarensis*)

# A hominin radiation



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



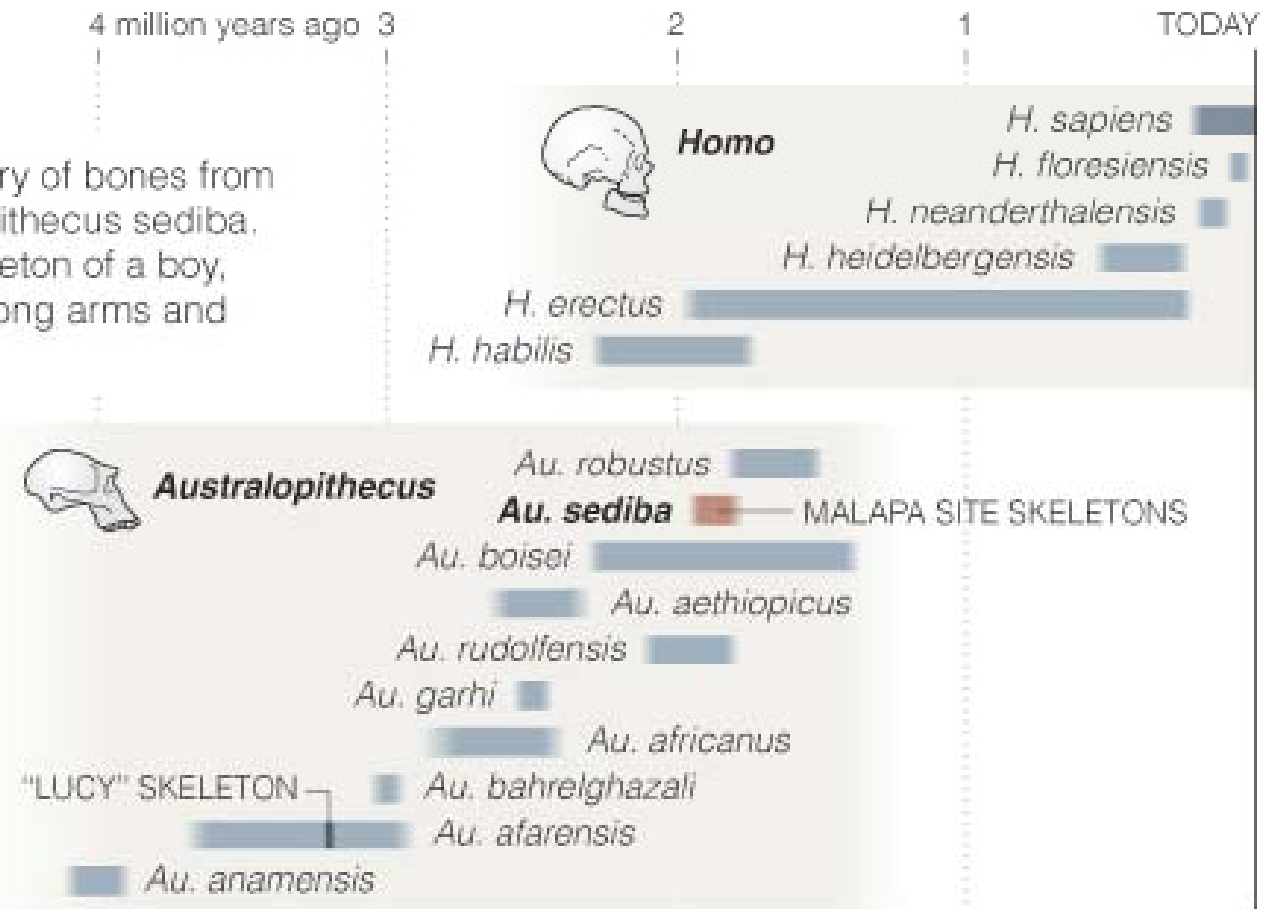
# *Australopithecus sediba* - the dawn of Homo?

The New York Times

April 9, 2010

## A New Hominid

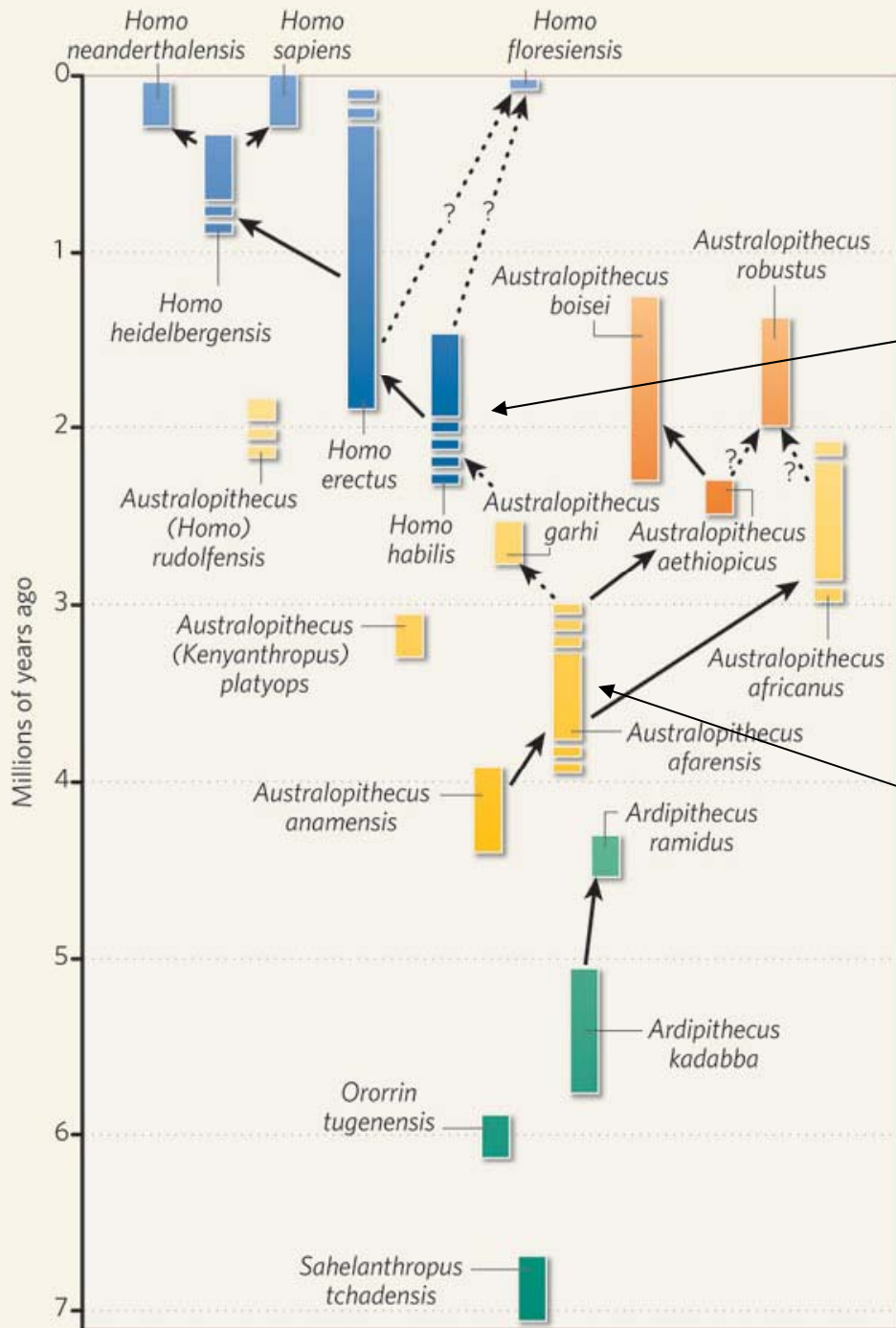
Scientists announced the discovery of bones from a new hominid species, *Australopithecus sediba*. The bones include the partial skeleton of a boy, who walked upright but retained long arms and hands for climbing trees.



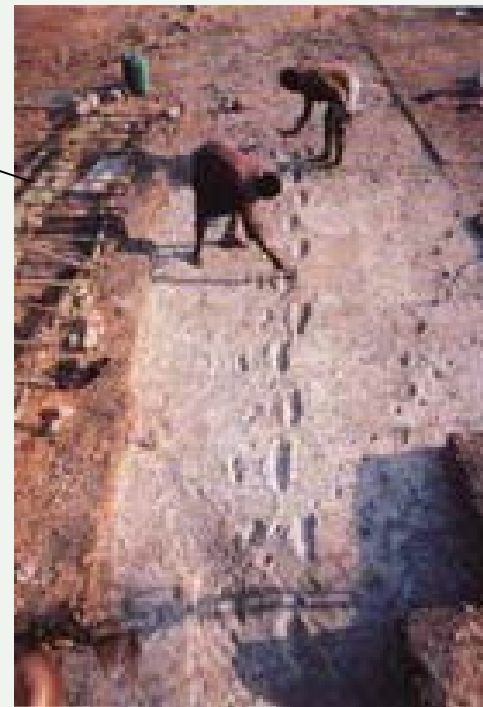
Additional fossils were described in 5 papers in September 9, 2011 issue of Science



For most of the last 4 My, hominid species have co-occurred.  
For example, *Australopithecus boisei* (left) and *Homo ergaster*  
(right)  
both lived 1.7 Mya at Koobi Fora, Kenya.



First manufactured stone tools



Upright walking



*Sahelanthropus tchadensis*

**6-7 Mya**

**Not clear if it was bipedal**

**Some suggest this was ancestral to chimps**



*H. sapiens sapiens*





<http://www.talkorigins.org>

**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**

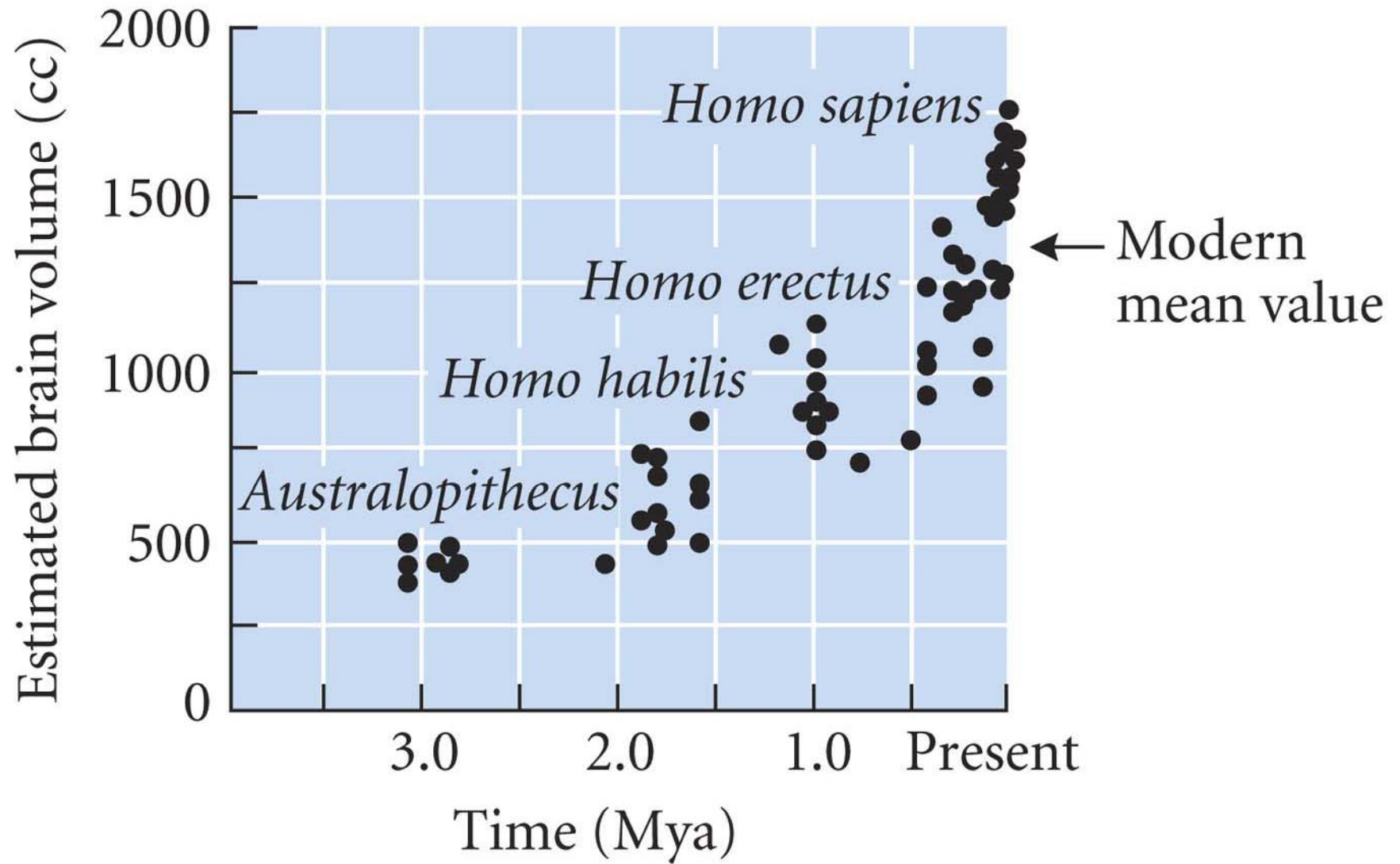
**K: *H. s. neanderthalensis*, 60K**

**L: *H. s. neanderthalensis*, 45K**

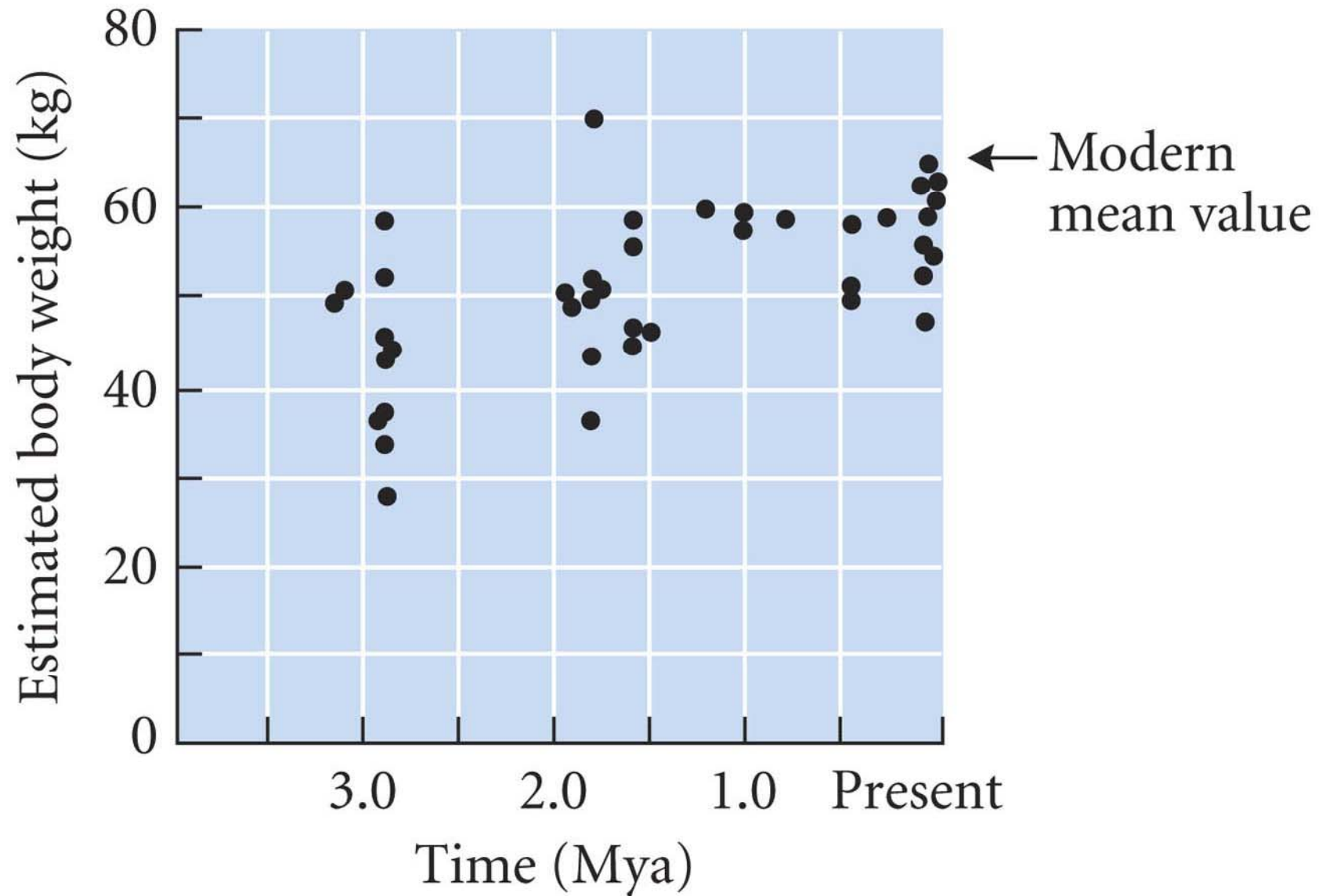
**M. *H. s. sapiens* (Cro-Magnon), 30K**

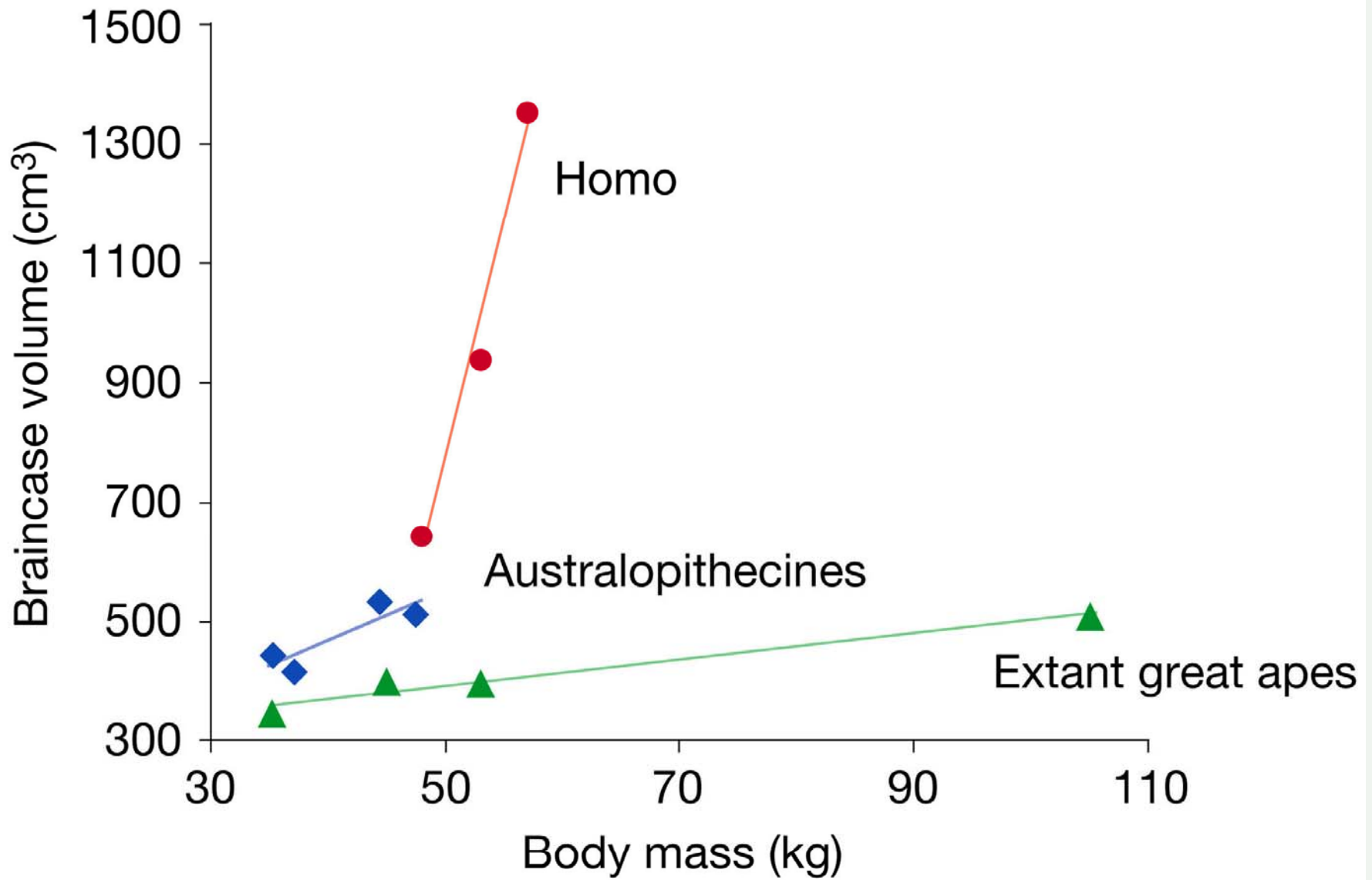
**N. *H. s. sapiens*, modern**

(B)



(A)





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# What makes humans human?

- Are there “quantitative” or just “qualitative” differences?

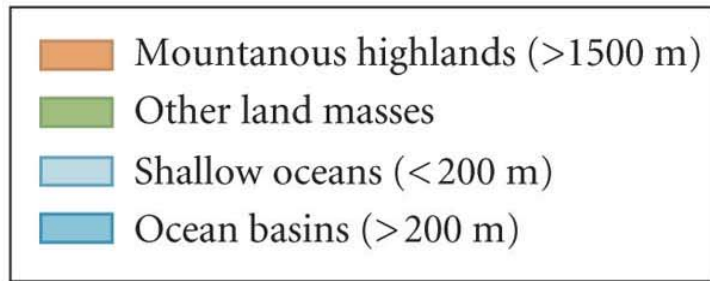
# How did we people Earth?



<http://cseligman.com>

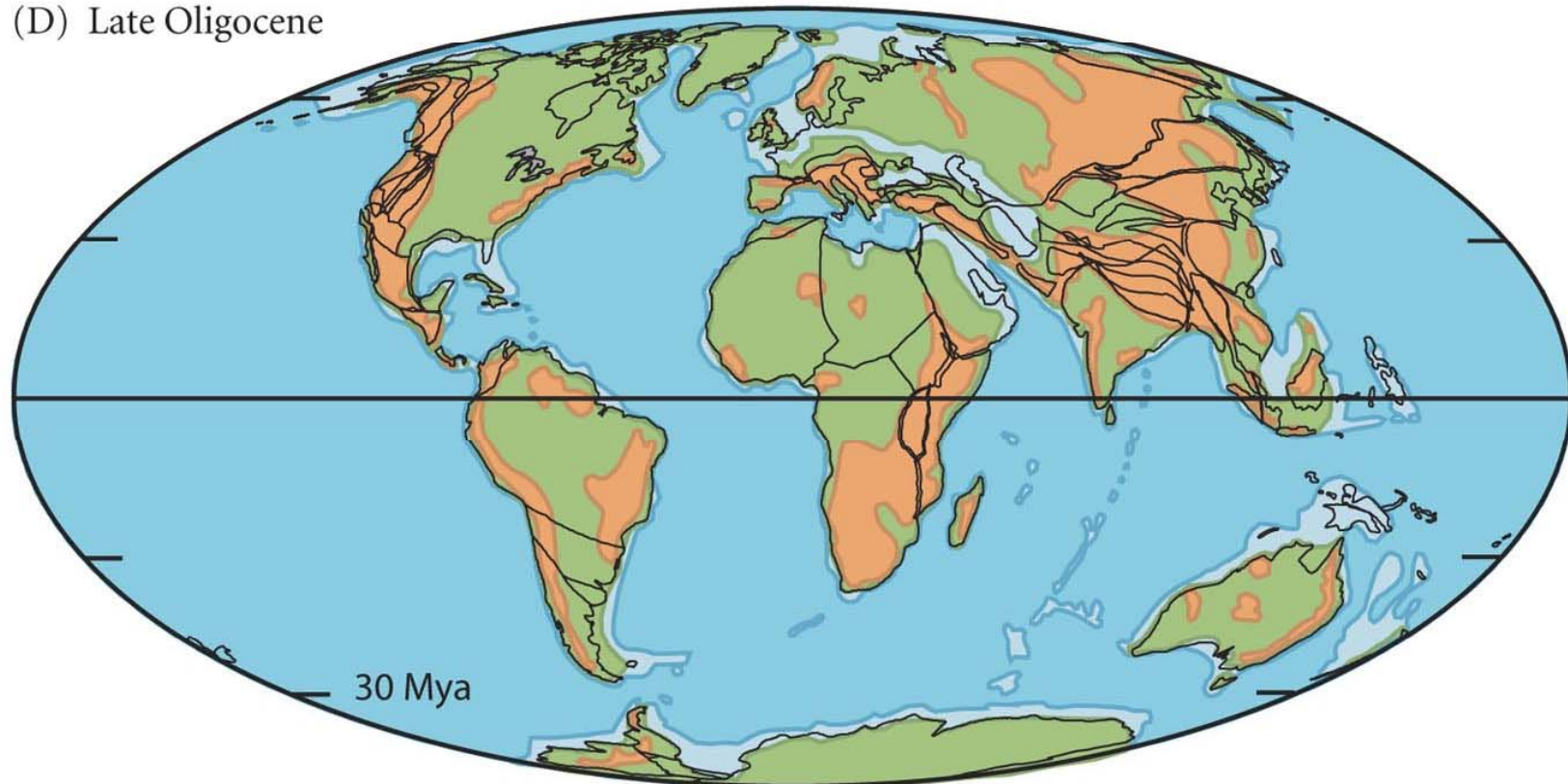
## When?

# The distribution of land masses at several points in geological time

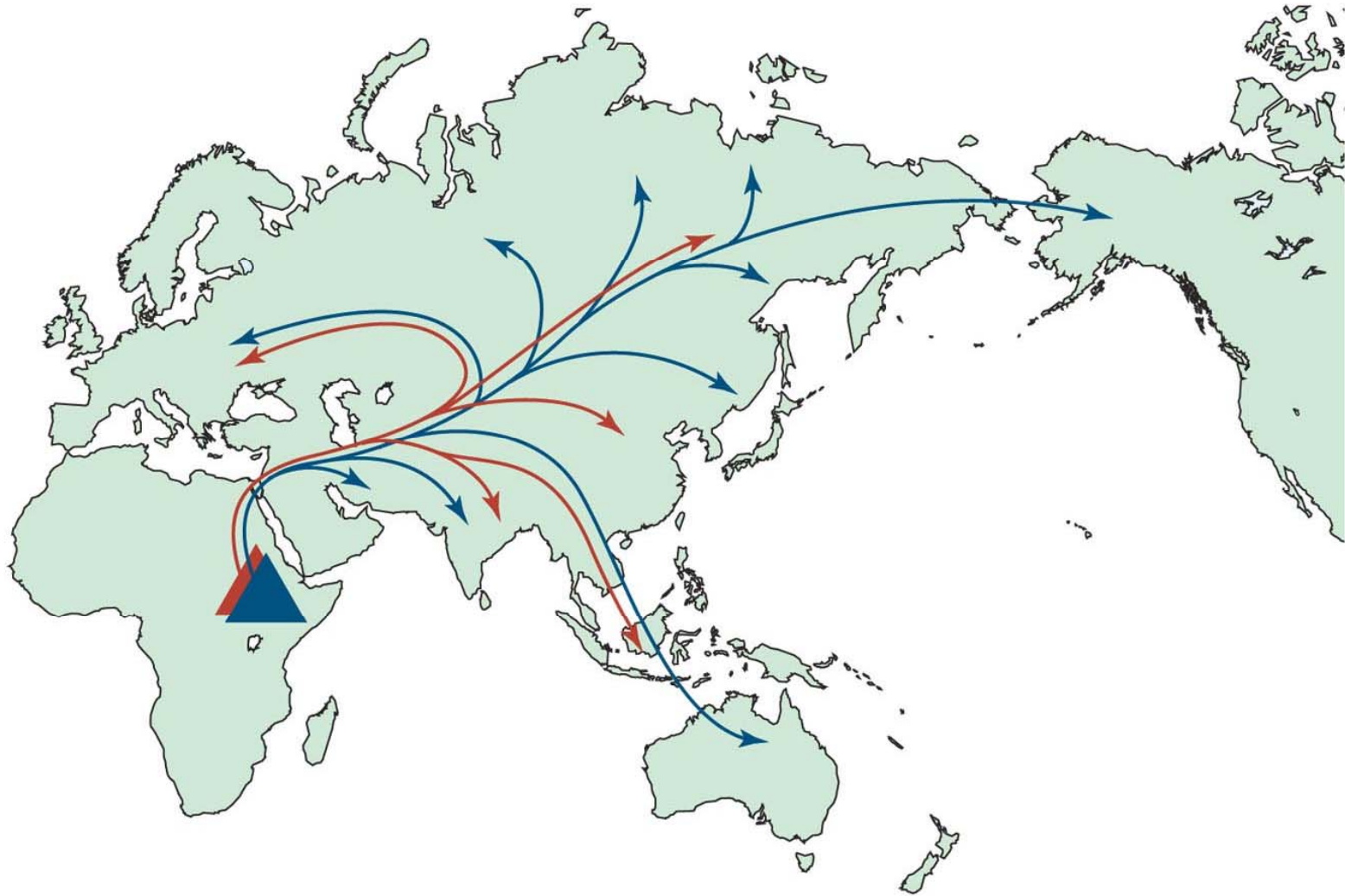


~25 Mya

(D) Late Oligocene



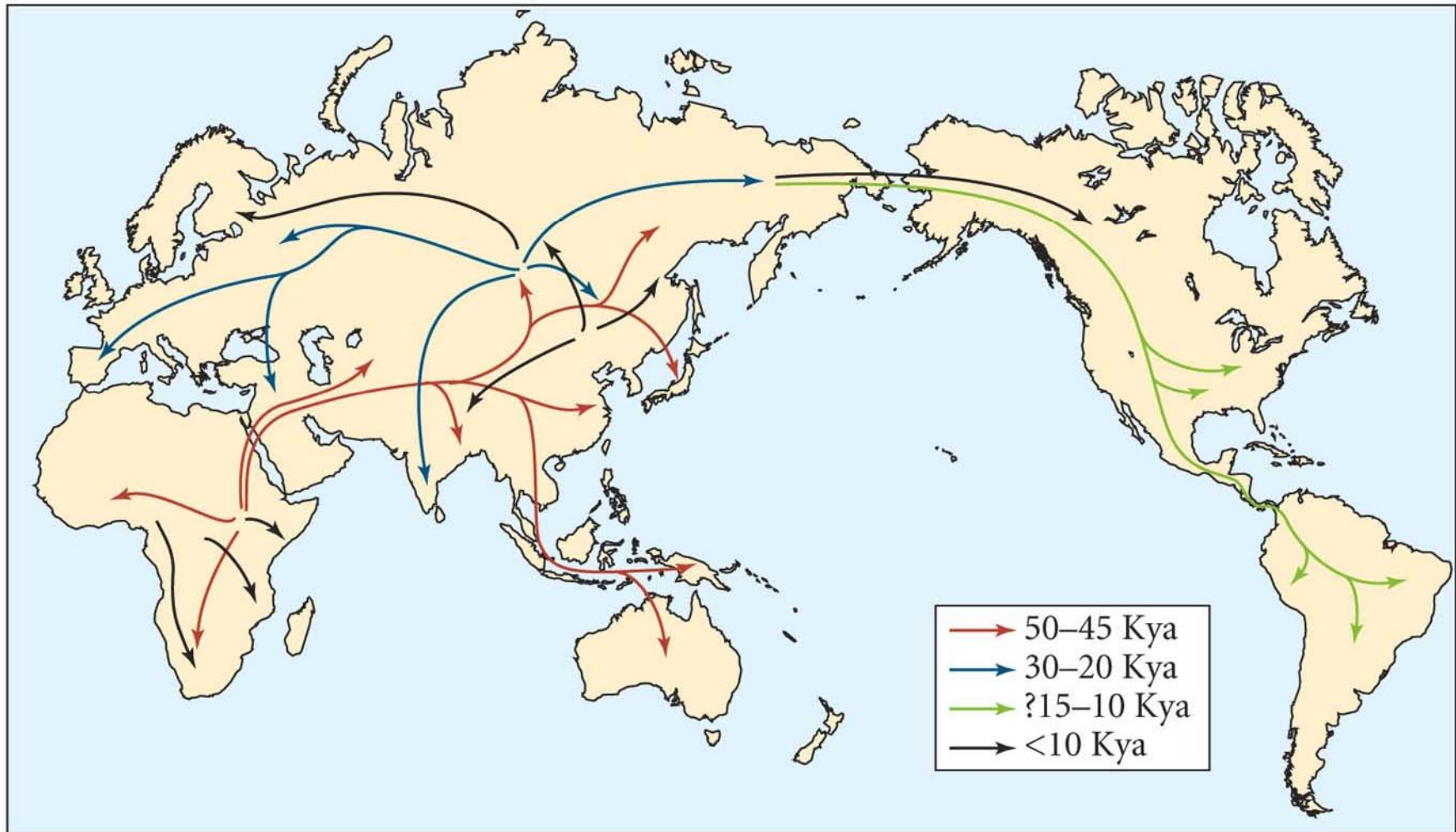
*Homo erectus* spread (~1.8 Mya) from Africa to Europe and Asia and evolved into *H. neanderthalensis*





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

(B)



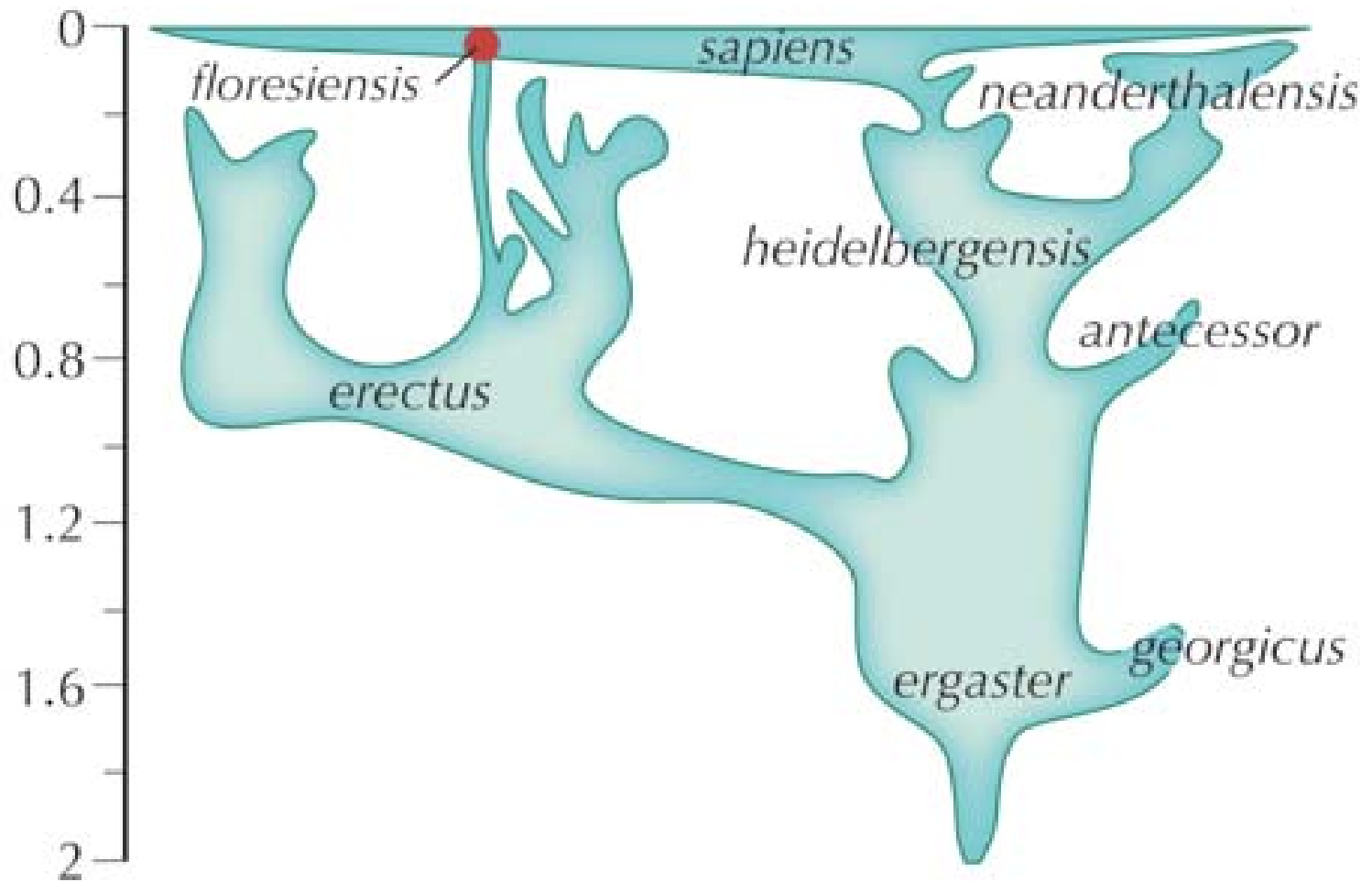
Age (Mya)

E. Asia

S.E. Asia

Africa

Europe



# The “Hobbit”

- *Homo floresiensis* or diseased *H. sapiens*?



Flores

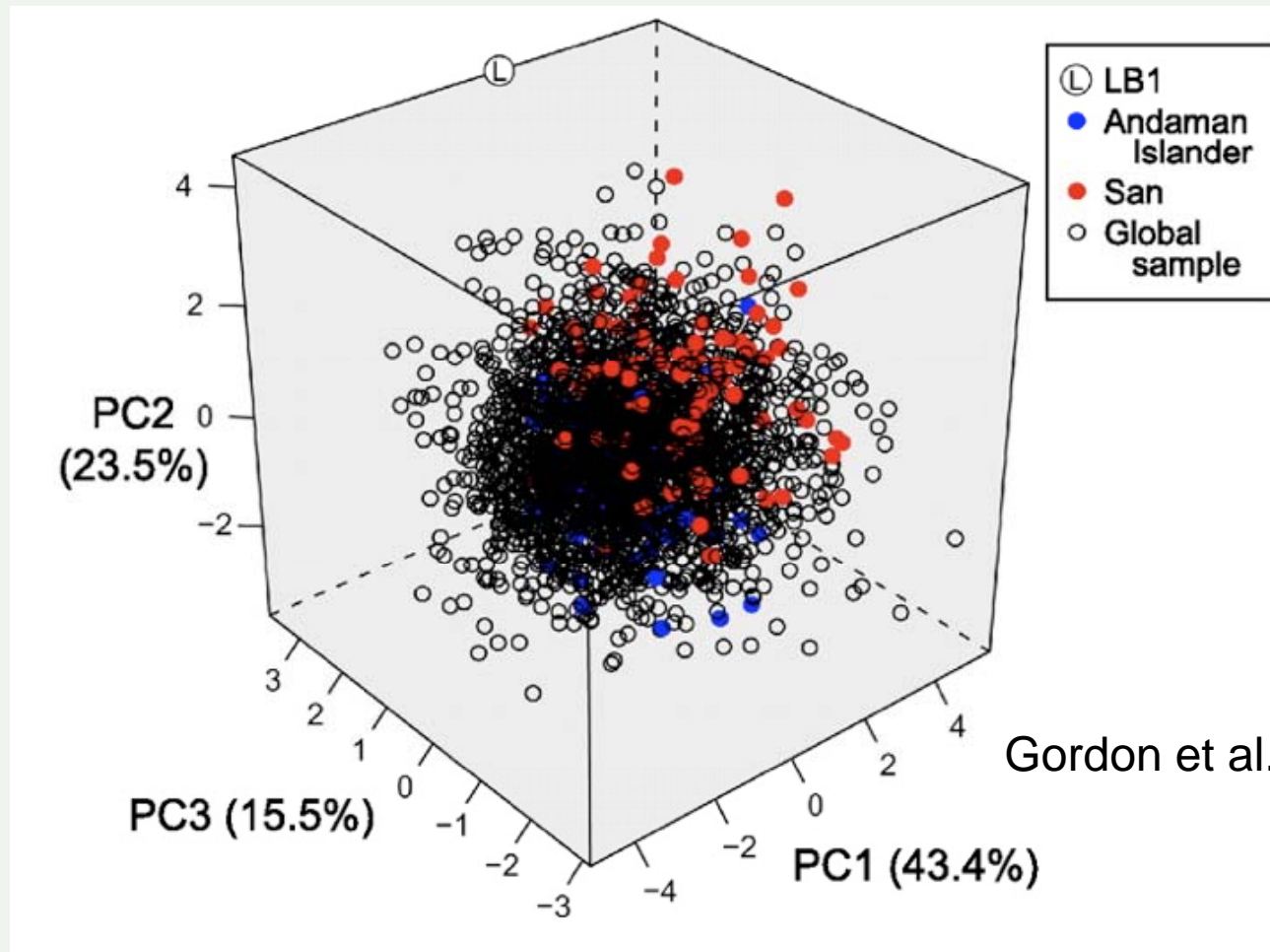
- Used most likely tools
- Two skeletons from ca. 80,000 and 17,000 years ago.



# Hypothesis: *H. floresiensis* is an island dwarf form that evolved from a hominin ancestor

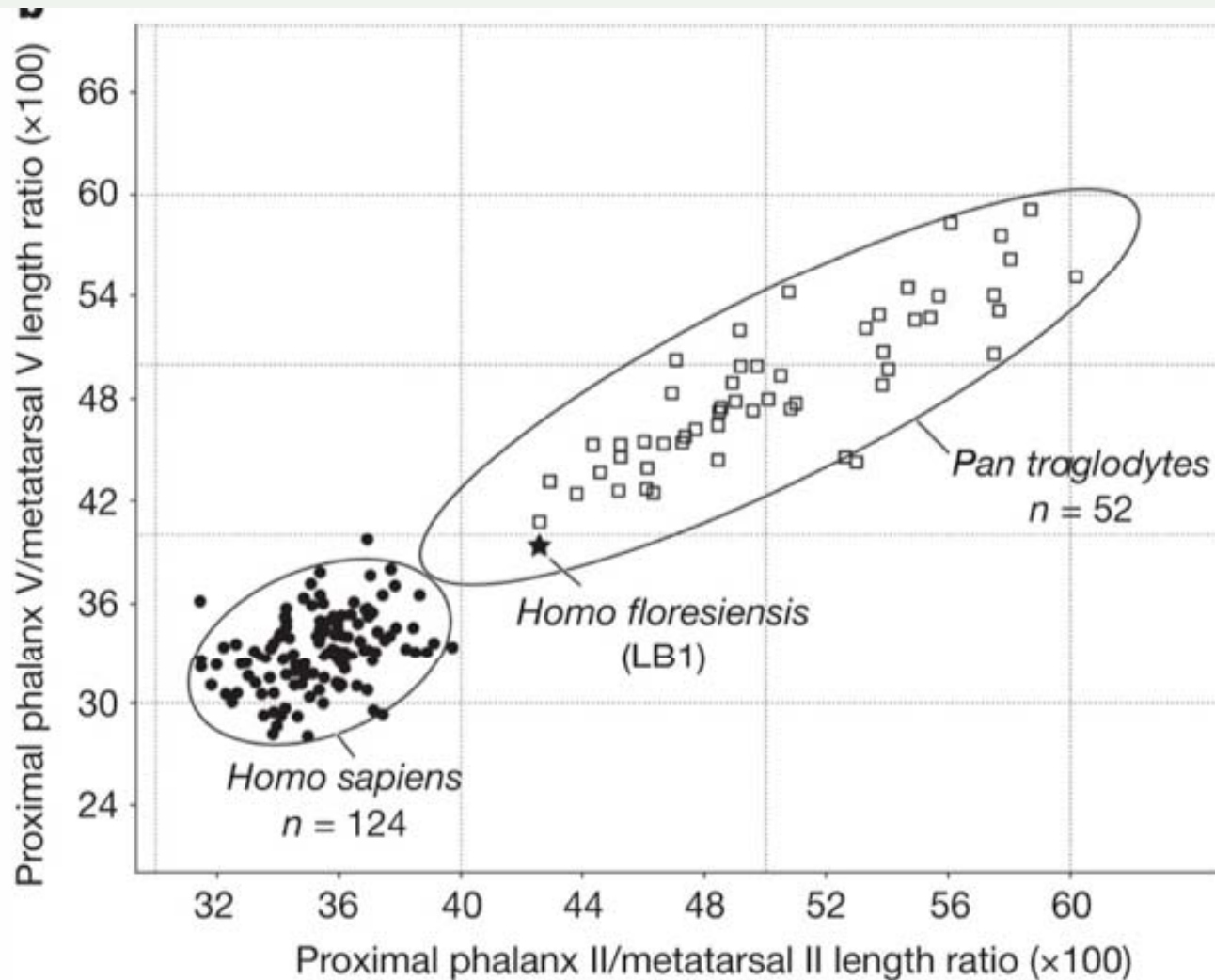
- Problem: The “hobbit” brain is too small to be simply a scaled down *sapiens* or *erectus* brain
- But... dwarf species of hippos show a similar disproportionate reduction in brain size

# Hobbit or modern human?



- Shape analysis of cranial morphology

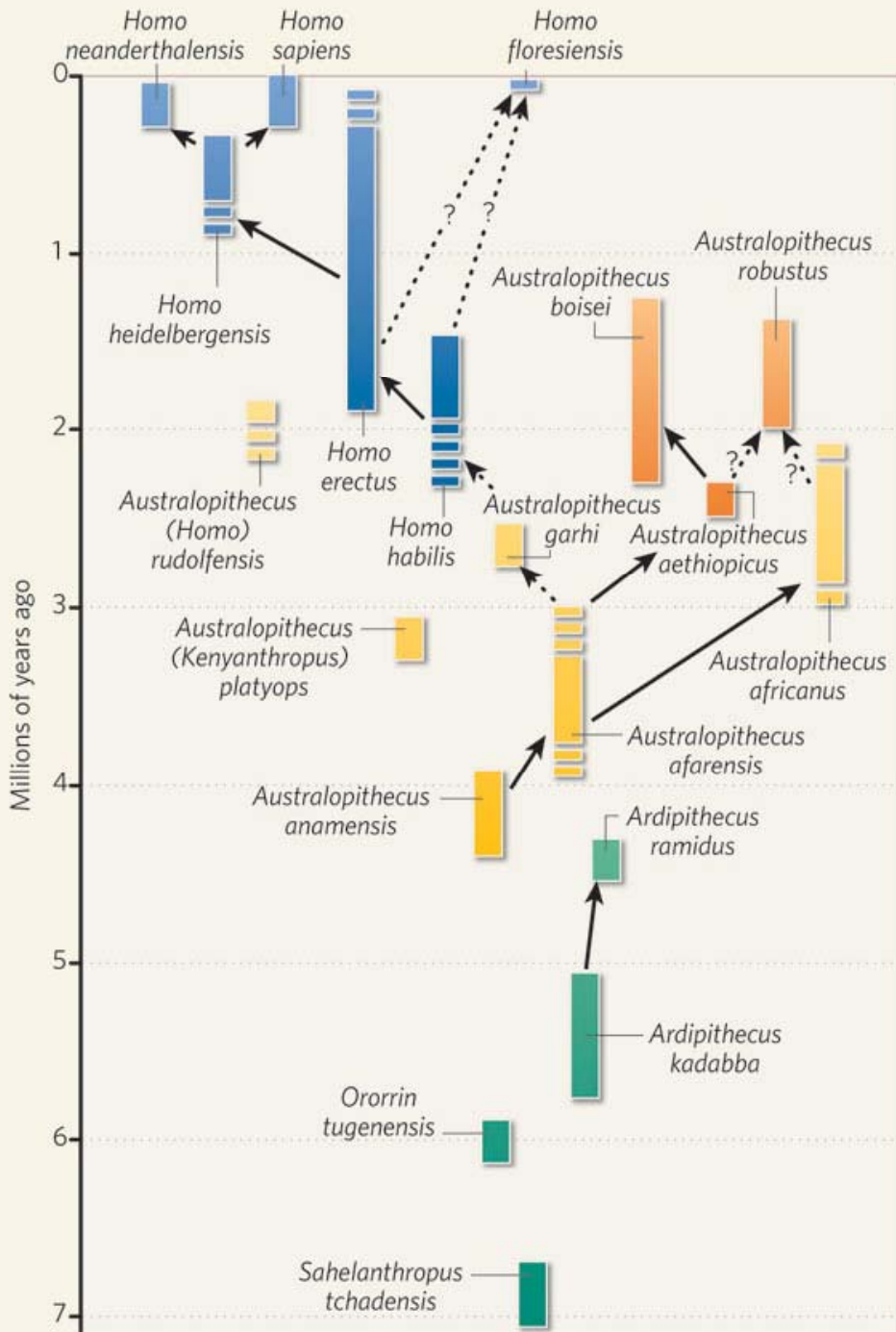
# Foot of *H. floresiensis* combines basal and derived features



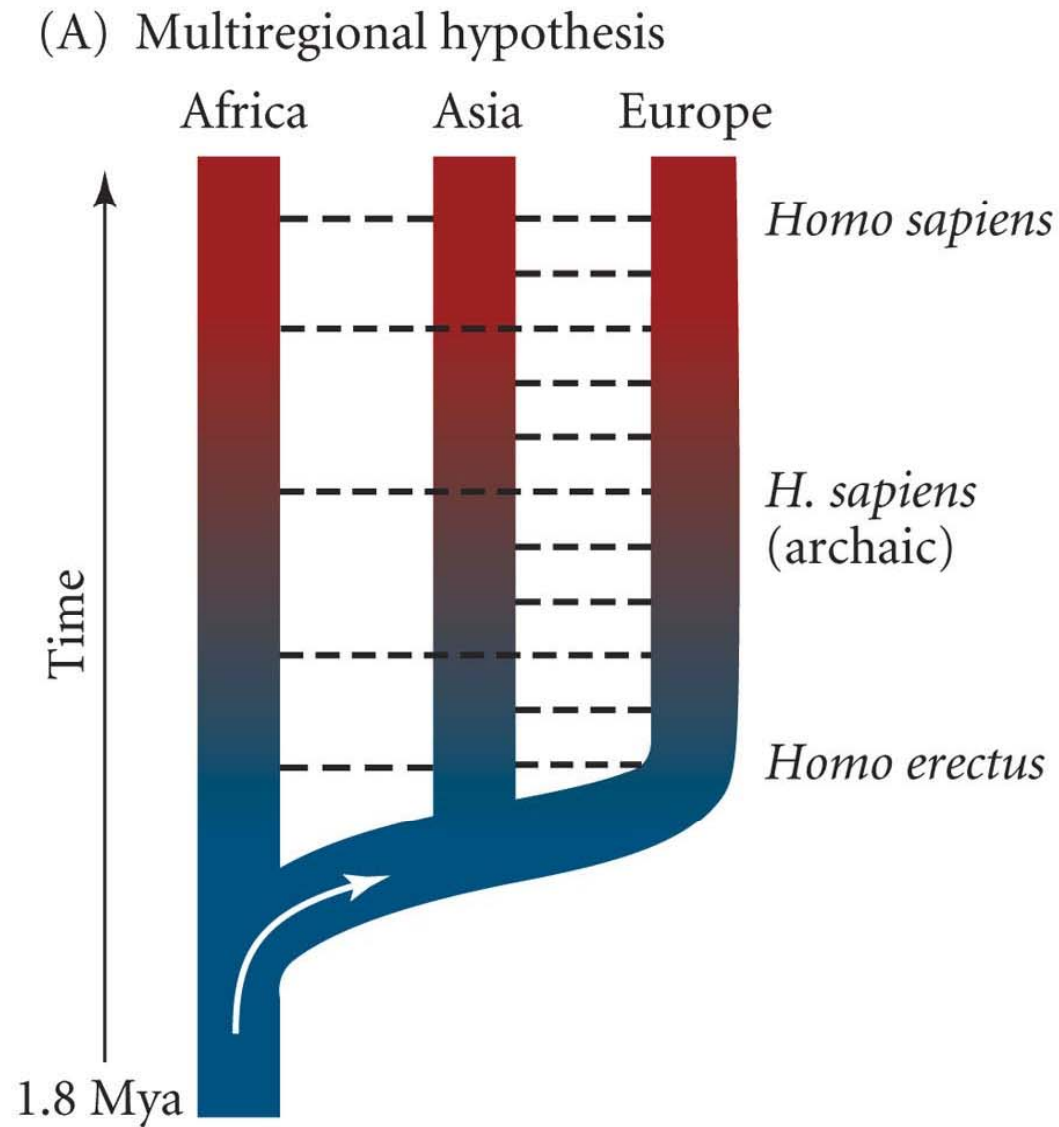
- Good for walking but not for running?

# Is the foot too ancestral for *H. erectus*?

- Cranial features are similar to *Homo erectus*



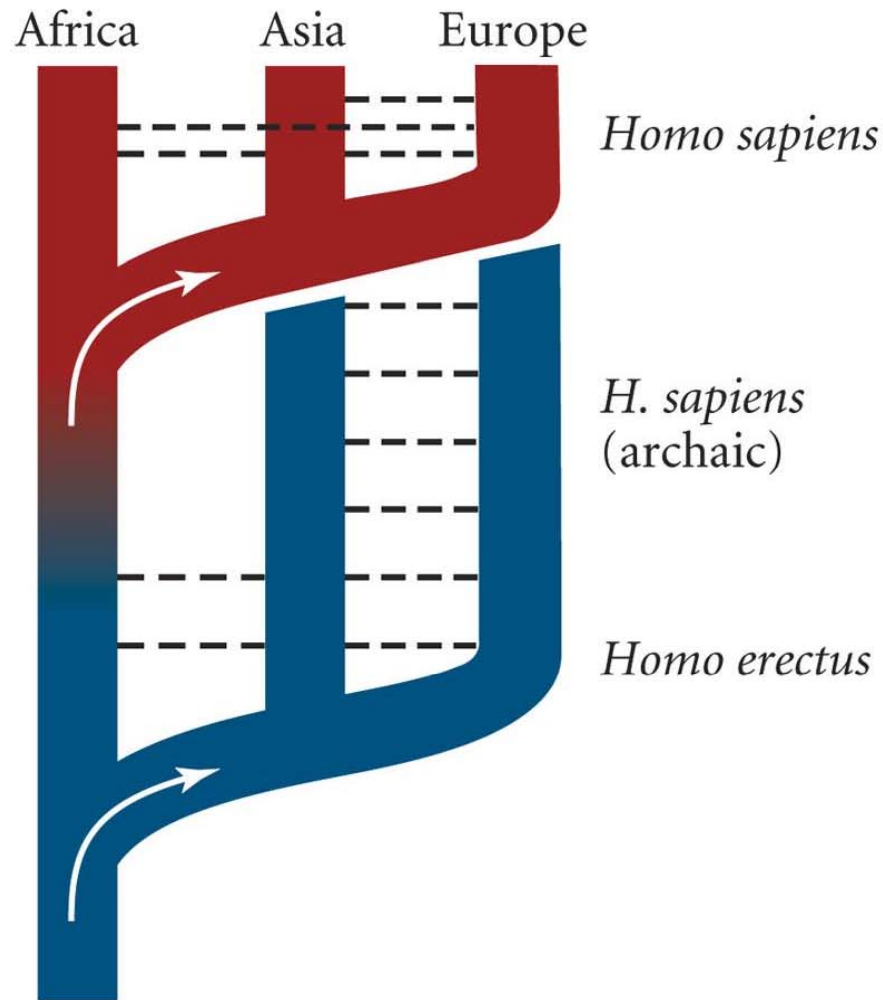
## 6.16(1) Two hypotheses on the origin of modern humans





## 6.16(2) Two hypotheses on the origin of modern humans

(B) Replacement hypothesis

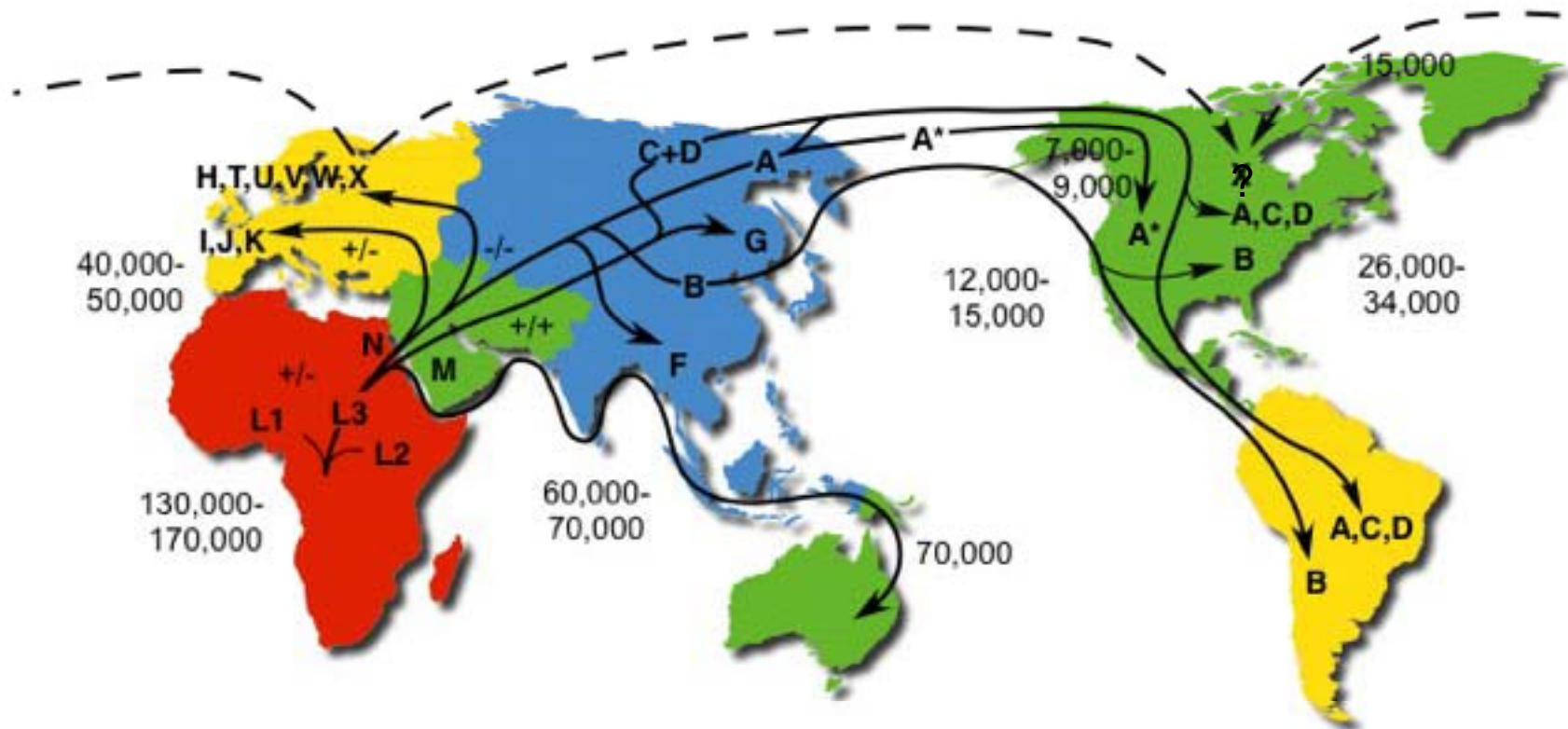


# Biogeography of *Homo sapiens*

## Human mtDNA Migrations

<http://www.mitomap.org/mitomap/WorldMigrations.pdf>

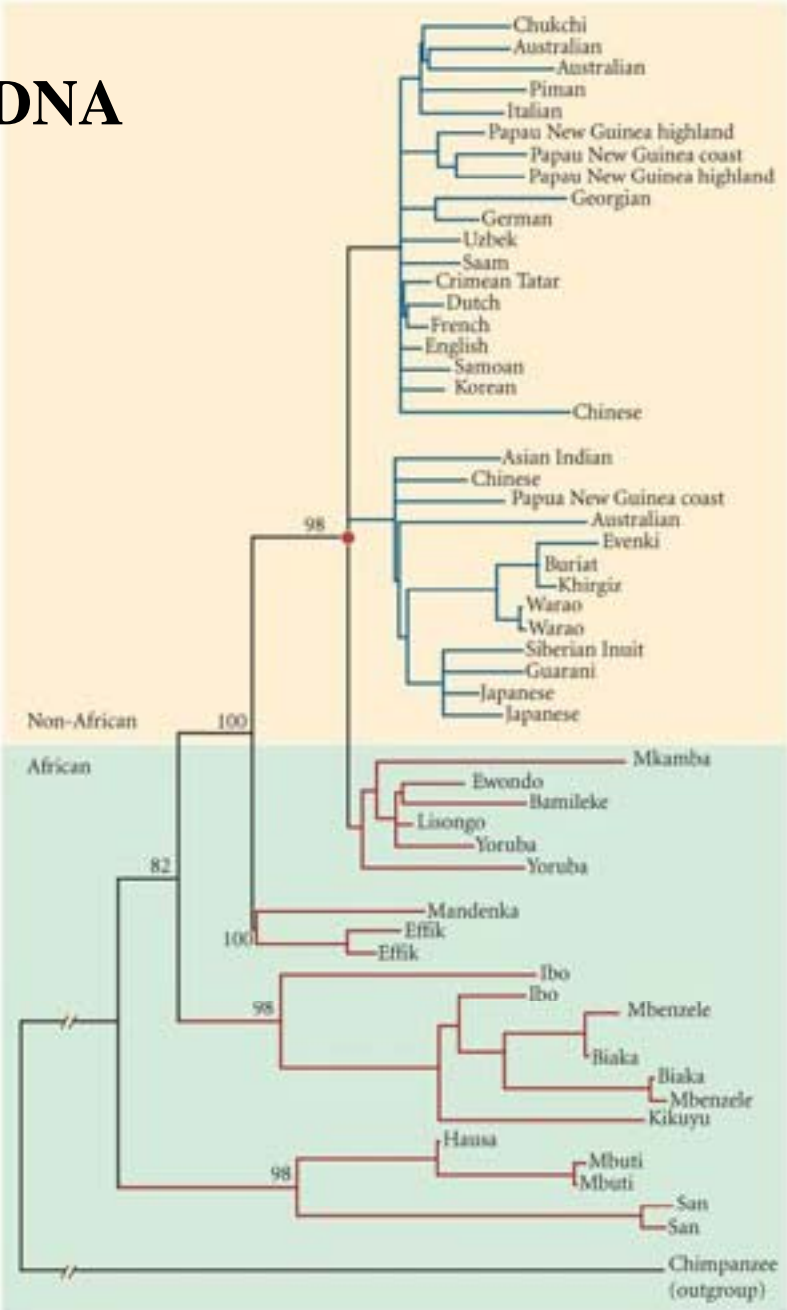
Copyright 2002 © Mitomap.org



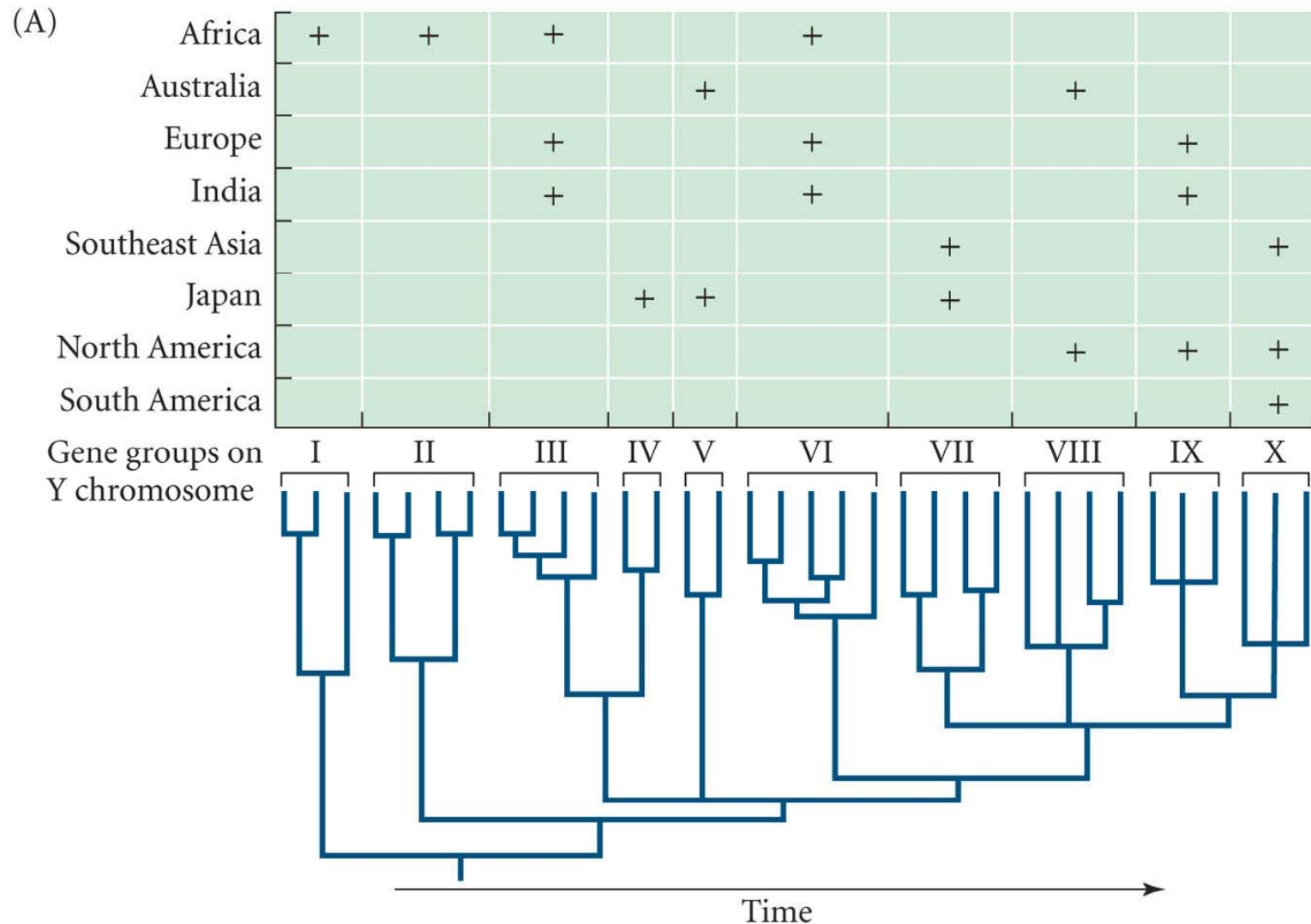
+/-, +/+, or -/- = Dde I 10394 / Alu I 10397  
\* = Rsa I 16329

Mutation rate = 2.2 - 2.9 % / MYR  
Time estimates are YBP

# Tree based on mtDNA



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



# Can we really exclude *sapiens-neanderthalensis* interbreeding?

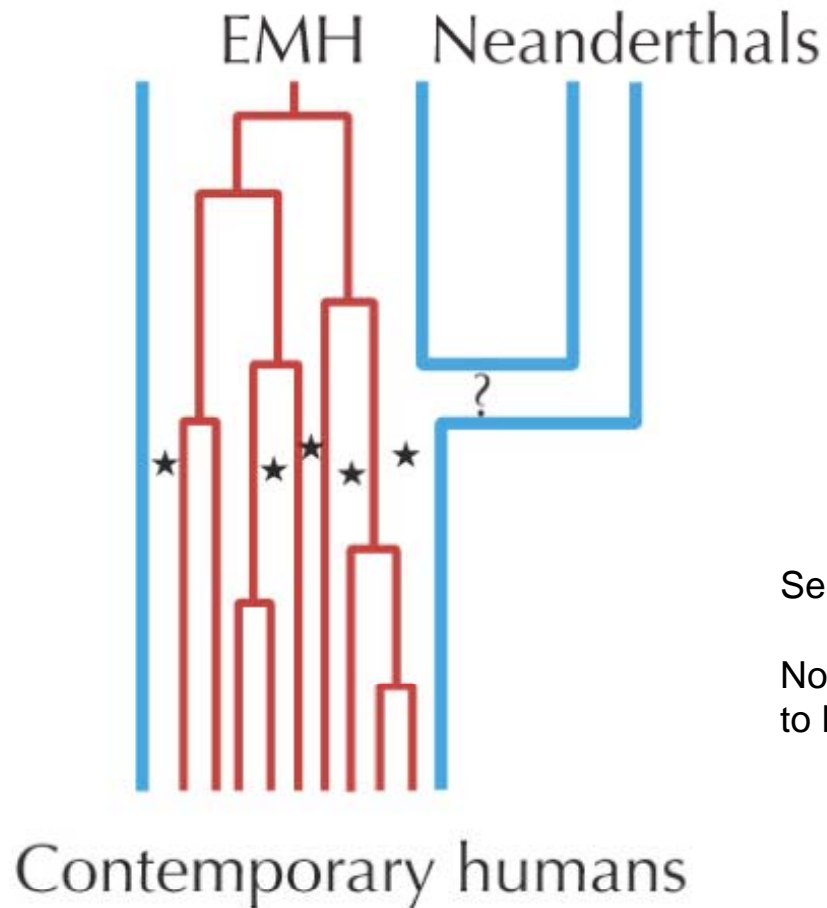


Figure from textbook!

Serre et al., 2004 PLoS Biology

No Evidence of Neanderthal mtDNA Contribution to Early Modern Humans

- Just a matter of mtDNA sampling error?

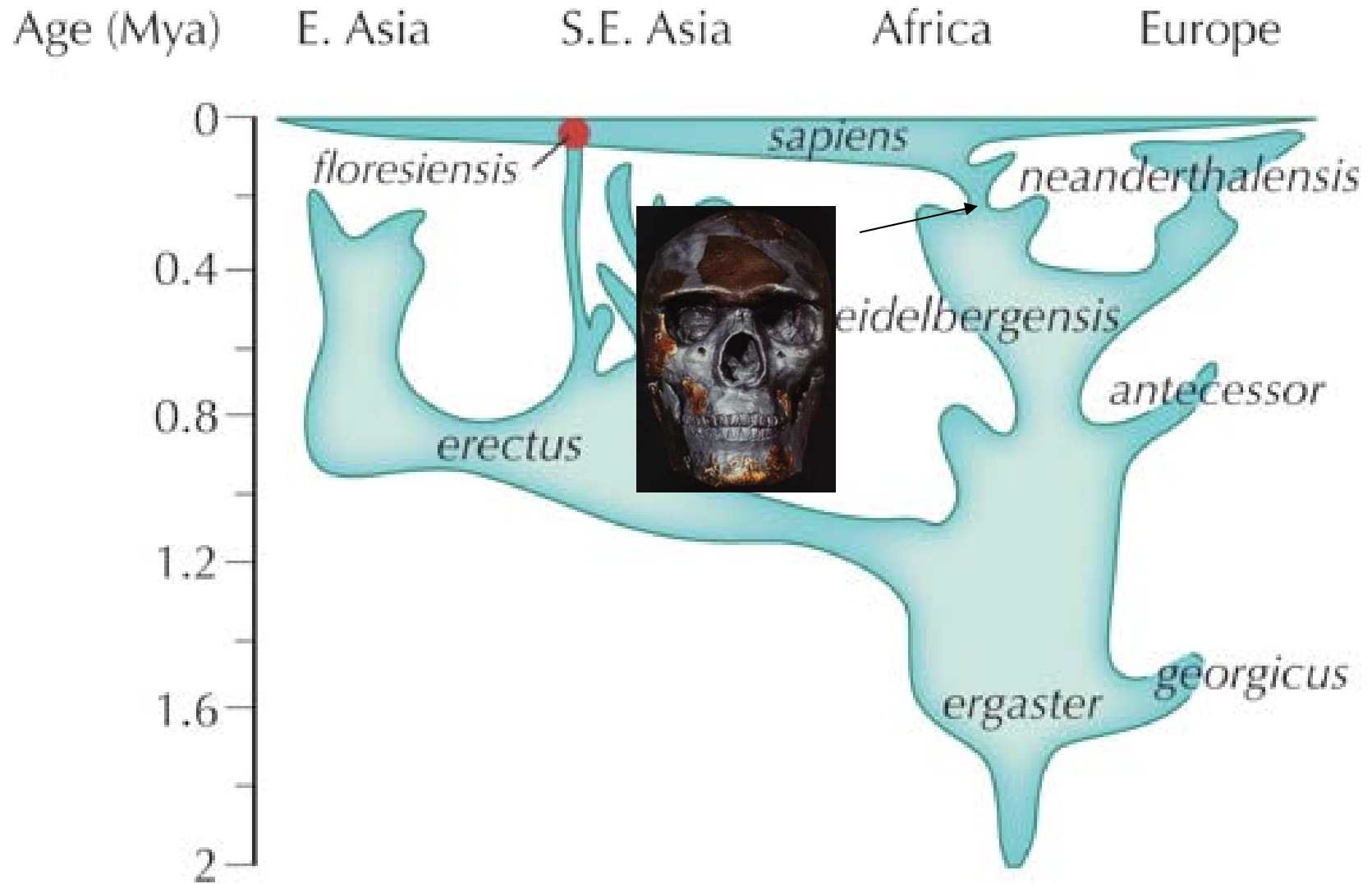
# A scientific revolution!

## RESEARCH ARTICLE

### A Draft Sequence of the Neandertal Genome

Richard E. Green,<sup>1\*</sup>†‡ Johannes Krause,<sup>1</sup>†§ Adrian W. Briggs,<sup>1</sup>†§ Tomislav Maricic,<sup>1</sup>†§ Udo Stenzel,<sup>1</sup>†§ Martin Kircher,<sup>1</sup>†§ Nick Patterson,<sup>2</sup>†§ Heng Li,<sup>2</sup>† Weiwei Zhai,<sup>3</sup>†|| Markus Hsi-Yang Fritz,<sup>4</sup>† Nancy F. Hansen,<sup>5</sup>† Eric Y. Durand,<sup>3</sup>† Anna-Sapfo Malaspinas,<sup>3</sup>† Jeffrey D. Jensen,<sup>6</sup>† Tomas Marques-Bonet,<sup>7,13</sup>† Can Alkan,<sup>7</sup>† Kay Prüfer,<sup>1</sup>† Matthias Meyer,<sup>1</sup>† Hernán A. Burbano,<sup>1</sup>† Jeffrey M. Good,<sup>1,8</sup>† Rigo Schultz,<sup>1</sup> Ayinuer Aximu-Petri,<sup>1</sup> Anne Butthof,<sup>1</sup> Barbara Höber,<sup>1</sup> Barbara Höffner,<sup>1</sup> Madlen Siegemund,<sup>1</sup> Antje Weihmann,<sup>1</sup> Chad Nusbaum,<sup>2</sup> Eric S. Lander,<sup>2</sup> Carsten Russ,<sup>2</sup> Nathaniel Novod,<sup>2</sup> Jason Affourtit,<sup>9</sup> Michael Egholm,<sup>9</sup> Christine Verna,<sup>21</sup> Pavao Rudan,<sup>10</sup> Dejana Brajkovic,<sup>11</sup> Željko Kucan,<sup>10</sup> Ivan Gušić,<sup>10</sup> Vladimir B. Doronichev,<sup>12</sup> Liubov V. Golovanova,<sup>12</sup> Carles Lalueza-Fox,<sup>13</sup> Marco de la Rasilla,<sup>14</sup> Javier Fortea,<sup>14</sup>¶ Antonio Rosas,<sup>15</sup> Ralf W. Schmitz,<sup>16,17</sup> Philip L. F. Johnson,<sup>18</sup>† Evan E. Eichler,<sup>7</sup>† Daniel Falush,<sup>19</sup>† Ewan Birney,<sup>4</sup>† James C. Mullikin,<sup>5</sup>† Montgomery Slatkin,<sup>3</sup>† Rasmus Nielsen,<sup>3</sup>† Janet Kelso,<sup>1</sup>† Michael Lachmann,<sup>1</sup>† David Reich,<sup>2,20\*</sup>† Svante Pääbo<sup>1\*</sup>†

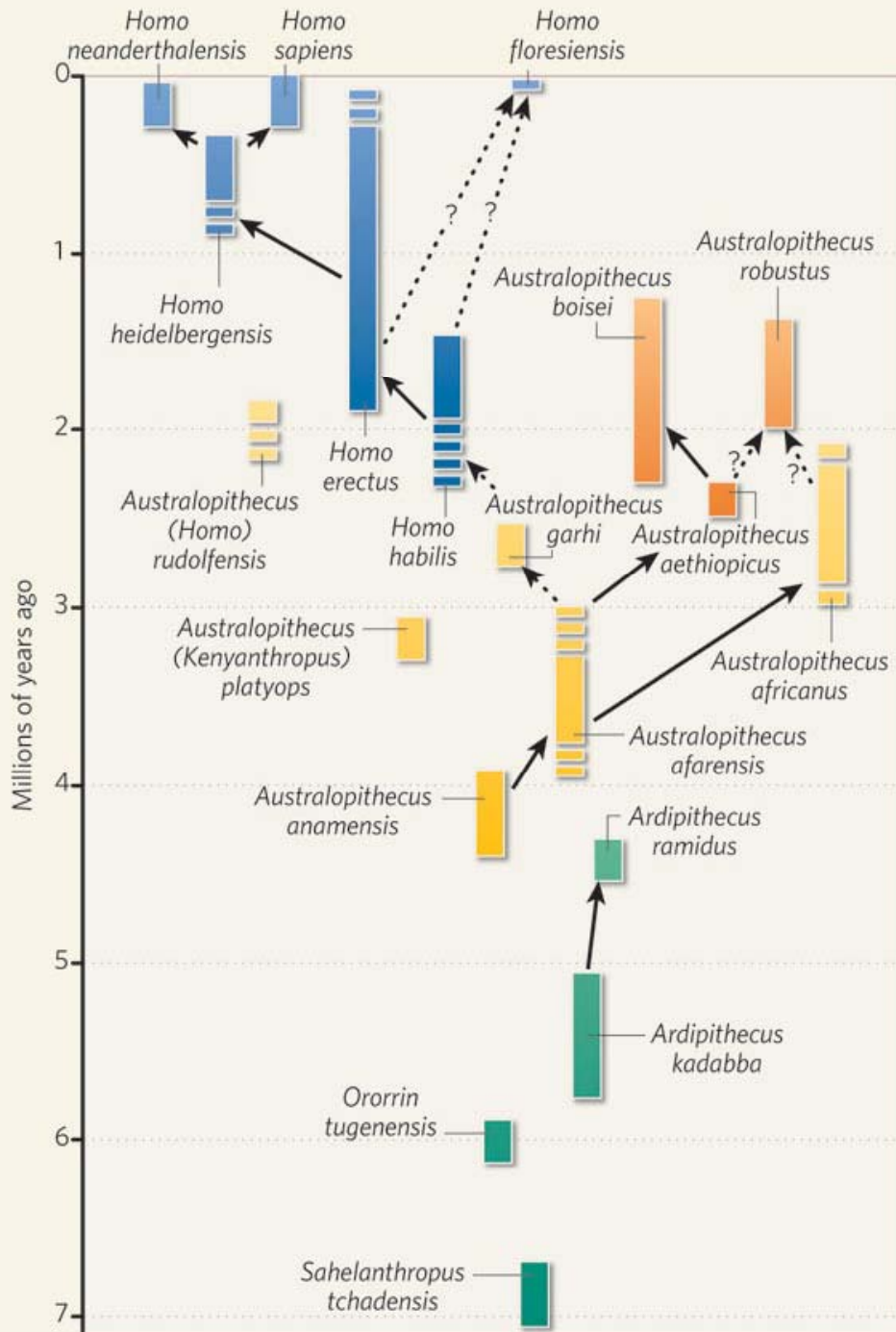
- Science 2010



- Oldest modern humans ca. 200,000 yrs old (Omo valley in Ethiopia)

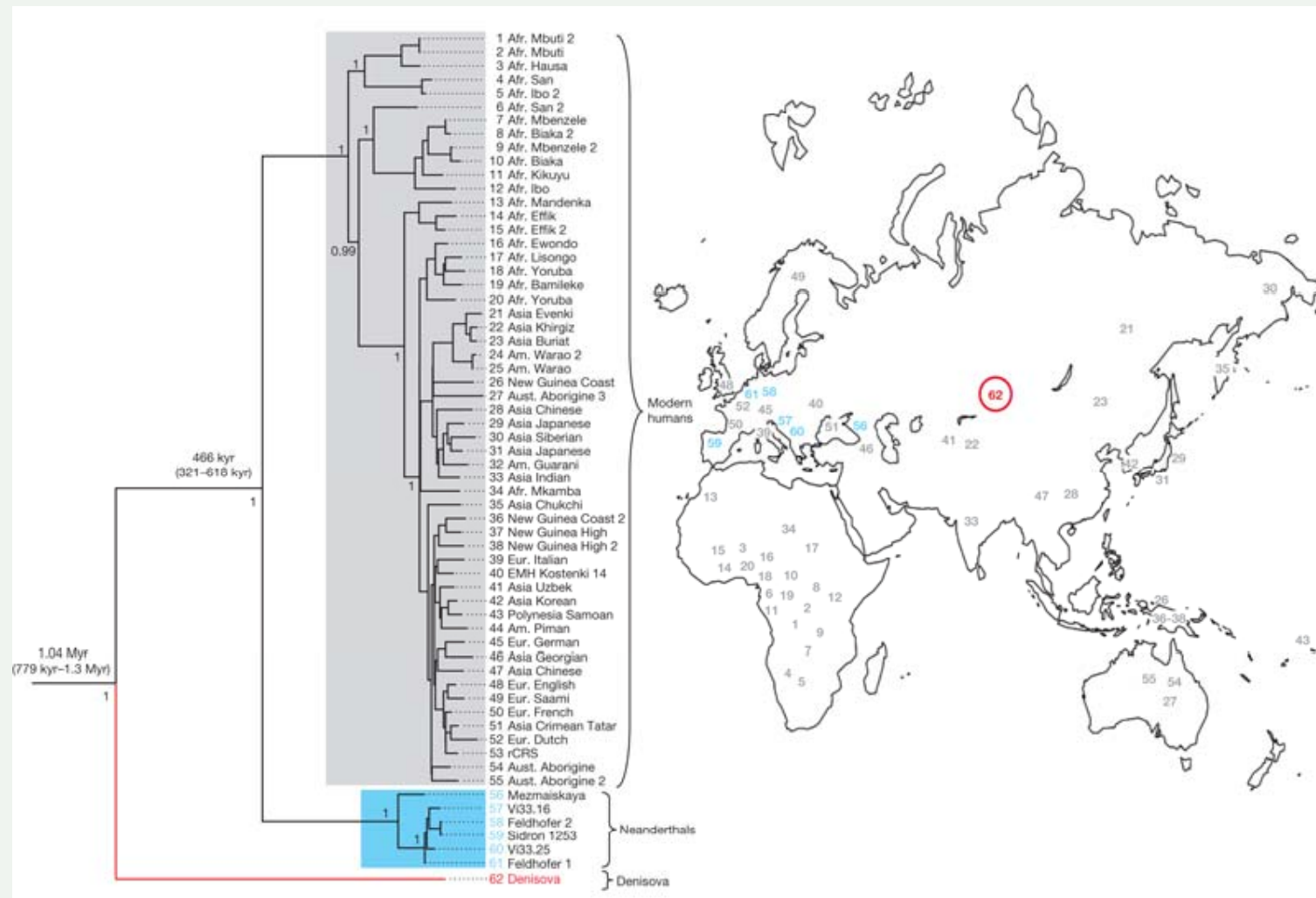
# The genetics of becoming human

- We split from most recent living relative (chimp) a long time ago





# 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

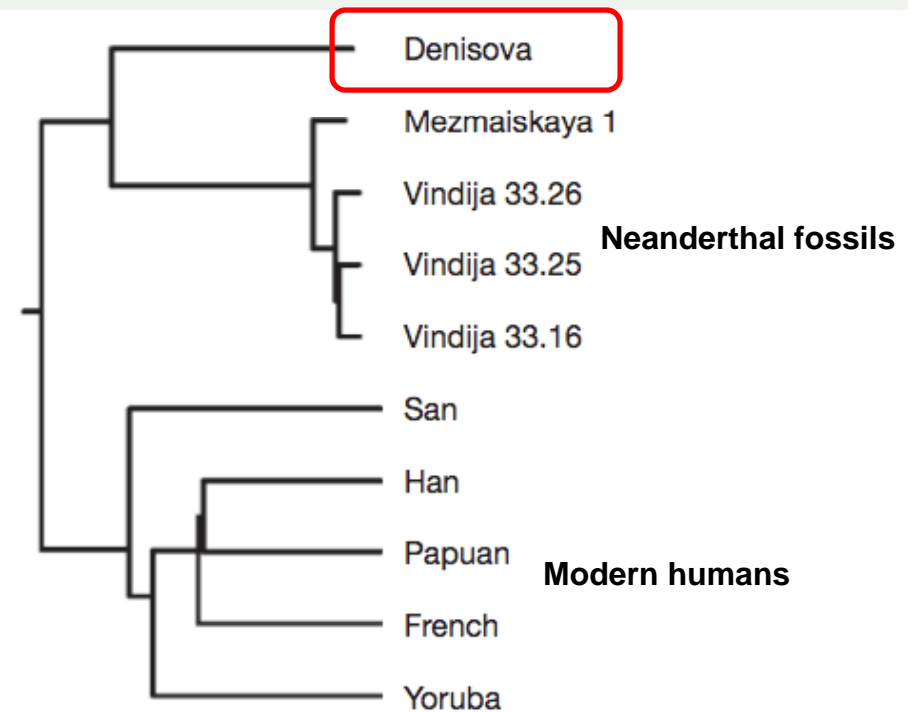
doi:10.1038/nature09710

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

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

### Genome sequence of finger bone

Phylogeny using multiple autosomal genes



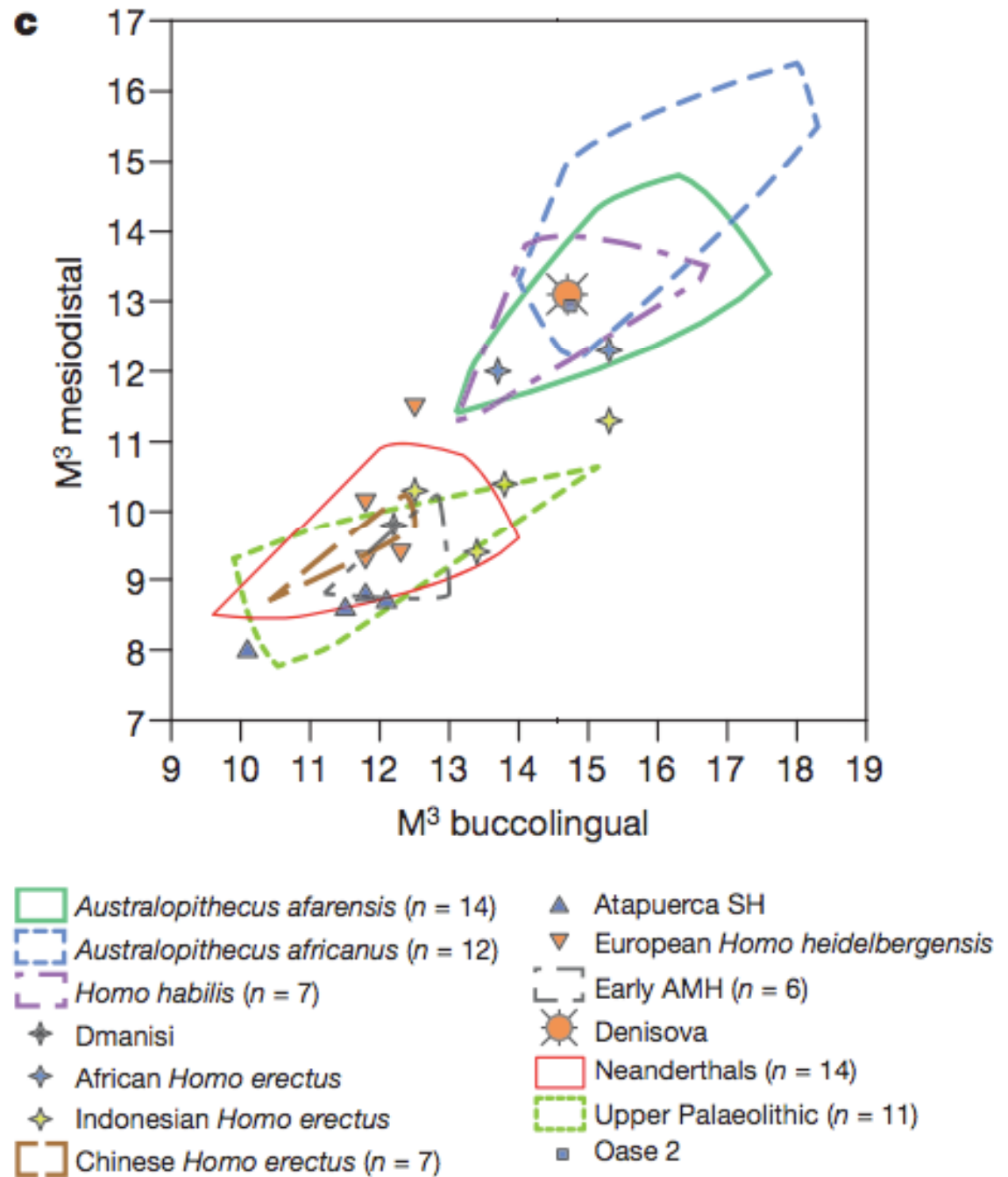
**Figure 1 | A neighbour-joining tree based on pairwise autosomal DNA sequence divergences for five ancient and five present-day hominins. Vindija 33.16, Vindija 33.25 and Vindija 33.26 refer to the catalogue numbers of the Neanderthal bones.**

- How can we explain the discrepancy?

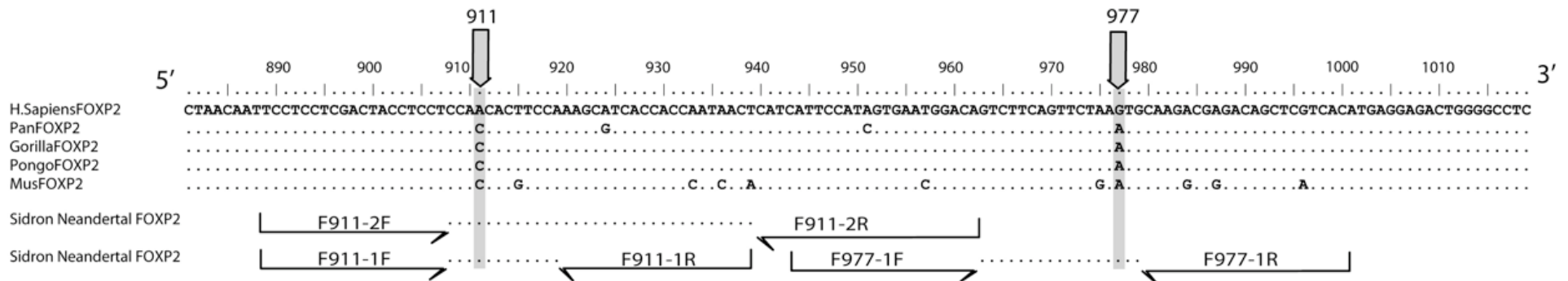
# Are the Denisovans separate from the Neanderthals?



- Population history
- Tooth morphology

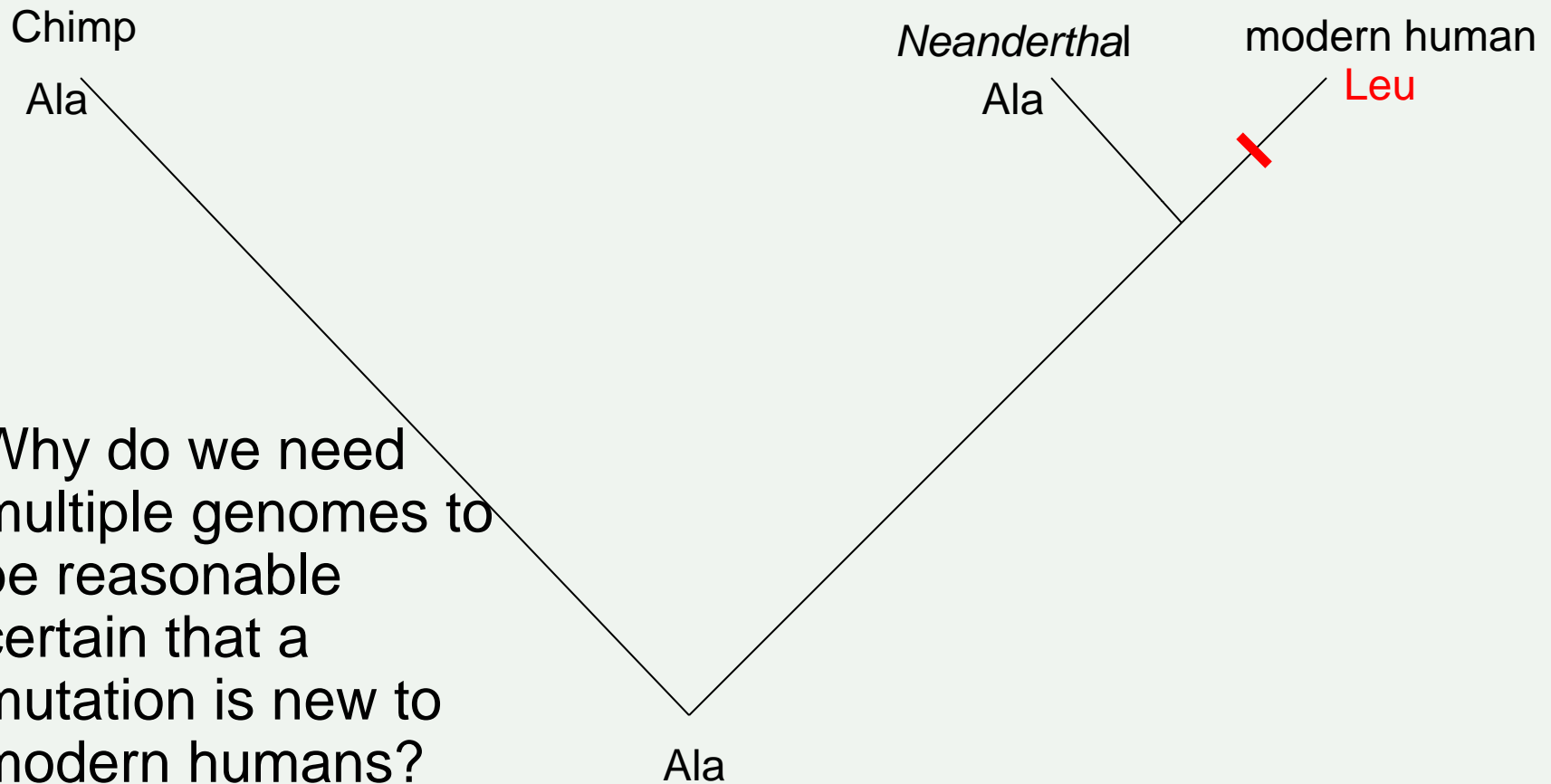


# *Homo neanderthalensis* and speech



- 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

# How the *Neanderthal* genome helps to find *sapiens* specific mutations



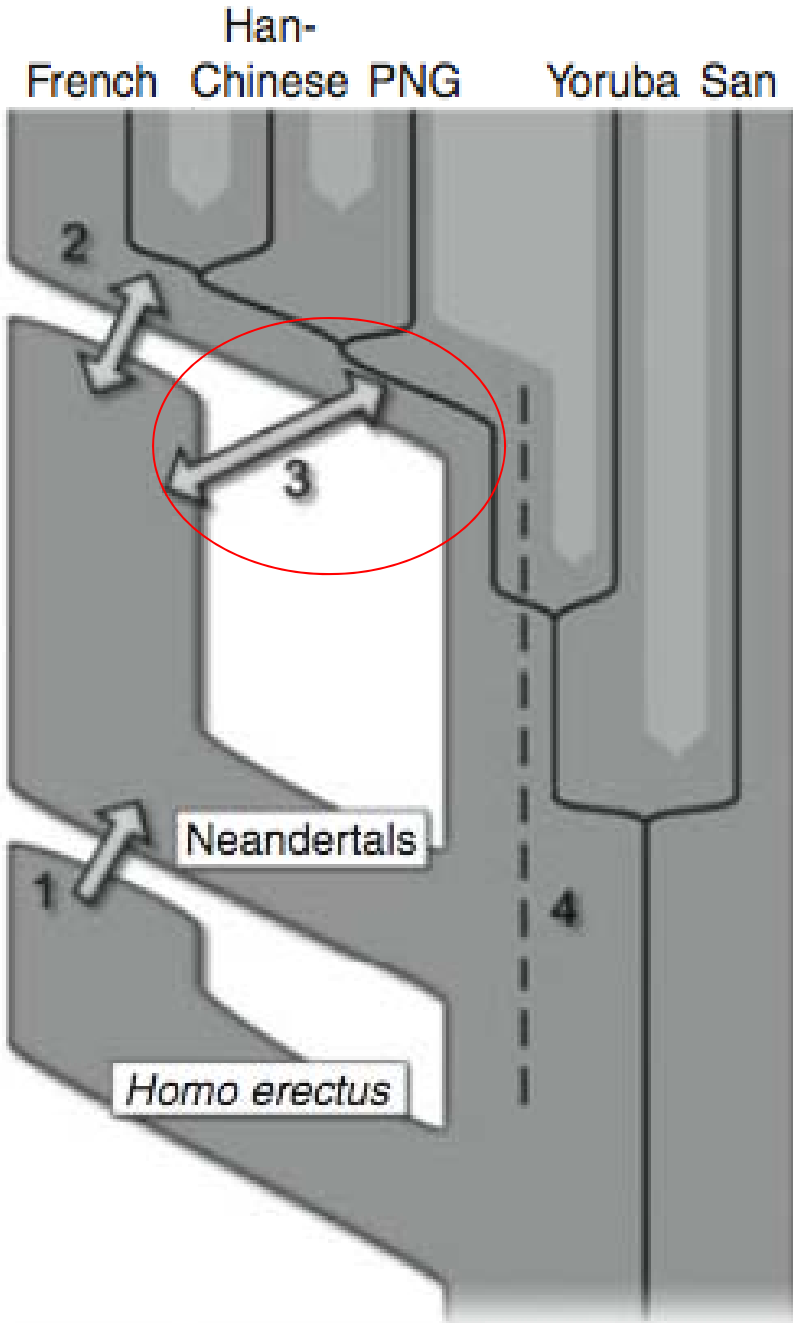
- Why do we need multiple genomes to be reasonable certain that a mutation is new to modern humans?

# Genes with sapiens-specific amino acid exchanges

**Table 2.** Amino acid changes that are fixed in present-day humans but ancestral in Neandertals. The table is sorted by Grantham scores (GS). Based on the classification proposed by Li *et al.* in (87), 5 amino acid substitutions are radical (>150), 7 moderately radical (101 to 150), 33 moderately conservative (51 to

100) and 32 conservative (1 to 50). One substitution creates a stop codon. Genes showing multiple substitutions have bold SwissProt identifiers. (Table S15 shows the human and chimpanzee genome coordinates, additional database identifiers, and the respective bases.) Genes with two fixed amino acids are indicated in bold.

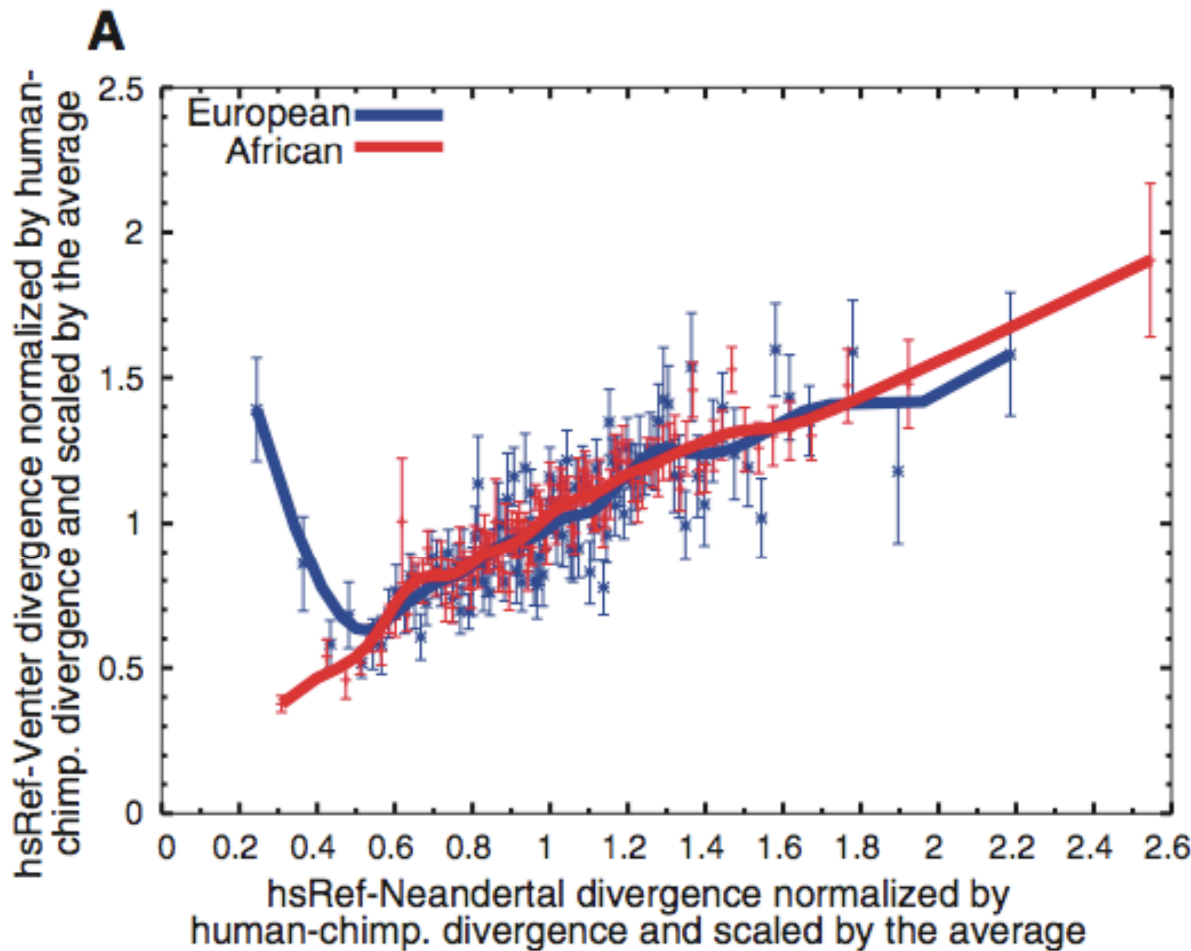
ID	Pos	AA	GS	Description/function
<b>RPTN</b>	785	*/R	–	Multifunctional epidermal matrix protein
GREB1	1164	R/C	180	Response gene in estrogen receptor–regulated pathway
OR1K1	267	R/C	180	Olfactory receptor, family 1, subfamily K, member 1
<b>SPAG17</b>	431	Y/D	160	Involved in structural integrity of sperm central apparatus axoneme
NLRX1	330	Y/D	160	Modulator of innate immune response
NSUN3	78	S/F	155	Protein with potential SAM-dependent methyl-transferase activity
RGS16	197	D/A	126	Retinally abundant regulator of G-protein signaling
BOD1L	2684	G/R	125	Biorientation of chromosomes in cell division 1-like
CF170	505	S/C	112	<i>Uncharacterized protein: C6orf170</i>
STEAP1	336	C/S	112	Metalloreductase, six transmembrane epithelial antigen of prostate 1
F16A2	630	R/S	110	<i>Uncharacterized protein: family with sequence similarity 160, member A2</i>
LTK	569	R/S	110	Leukocyte receptor tyrosine kinase
BEND2	261	V/G	109	<i>Uncharacterized protein: BEN domain-containing protein 2</i>
O52W1	51	P/L	98	Olfactory receptor, family 52, subfamily W, member 1
<b>CAN15</b>	427	L/P	98	Small optic lobes homolog, linked to visual system development
SCAP	140	I/T	89	Escort protein required for cholesterol as well as lipid homeostasis
<b>TTF1</b>	474	I/T	89	RNA polymerase I termination factor



# Gene flow with *neanderthalensis*

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

# European genome segments most similar to Neanderthals differ strongly from other human sequences



- Comparable results for Asian sequence
- Now, more diversity outside of Africa than within!



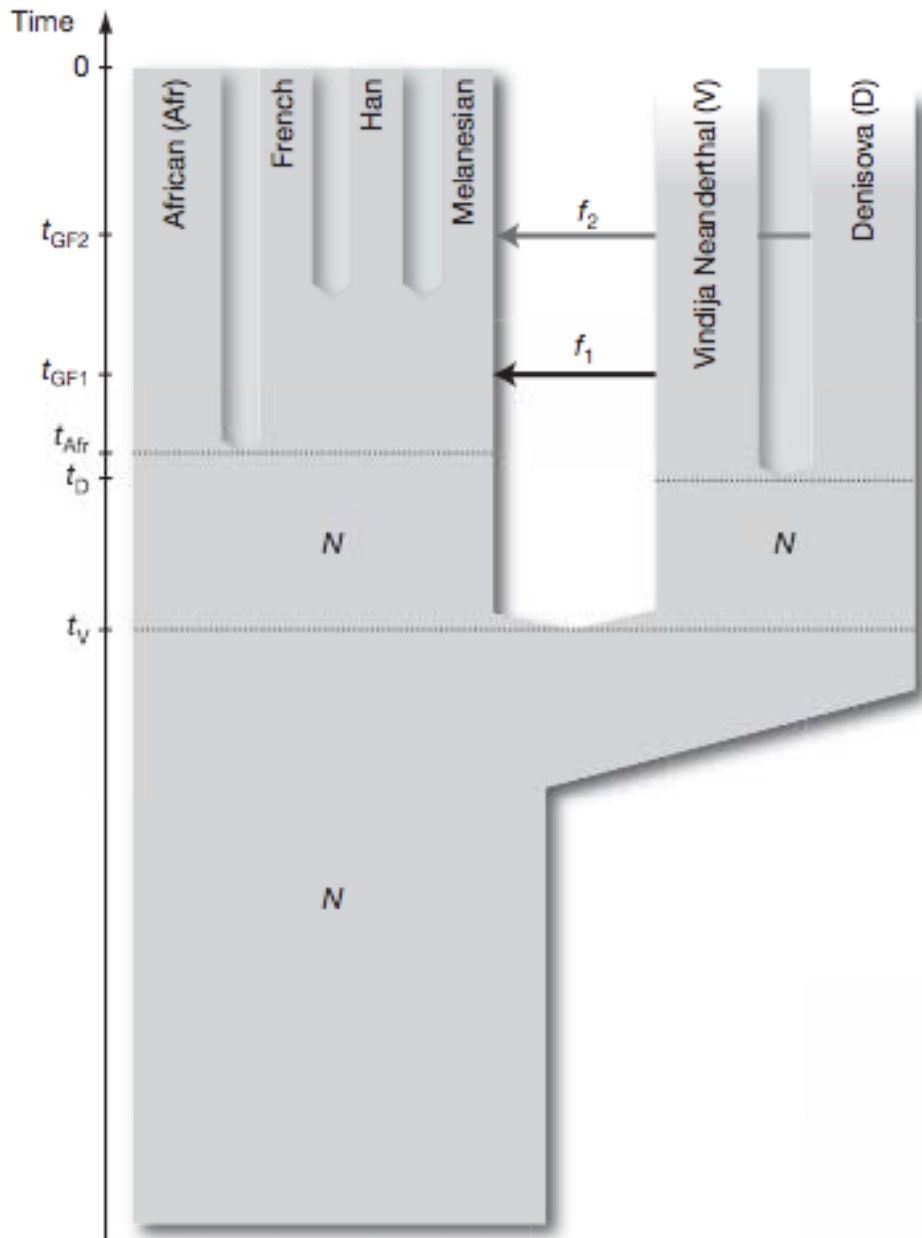


Figure 3 | A model of population history compatible with the data.  $N$  denotes effective population size,  $t$  denotes time of population separation,  $f$  denotes amount of gene flow and  $t_{GF}$  denotes time of gene flow.

# What about gene flow from Denisovans?

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

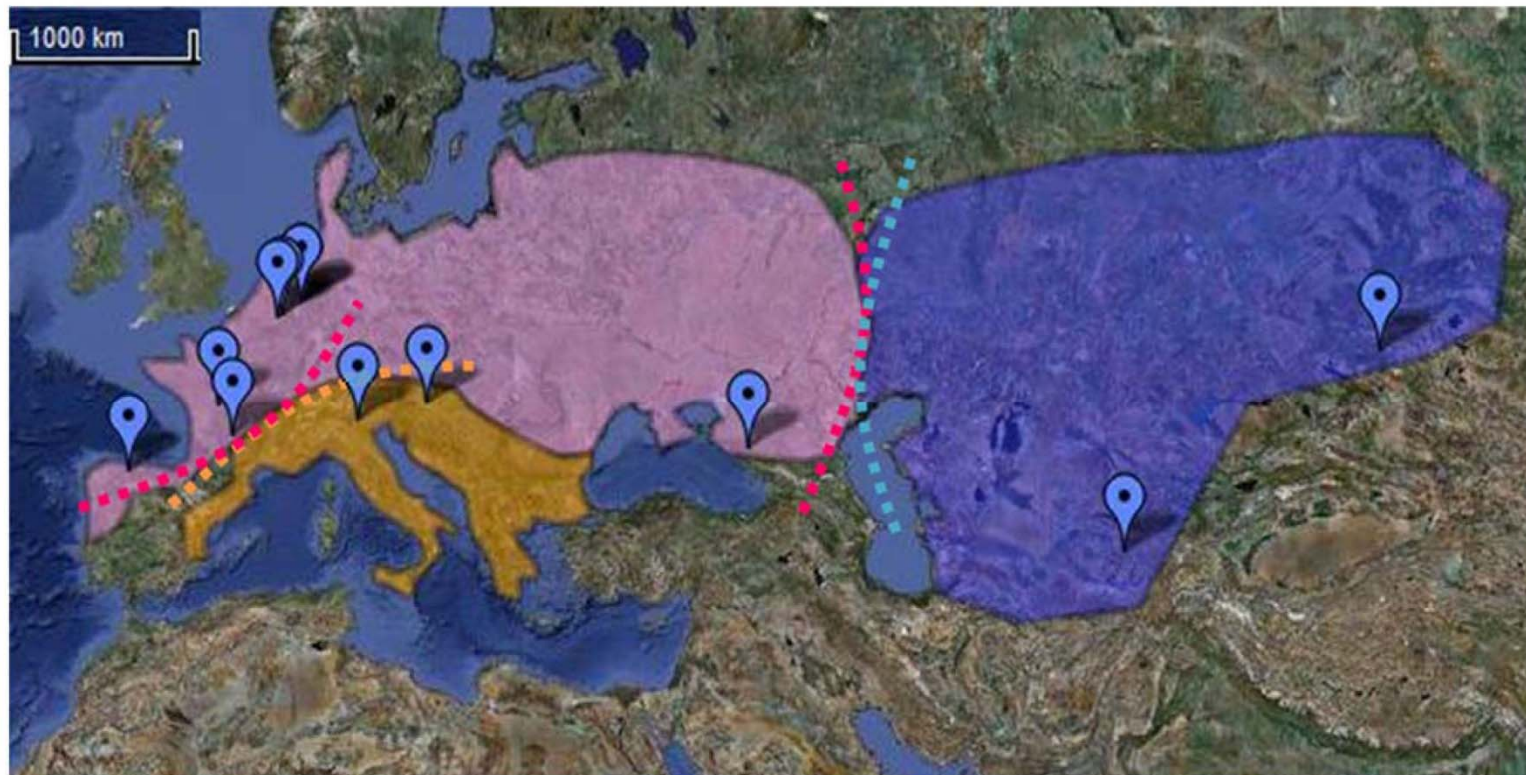


# Take Home Message

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

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

Fabre et al., 2009 PloS One.

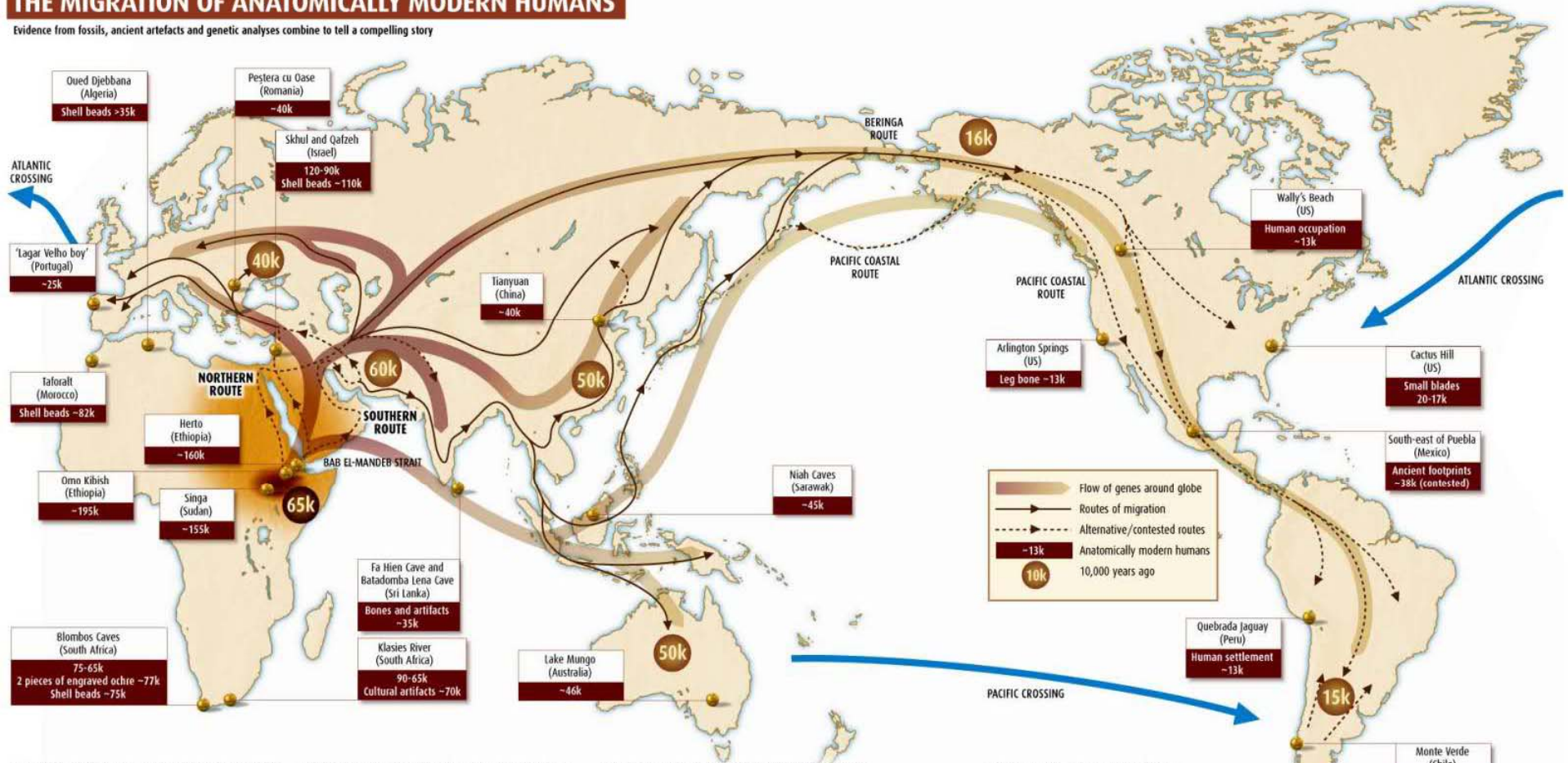


**Figure 2. Map representing Neanderthal geographical distribution in groups.**

doi:10.1371/journal.pone.0005151.g002

# 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.

