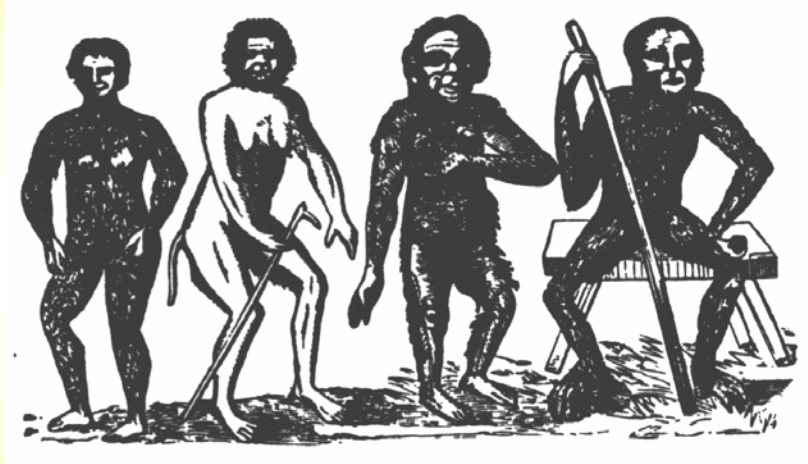


Human evolution

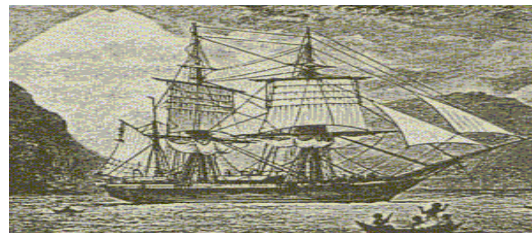


Linnean hominids

Closing the gap between humans and animals

Darwin meets Fuegians

It is a common subject of conjecture what pleasure in life some of the less gifted animals can enjoy: how much more reasonably the same question may be asked with respect to these barbarians. At night, five or six human beings, naked and scarcely protected from the wind and rain of this tempestuous climate, sleep on the ground coiled up like animals.



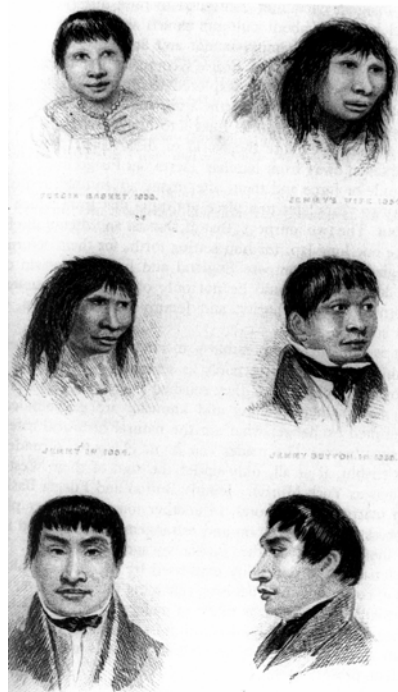
The issue: determinism and human nature

S.Americans kidnapped on Beagle and later returned after several years in Victorian environments

Cpt Fitzroy meets 'Jemmy' again:

This poor man was Jemmy, - now a thin, haggard savage, with long disordered hair, and naked, except a bit of blanket round his waist.

... We had left him plump, fat, clean, and well dressed; - I never saw so complete and grievous a change.

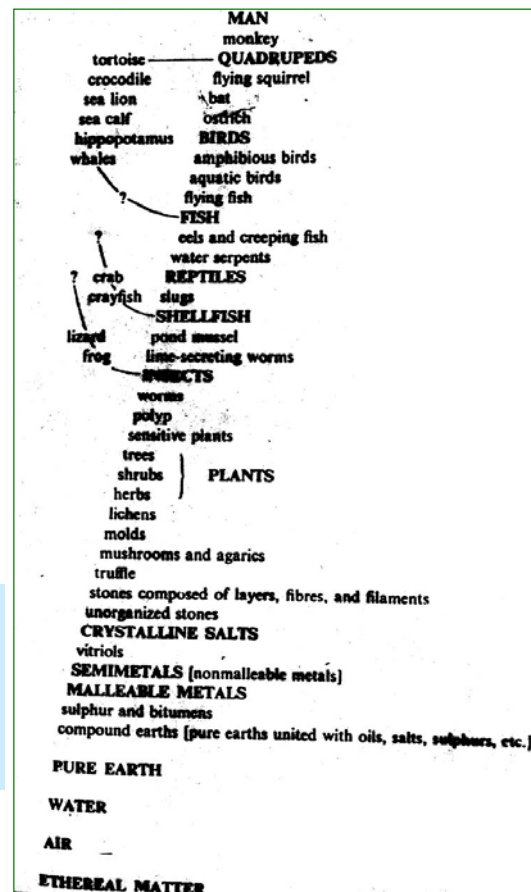


Long standing preevolutionary ideas - *scala naturae*

Evolution as progress.

- non-europeans
 - women
 - lower classes
 - criminals
- have still not evolved to higher levels

Eugenics movement: assist natural selection in purification of higher intelligent and moral order



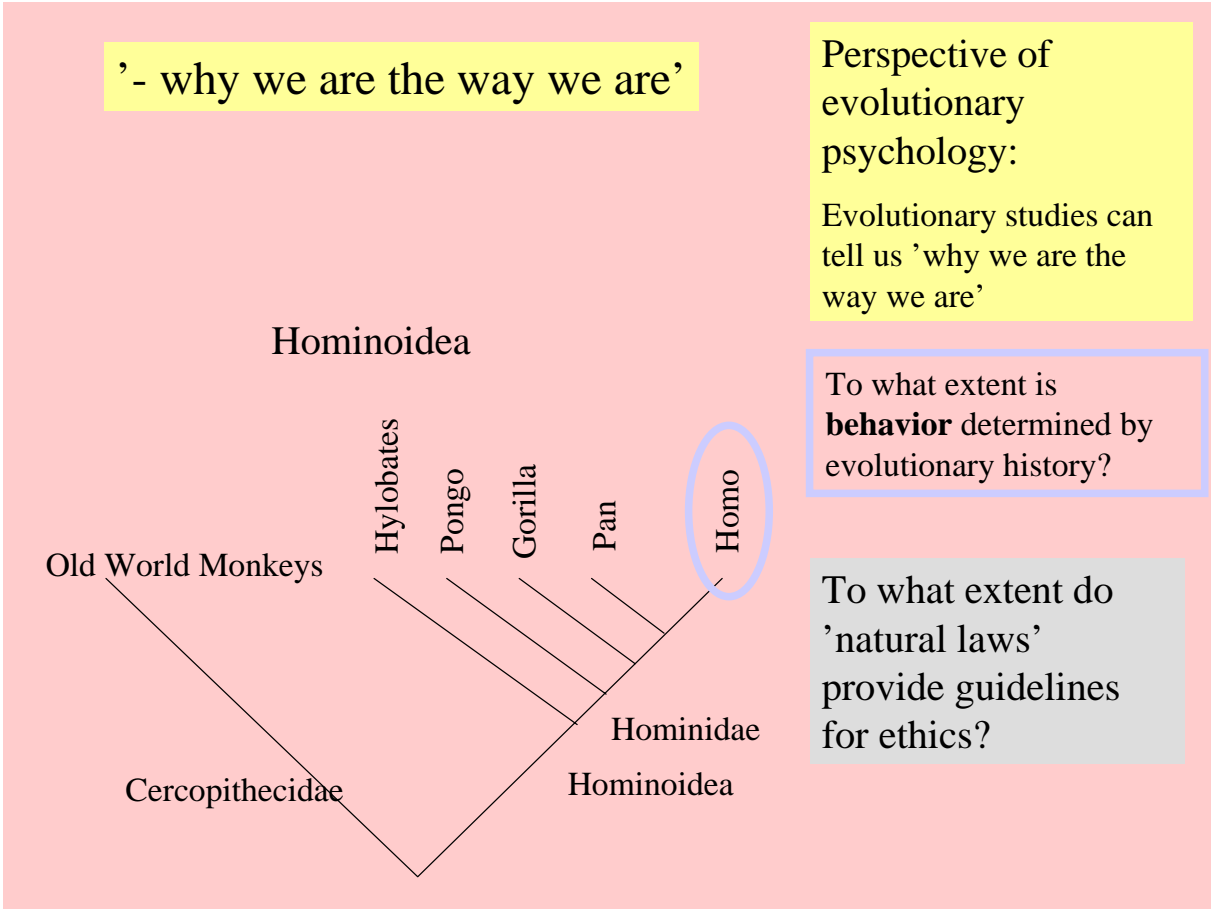
'- why we are the way we are'

Perspective of evolutionary psychology:

Evolutionary studies can tell us 'why we are the way we are'

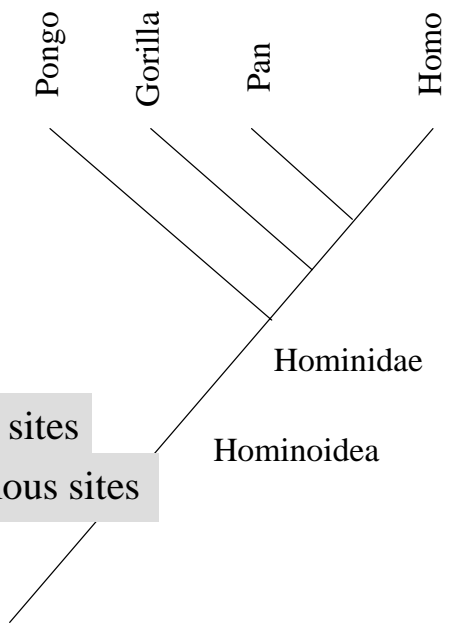
To what extent is **behavior** determined by evolutionary history?

To what extent do 'natural laws' provide guidelines for ethics?



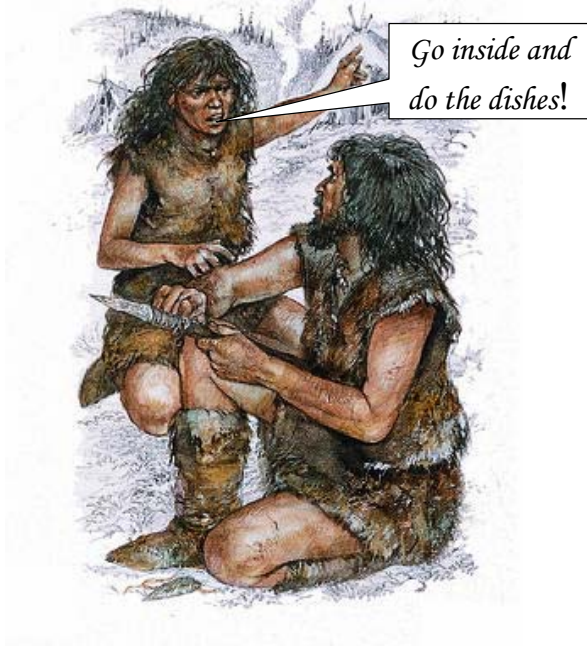
Hominidae

Wildman *et al* 2003 (PNAS):
'family Hominidae should include all extant apes; and genus *Homo* should include three extant species and two subgenera, *Homo* (*Homo*) *sapiens* (humankind), *Homo* (*Pan*) *troglodytes* (common chimpanzee), and *Homo* (*Pan*) *paniscus* (bonobo chimpanzee)'



97 genes *Pan* and *Homo*
98.4% identity at synonymous sites
99.4% identity at nonsynonymous sites

Is our genetic make-up 'frozen' by selection that took place in a 'hunter-gatherer' environment?



Nature – nurture conflict

Does sociobiology and evolutionary psychology construct ideologically biased gender roles that reflect conservative western family values from the 1950ies?



Family portrait: Hominoidea

Hylobates spp gibbons (8 species)



monogamy

Symphalangus siamang



Hominidae

Pongo pygmaeus orangutang



unimale polygyny (exploded)

wristwalker

Man and apes

morphological synapomorphies:

elongate skull, large brain

tail reduced

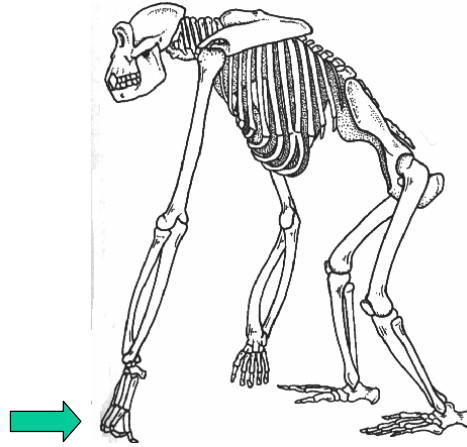
flexibility of joints (hips, ankles, wrist, thumb)

Hominidae

Gorilla gorilla gorilla, gorilla

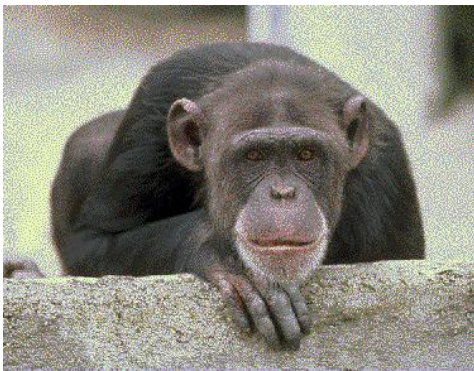


unimale polygyny
knucklewalker



Hominidae

Pan troglodytes common chimpanzee, sjimpanse



multimale polygyny
knucklewalker

Hominidae

Pan paniscus bonobo, pygmy chimpanzee, dvergsjimpanse



unconstrained sexlife substitutes aggression
sex partly separated from reproduction

several similarities with australopithecines

knucklewalker

Hominidae

Homo sapiens



polygyny, (serial) monogamy, polyandry

advanced bipedalism

large brain

complex social structures

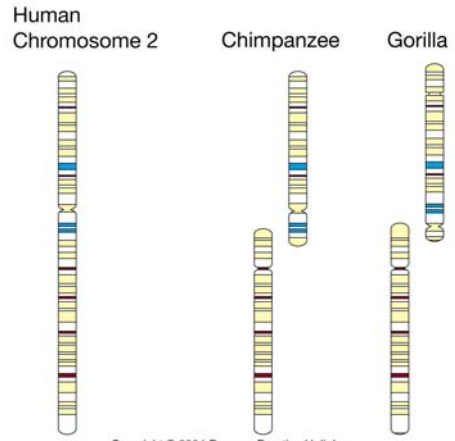
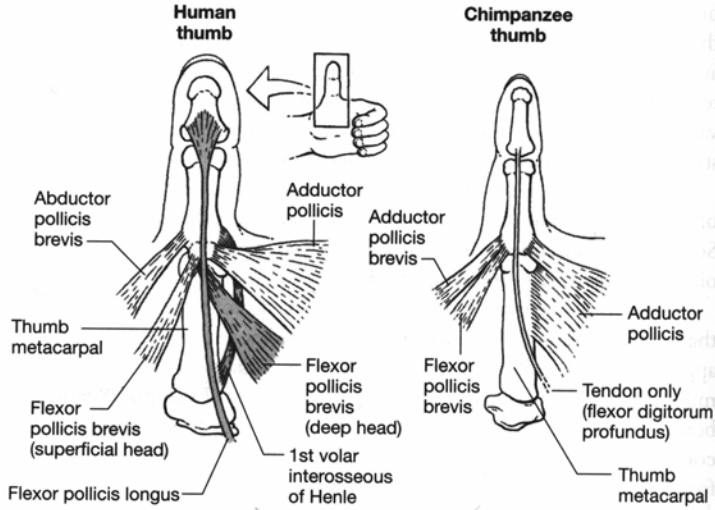
flexible thumb

advanced mythologies and rituals

advanced communication systems

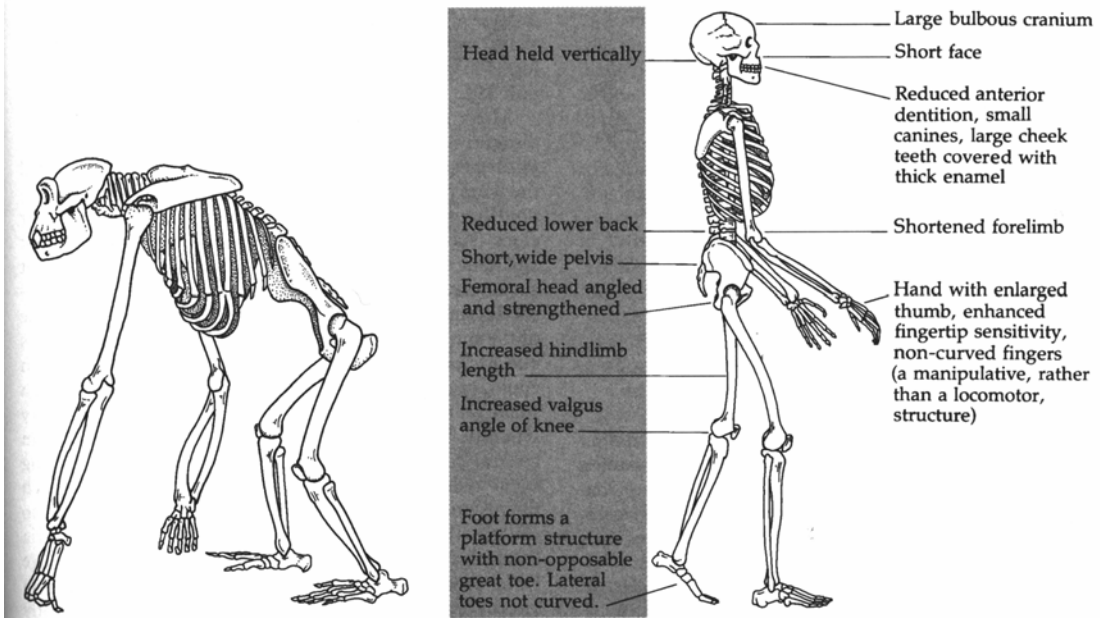
advanced technologies

How much is 0.6 % difference?



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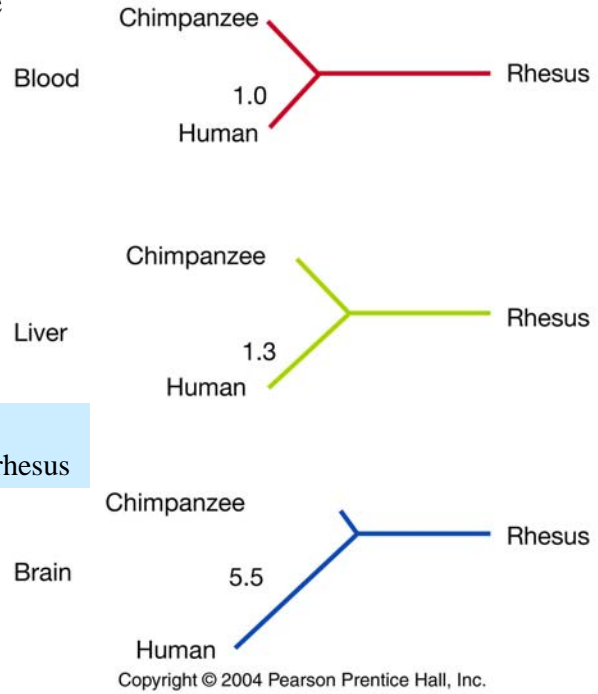
Adaptations to bipedal locomotion



0.6% structural genetic difference

but **striking differences in gene expression** as measured from ca 12,000 genes (Enard et al. 2000)

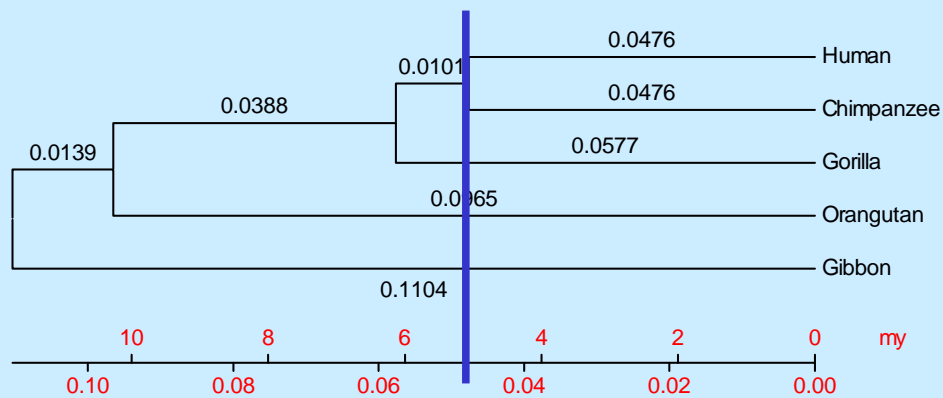
Branch lengths:
human divergence / chimp divergence from rhesus



Molecular clock -mitochondrial data

from Brown et al 1982

Mitochondrial difference
chimp-human amounts to
ca 10%



Fossile hominids

The oldest hominid fossils are found in Africa:

Sahelanthropus tchadensis (6-7 Mya)

Orrorin tugenensis (6 Mya)

Kenyanthropus platyops (3.5 Mya)

Ardipithecus

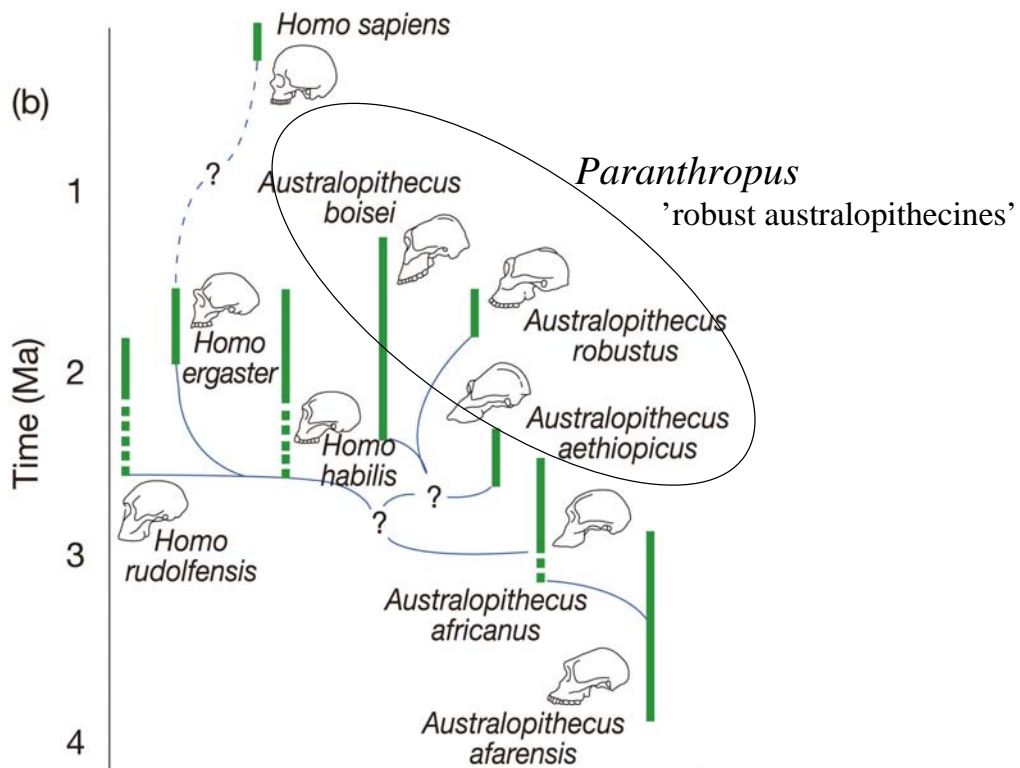
Australopithecus

Paranthropus

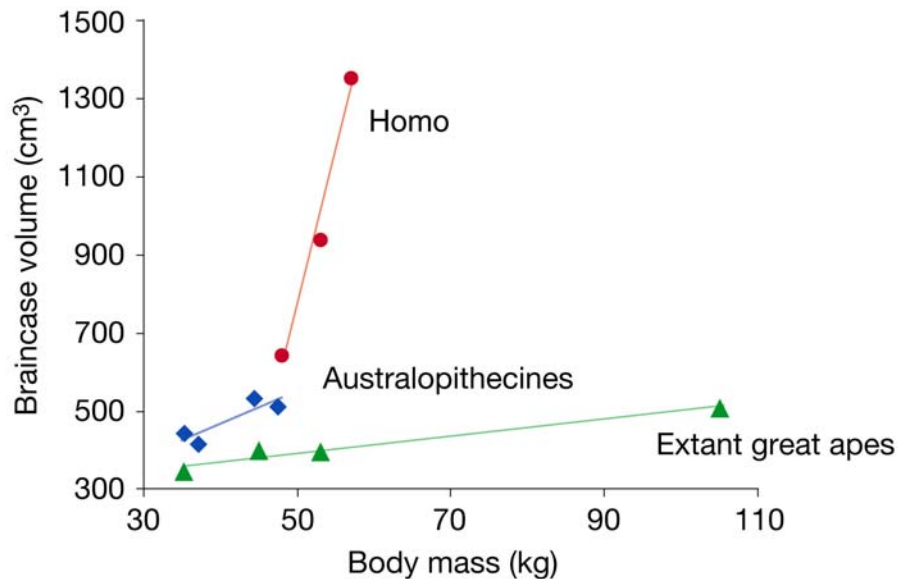
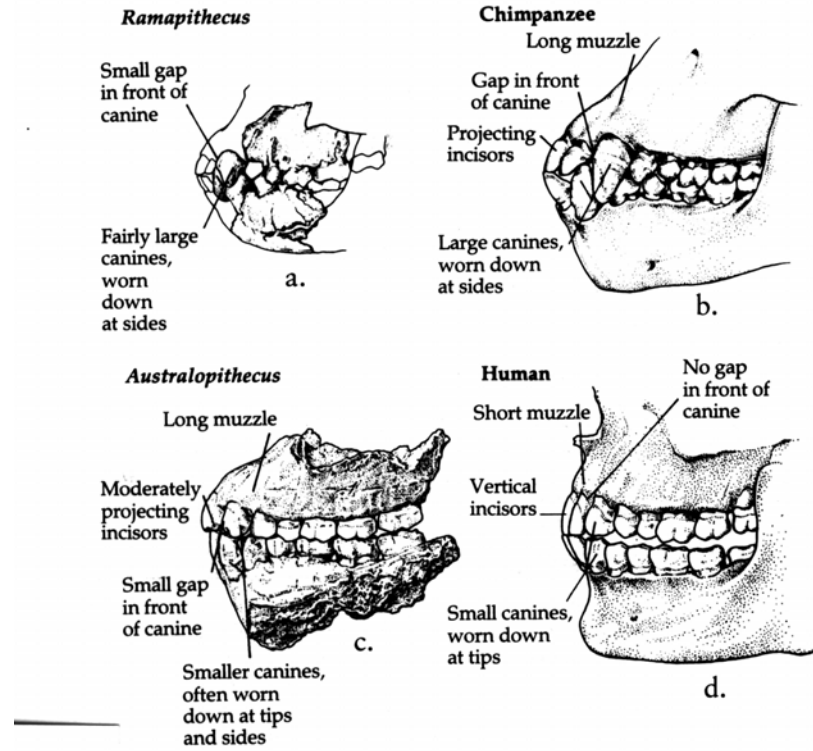
Homo spp

Human - chimp
- gorilla
ancestors?
recall mol. clock
divergence

Australopithecus, *Paranthropus* and *Homo spp* have overlapping time zones (~ 1 my coexistence)



Teeth and jaw



australopithecines and *Ardipithecus* (~2.4 - 4.4 MY)



A. africanus

Two groups: 'gracile' and 'robust'
Not monophyletic
prognathous, large teeth, small bodies (<1.5m),
small brain size (<500cm³), mostly bipedal

Gracile group: *Australopithecus*

A. africanus: 2.4 - 3.5 Mya

A. afarensis: 3.0 - 3.9 Mya (fossil footprints)

A. anamensis: 3.9 - 4.2 Mya



P. aethiopicus

Robust group: *Paranthropus*

large face, sagittal crest

P. robustus: 1.0 - 2.0 Mya

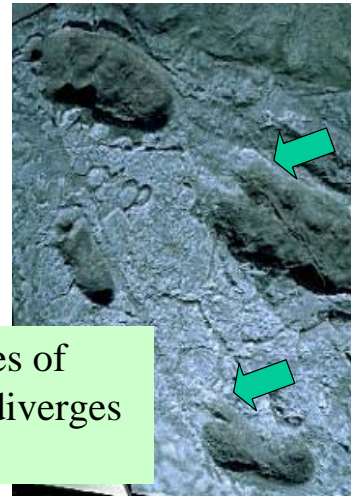
P. boisei: 1.4 - 2.3 Mya

P. aethiopicus: 1.9 - 2.7 Mya

Ardipithecus ramidus: 4.4 Mya

Arboreality of australopithecines?

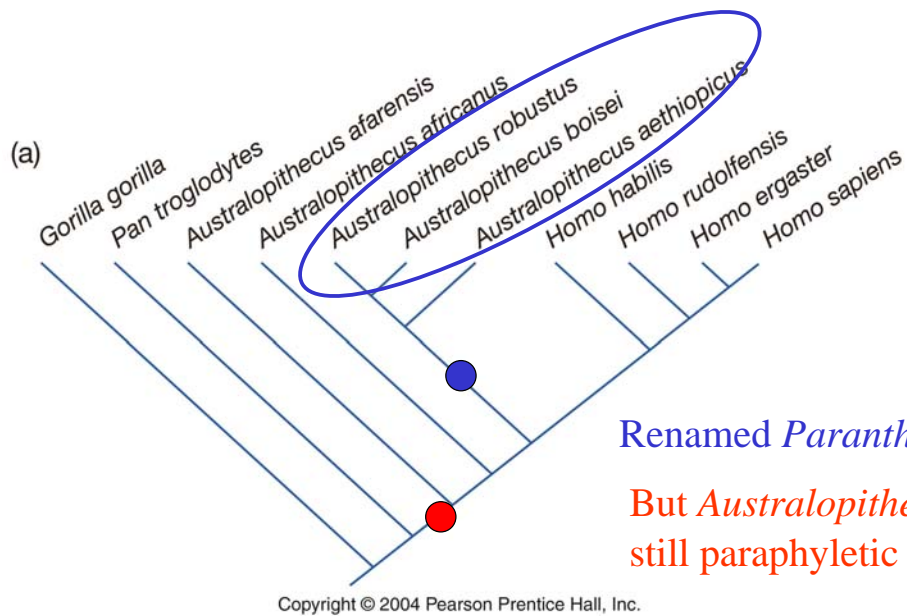
3.6 mya
fooprints of
A.afarensis,
Tanzania



More robust limbs. Four articulating foot bones of *A.africanus* (3.5 my) imply that the great toe diverges from other toes as in *A.afarensis* and in apes

Vestibular system (balance organs): in humans the anterior and posterior canals are relatively larger than in apes

computer tomography of *Homo* and australopithecine fossils shows that the latter are apelike (Spoor *et al* 1996)



Renamed *Paranthropus*:

But *Australopithecus* is still paraphyletic

Earliest *Homo* spp



Homo habilis (handy man) 1.6 - 1.9 mya

first fossil found in E.Africa early 1960ies

Homo rudolfensis, 1.8 - 2.4 mya, has been considered by some to be the same species, but most anthropologists think of *rudolfensis* as a species with larger brain and differences in skull shape

early *Homo* had larger brains (ca.640cm³) than australopithecines (ca.400cm³).

Estimated body weight

50 kg males

30 kg females

Homo erectus ~ 0.4-1.2Mya (1.8 Mya*)



'Java man': 1891, skull cap and thigh bone

'Peking man': 1927, a tooth

More fragments in Java and China later

Other findings since 1950ies: Algeria, Morocco, Georgia and E. Africa*

H. erectus is considered as a wide spread species with considerable morphological variability. Many datings (particularly Java) are uncertain and have been questioned in later years. Chinese and Java may be up to 0.7 my.

**Homo ergaster* - including 'the Turkana boy' is regarded by some researchers to be the same species as *H. erectus* ('African *H. erectus*')

Homo ergaster 1.5- 1.8 Mya

East Africa and Chad.

Almost complete skeletons available.

males nearly 1.80 m high

females about 1.55

Findings of *erectus* in Georgia were dated up to 1.8 my old. This may be an overestimate. If not, some antropologists say, *H. erectus* may have originated in Eurasia.



Homo heidelbergensis 0.2-0.6 (0.78?) Mya

No fossils to suggest the presence of *ergaster* / *erectus* in Europe.

But, many examples of so called *archaic Homo*

Many of these have been assigned to *H.heidelbergensis*, first found in 1907 in Germany

Recent findings in Atapuerca, N.E.Spain were first regarded as *H.heidelbergensis*, but have now (1997) been named *Homo antecessor*. These remains contain many individuals, some of which may be 780.000 y old.

Notice that neanderthal - modern human has been dated 317.000 - 741.000 y with molecular clock

Homo neanderthalensis ~ 35.000 - 150.000 y*



First discovered in 1856. Named in 1864.

Presently known distribution: Europe, Middle East to W.Central Asia

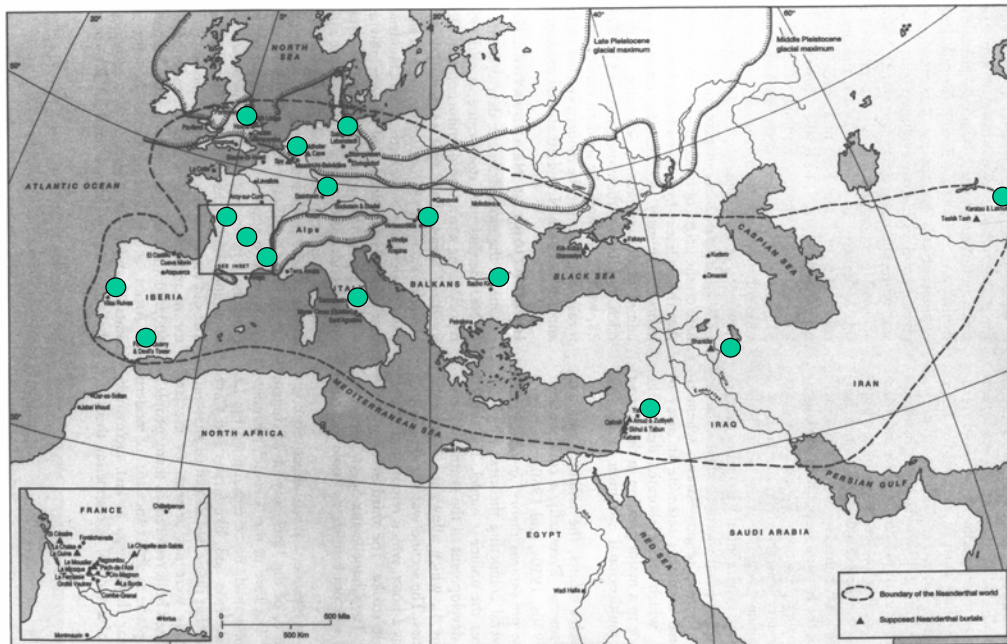
Tools, houses, and other artefacts have been recovered by archaeologists

H.neanderthalensis has been considered as either

- 1) a direct ancestor of European *H.sapiens*
- 2) a side branch of *H.sapiens* (*H. sapiens neanderthalensis*)
- 3) descendant from *H.erectus* - driven to extinction or swamped by the genepool of expanding *Homo sapiens*

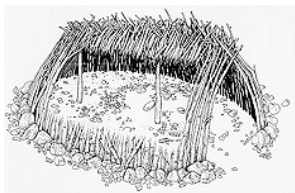
*328 base pair mtDNA indicate that *H. neanderthalensis* was very different from modern humans, and molecular clock estimates suggest divergence from *H.sapiens* about 600.000 years ago .

H. neanderthalensis distribution



GEOGRAPHICAL DISTRIBUTION: Neanderthal populations were confined to Europe, the Middle East, and western Asia. (Courtesy of Chris Stringer.)

Changing neanderthal reconstructions



From discovery of bone remains at La Chapelle-aux-Saints (1908), M. Boule at Mus. Natn. d'Hist. Nat. painted out the picture of Neanderthals as evolutionary dead end, semi-idiot brutes. This became dominant understanding of 'cave men' until the late 1960ies.

Modern reconstructions suggest that the fur was rather obtained from somebody else's bodies. Neanderthals had bigger brains than modern humans.

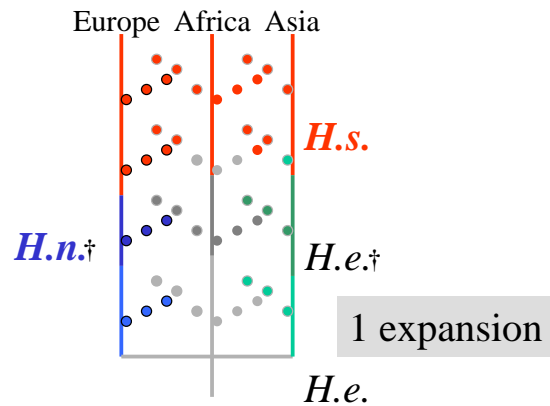
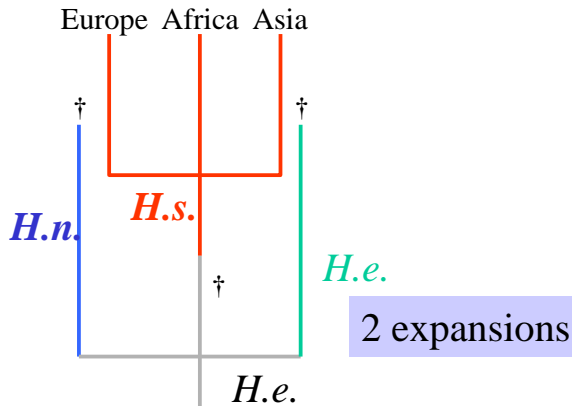
Competing hypotheses on *H.sapiens*

Out of Africa

Ancient populations of Europe (e.g. *H.neanderthalensis*) and Asia (*H.erectus*) **replaced** by expanding *H.sapiens*.
(‘Noah’s Ark’-hypothesis’)

Multiregional origin

H.sapiens gradually evolves from ancient populations of *H.erectus* in different regions. Gene flow between regional populations.
(‘modified Candelabra model’)



Palaeontological predictions of each hypothesis

Out of Africa

- Earliest fossils of *H. sapiens* should appear in Africa.
- Transitional morphologies should be found only in Africa, i.e. the most recent ancestor of *H. sapiens* should appear only there.

Multiregional origin

- Fossils of *H.sapiens* from the same period should be found in several regions of Eurasia
- Transitional morphologies should be found in several regions of Eurasia.

Testability of both hypotheses depend on *taxonomy*, location, age, and representativeness of the fossil record

Problems: sparse record of fossils

- fossils fragmented
- taxonomy not clear-cut: e.g. ‘.. primitive looking moderns’
- phylogenies fragile
- datings uncertain

Genetic predictions of each hypothesis

Out of Africa

- ancestral neutral alleles mostly in Africa.
- European and Asian alleles are subsets of African.
- divergence time African /non-African *H.s* < 200.000 years
- greater diversity in Africa

Multiregional origin

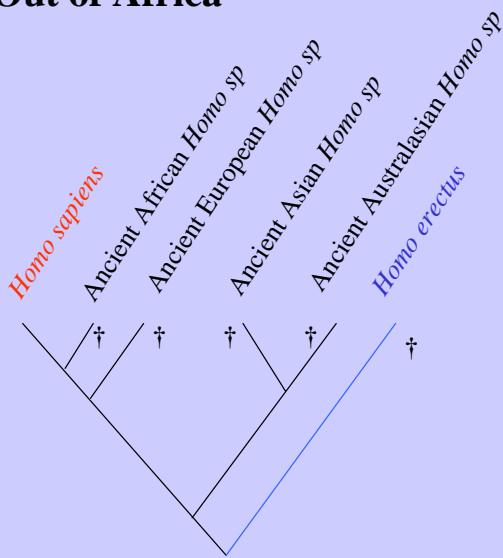
- randomly distributed alleles
- some European, Asian, alleles are not subsets of African.
- divergence time > 1 My
- about equal diversity over all

Problems: with at least two expansions it may be difficult to separate between ancient *H.sapiens* and *H.erectus/ergaster* alleles.

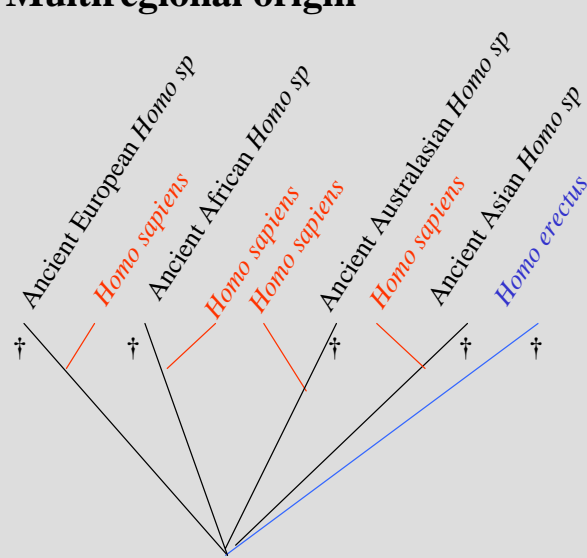
- Gene flow can reduce apparent age
- Genetic splits may be older than species splits
- Do all morphospecies actually reflect speciation events?

Species concepts?

Out of Africa



Multiregional origin



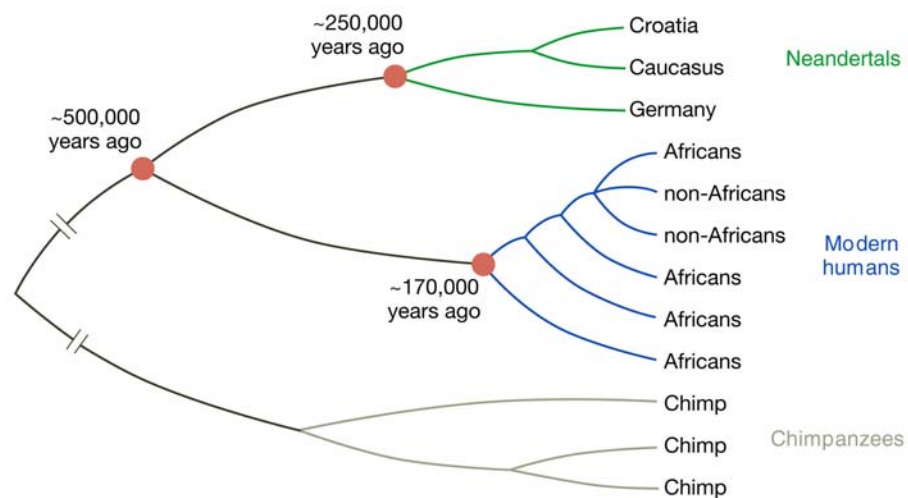
What sort of biological realities would allow for **the same species** to be formed **four times in different lineages (polyphyletic species)**?

Dating the neanderthal divergence

- short sequence recovered from bones with PCR (Pääbo *et al.*)
- compared with 663 modern humans, 7 chimps and 2 bonobos
- all moderns are more closely related
- neanderthal sequence more than 3 times different than the span of differences between modern humans

•using divergence time 4-5 My for chimp - human, the divergence neanderthal - modern human is estimated between 317.000 - 741.000 years ago

•supports Out of Africa for *H.sapiens*



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Evidence from population differences

Data from Nei &
Roychoudhury (1993):
15 populations,
33 polymorphic loci

Largest difference within groups: African

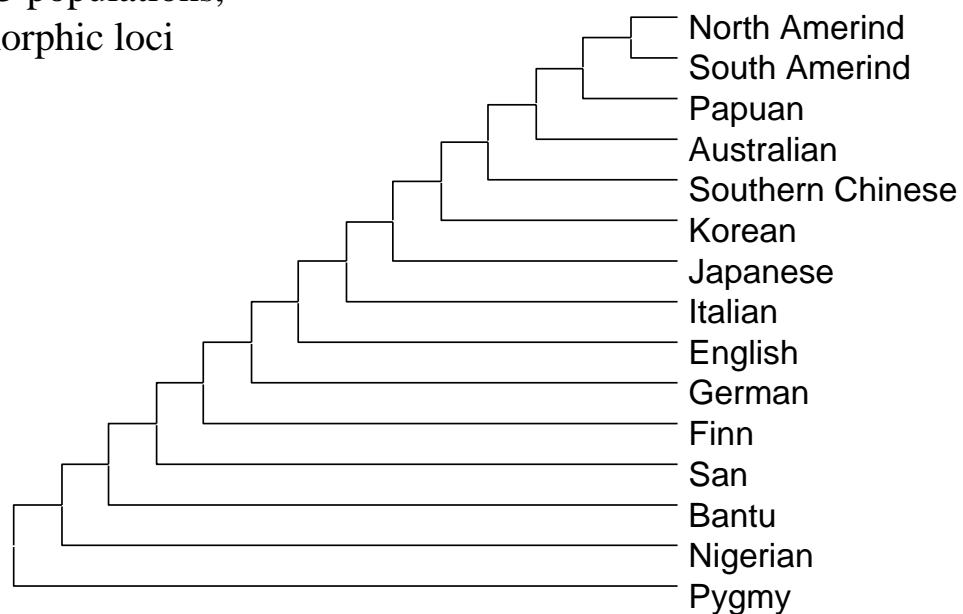
Largest difference between groups:
African versus Australian-New Guinean

Smallest difference between groups:
Asian versus American Indian

Distances within groups	Between groups				
	1	2	3	4	5
African 0.0436	[1] African -				
European 0.0049	[2] European 0.0804	-			
Asian 0.0148	[3] Asian 0.0875	0.0441	-		
AusNG 0.0396	[4] AusNG 0.1037	0.0774	0.0285	-	
Amind 0.0313	[5] Amind 0.0879	0.0476	0.0252	0.0478	-

Population differences

Nei & Roychoudhury
(1993): 15 populations,
33 polymorphic loci



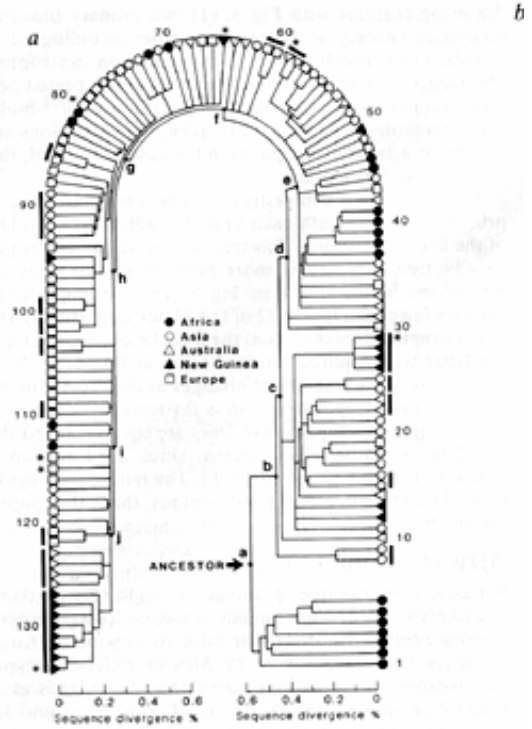
Mitochondrial DNA

Potentially a powerful tool for tracing population history. Not recombining (or less so than nDNA).

A. Wilson *et al.* (1987): 147 individuals from different regions. The root in Africa.

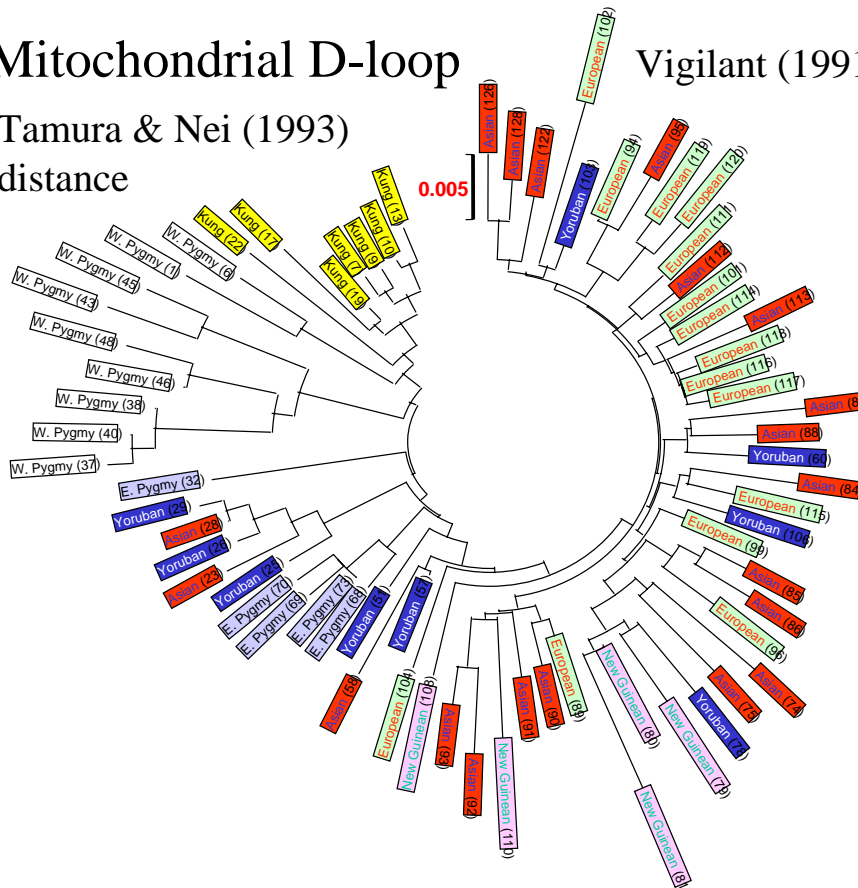
African populations seen as older due to larger variability.

The mitochondrial Eve theory: all moderns can be traced back to a single female in a population of ca. 10.000 living ca. 200.000 years ago in Africa



Mitochondrial D-loop

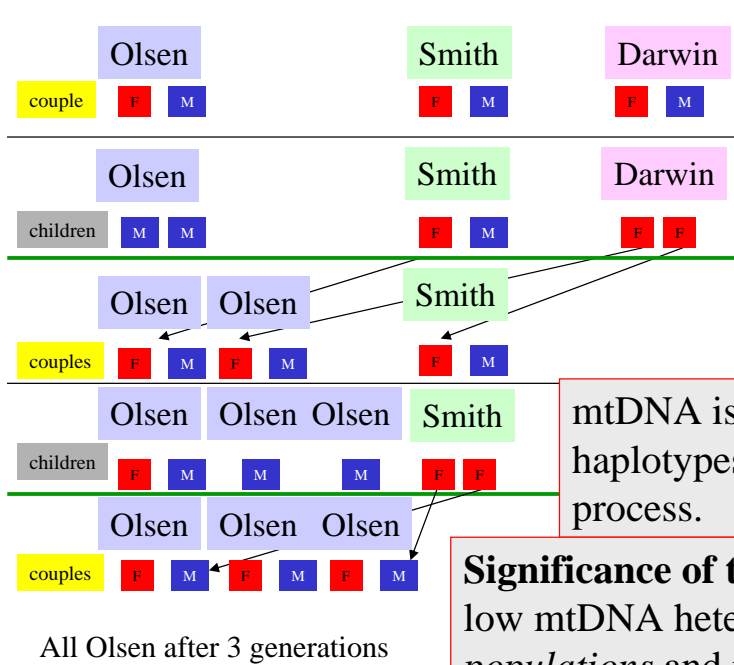
Tamura & Nei (1993) distance



Vigilant (1991) data

- New Guinean
- Asian
- European
- Yoruban
- E. Pygmy
- W. Pygmy
- Kung

mitochondrial Eve



Patrilineal family names may go extinct in a stable population where each couple produces two offspring. If, on average, 1/4 has 2 girls, 1/4 has 2 boys, 1/2 has 1 boy and 1 girl: **only one family name remains** after 2N generations, where N is the original number of females.

mtDNA is inherited *matrilinearly* and haplotypes may be lost in a similar process.

Significance of this:
 low mtDNA heterogeneity *may reflect small populations* and not necessarily

- young age or
- a single stem mother

All Olsen after 3 generations

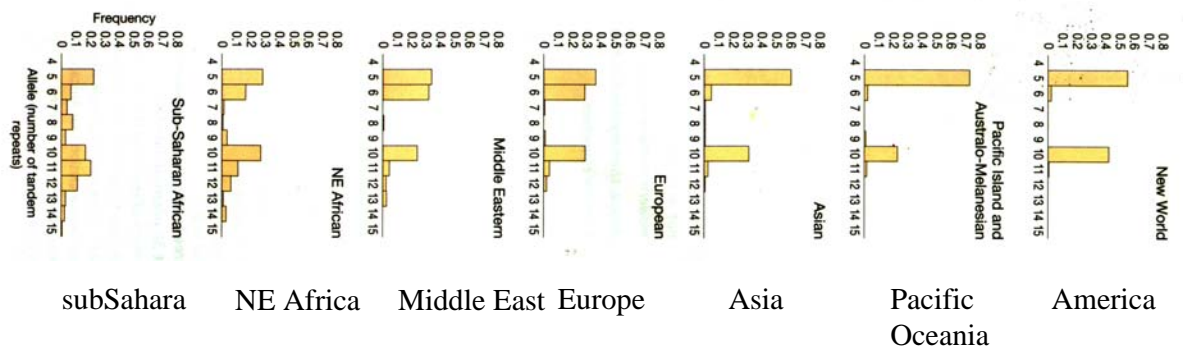
Microsatellites

Tishkoff et al (1996): short tandem repeat polymorphism on chromosome 12

TTTTC repeated 4 - 15 times. TTTTCTTTTCTTTTCTTTTC

Thus possible to score for 12 alleles for more than 16000 samples

Highest diversity in Africa. Least in New World



Conclusions

Out of Africa seems well supported

Clear geographical gradient in genetic diversity

However, still unclear which species of *Homo* expanded