

Evolution of Modern Humans

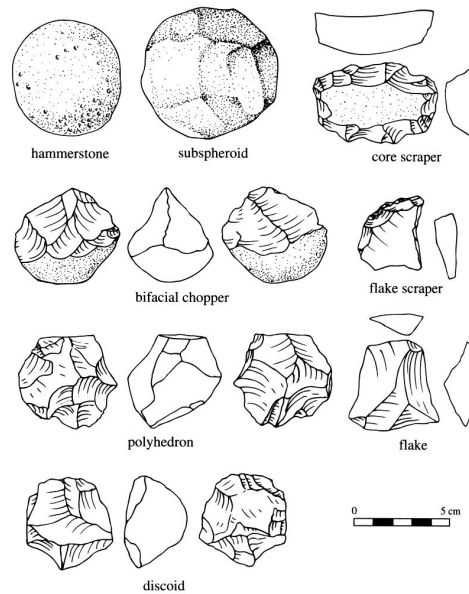
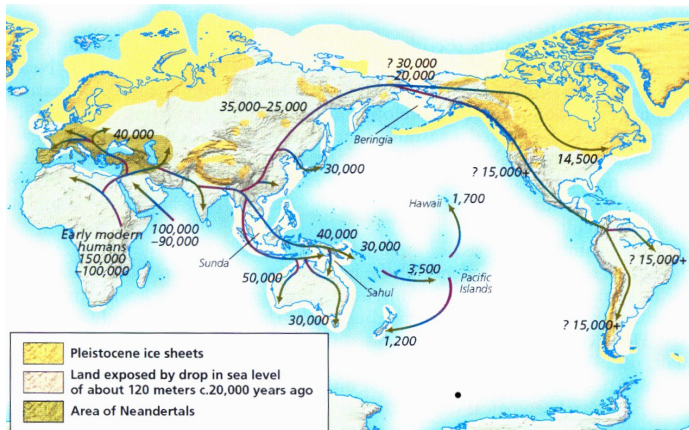
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June 25, 2012

Evolution of Modern Humans

- ▶ Tool traditions
- ▶ Morphology
- ▶ Hypotheses
- ▶ Genetic evidence

Moderns invade Eurasia



- ▶ Oldowan tools
- ▶ 2.6–1.7 mya
- ▶ Earliest stone tools
- ▶ Probably made by *Homo habilis/ rudolphensis*

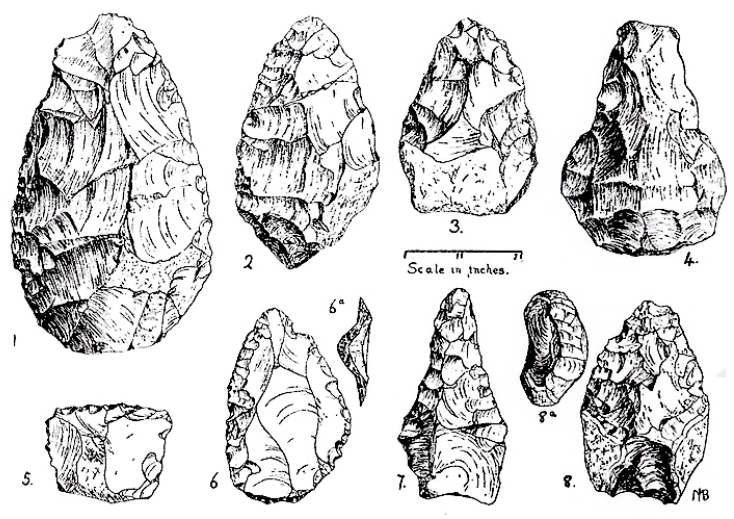


Oldowan tools
2.6–1.7 mya

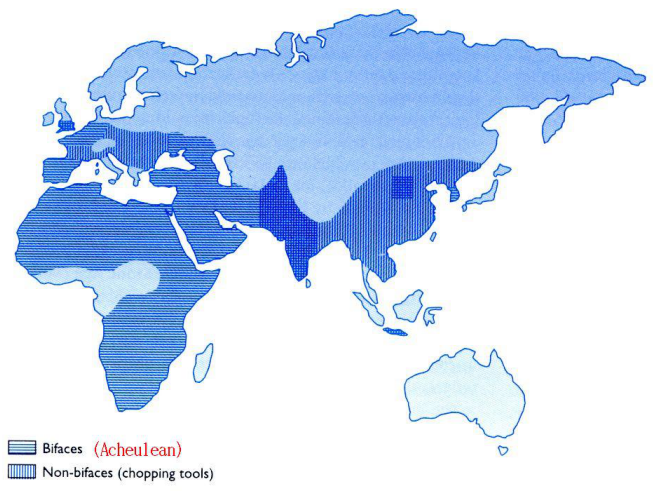
Acheulean hand axe (1.5–0.3 mya)



Acheulean tools (1.5–0.3 mya)



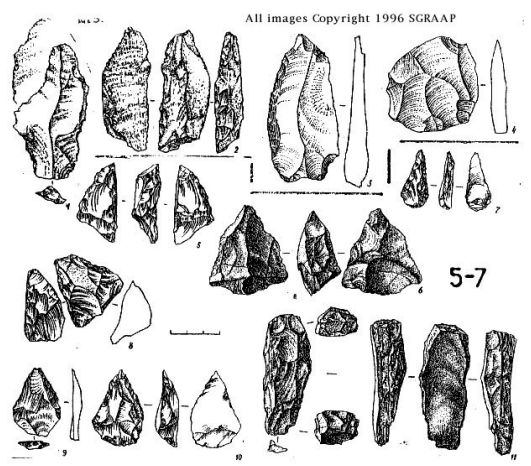
Distribution of Acheulean tools



Acheulean tools

- ▶ Associated with *Homo ergaster/erectus*
- ▶ 1.5–0.3 myr ago
- ▶ Essentially unchanged for 1.2 myr
- ▶ Wide distribution in space

Mousterian tools



- ▶ 300–30 kya
- ▶ Europe and western Asia
- ▶ Neandertals

Neandertal sites



Mousterian tools

- ▶ Neandertals
- ▶ 300–30 kya
- ▶ Little change in 270 kyr
- ▶ Wide distribution in space



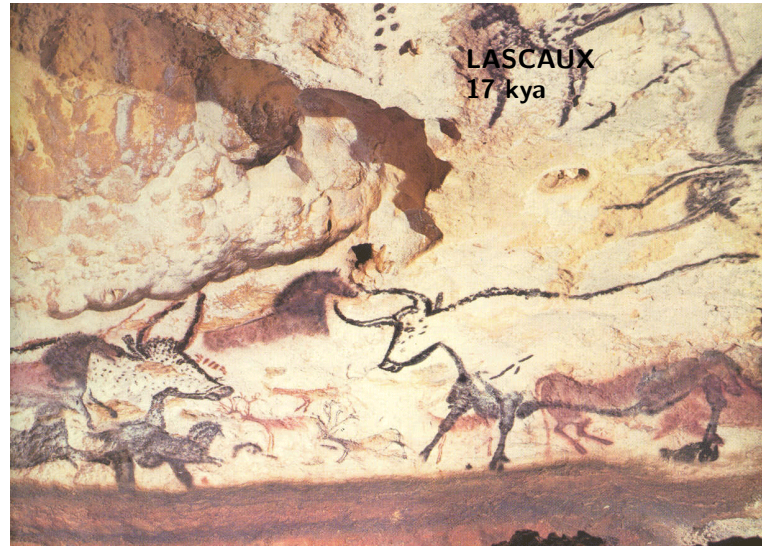
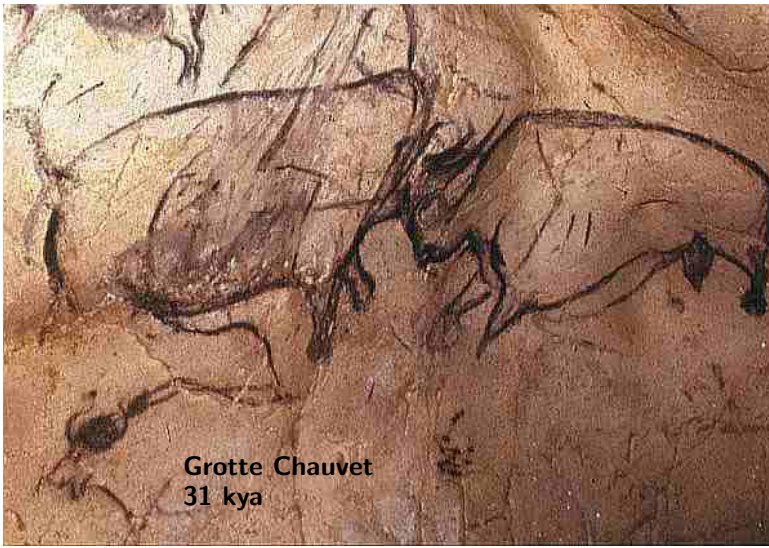
Aurignacian tools

- ▶ 34–23 kya
- ▶ Earliest Upper Paleolithic, Europe
- ▶ Modern humans

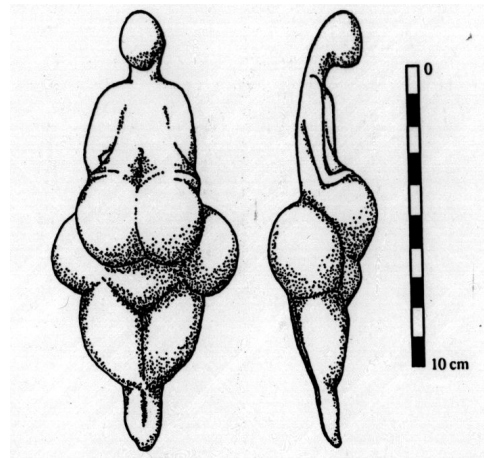


Solutrean tools

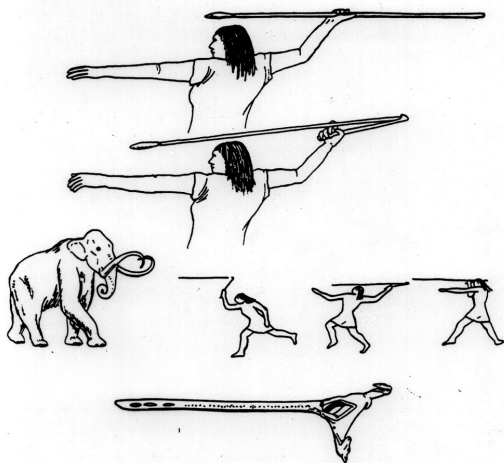
- ▶ 19–15 kya
- ▶ Laurel-leaf points
- ▶ Later Upper Paleolithic, Europe
- ▶ Modern humans



Art
Deer's head
18–10 kya

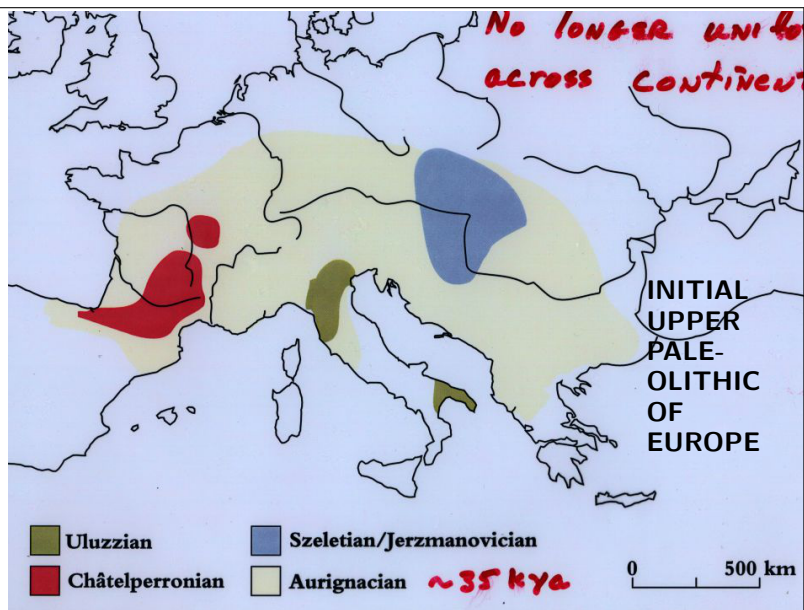


Venus of Lespugue
(28 kya)



Spear thrower

- ▶ increases force of throw
- ▶ penetrated Spanish armor
- ▶ kill at 70 m
- ▶ by 14 kya



Tool traditions of the Upper Paleolithic

Age	Tradition
35–29 kya	Chatelperronian
34–23 kya	Aurignacian
28–22 kya	Gravettian
19–15 kya	Solutrean
18–10 kya	Magdalenian

- ▶ Change is rapid.
- ▶ Each tradition occupies a small region.
- ▶ Culture varies in space.



- Neandertal & Modern**
Modern (at right):
- ▶ small
 - ▶ long-limbed
 - ▶ gracile
 - ▶ flat face
 - ▶ chin
 - ▶ forehead
 - ▶ domed skull

Herto, Ethiopia (160 kya)



Outline

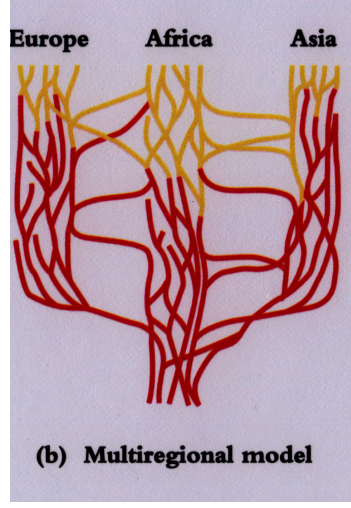
- Tool traditions
- Morphology
- ▶ Hypotheses
- ▶ Genetic evidence

How did modern humans evolve?

In the 1980s and 90s, there were two main hypotheses

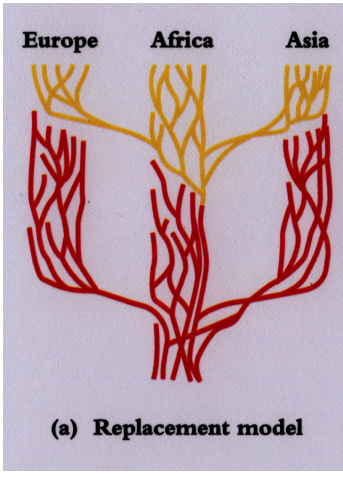
- ▶ Multiregional
- ▶ Replacement

Multiregional hypothesis



- ▶ *Homo erectus* expands into Eurasia 1.8 mya
- ▶ Strong gene flow
- ▶ Favorable mutations spread in every direction.
- ▶ Moderns have no geographic origin.

Replacement hypothesis



- ▶ *Homo erectus* expands into Eurasia 1.8 mya
- ▶ Moderns evolve in Africa by 100 kya
- ▶ Expand into Eurasia btw 100 and 30 kya
- ▶ No mixing with archaics

The next lecture will evaluate these (and other) hypotheses.

Genetic Evidence on Modern Human Origins

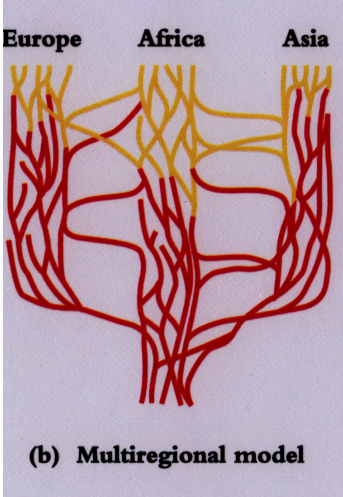
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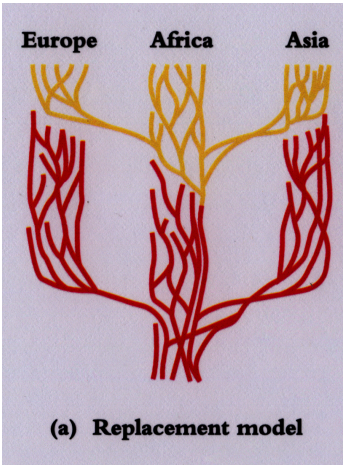
- ▶ Genetic differences within and between pops
- ▶ Why genes inform us about history.
- ▶ Evidence for a Pleistocene population explosion.
- ▶ Grounds for skepticism: the selection hypothesis
- ▶ Diffusion wave

Multiregional hypothesis



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What the hypotheses predict

- Multiregional** All populations are ancient, and they separated long ago.
- ▶ Big genetic diffs w/i and btw populations
- Replacement** Eurasia is recent; Africa is ancient
- ▶ Small diffs btw pops and w/i Eurasia
 - ▶ Big diffs w/i Africa

Mitochondrial DNA

- ▶ inherited from mother only
- ▶ evolves fast
- ▶ mean pairwise difference: average number of nucleotide site differences between mitochondria of pairs of individuals
- ▶ we will look at about 300 base pairs of mitochondrial DNA

Mitochondrial nucleotide differences (D-loop)

Mean pairwise diff: between\within\net

Major Human Populations

	European (N = 20)	Asian (N = 71)	African (N = 10)
Eur	0.0094	0.0012	0.0028
As	0.0128	0.0137	0.0015
Af	0.0194	0.0203	0.0238

Chimpanzee Subspecies

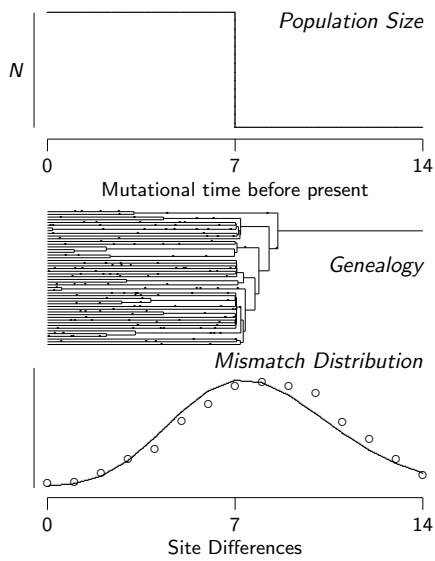
	Pts (N = 40)	Ptt (N = 18)	Ptv (N = 8)
Pts	0.029	0.030	0.137
Ptt	0.072	0.055	0.087
Ptv	0.192	0.155	0.081

Genetic differences between human mitochondria are

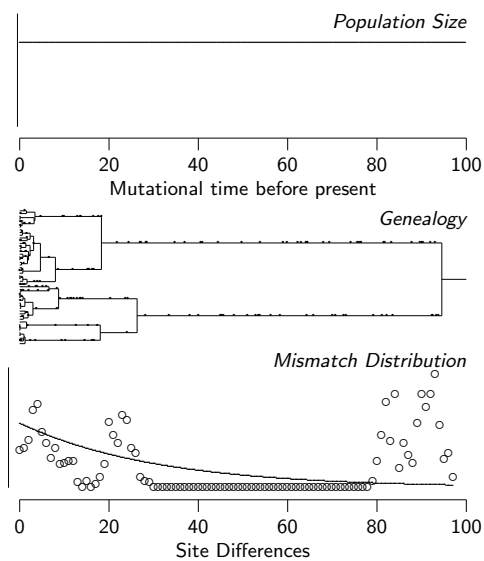
- ▶ small between populations
- ▶ small within Eurasian populations
- ▶ somewhat larger within Africa

Suggests

- ▶ populations separated recently
- ▶ Eurasian populations less ancient

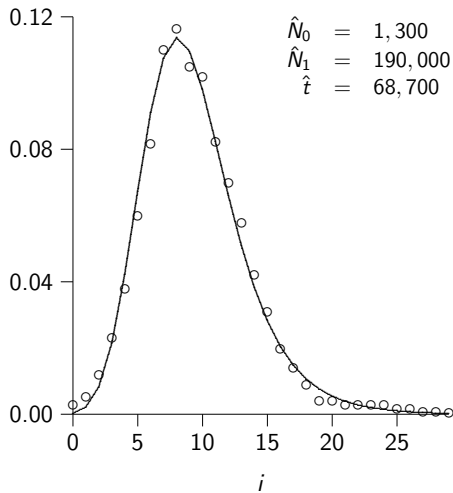


- ▶ Simulation of expanded population
- ▶ Pop expands 7 units of "mutational time" ago
- ▶ 1 mutational diff per time unit
- ▶ Comb-shaped genealogy
- ▶ Mismatch distribution has wave
- ▶ Peak just above 7



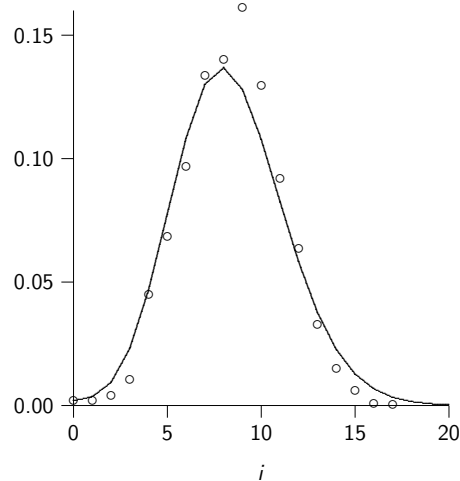
- ▶ Simulation of equilibrium population
- ▶ No history of growth
- ▶ Deep genealogy
- ▶ Ragged mismatch distribution

Mitochondrial Mismatch Distribution



- ▶ open circles: data of Cann, Stoneking, & Wilson (1987).
- ▶ solid line: fit to expansion model (Rogers & Harpending 1992)
- ▶ implies expansion ~70 kyr ago
- ▶ coincident with origin of modern humans

Mismatch Distribution: 77 Asian Subjects



- ▶ open circles: Asian data
- ▶ solid line: fit to expansion model (Rogers & Harpending 1992)
- ▶ implies expansion ~70 kyr ago
- ▶ coincident with origin of modern humans

Outline

- Models of modern human origins
- Why genes inform us about history.
- Evidence for a Pleistocene population explosion.
- ▶ Grounds for skepticism: the selection hypothesis
- ▶ Mismatch distributions of human and chimp
- ▶ Comparing loci

The Selection Hypothesis

- Suppose that a favorable mitochondrial mutation
- ▶ arose 60,000 years ago, and
 - ▶ increased in frequency until everyone had it.
- This is called a "selective sweep."

Outline

A selective sweep in the mitochondrion would

- ▶ produce a wave in the mismatch distribution,
- ▶ just like one produced by population growth.

How can we tell the difference?

Compare other loci.

- Genetic differences within and between pops
- Why genes inform us about history.
- Evidence for a Pleistocene population explosion.
- Grounds for skepticism: the selection hypothesis
- ▶ Diffusion wave

Mitochondrial story, circa 1996

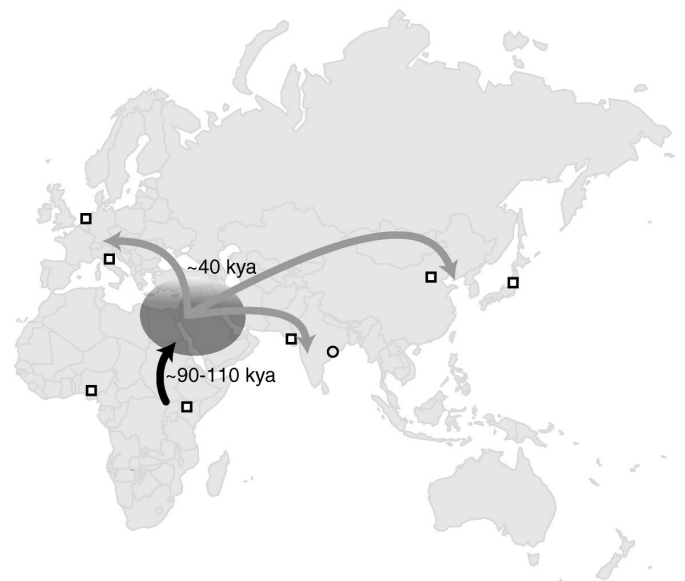
- ▶ Population expansion 50–100 kya
- ▶ Early population ≤ 5000 females
- ▶ Late population $\geq 1,000,000$ females
- ▶ Consistent with replacement hypothesis
- ▶ but not multiregional hypothesis

Nuclear genes

Since 1997, we have relied more and more on nuclear genes.

Xing et al 2010

- ▶ studied large sample of nuclear DNA from populations in Africa, Europe, East Asia, and India.
- ▶ Eurasian populations left Africa about 100 thousand years ago
- ▶ Did not separate until 25–40 thousand years ago



Did moderns mix with archaics?

Fossils From Vindija Cave, Croatia



Hominin tooth from Denisova Cave, Altai Mtns, southern Siberia

Patterns of nucleotide site differences



Compare 4 genomes:

	Pattern		
	1	2	3
French	D	D	A
African	D	A	D
Neanderthal	A	D	D
Chimpanzee	A	A	A
# sites	303,340	103,612	95,347

Common pattern (1) reflects history of population splits.

Absent admixture, the other two should be equally common

Excess of pattern 2 reflects admixture.

Estimate from Neandertal DNA

Eurasians share some derived alleles with archaics

- ▶ DNA of modern Europeans is 1.3–2.7% Neandertal.
- ▶ Same is true for modern people of east Asia and Papua New Guinea, but not Africa. Green et al (2010)
- ▶ Admixture must have occurred *after* moderns left Africa but *before* they expanded throughout the world.

Neandertal matches French 4.6% more often than Yoruban (African).

Denisova matches French 1.8% more often than Yoruban (African).

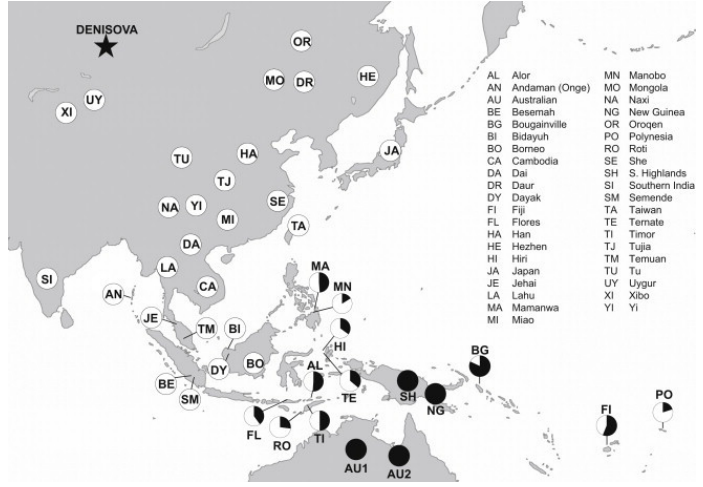
Archaic component of Eurasian genome more Neandertal than Denisovan.

Green et al 2010; Reich et al. 2010.

So do Asians and Papuans

Asians and Papuans carry as many Neanderthal alleles as Europeans do: 1.3–2.7%.

Denisovan DNA most common in Australia, NG, and Oceania



Summary

- ▶ Our ancestors expanded out of Africa 50 kya,
- ▶ and mated with surrounding archaic populations.
- ▶ Yet only a few archaic genes entered the modern population.
- ▶ Explains the contradictory signals given by different genetic loci.
- ▶ Europeans are part Neandertal, and Melanasiens are part Denisovan.