

Modern Human Origins

Hugo Reyes-Centeno, Yonatan Sahle, Christian Bentz



Last week:

- ❑ **Hominin taxonomy**
How do we classify human fossils?
- ❑ **Modern human fossils**
When and where do we find anatomically modern fossils?
- ❑ **Populations and demes**
Are population models better than species models?



For today:

- ❑ **Genomics of modern human origins**
What does (ancient) DNA tell us about the origins and evolution of modern humans?
- ❑ **Models of anthropogeny**
What model of modern human origins is best supported with the current fossil and genomic evidence?
- ❑ **Modern human dispersals**
When, how, and why did anatomically modern humans disperse out of Africa?



Species concepts and speciation

- ☐ **Biological species**
Reproductively isolated populations.
Interbreeding is possible by species
recognition and compatible
fertilization system.
- ☐ **Morphological species**
Phenetic clustering of organisms
based on anatomical traits
- ☐ **Genetic species**
Genetic clustering of organisms
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- ☐ **Phylogenetic species**
- ☐ **Evolutionary species**
Ancestral-descendant sequence of
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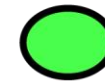
□ Phylogenetic species

□ Evolutionary species

Ancestral-descendant sequence of populations terminating by extinction

Allopatric

Original population



Initial step of speciation



Barrier formation

Evolution of reproductive isolation



In isolation

New distinct species after equilibration of new ranges

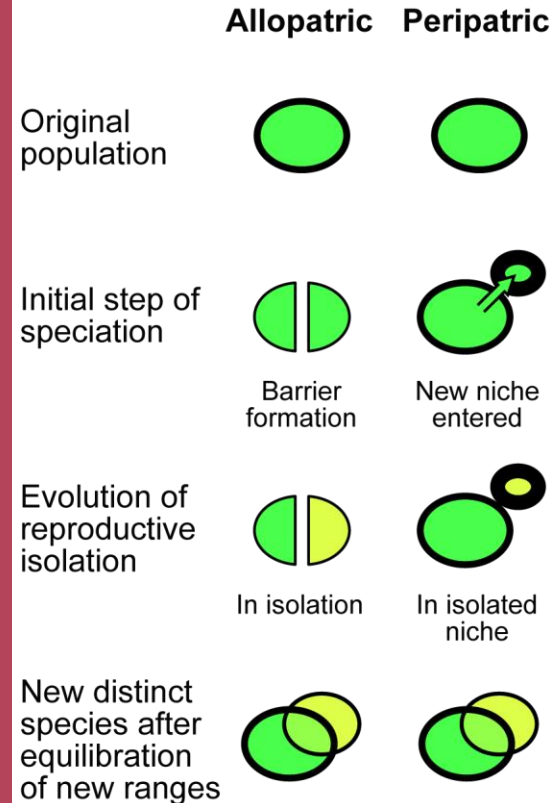


I. Karonen 2006



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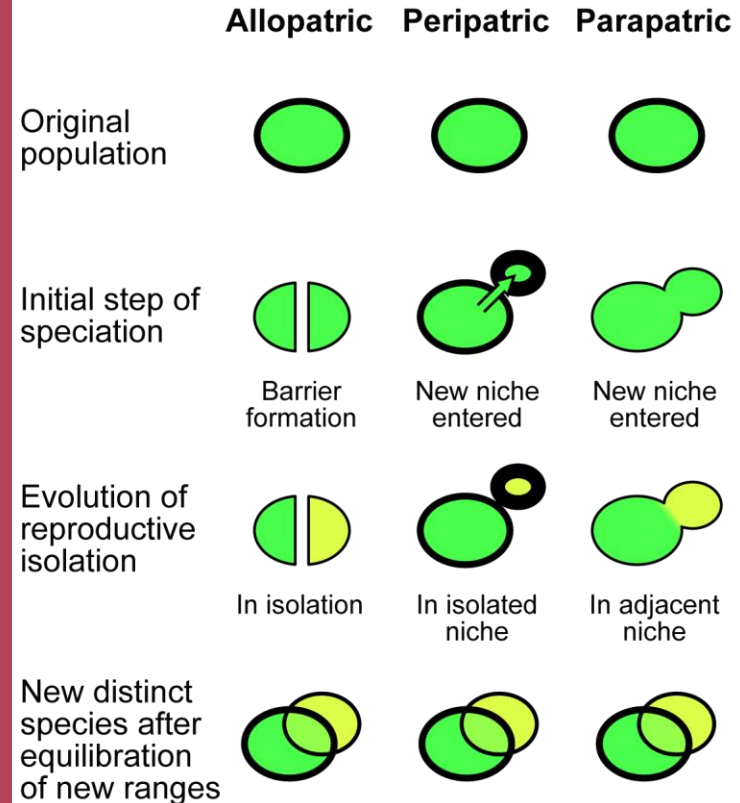
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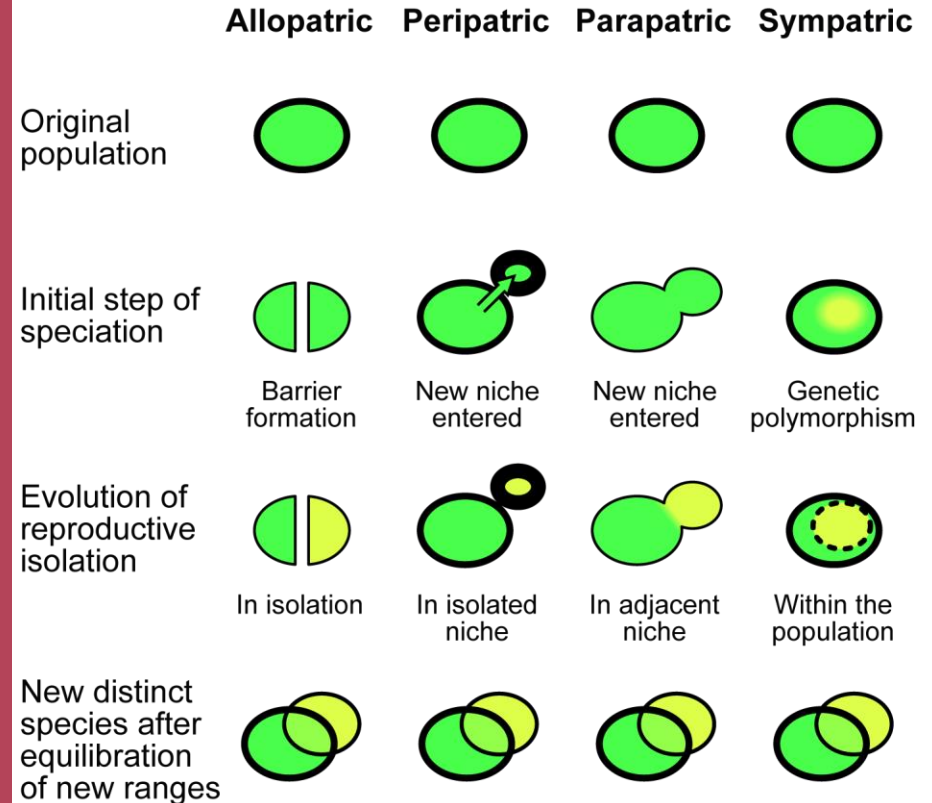


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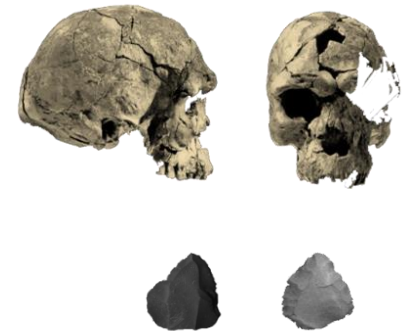


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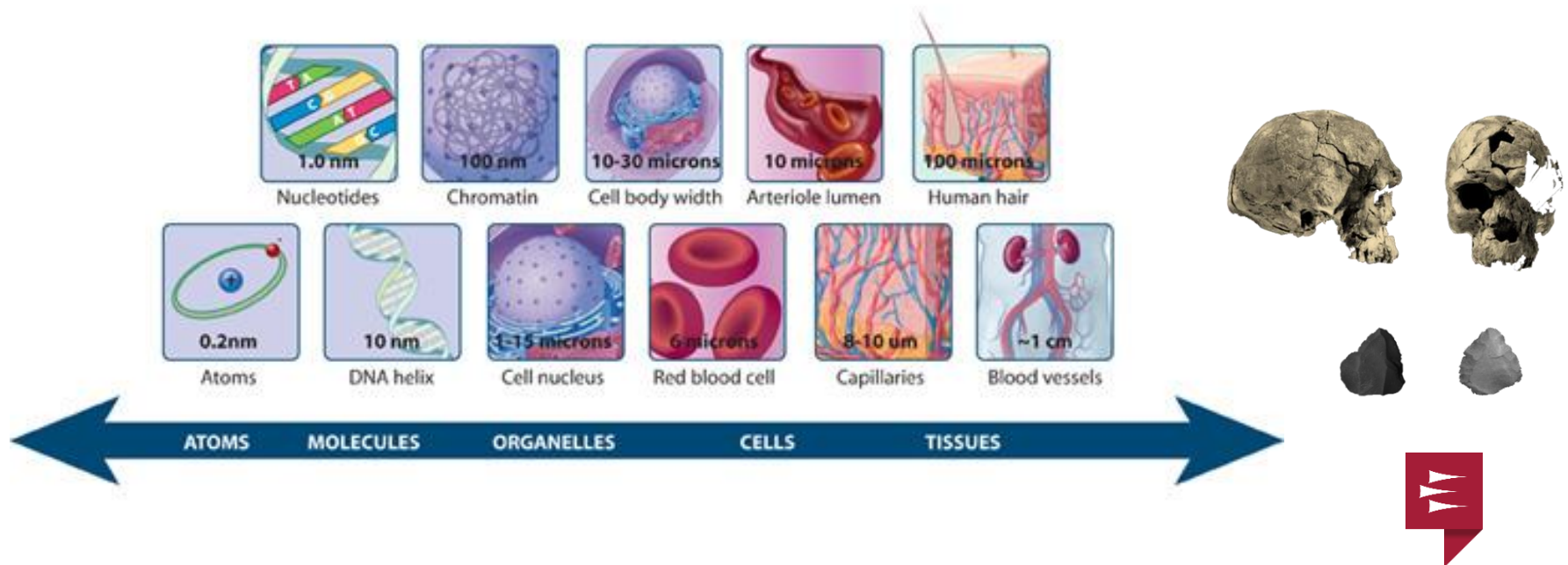


Modern human genomics

What does (ancient) DNA tell us about the origins and evolution of modern humans?



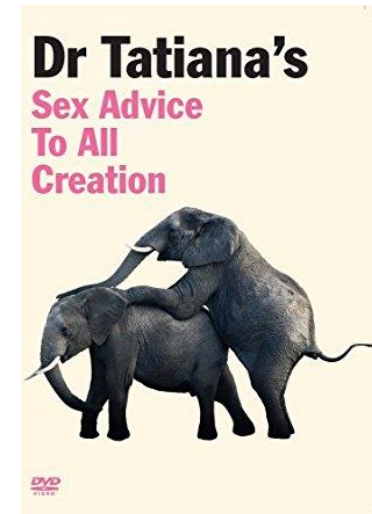
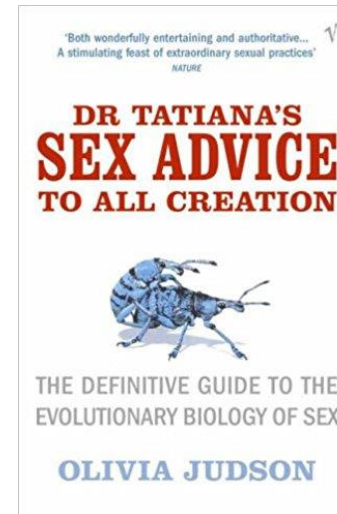
White *et al.* 2003; Beyin 2013



Nature Education 2010; White *et al.* 2003; Beyin 2013

Basics of inheritance

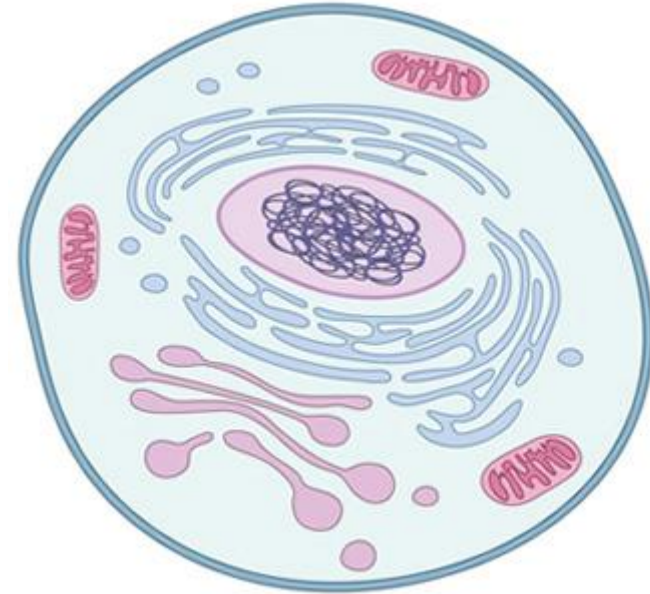
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Nature Education 2010

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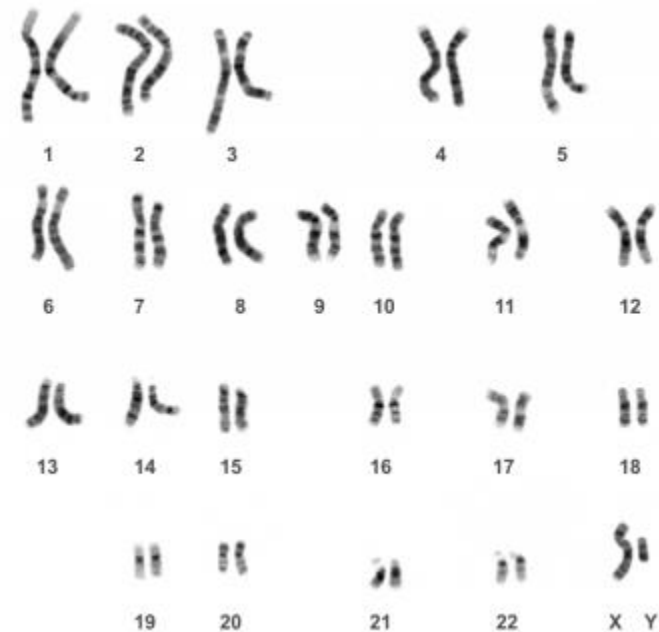
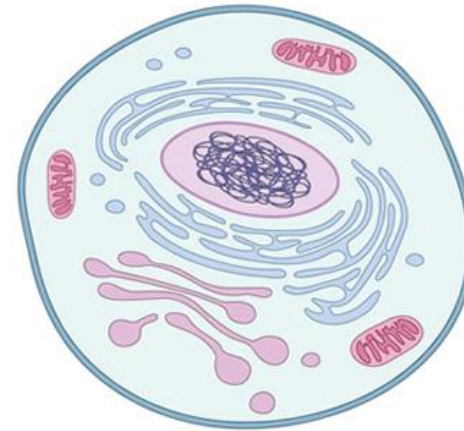
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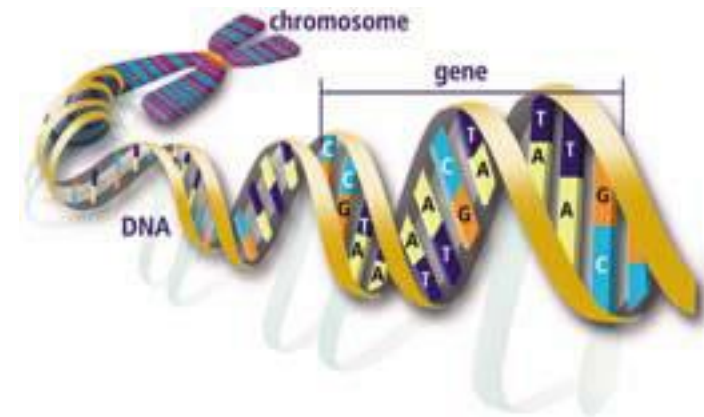
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Nature Education 2010; [23andMe](#)

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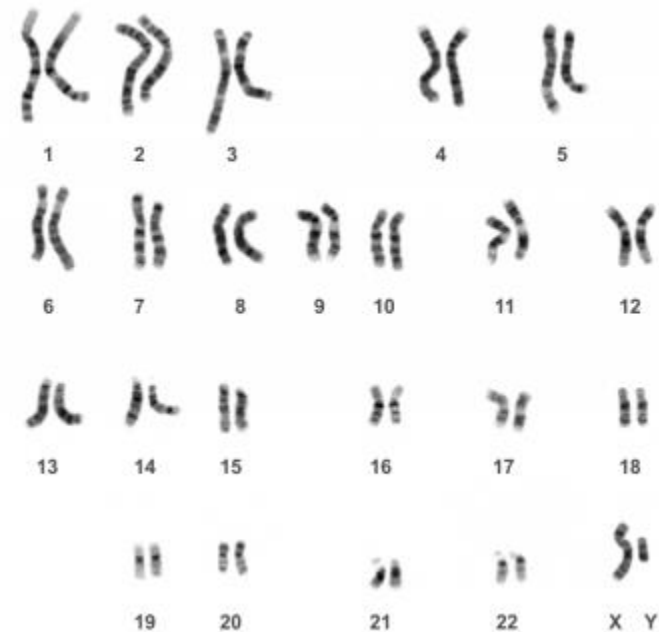
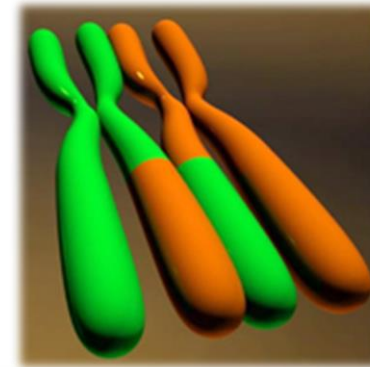
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US Department of Energy

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- ❑ **Recombination**
at the cellular level, genetic diversity
is produced by the process of
recombination



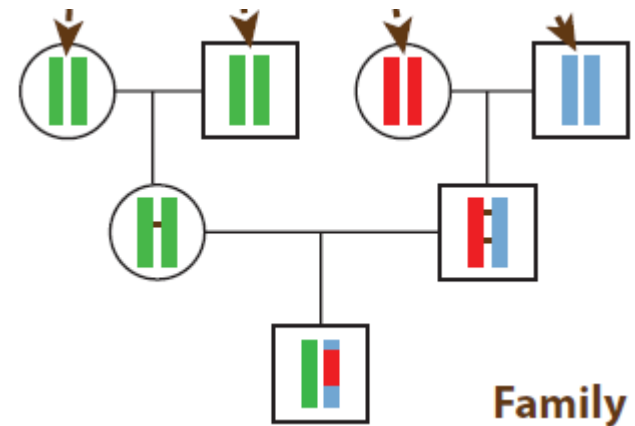
Nature Education 2010; 23andMe



Basics of inheritance

□ Genealogy

In theory, you can trace ancestry based on genetic inheritance, but recombination makes this difficult



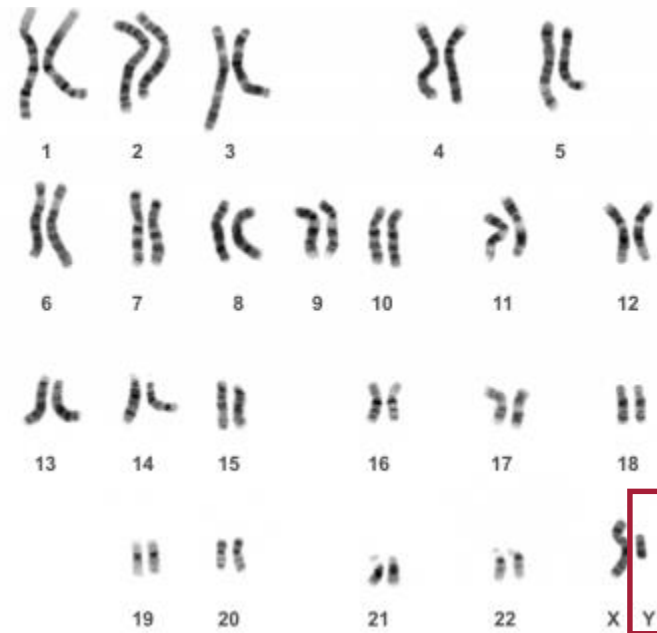
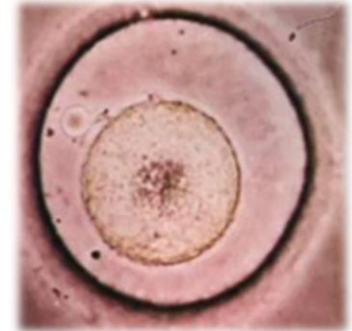
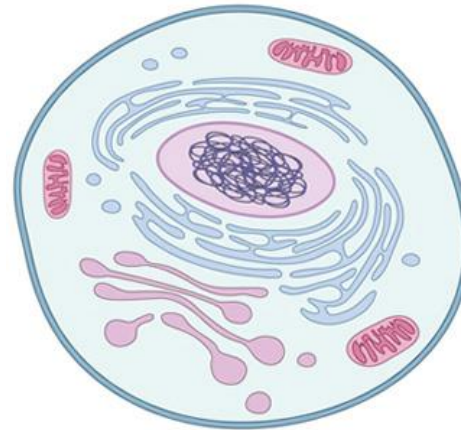
Novembre & Ramachandran 2011

Basics of inheritance

Two regions that do not recombine are:

- ❑ **mitochondria**
inherited maternally
- ❑ **Y-chromosome**
inherited paternally

*some regions do recombine, but not to the same degree as other chromosomes



Nature Education 2010; 23andMe

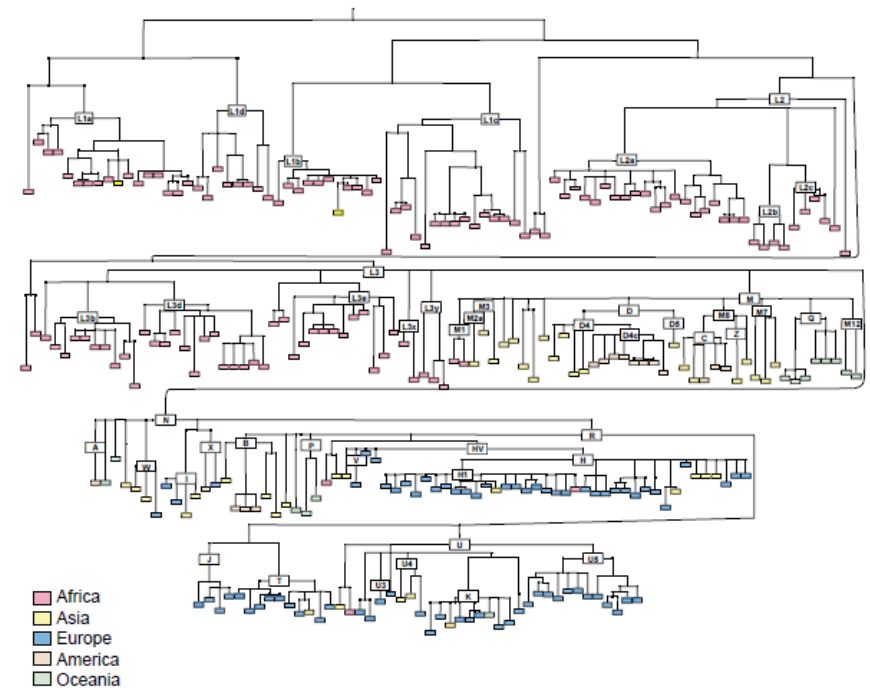


Phylogeography

Phylogeography: a method to analyze the geographical distribution of different clades within a phylogeny

- Optimal for uni-parental loci (mitochondrial DNA and Y-Chromosome DNA)

mtDNA



Cavalli-Sforza & Feldman 2003

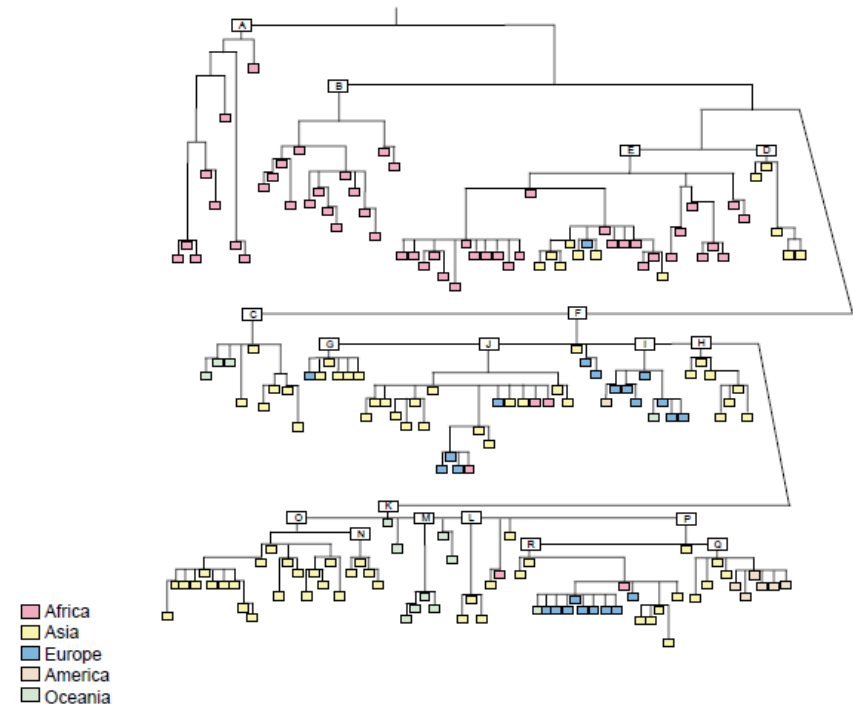


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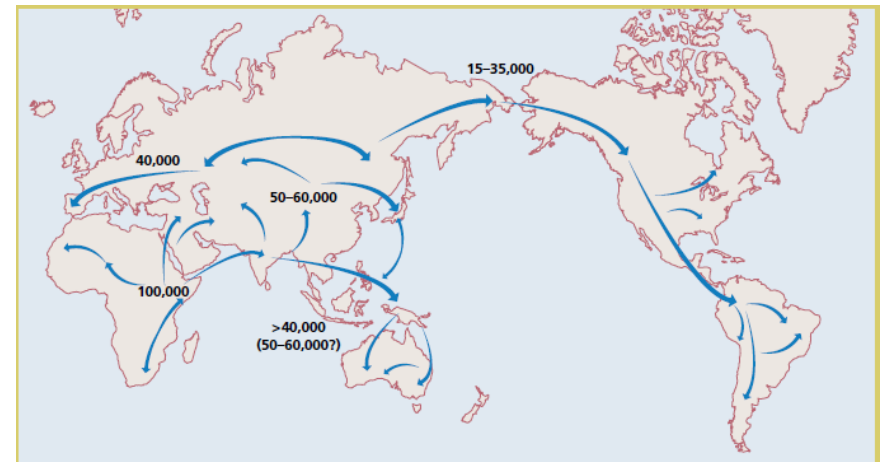
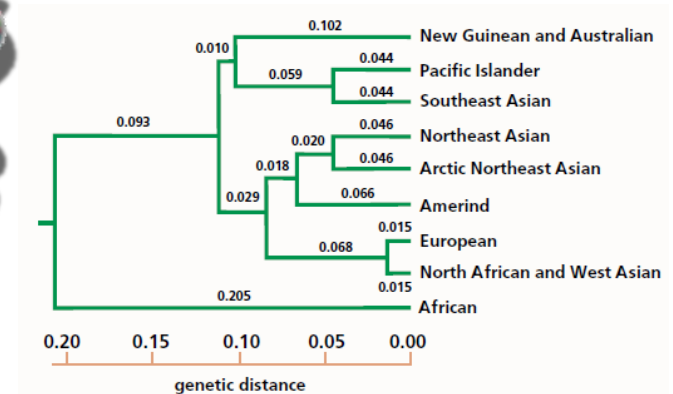


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- Geographical distribution and dating theoretically together allow inferences on key events in human evolution



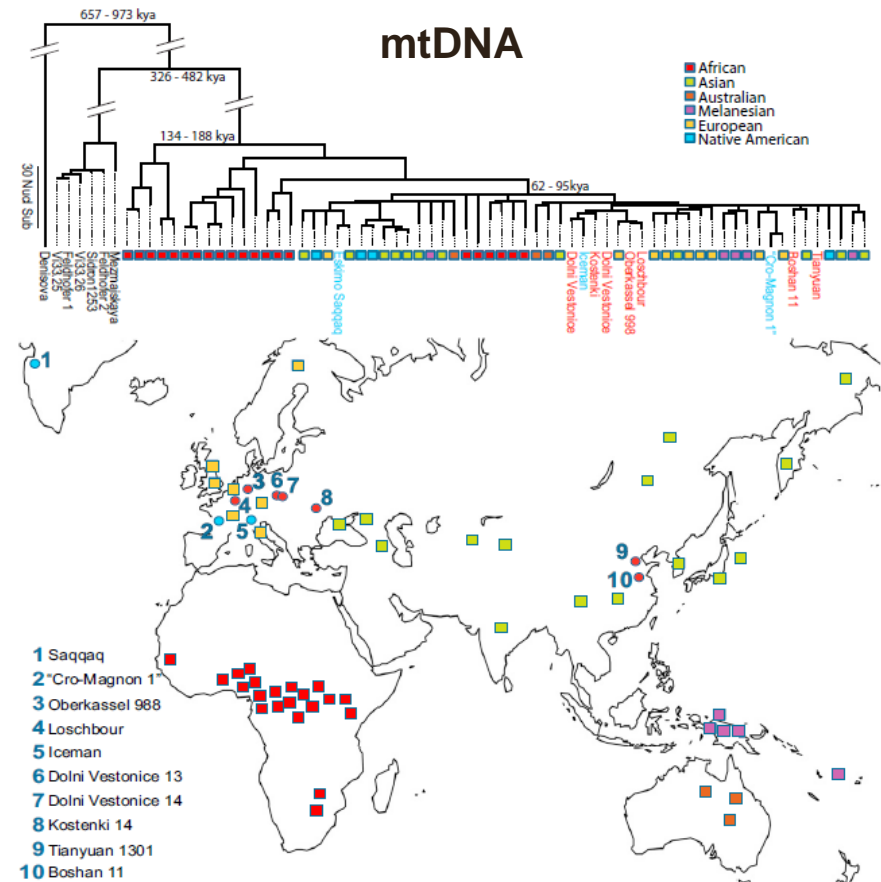
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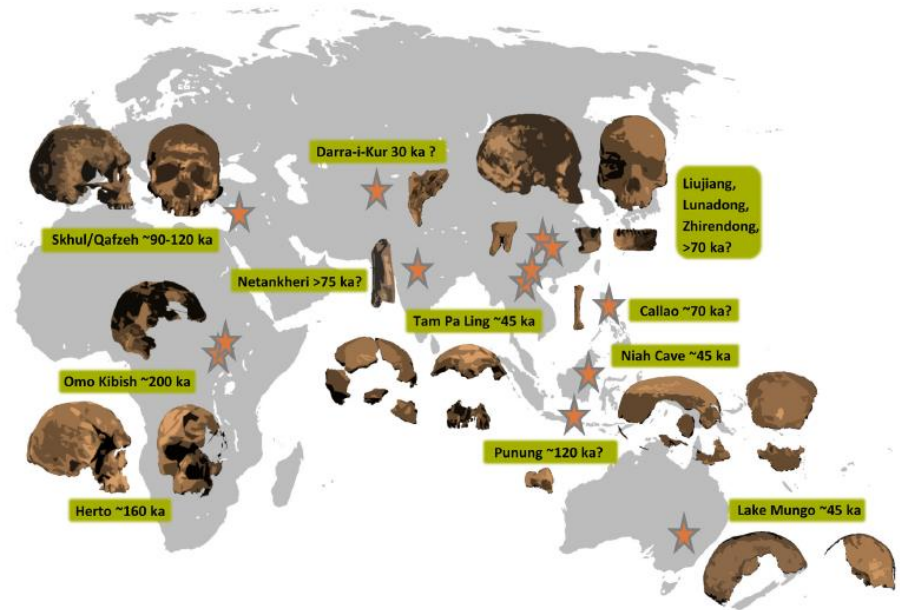
Fu et al 2013

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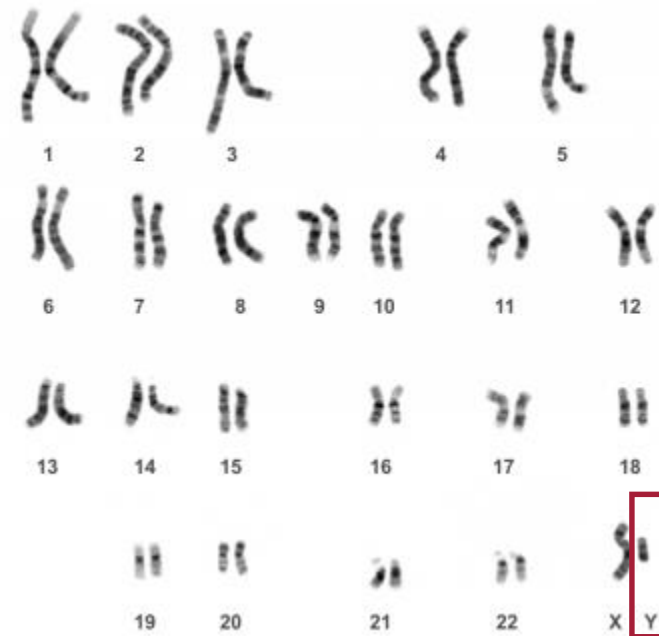
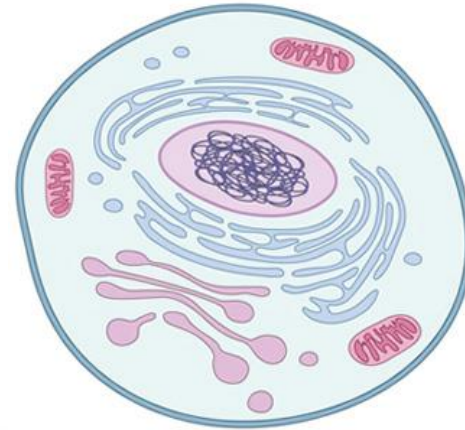
Fossils



Reyes-Centeno 2016

Limitations of uni-parental loci

- A tiny part of our total inheritance!
- The autosome (non-sex chromosomes) are excluded
- Y-chromosome changes depend to some extent on father's age during conception (mutations are higher with older age, which could inflate dates of divergence)



Nature Education 2010; 23andMe

Genome-wide approaches

❑ Microsatellites

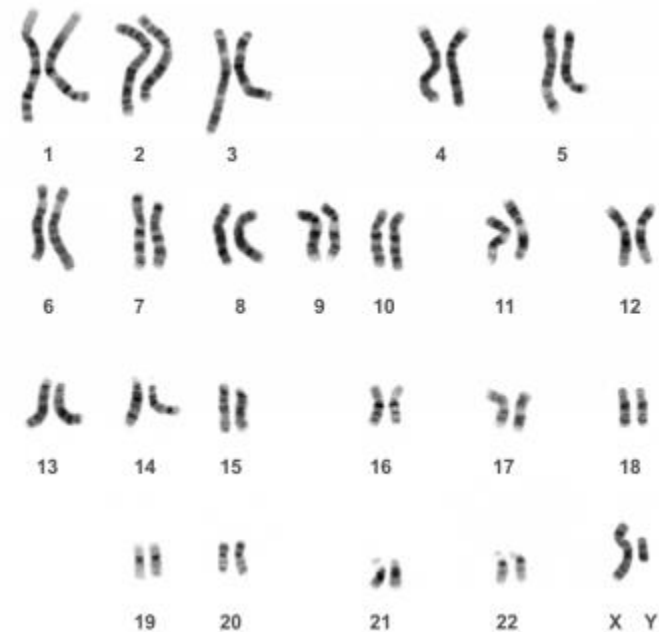
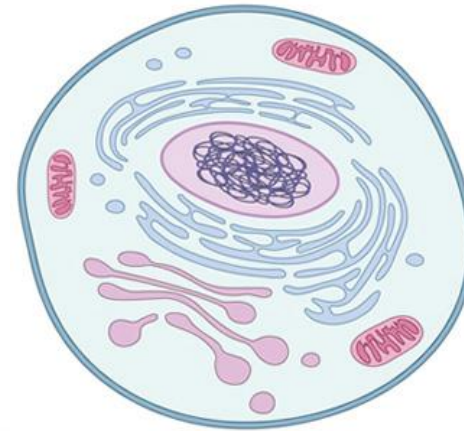
Non-functional regions of the genome, consisting of repeating 2-6 basepairs; also referred to as short-tandem repeats (STRs)

❑ Single-nucleotide polymorphisms (SNPs)

Base substitutions, deletions, or insertions at functional and non-functional regions

❑ Genomes

The entire genetic information of an organism's nucleus (both autosomal and sex chromosomes; both functional and non-functional)



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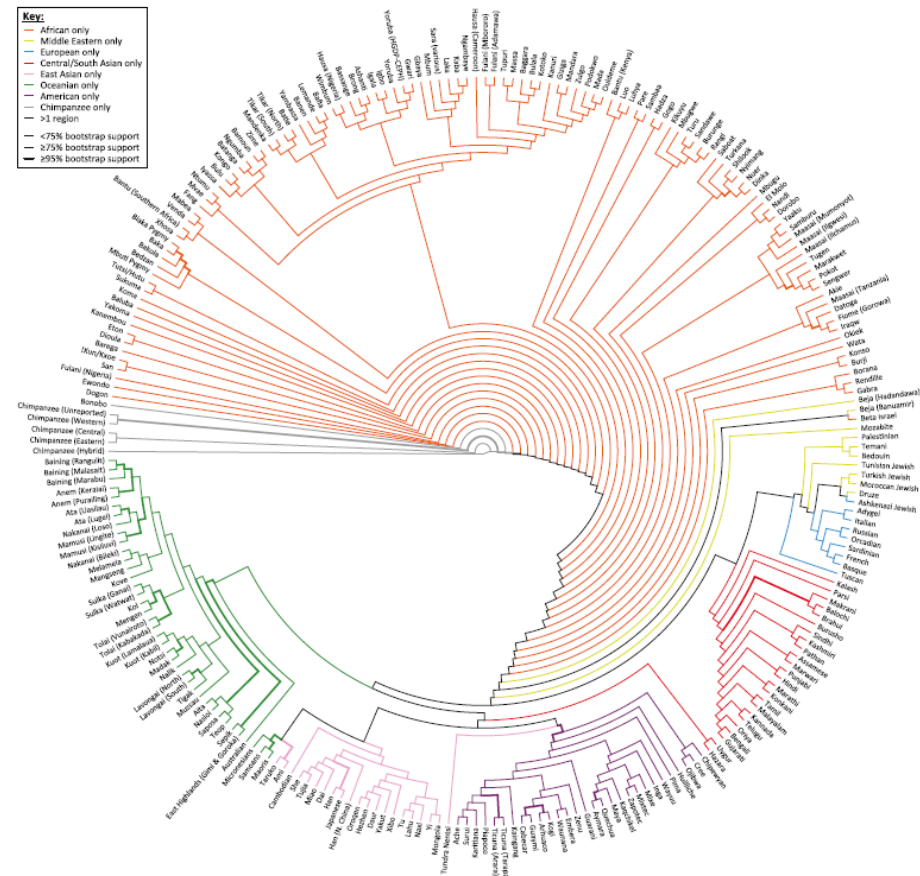
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Pemberton et al 2013

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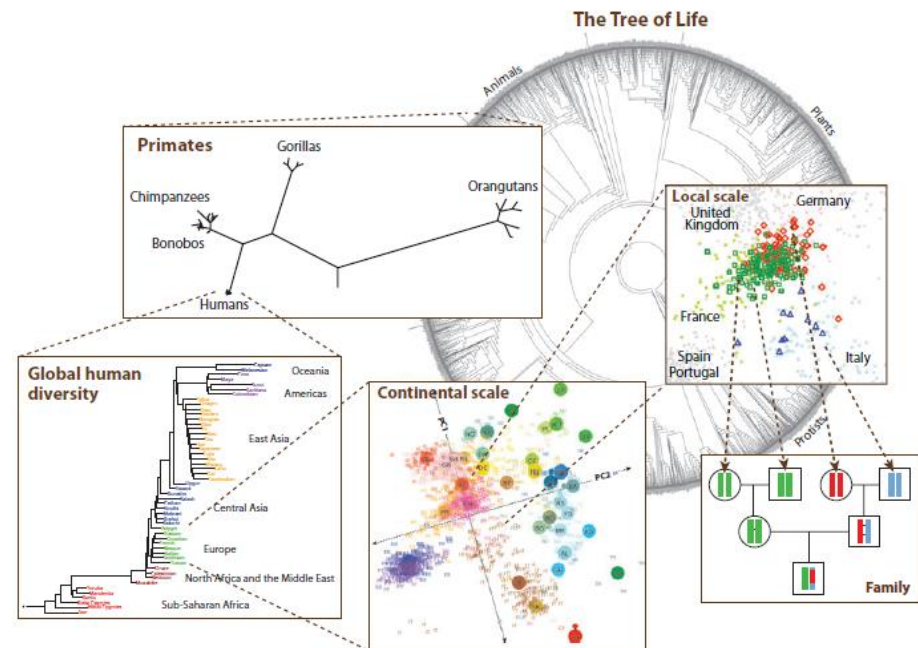
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Novembre & Ramachandran 2011

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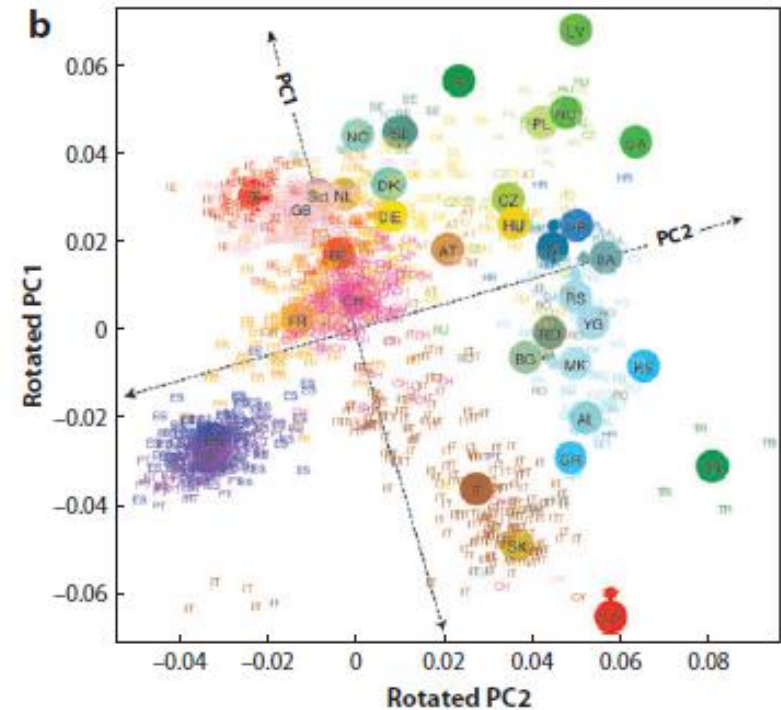
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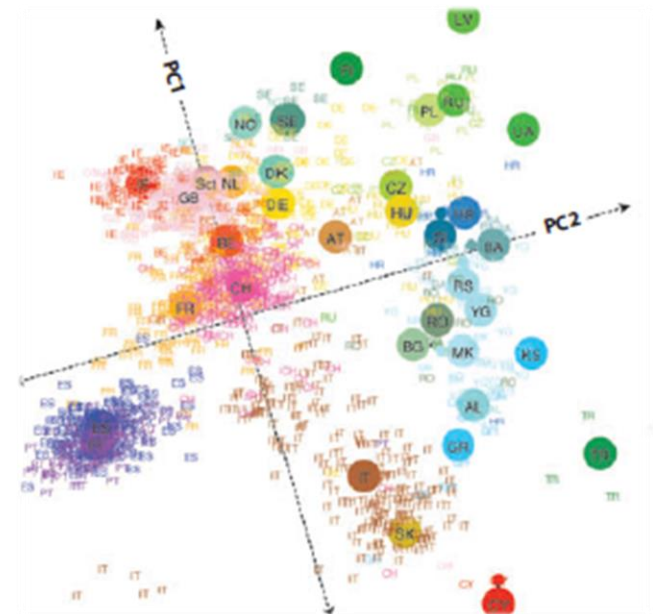
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November & Ramachandran 2011



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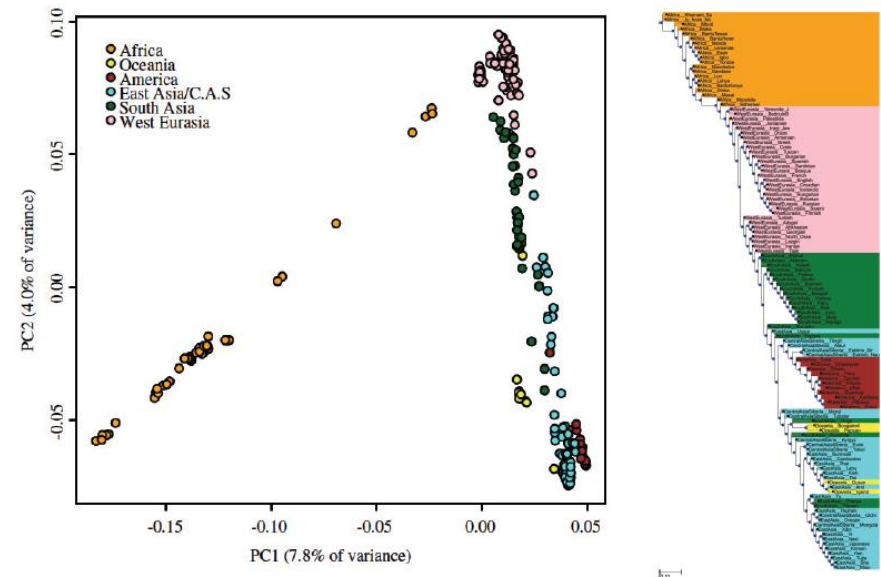
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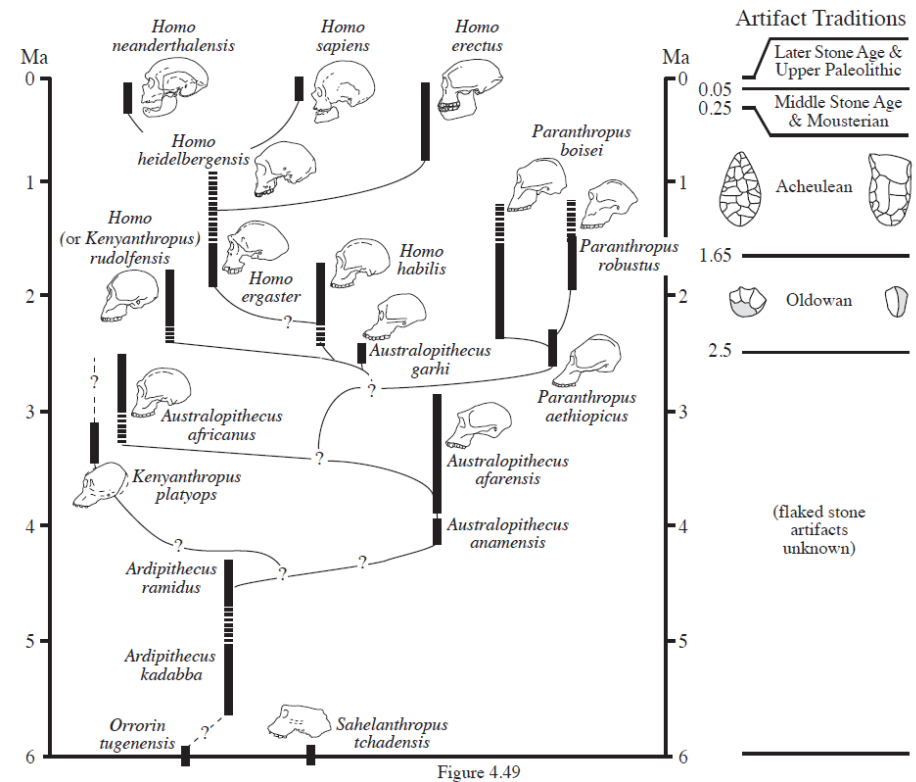


Mallick *et al.* 2017



Ancient genomes and fossils fill in the gaps...

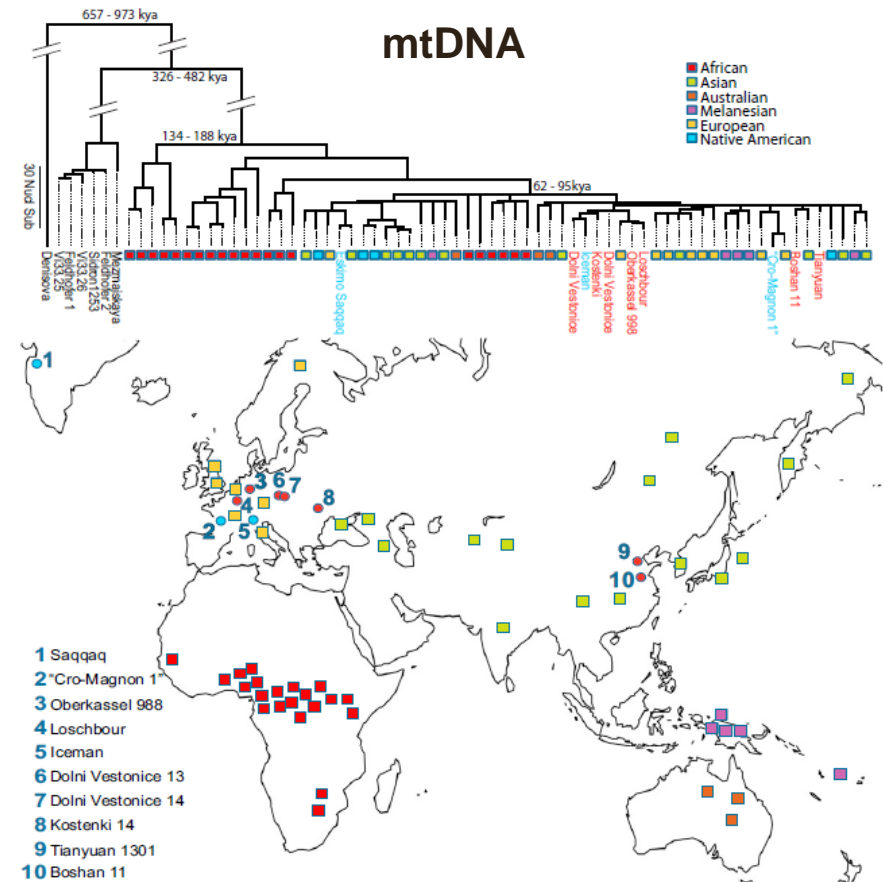
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Klein 2009

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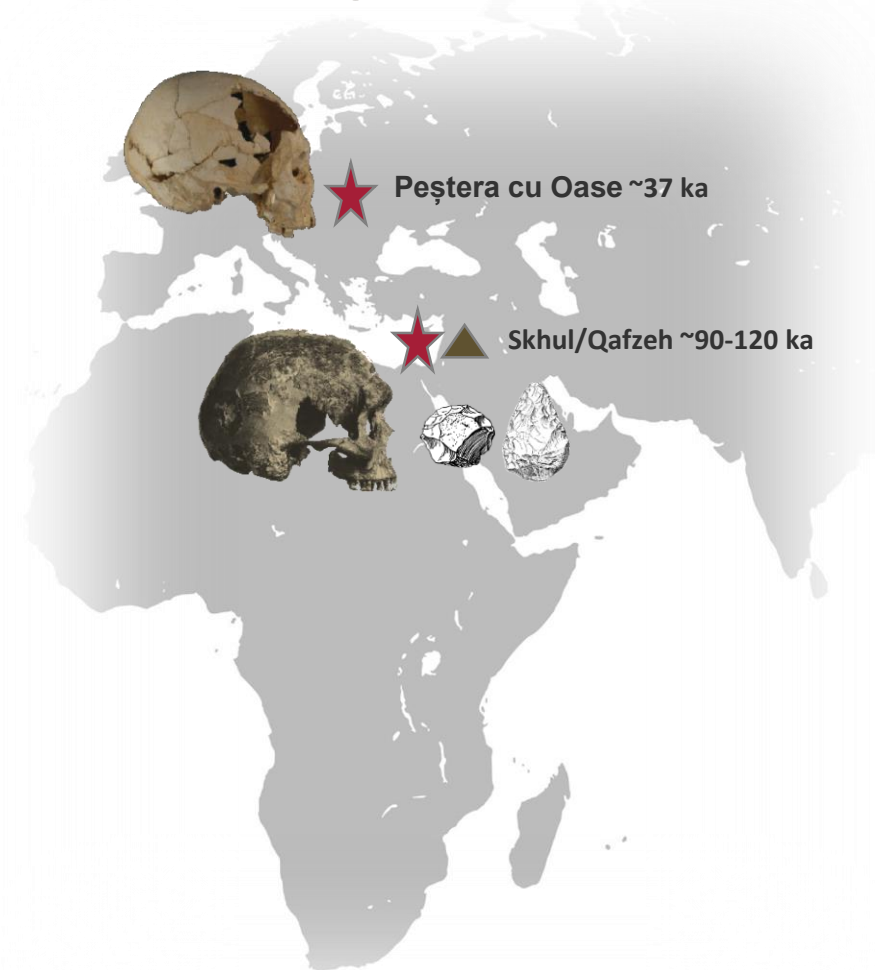


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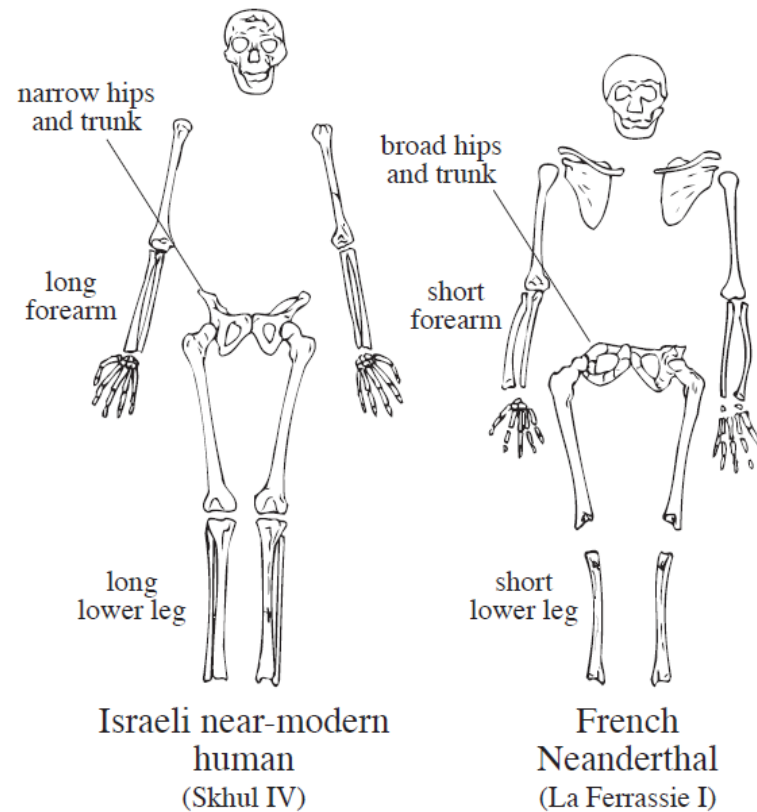
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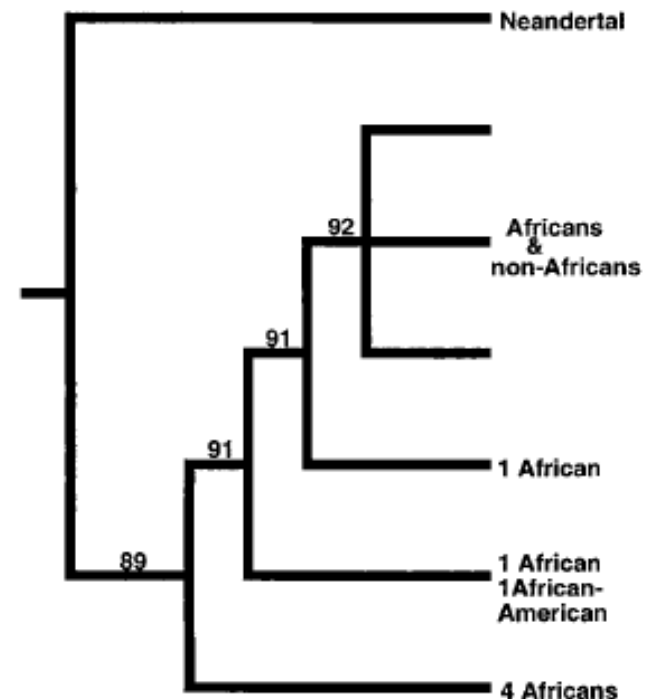
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Krings et al 1997



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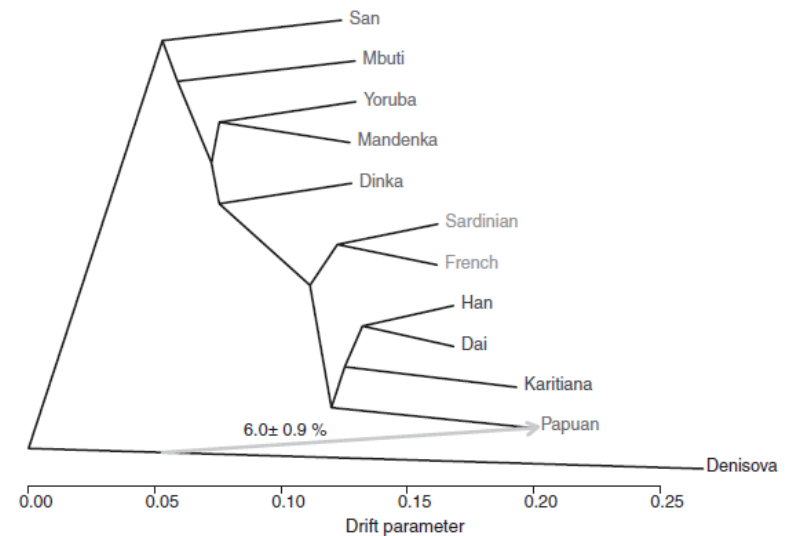
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...and break down the tree



Meyer *et al.* 2012

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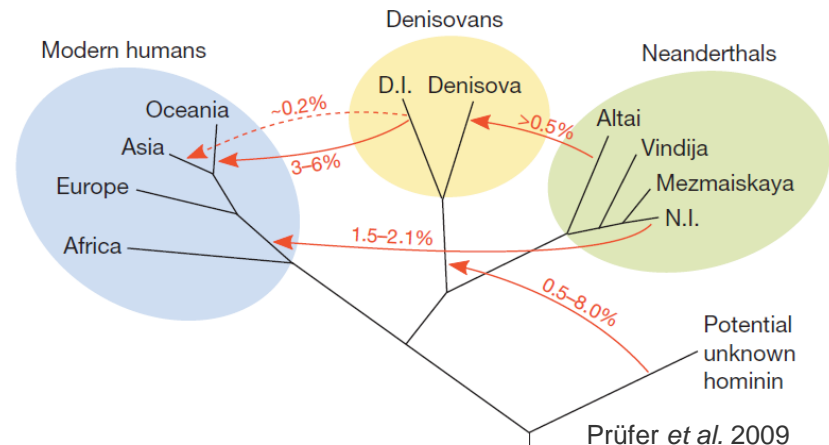
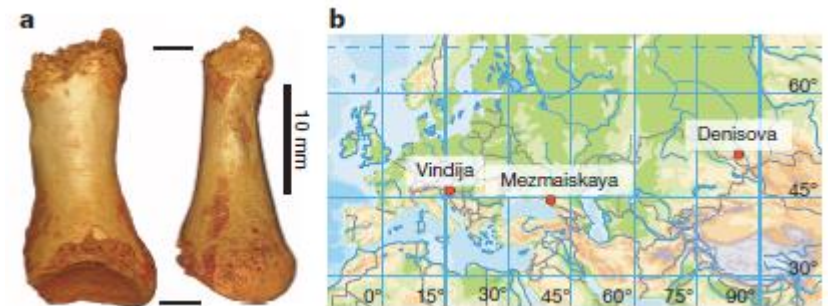
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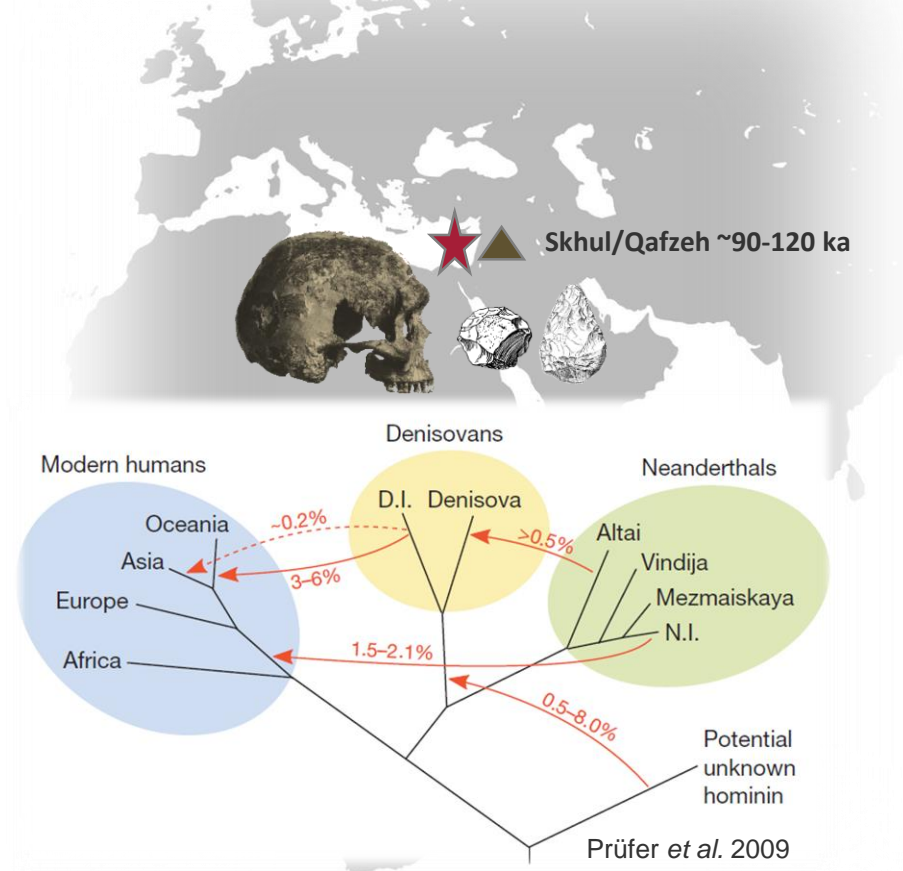
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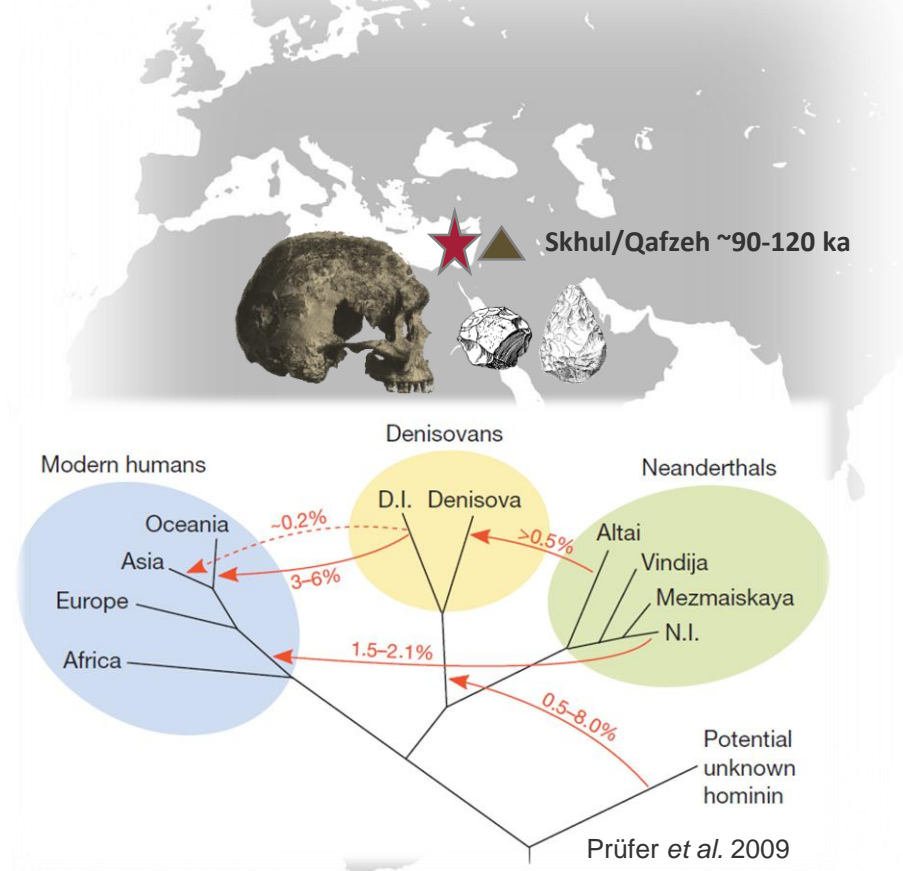
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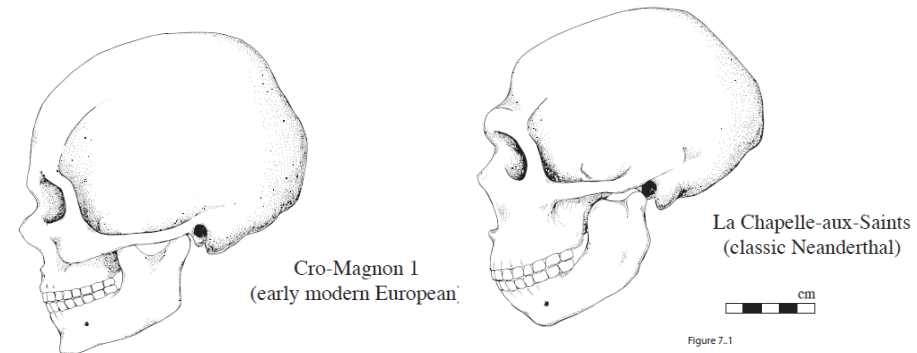
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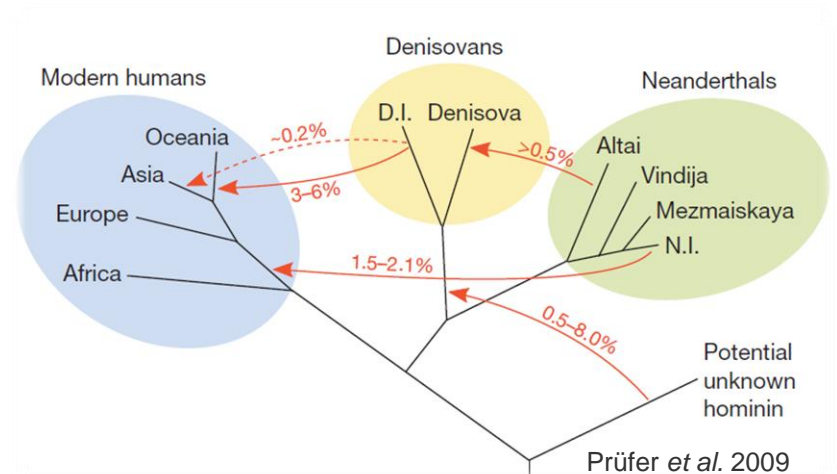


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Klein 2009





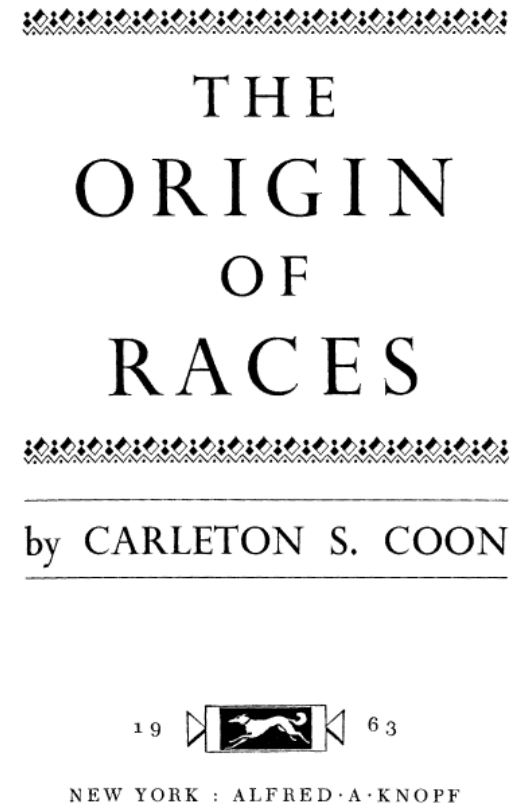
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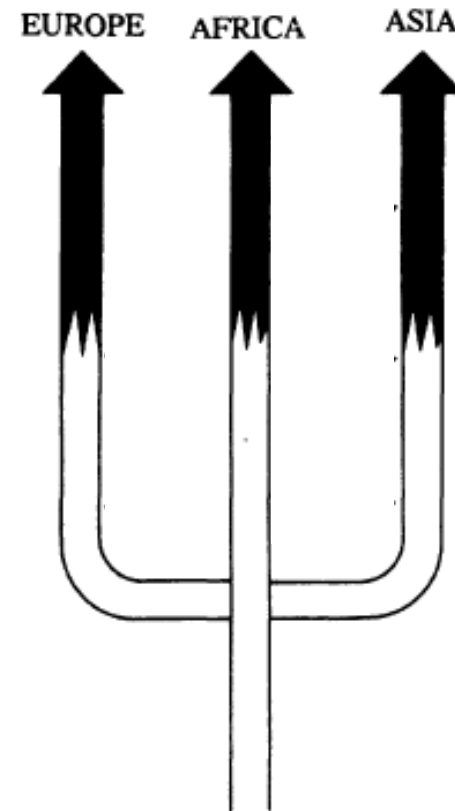
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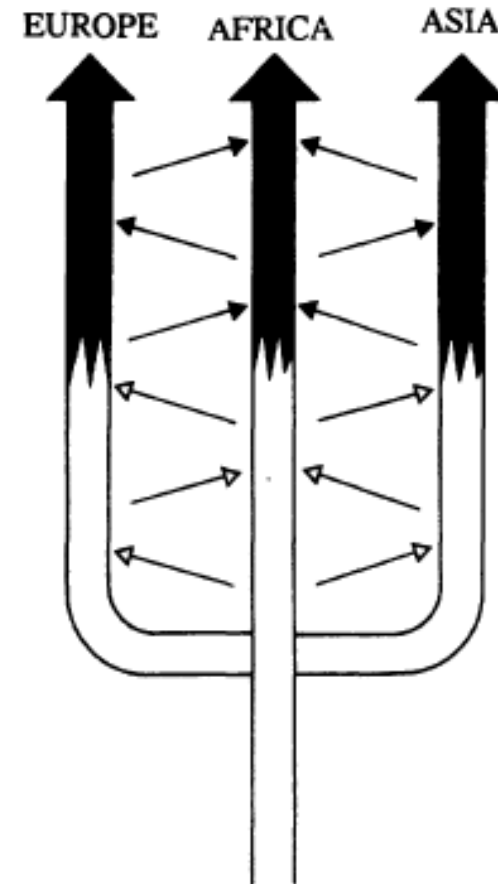


modified from Aiello 1993



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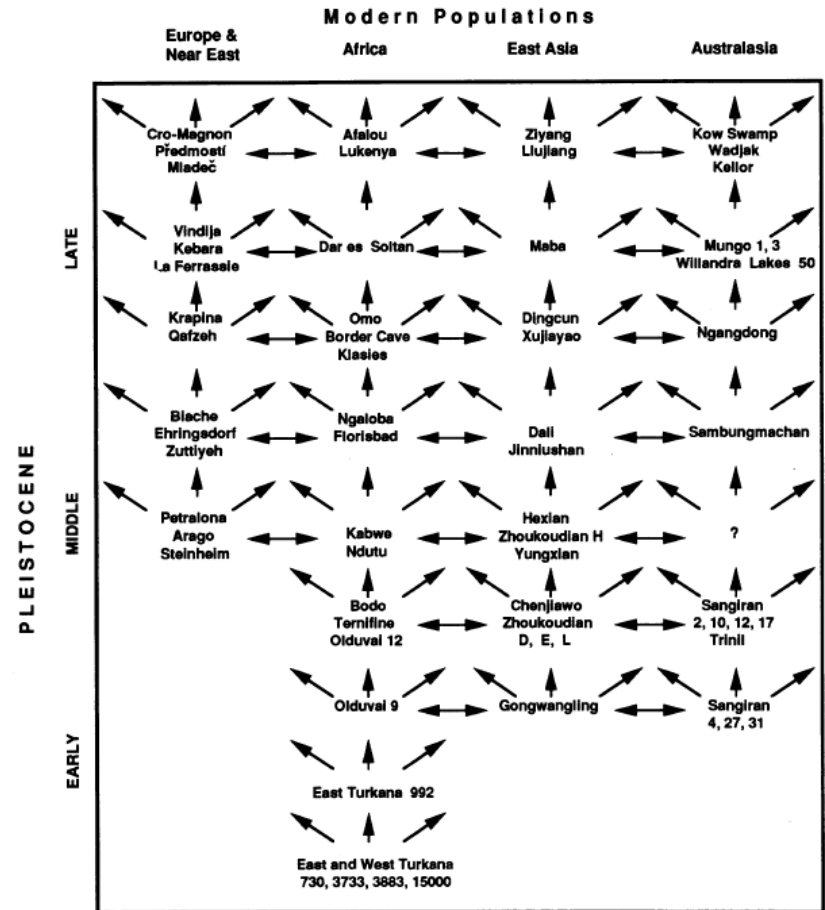


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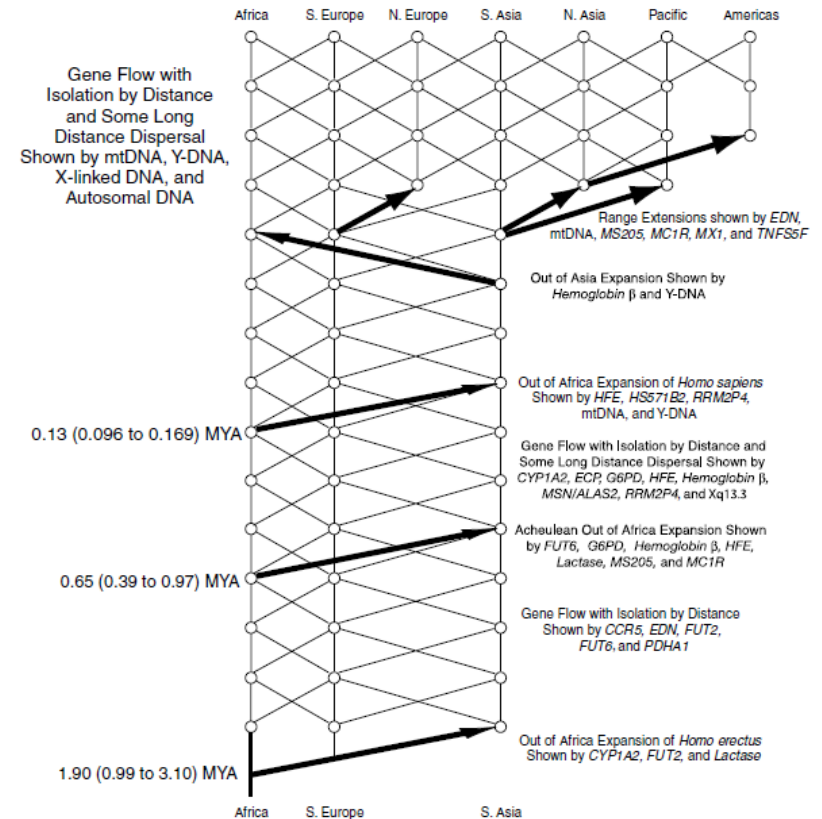


Frayer et al. 1993



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Multiple origins in different continents and convergent evolution
- ❑ **Multiregional Evolution**
Dynamic admixture within between populations across time and space

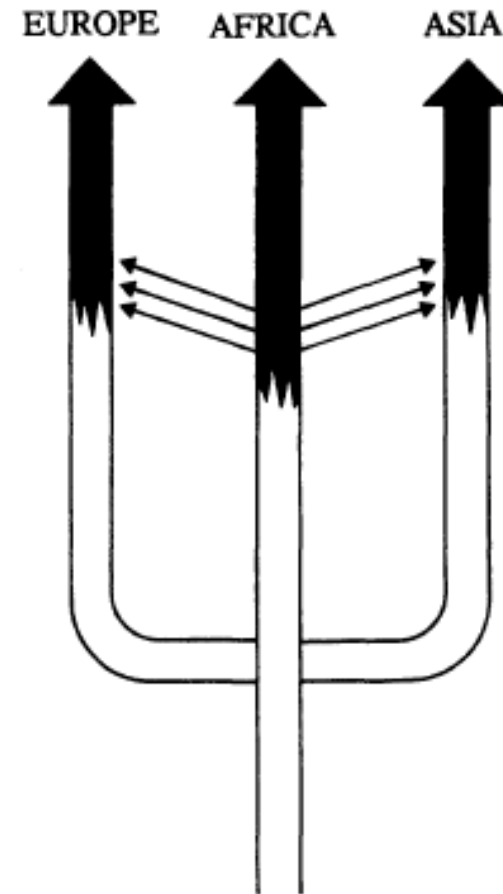


Templeton 2007



Hypotheses on modern human origins

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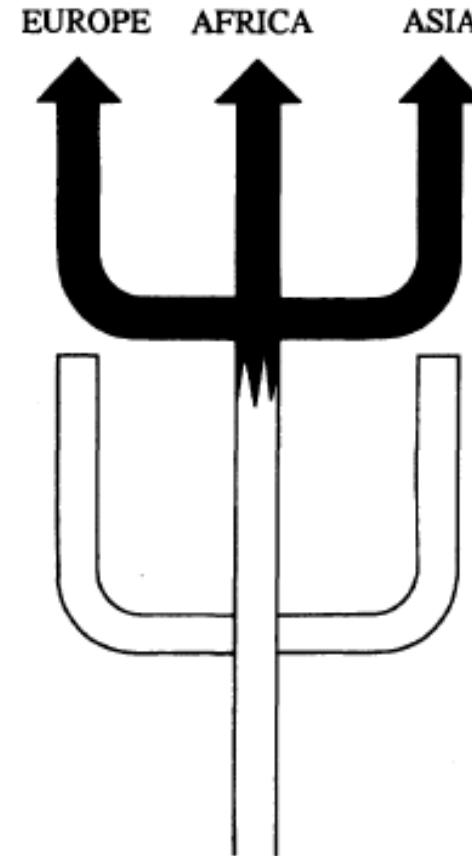


Aiello 1993



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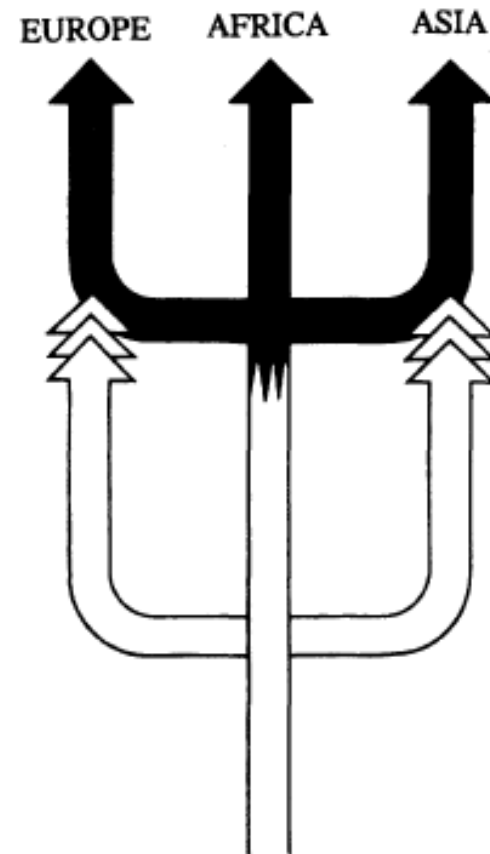


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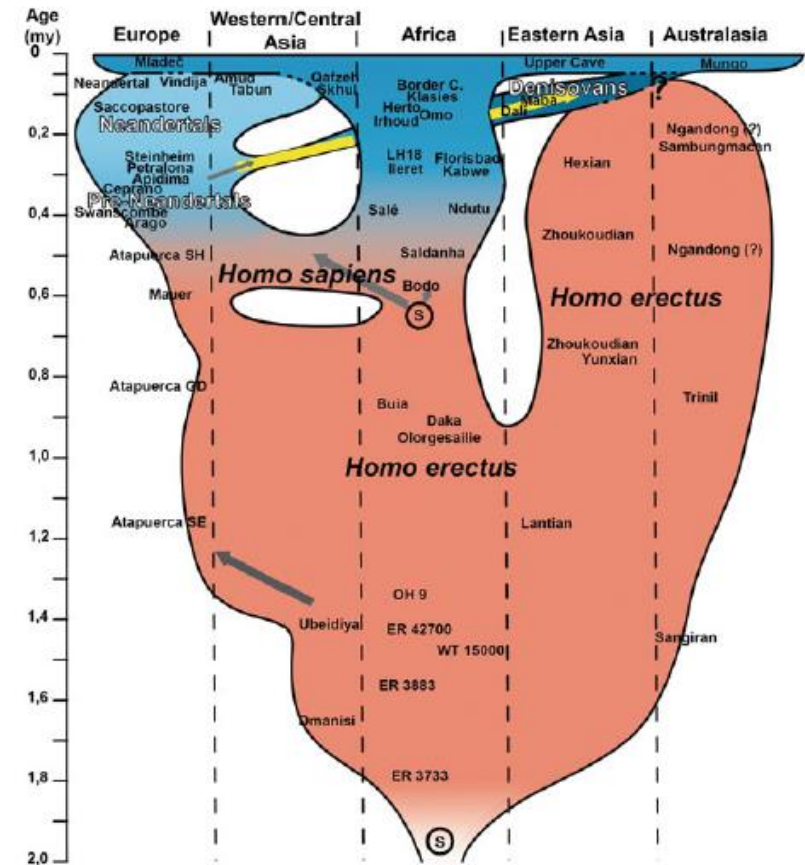
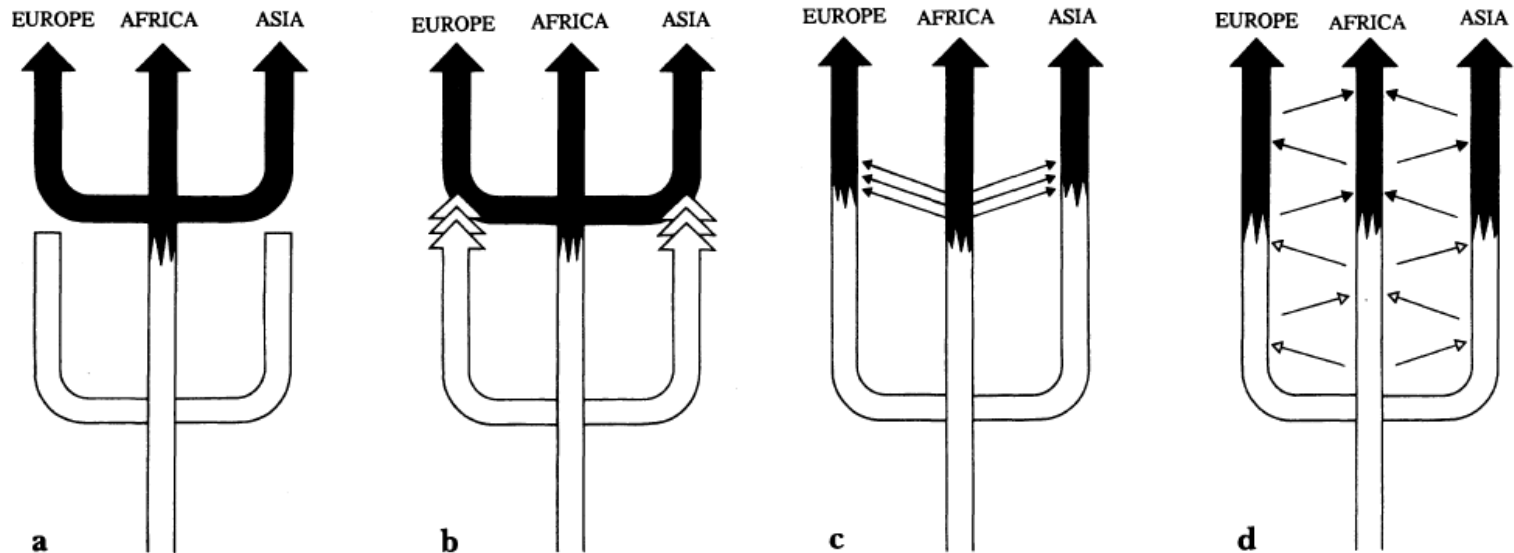


Fig. 7 Origin and evolution of *Homo sapiens*

Bräuer 2015



Hypotheses on modern human origins

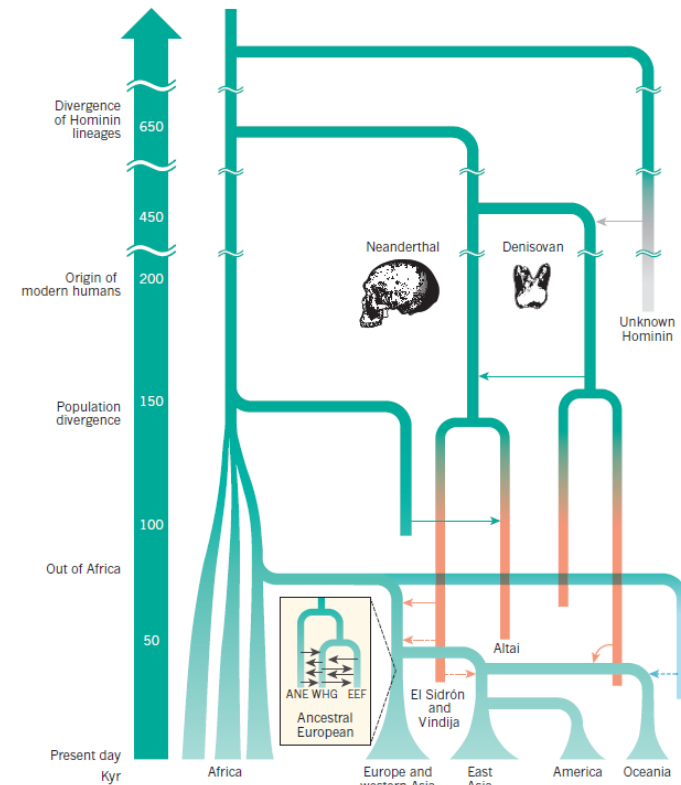


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Nielsen et al 2017



Hypotheses on modern human origins

□ Biological species

Reproductively isolated populations. Interbreeding is possible by species recognition and compatible fertilization system.

□ Morphological species

Phenetic clustering of organisms based on anatomical traits

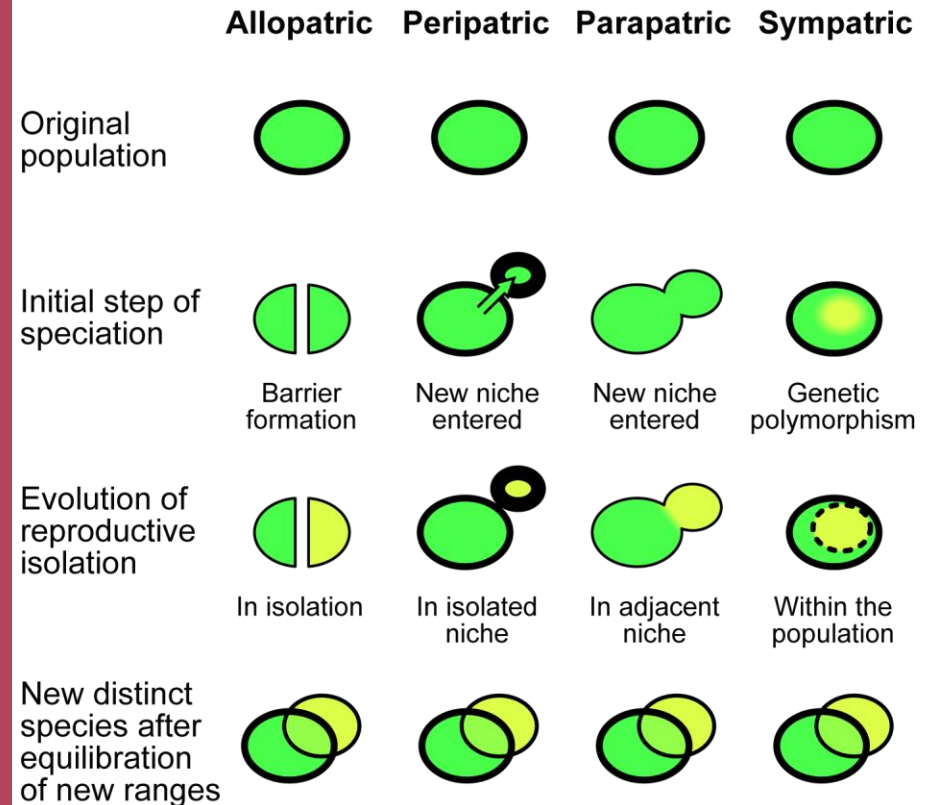
□ Genetic species

Genetic clustering of organisms based on genetic frequencies

□ Phylogenetic species

□ Evolutionary species

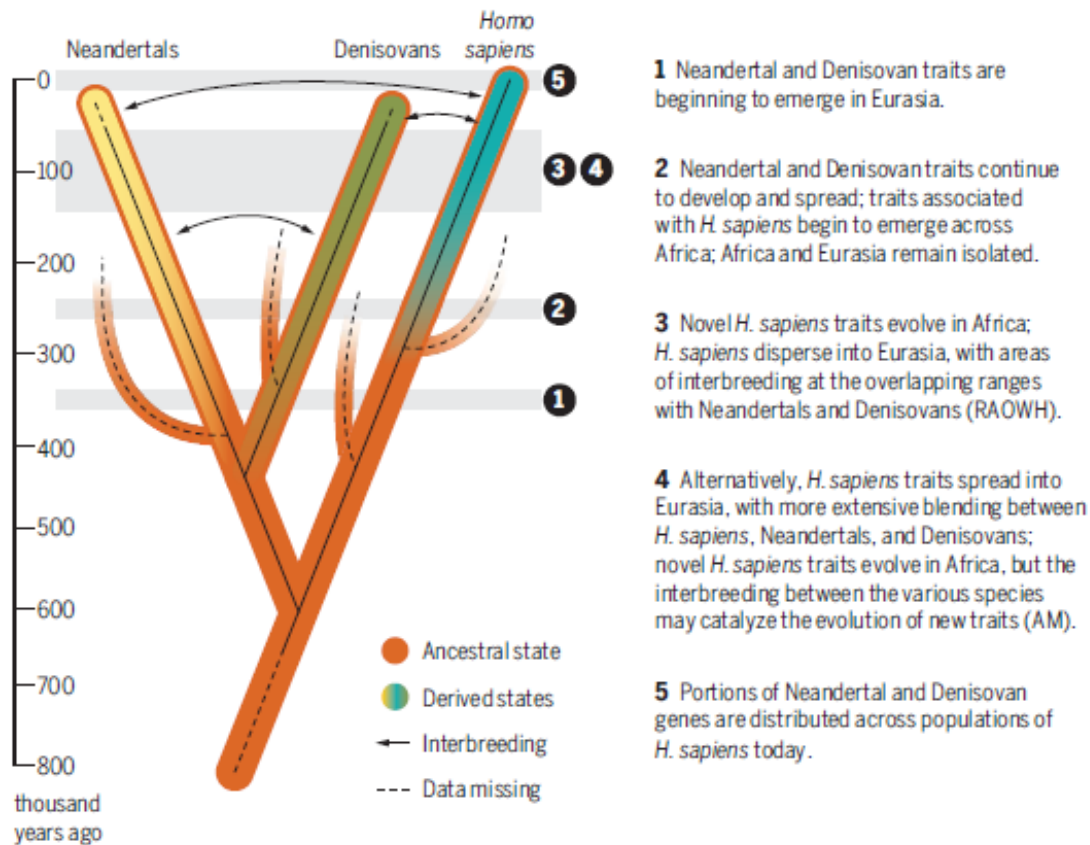
Ancestral-descendant sequence of populations terminating by extinction



I. Karonen 2006



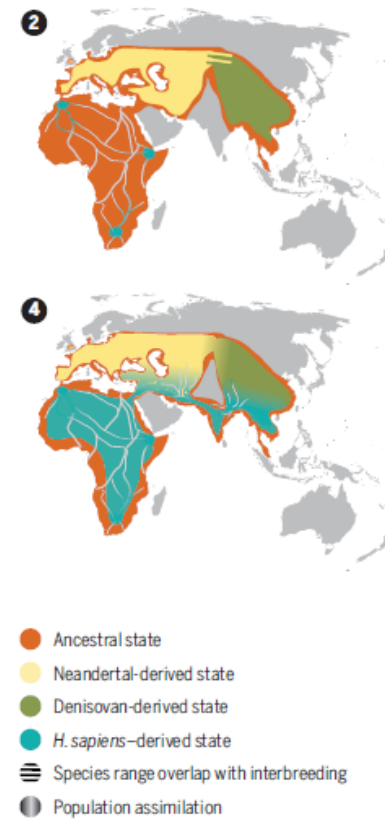
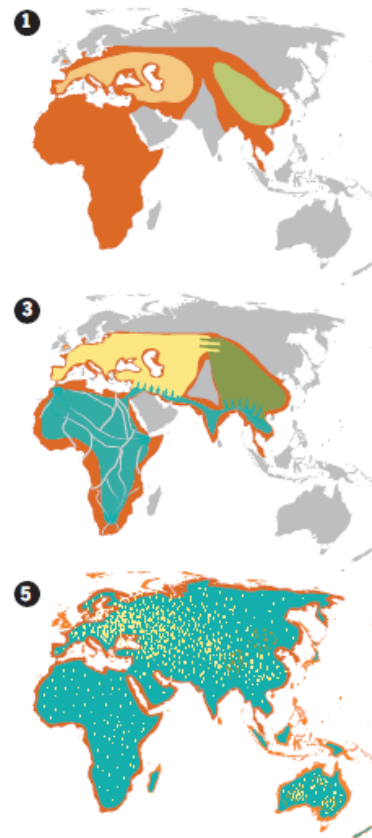
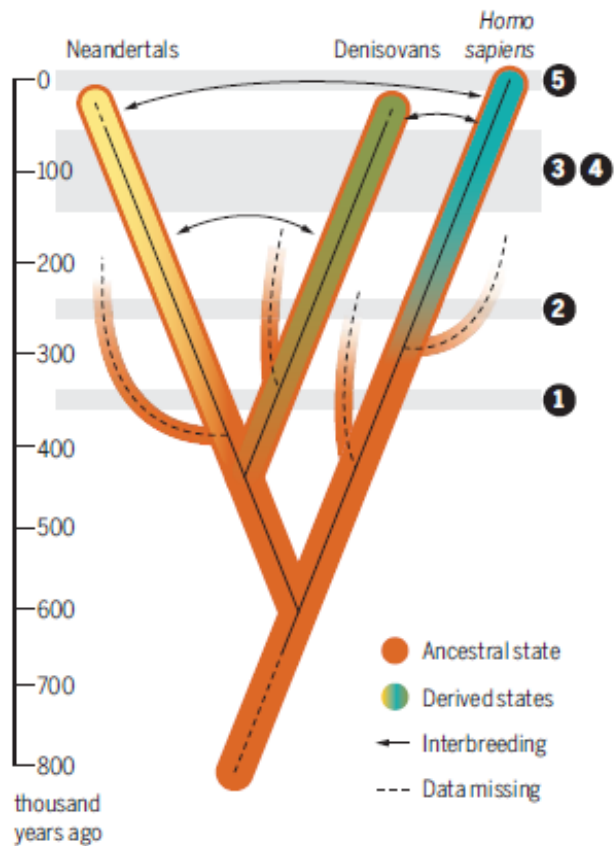
Hypotheses on modern human origins



Galway-Witham & Stringer 2018



Hypotheses on modern human origins



Galway-Witham & Stringer 2018



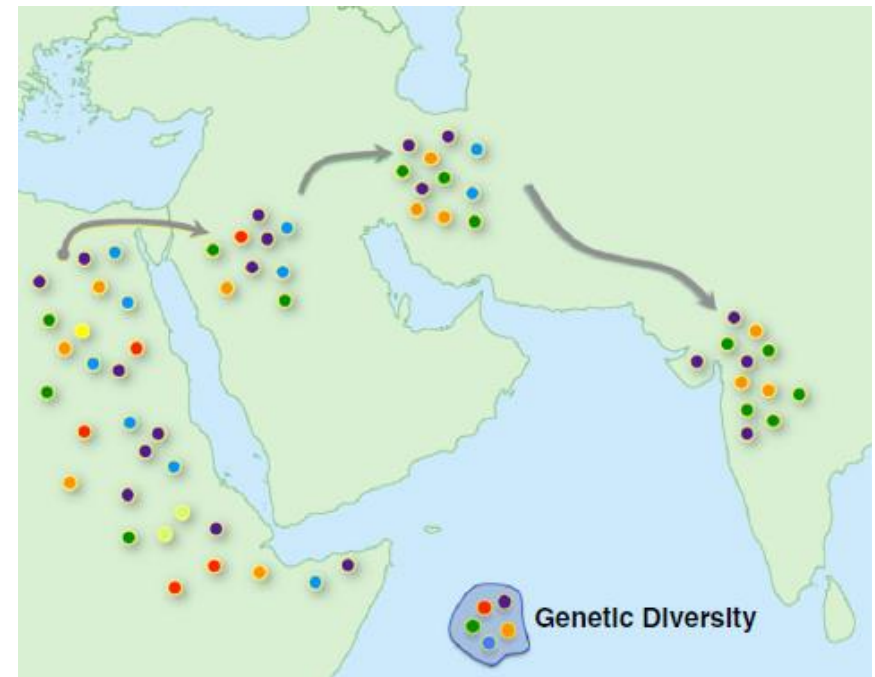
Modern human dispersals

When, how, and why did anatomically modern humans disperse out of Africa?



The serial founder effect model

- ❑ Cascading bottlenecks or serial founding events

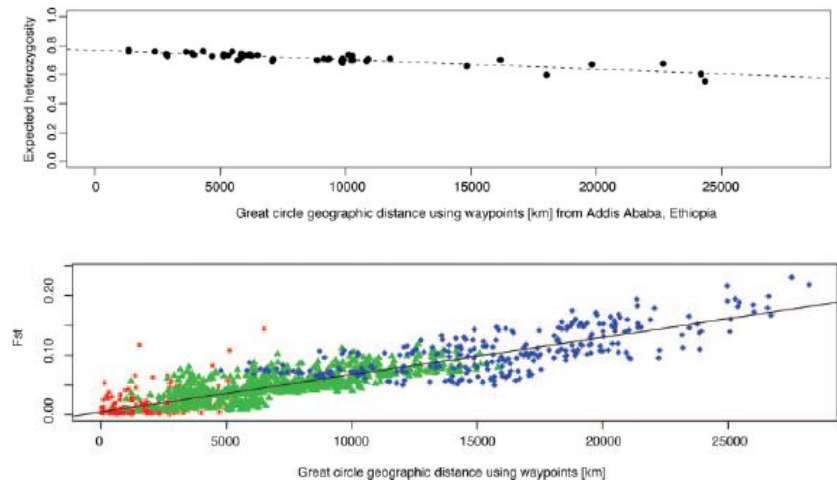


Henn et al. 2012



The serial founder effect model

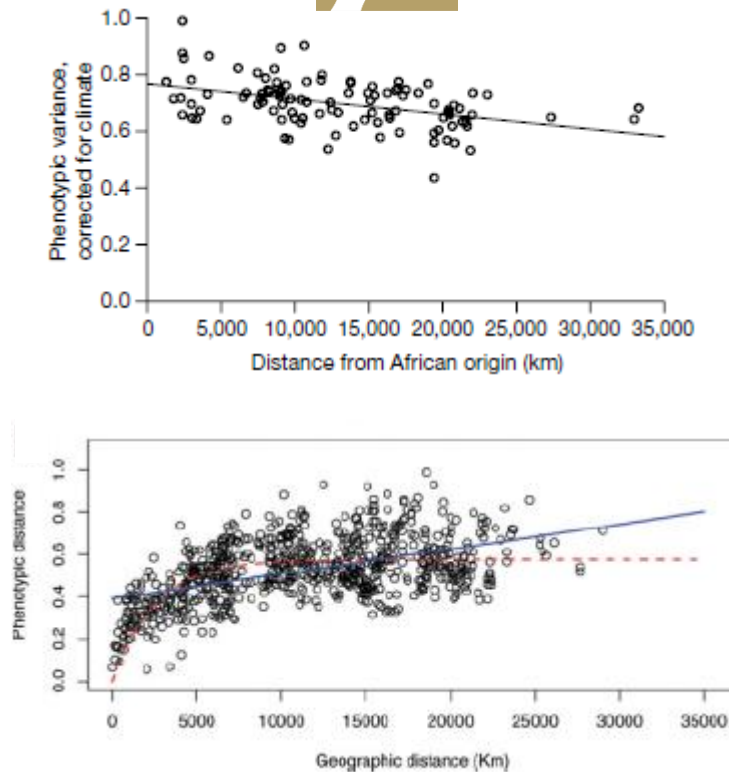
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 1. Decreasing intra-population diversity with geographical distance from Africa
 2. Increasing inter-population diversity between populations with geographical distance separating them



Ramachandran et al. 2005

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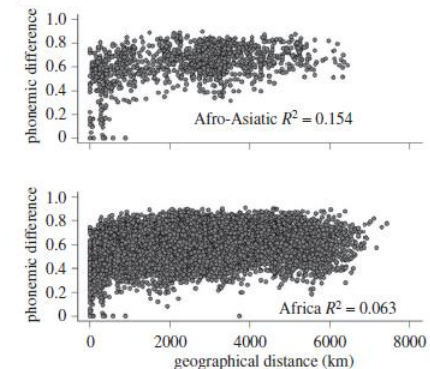
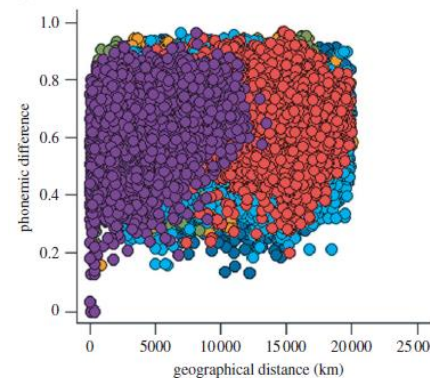
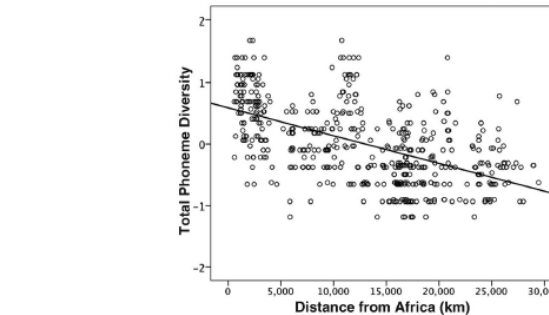


Manica et al. 2007; Betti et al. 2011



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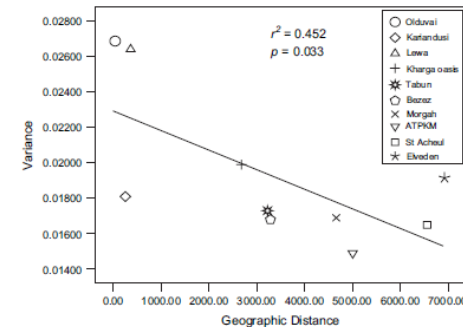
Atkinson 2011; Hunley et al. 2012



The serial founder effect model

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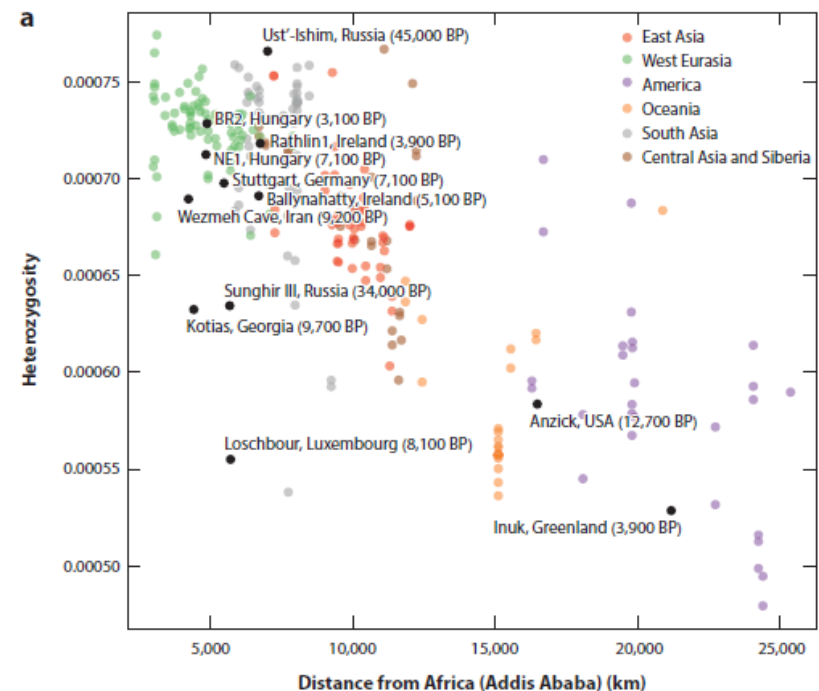


Lycett & von Cramon-Taubadel 2008



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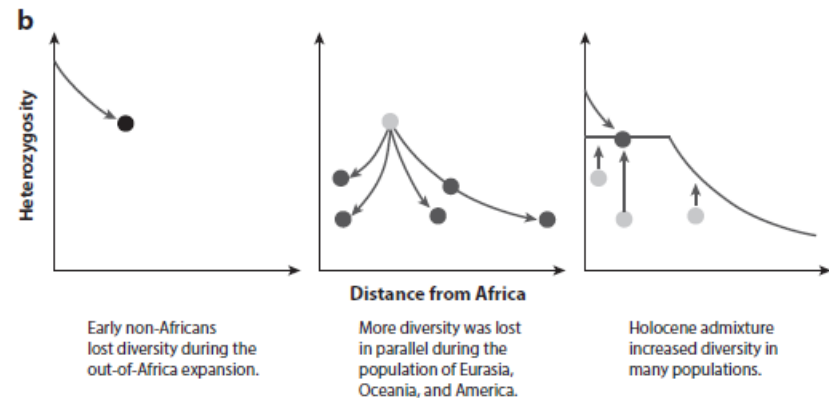


Skoglund & Mathieson 2018



The serial founder effect model

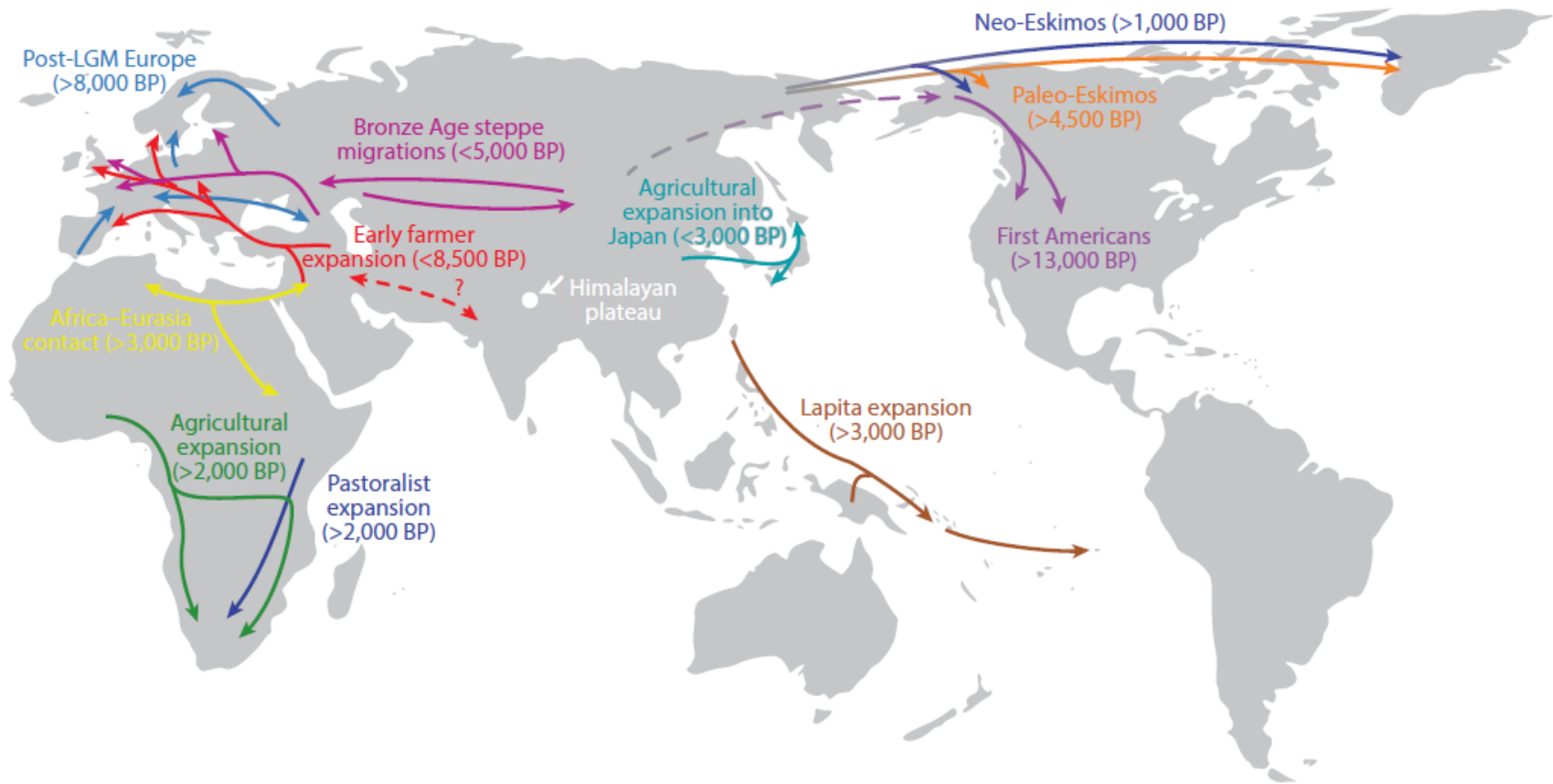
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Skoglund & Mathieson 2018



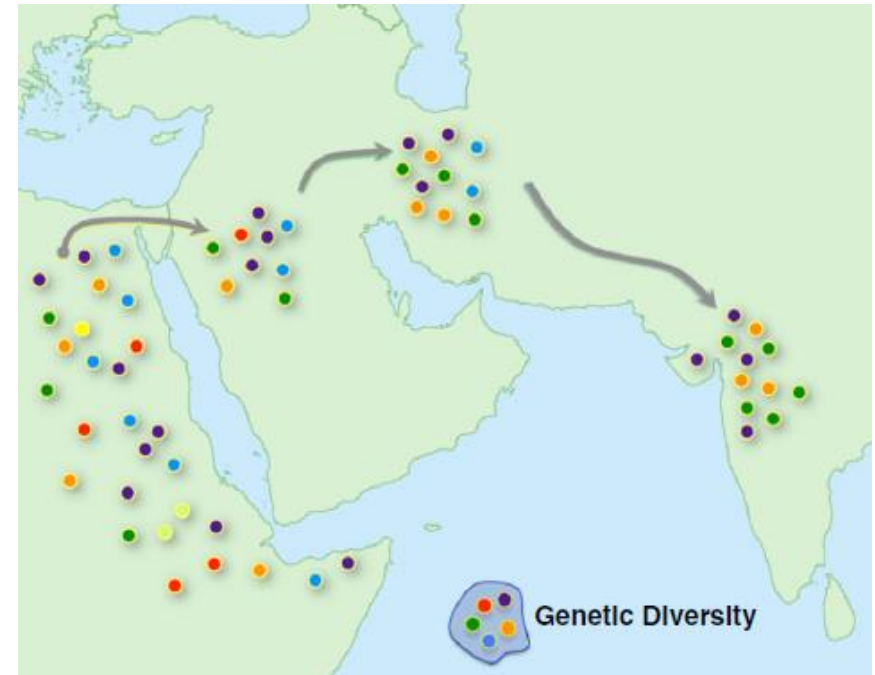
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Skoglund & Mathieson 2018

Competing modern human dispersal models

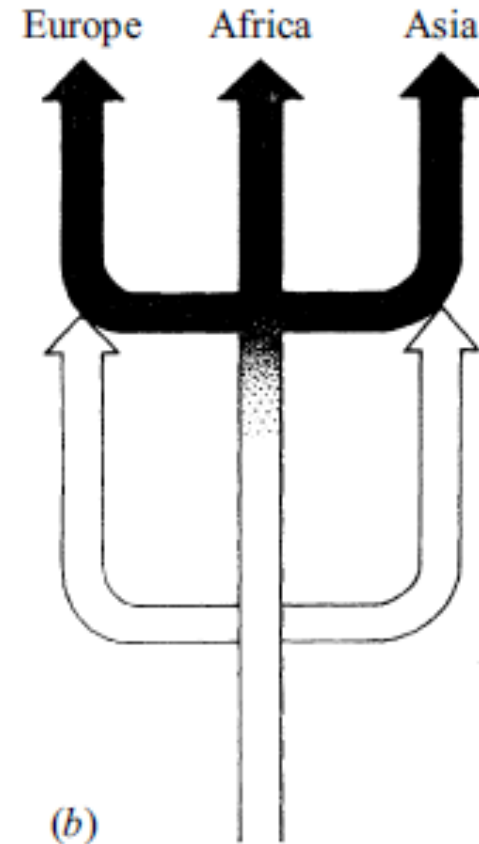
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 - 1 Out-of-Africa event
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- ❑ **Mode: Route of dispersal**
 - Southern (to Arabian Peninsula)
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Henn et al. 2012

Competing modern human dispersal models

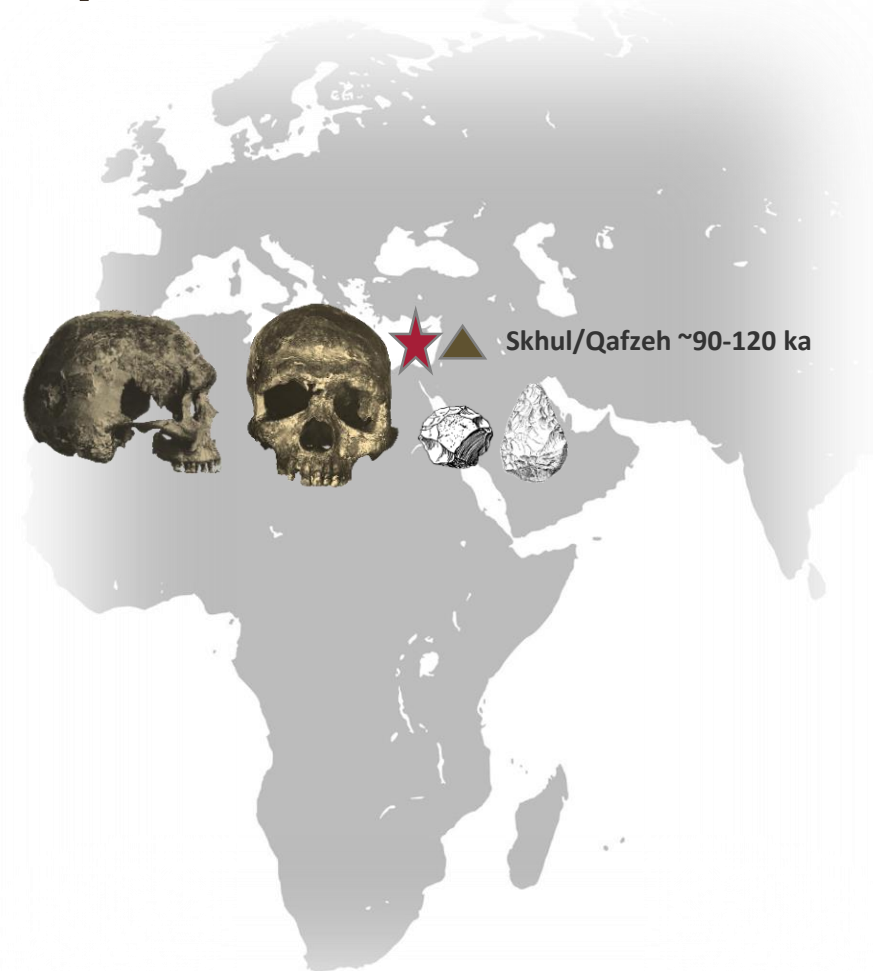
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Stringer 2001

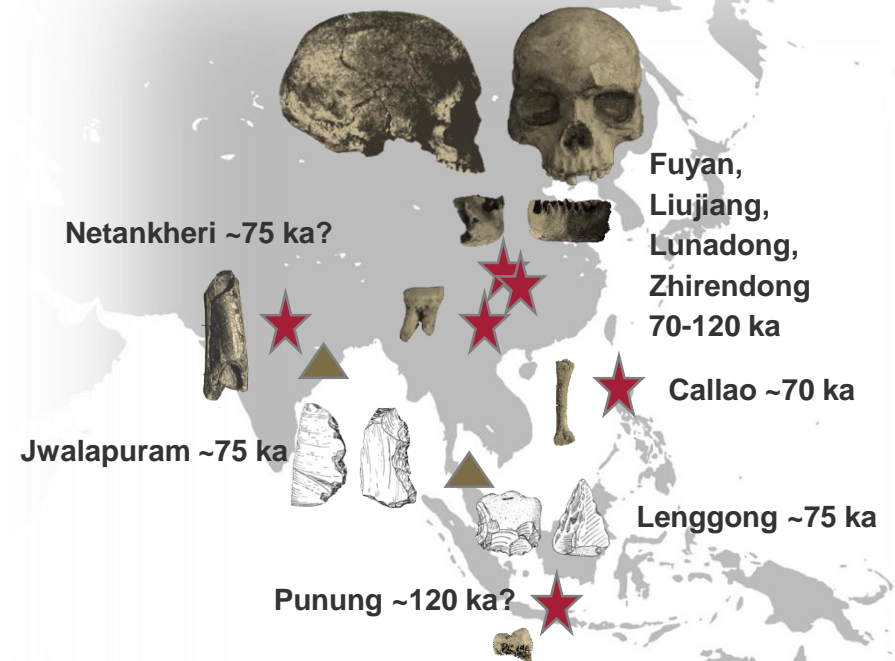
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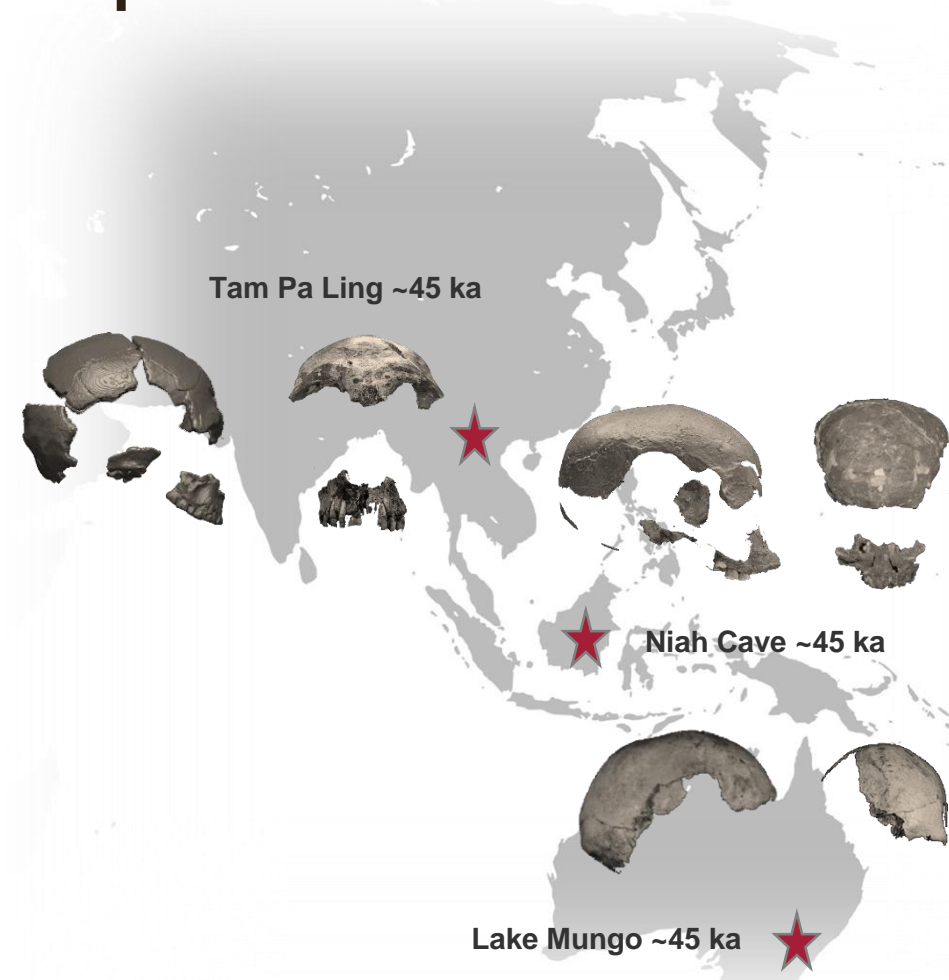
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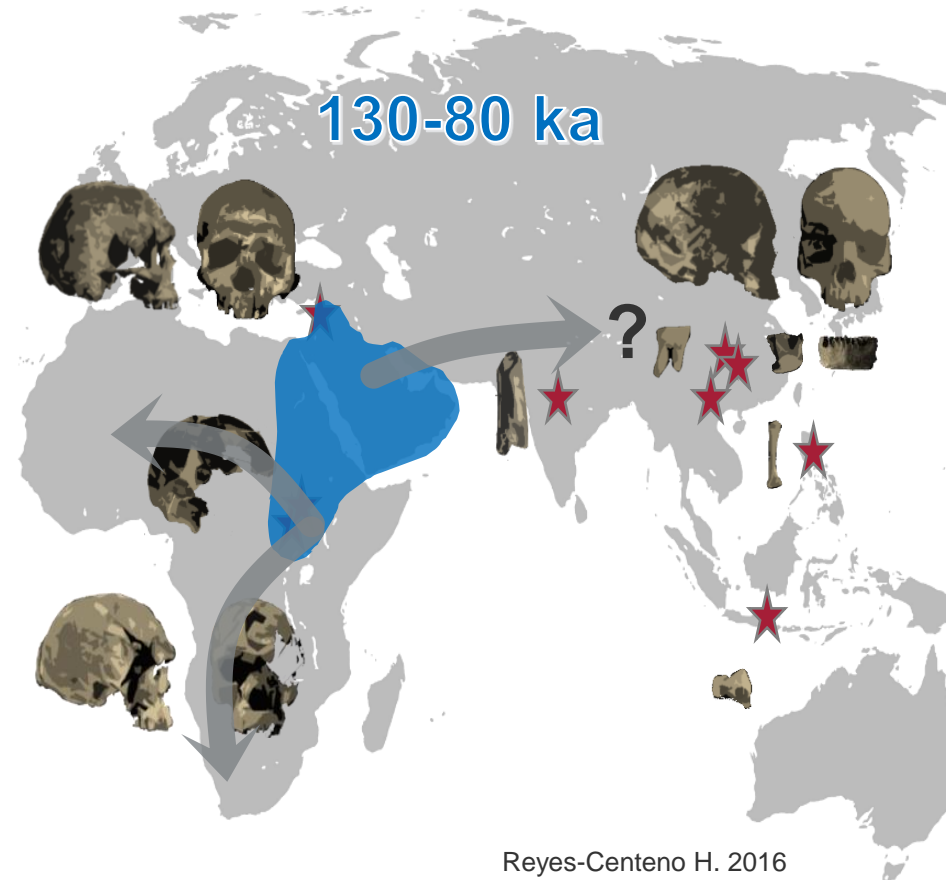
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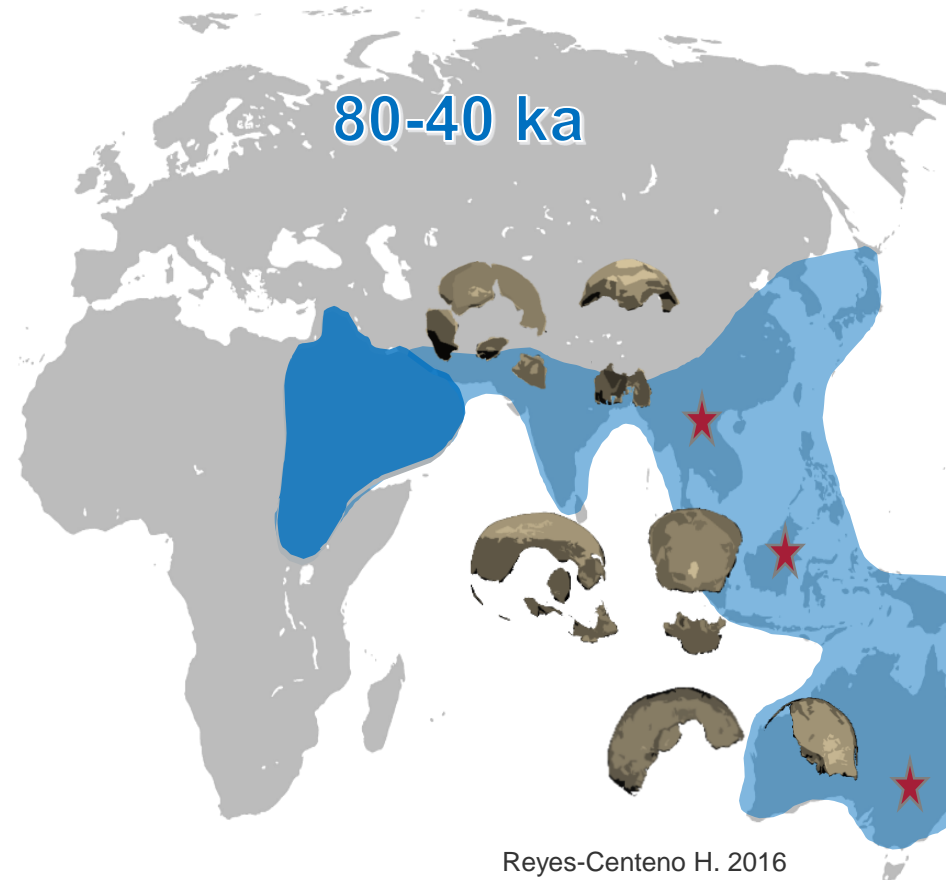


Reyes-Centeno H. 2016



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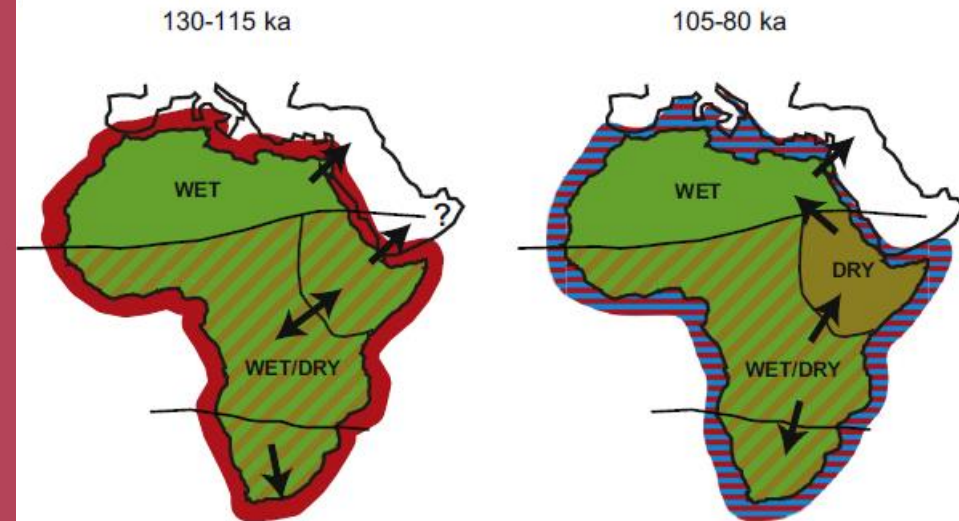


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Competing modern human dispersal models

□ Mode: Route of dispersal

- Southern (to Arabian Peninsula)
 - Paleoenvironment: passage more likely between 145-115 ka and again between 80-65 ka
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 - Paleoenvironment: passage more likely between 140-75 ka



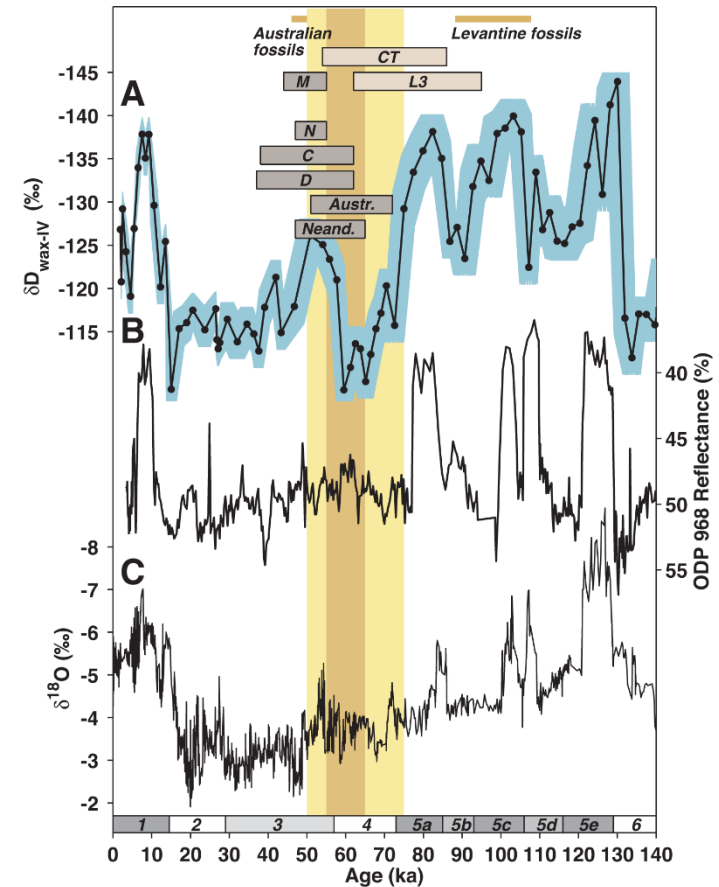
Blome et al. 2012



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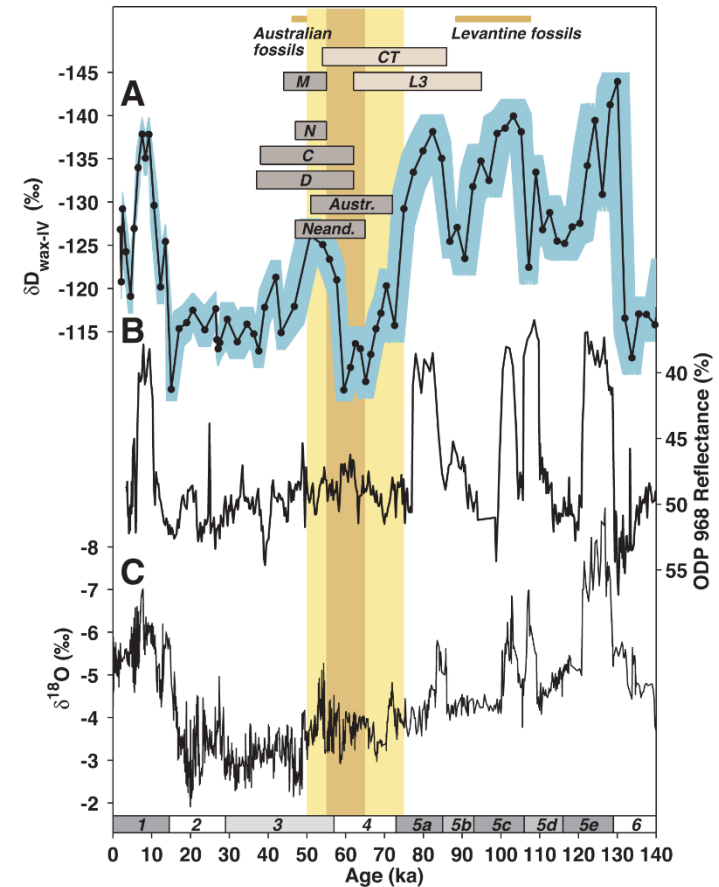
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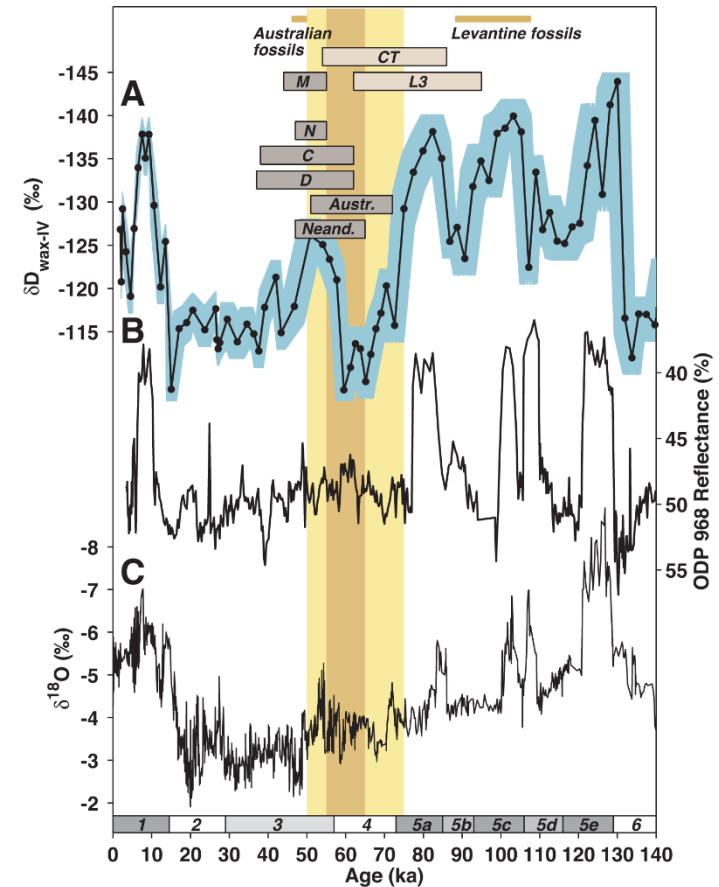
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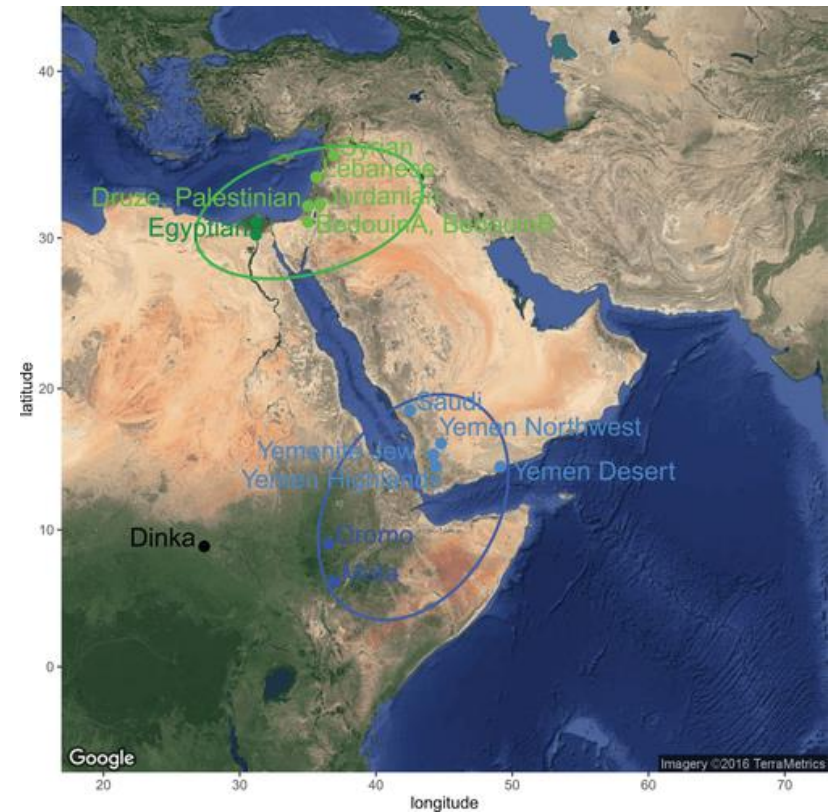
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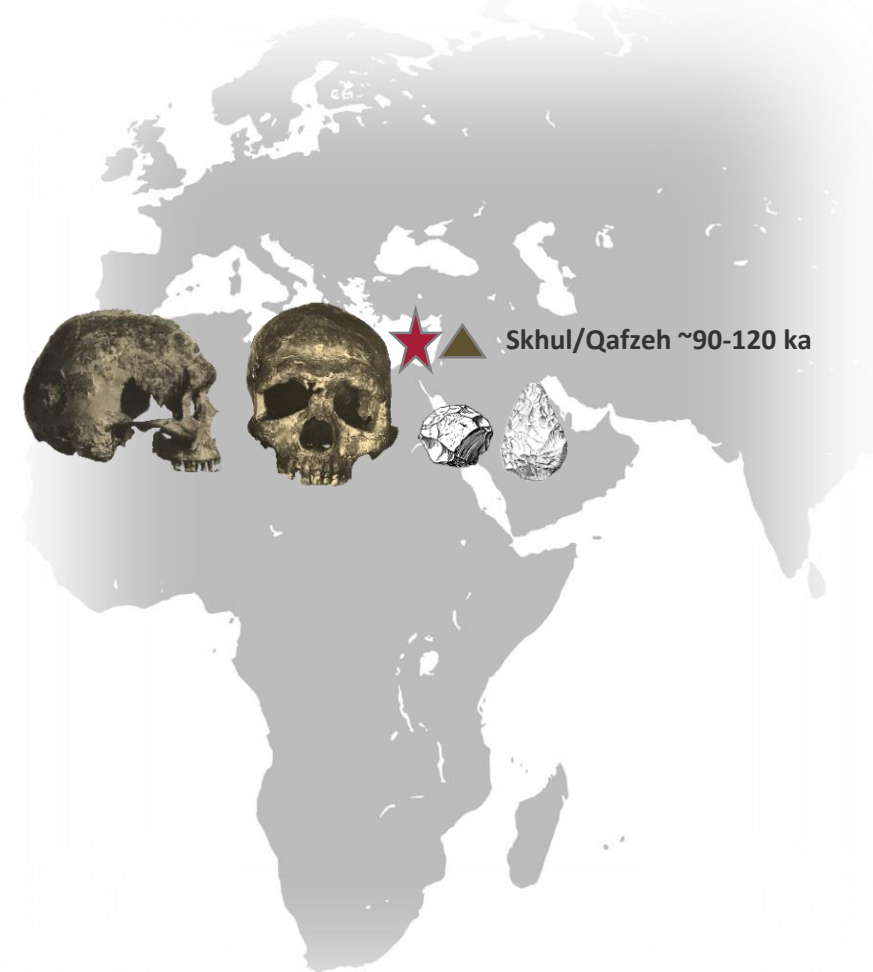
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 - Genomics of recent/living populations do not resolve debate



Vyas et al. 2017

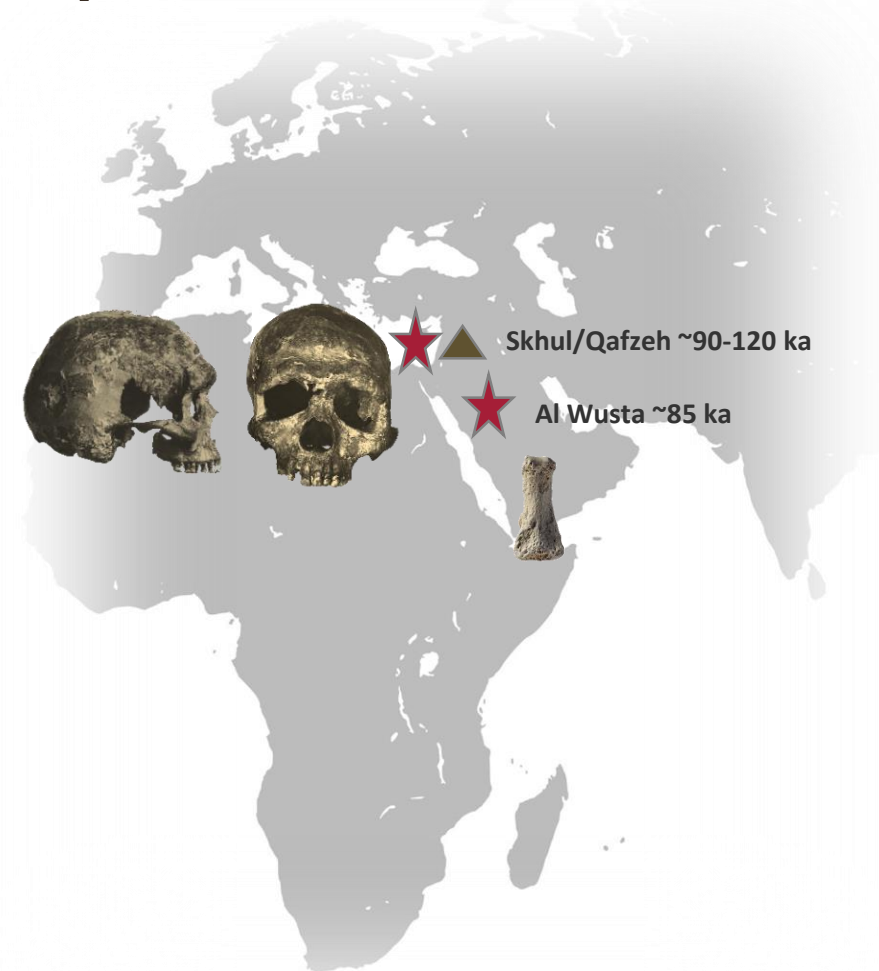
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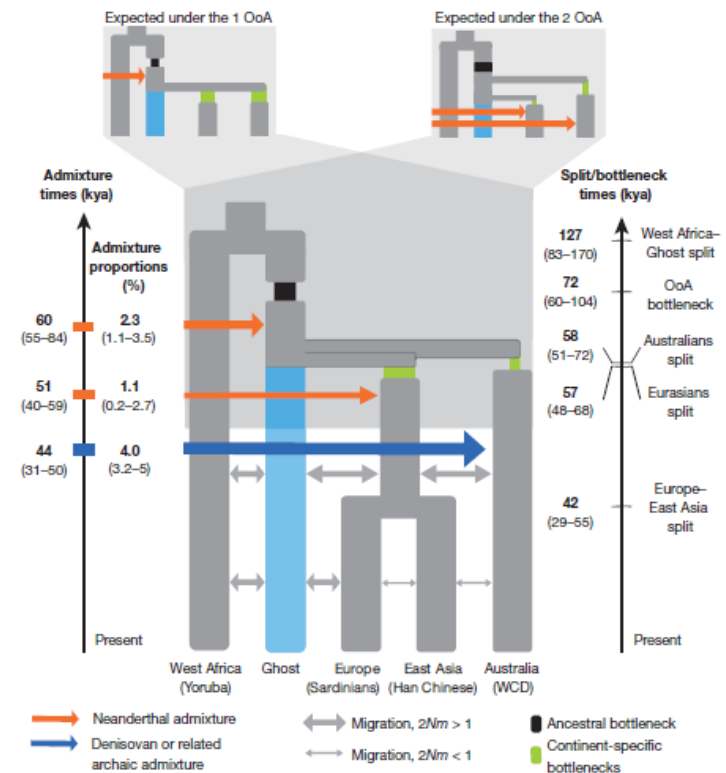
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 - Evidence by ~55 ka. Possible hybrid?





Competing modern human dispersal models

- **Current genomic consensus:**
 - Single out of Africa ~104-60 ka
 - Early split of Australo-melanesians?

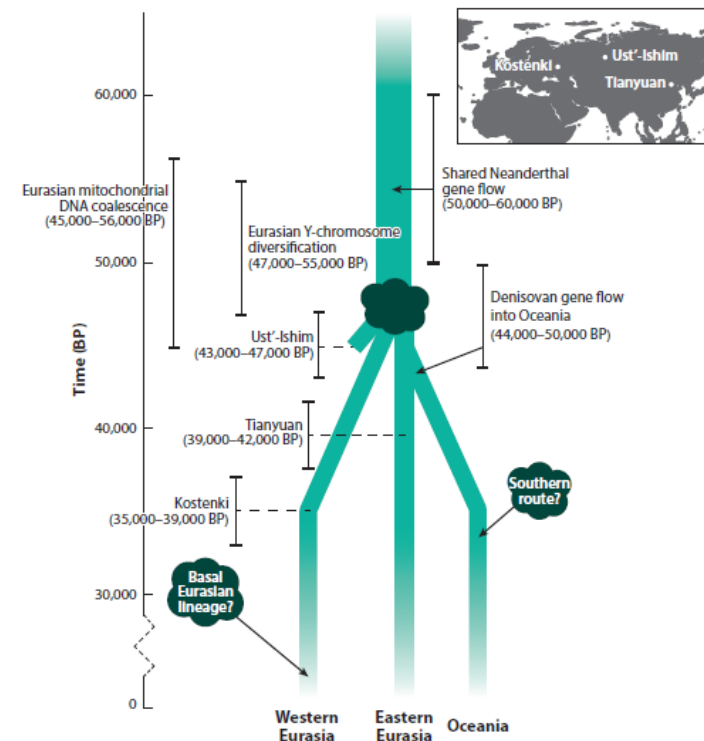


Malaspinas et al. 2016

Competing modern human dispersal models

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- Additional ancient genomes will continue to constrain dates

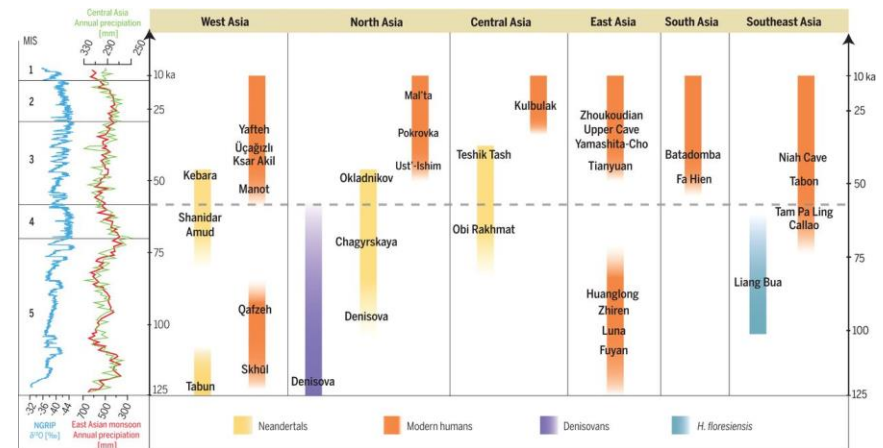
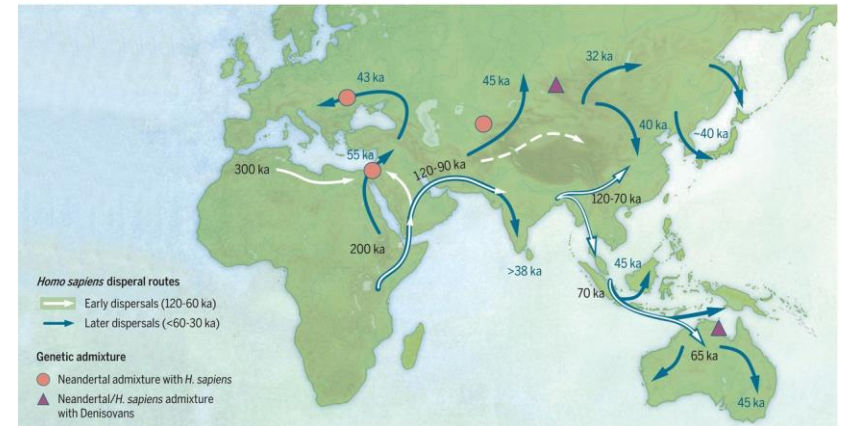


Skoglund & Mathieson 2018

Competing modern human dispersal models

□ Revised view:

- Expansion ~130 ka to the Levant and possibly further into Eurasia, followed by extinction
 - Small populations?
 - Contributions to Neanderthals?
 - Competition with other hominins?
 - Middle Paleolithic / MSA toolkit?
- Major dispersal between ~80-50 ka



Bae et al 2017



Next week

- ❑ **Neutral and adaptive evolution**
What is the difference between evolution by chance and evolution under selection?
- ❑ **Co-evolution**
Do the genotype and phenotype co-evolve?
- ❑ **Evolution of language**



Reminder: no class next week; lectures resume 10 December

DFG Center Symposium 14-15 December:

<http://www.wordsandbones.uni-tuebingen.de/symposium2018>

Late sign-ups: contact Dr. Monika Doll

