Evolution of Modern Humans

Alan R. Rogers

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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

Acheulean hand axe (1.5–0.3 mya)

Oldowan tools
2.6–1.7 mya
Acheulean tools (1.5–0.3 mya)

- 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

- 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

**Grotte Chauvet**
- 31 kya

**LASCAUX**
- 17 kya

**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

<table>
<thead>
<tr>
<th>Age</th>
<th>Tradition</th>
</tr>
</thead>
<tbody>
<tr>
<td>35–29 kya</td>
<td>Chatelperronian</td>
</tr>
<tr>
<td>34–23 kya</td>
<td>Aurignacian</td>
</tr>
<tr>
<td>28–22 kya</td>
<td>Gravettian</td>
</tr>
<tr>
<td>19–15 kya</td>
<td>Solutrean</td>
</tr>
<tr>
<td>18–10 kya</td>
<td>Magdalenian</td>
</tr>
</tbody>
</table>

▶ 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.

Outline

- 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

- Homo erectus expands into Eurasia 1.8 mya
- Strong gene flow
- Favorable mutations spread in every direction.
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Replacement 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)

<table>
<thead>
<tr>
<th>Major Human Populations</th>
<th>European</th>
<th>Asian</th>
<th>African</th>
</tr>
</thead>
<tbody>
<tr>
<td>(N = 20)</td>
<td>(N = 71)</td>
<td>(N = 10)</td>
<td></td>
</tr>
<tr>
<td>Eur</td>
<td>0.0094</td>
<td>0.0012</td>
<td>0.0028</td>
</tr>
<tr>
<td>As</td>
<td>0.0128</td>
<td>0.0137</td>
<td>0.0015</td>
</tr>
<tr>
<td>Af</td>
<td>0.0194</td>
<td>0.0203</td>
<td>0.0238</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Chimpanzee Subspecies</th>
<th>Pts</th>
<th>Ptt</th>
<th>Ptv</th>
</tr>
</thead>
<tbody>
<tr>
<td>(N = 40)</td>
<td>(N = 18)</td>
<td>(N = 8)</td>
<td></td>
</tr>
<tr>
<td>Pts</td>
<td>0.029</td>
<td>0.030</td>
<td>0.137</td>
</tr>
<tr>
<td>Ptt</td>
<td>0.072</td>
<td>0.055</td>
<td>0.087</td>
</tr>
<tr>
<td>Ptv</td>
<td>0.192</td>
<td>0.155</td>
<td>0.081</td>
</tr>
</tbody>
</table>

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
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.”

Mitochondrial Mismatch Distribution

\[
\hat{N_0} = 1,300 \\
\hat{N_1} = 190,000 \\
\bar{i} = 68,700
\]

- solid line: fit to expansion model (Rogers & Harpending 1992)
- implies expansion \(~70 \text{ kyr ago}\)
- 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 \(~70 \text{ kyr ago}\)
- coincident with origin of modern humans
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.

Outline
◦ 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 ≥ 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?

- 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.

Fossils From Vindija Cave, Croatia

Patterns of nucleotide site differences

<table>
<thead>
<tr>
<th>Pattern</th>
<th>1</th>
<th>2</th>
<th>3</th>
</tr>
</thead>
<tbody>
<tr>
<td>French</td>
<td>D</td>
<td>D</td>
<td>A</td>
</tr>
<tr>
<td>African</td>
<td>D</td>
<td>A</td>
<td>D</td>
</tr>
<tr>
<td>Neanderthal</td>
<td>A</td>
<td>D</td>
<td>D</td>
</tr>
<tr>
<td>Chimpanzee</td>
<td>A</td>
<td>A</td>
<td>A</td>
</tr>
<tr>
<td># sites</td>
<td>303,340</td>
<td>103,612</td>
<td>95,347</td>
</tr>
</tbody>
</table>

Common pattern (1) reflects history of population splits.
Absent admixture, the other two should be equally common
Excess of pattern 2 reflects admixture.

Eurasians share some derived alleles with archaics

- Neanderthal 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 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 Melanasians are part Denisovan.