## ORIGIN OF MODERN HUMANS

## Paleoanthropology: How Old Is the Oldest Human?

Jean-Jacques Hublin

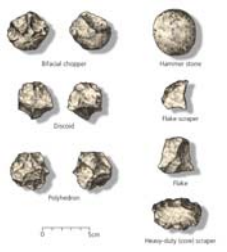
Figure 1. The LD 350-1 mandible in hands of its discover, Chalachew Seyoum.
The Ledi-Geraru area provides an invaluable material documenting a critical period of hominin evolution for which the East African fossil record is still very scarce. (Photo credit: Brian Villmoare.)

A 2.8 Ma old mandible unearthed in Ethiopia fills the gap between ape-like australopithecines and representatives of the genus *Homo*. It pushes the origin of large-brained hominins further back in time and highlights the complexity of the human evolutionary tree.

Current Biology 25, R448–R469, June 1, 2015

Cut marks in bone
3.4 mya

Stone tools
3.3 mya



Harmand *et al. Nature* **521**, 310-315 (2015)

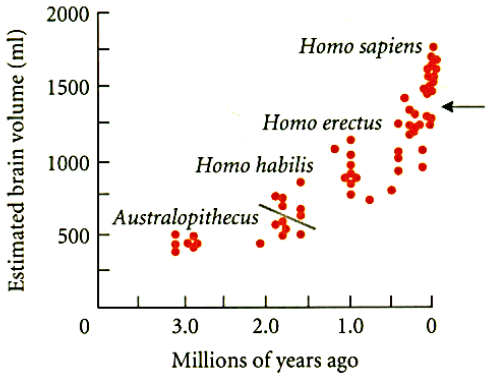
Oldowan tools
2.6 - 1.5 mya

Figs. 17.13 & 17.14 Z&E

## APPEARANCE OF THE GENUS *HOMO*

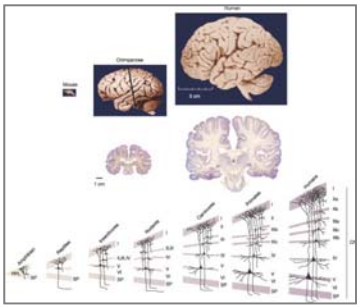
- **Increasingly large brain**
  - *habilis* - 650-800 cc
  - *erectus* - 900-1200 cc
  - *sapiens* - 1200-1400 cc
- **Stone tool use**
- **Number of biological species???**

***Homo habilis* 1.9 mya**




**Molecular insights into human brain evolution**

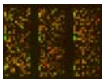
Robert Sean Hill and Christopher A. Walsh

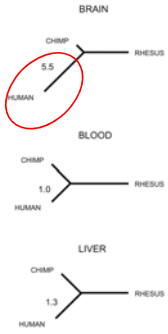


**Differences in cerebral cortical size are associated with differences in the cerebral cortex circuit diagram.**

*Nature* **437**, 64-67 (1 September 2005)

## Intra- and Interspecific Variation in Primate Gene Expression Patterns






- **Enard et al. used an AFFIMETRIX gene chip with 12,000 human genes to analyze differences in expression patterns among 3 primates.**
- **No significant differences were noted in blood or liver assays *BUT* large differences were observed in brain expression patterns.**
- **Rapid evolution of gene expression patterns in the human brain.**

**FROM: Enard et al., *Science* April 12, 2002 296:340-343**

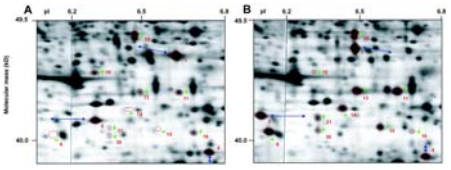


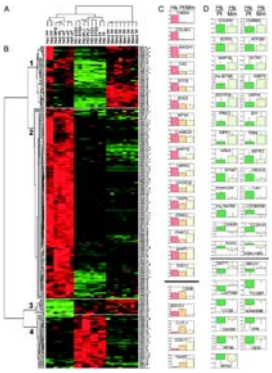

**Table 1. Brain protein pattern differences between humans and chimpanzees as analyzed by 2D gel electrophoresis**. Differences between humans and chimpanzees were scored if confirmed in three individual human-chimpanzee pairs and were analyzed in the same way as in a larger mouse study comparing *M. musculus* and *M. spretus*. **Qualitative differences** represent changes in electrophoretic mobility of spots, which likely result from amino acid substitutions, whereas **quantitative differences** reflect changes in the amount of protein.

| Comparison | Analyzed spots | Differences | |
|---|---|---|---|
| | | Qualitative | Quantitative |
| Human-chimpanzee | 538 | 41 (7.6%) | 169 (31.4%) |
| *M. musculus-M. spretus* | 8767 | 668 (7.6%) | 656 (7.5%) |

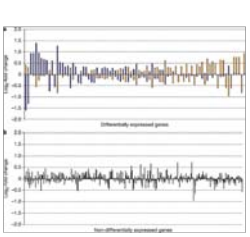
**FROM: Enard et al., *Science* April 12, 2002 296:340-343**

**Elevated gene expression levels distinguish human from non-human primate brains**

Caceres *et al.* (*PNAS* 2003) identified 169 genes that exhibited gene expression differences between human and chimpanzee lineages. 91 of these genes differentiated in the human lineage. **Most differences involved up-regulation with higher expression levels humans.**



**Expression profiling in primates reveals a rapid evolution of human transcription factors**
Yoav Gilad *et al.*



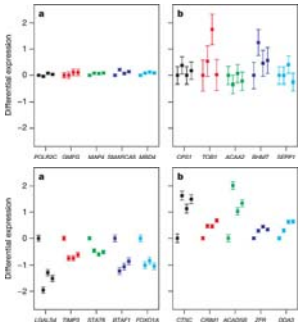


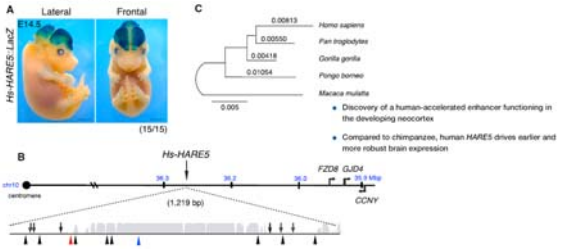
**Table 1 | Inter-species differentially expressed genes**

| | Chimpanzee | Orangutan | Rhesus macaque |
|---|---|---|---|
| Human | 110 | 128 | 176 |
| Chimpanzee | - | 150 | 141 |
| Orangutan | - | - | 129 |

humans, chimpanzees, orangutans and rhesus macaque (left to right)

*Nature* **440**, 242-245 (9 March 2006)

**Human-Chimpanzee Differences in a *FZD8* Enhancer Alter Cell-Cycle Dynamics in the Developing Neocortex** (Boyd *et al.* 2015)



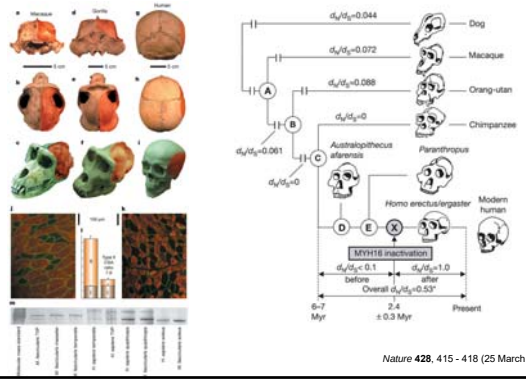

The neocortex expanded spectacularly during human evolution, giving rise to distinctively human anatomical and cognitive capabilities **Yet to date, just a handful of genetic loci have been associated with human-specific brain traits** and none have been shown to functionally impact corticogenesis in an evolutionarily divergent fashion. In this study, we report the discovery of the first human-accelerated enhancer that functions in brain development… **Our study suggests the intriguing hypothesis that evolutionary changes in HARE5 sequence and activity contributed to the origin of unique features of the human brain.**

Current Biology 25, 772-779, March 16, 2015


*NATURE* March 25, 2004

**Myosin gene mutation correlates with anatomical changes in the human lineage**

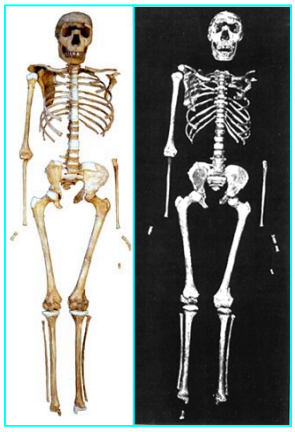
STEDMAN et al.




*Nature* **428**, 415 - 418 (25 March 2004)

***Homo (Kenyanthropus) rudolfensis***
**2.5 – 1.9 mya**

***Homo ergaster***
**1.8 – 1.4 mya**



**"Turkana boy"**

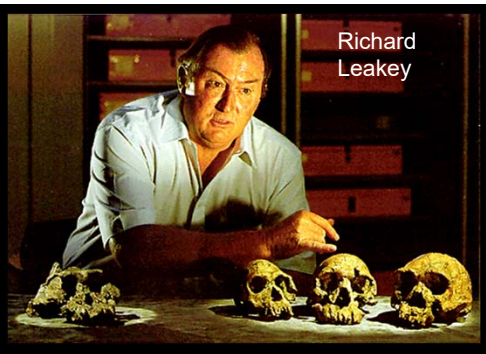
- 10-12 years old
- 1.6 million years ago
- Kenya
- called early African *H. erectus* or *H. ergaster*

**"Turkana boy"**

**10-12 years old**

**1.6 million years ago**

Starting ~1.6 mya a more sophisticated style of tool emerged



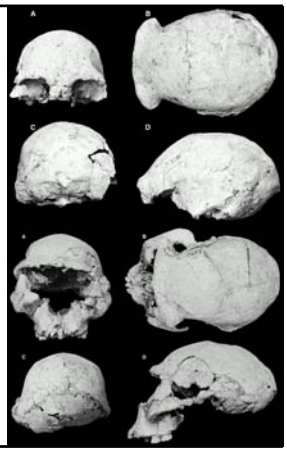
Richard Leakey

Eastern Africa - Lake Turkana region

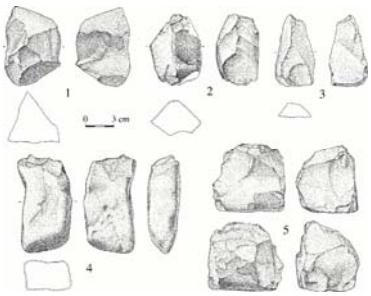
coexistence of different hominids

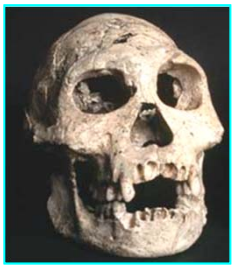
## DMANISI, REPUBLIC OF GEORGIA

- 1.7 mya
- Shortly after the origin of *Homo*, there is a migration out of Africa.

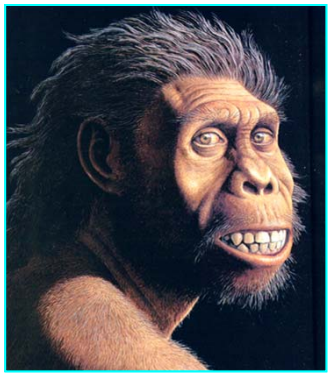


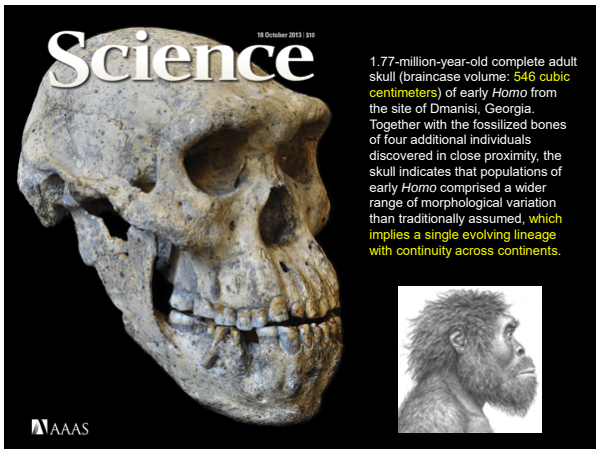
## DMANISI STONE TOOLS





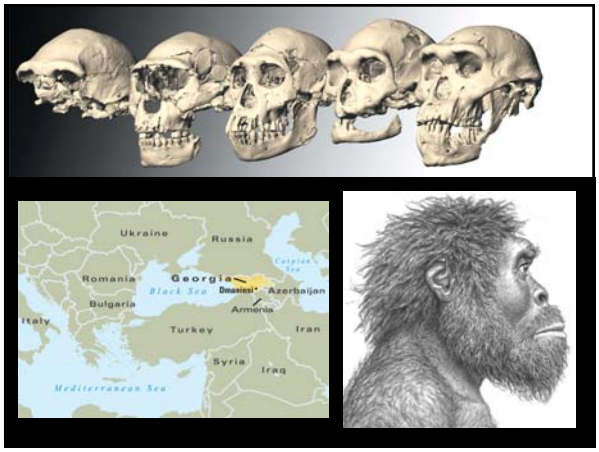
clearly not close to anatomically modern *H. sapiens* - like Turkana boy

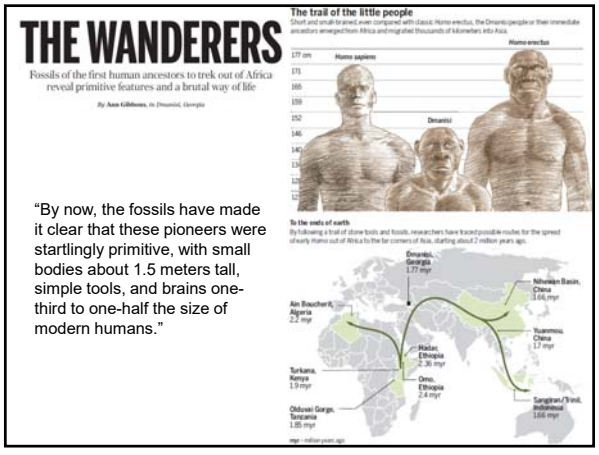





1.77-million-year-old complete adult skull (braincase volume: 546 cubic centimeters) of early *Homo* from the site of Dmanisi, Georgia. Together with the fossilized bones of four additional individuals discovered in close proximity, the skull indicates that populations of early *Homo* comprised a wider range of morphological variation than traditionally assumed, which implies a single evolving lineage with continuity across continents.

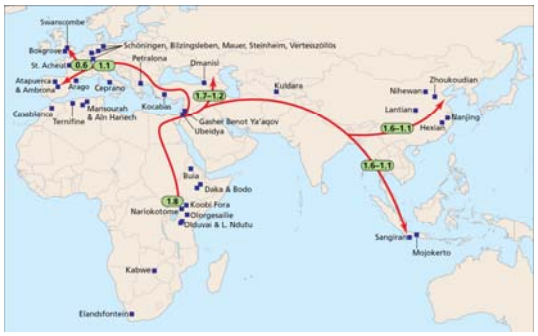





"By now, the fossils have made it clear that these pioneers were startlingly primitive, with small bodies about 1.5 meters tall, simple tools, and brains one-third to one-half the size of modern humans."

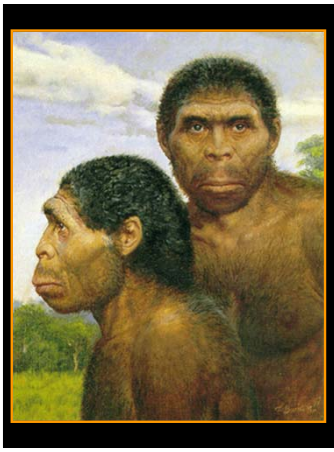
First migration out of Africa did not include the modern human lineage




## Asian *Homo erectus*

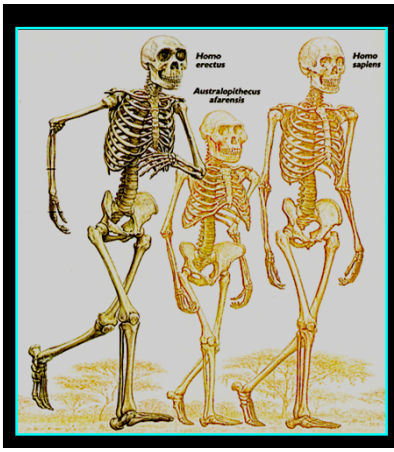
**"Java Man"**
**0.75 mya**

**Peking Man**
**China**
**0.77 mya**



**RECONSTRUCTION of Indonesian**

***H. erectus***




**Brain Size:**

***A. afarensis***

**500cc**

***H. erectus***

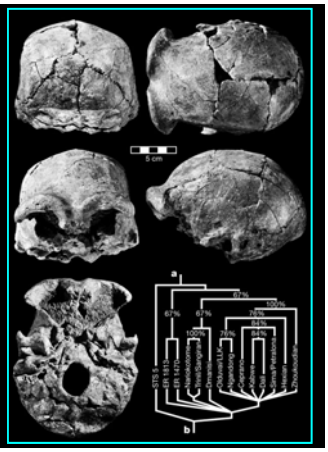
**900 – 1200 cc**

***H. sapiens***

**1100 – 1400 cc**

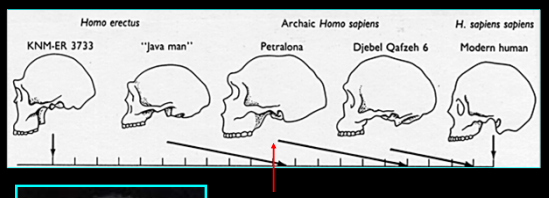
## 'Daka' Ethiopian Skull

- 1 million-year-old remains from Ethiopia show clear link between Asian *Homo erectus* and African *H. erectus* (widespread paleospecies)
- intermediate between earlier and later African fossils



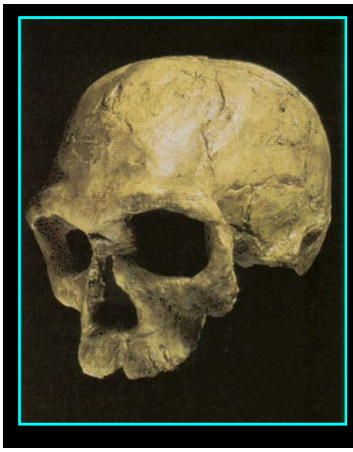
- **There is a growing realization that there may have been a high degree of sexual dimorphism in this archaic lineage compared to more modern groups.**

- Comparison of two *H. erectus* skulls found in Kenya showing the huge variation in size




**Petralona Skull – 250,000 years old**

- ***H. erectus* or archaic *H. sapiens*?**



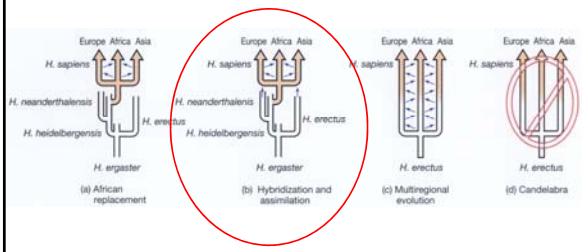
**JEBEL IRHOUD 1**

**MOROCO**

**100,000 – 200,000 YEARS OLD**

***H. erectus* or *H. sapiens*?**

**COMPETING HYPOTHESES FOR THE DEVELOPMENT OF MODERN HUMANS**

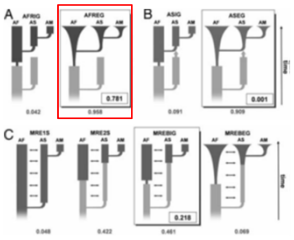


## COMPETING HYPOTHESES FOR THE DEVELOPMENT OF MODERN HUMANS

- **Multiregional model: archaic *H. sapiens* (or *H. erectus*) dispersed throughout the Old World and simultaneously evolved to modern form with abundant gene flow.**
- **Replacement Model (Out – of– Africa): single group that relatively recently dispersed from Africa, evolved into modern form and replaced all archaic forms, including Neanderthals.**
- **Hybridization & Assimilation Model: This model suggests that archaic lineages spread out from Africa early, followed later by a second wave of dispersal from a more derived lineage. Some amount of hybridization accompanied the replacement of the archaic lineages.**

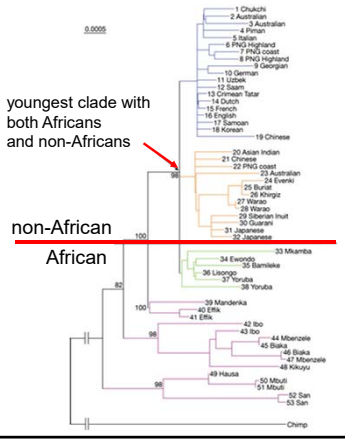
## Statistical evaluation of alternative models of human evolution

Fangundes et al. 2007 PNAS 17614-17619



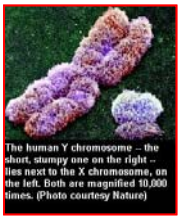

Using DNA data from **50 nuclear loci** sequenced in African, Asian and Native American samples…**a simple African replacement model with exponential growth has a higher probability (78%) as compared with alternative multiregional evolution or assimilation scenarios.** A Bayesian analysis of the data under this best supported model points to an origin of our species **141 thousand years ago (Kya), an exit out-of-Africa 51 Kya, and a recent colonization of the Americas 10.5 Kya.** We also find that the African replacement model explains not only the shallow ancestry of mtDNA or Y-chromosomes but also the occurrence of deep lineages at some autosomal loci, which has been formerly interpreted as a sign of interbreeding with *Homo erectus*.

**Recent comparisons of ENTIRE mtDNA genome indicate a recent (0.2 mya), African origin of anatomically modern humans.**



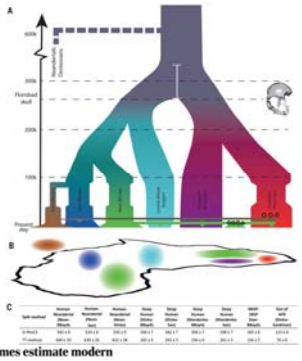
## Y CHROMOSOME STUDIES

| | |
|---|---|
| Dorit et al. 1995 | 173,000 |
| Hammer et al. 1995 | 188,000 |


The human Y chromosome -- the short, stumpy one on the right -- lies next to the X chromosome, on the left. Both are magnified 10,000 times. (Photo courtesy Nature)

- **mtDNA and Y chromosome studies yield similar dates for the MRCA of modern humans.**
- **Taken together, these studies strongly suggest that the *multiregional model* cannot be correct.**

And maybe the origin of modern humans goes back even a bit farther….



**Southern African ancient genomes estimate modern human divergence to 350,000 to 260,000 years ago**

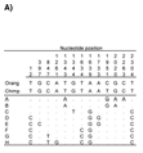
Carina M. Schlebusch,[1*] Helena Malmström,[1*] Torsten Günther,[1] Per Sjödin,[1] Alexandra Coutinho,[1] Hanna Edlund,[1] Arielle R. Munters,[1] Mário Vicente,[1] Maryna Steyn,[2] Himla Soodyall,[3] Marlize Lombard,[4†‡] Mattias Jakobsson[1†‡]

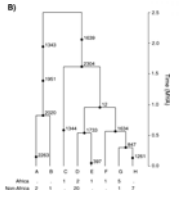
*Science* 28 Sep 2017

## Evidence for Archaic Asian Ancestry on the Human X Chromosome

Garrigan et al (2005) Mol. Biol. Evol. 22:189-192


Geographical distribution of the archaic *RRM2P4* lineage in 17 population samples



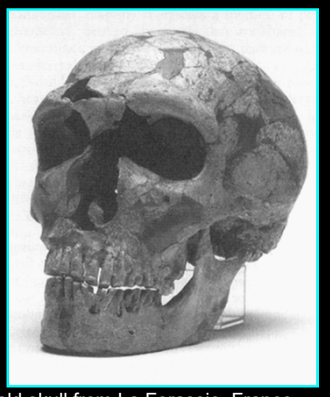



## WHAT ABOUT NEANDERTHALS???

*H. sapiens neanderthalensis*
**50,000 years ago**
**France**

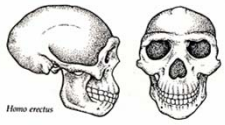
*H. sapiens sapiens*
**Present**

- **Neanderthal fossils are found from 400,000 to about 30,000 years ago in Europe and western Asia.**

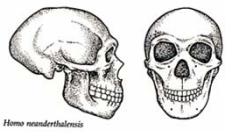


50,000 year old skull from La Ferassie, France

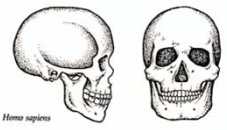
*Homo erectus*

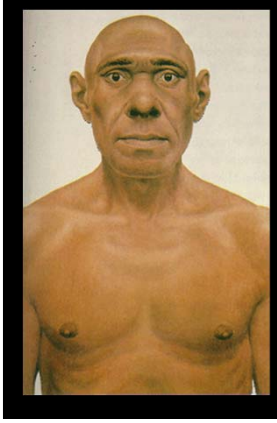



*Homo neanderthalensis*




*Homo sapiens*

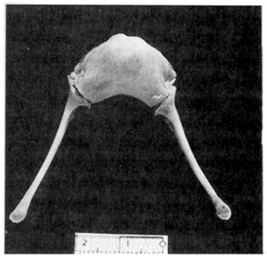




## RECONSTRUCTION BASED ON SKULLS FROM SHANIDAR CAVE IN IRAQ

- Prominent brow ridge
- Large bulbous nose
- Powerful build
- Possible advanced culture: sophisticated tools, burials, language?

## HYOID BONES CLOSELY RESEMBLE MODERN HUMANS

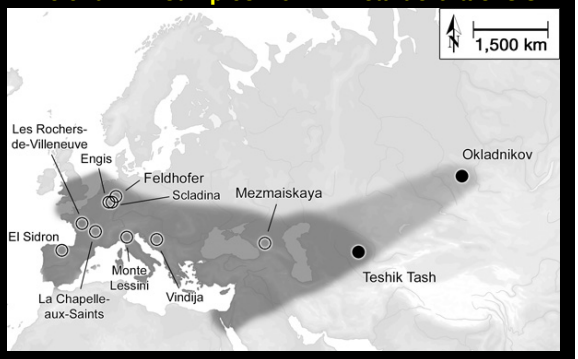


Chimpanzee

Neanderthal

## Sympatry *H. neanderthalensis* and *H. sapiens*

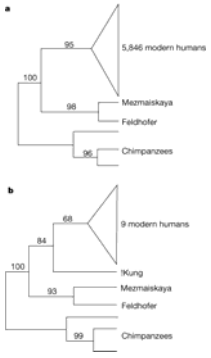
## Ancient DNA samples from *H. neanderthalensis*




Krause et al. *Nature* **449**, 902-904 (18 October 2007)

## mtDNA SEQUNCE ANALYSIS FROM NEANDERTHAL BONE (>30, 000 YEARS OLD)

- **Neanderthal sequences are 3 times as divergent from modern human sequences than are the most divergent modern humans.**
- **It is unlikely that Neanderthals were assimilated into human populations.**





1% to 4% of the DNA of Europeans and Asians, but not of Africans, was shared with Neandertals and concluded that modern humans interbred with Neandertals at low levels (*Science,* 7 May 2010, pp. 680, 710)

**Denisova human**

This view of the Altai Mountains is from just above Denisova Cave, where the fragment of bone analysed by Krause *et al*. was discovered. The excavation field camp is visible in the valley below.

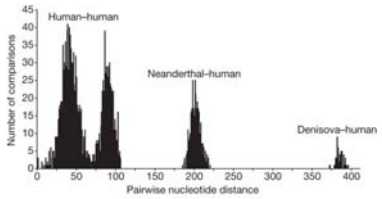
HUMAN EVOLUTION

## Stranger from Siberia

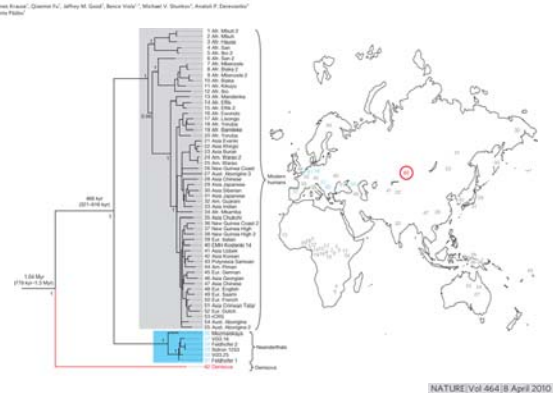
Terence A. Brown

**The sequencing of ancient DNA is generating dramatic results. The sequence from a bone fragment has revealed the existence of an unknown type of extinct human ancestor that lived in Asia 40,000 years ago.**

- Pairwise nucleotide differences from all pairs of complete mtDNAs from 54 present-day and one Pleistocene modern human, six Neanderthals and the Denisova hominin are shown.



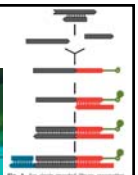

**The complete mitochondrial DNA genome of an unknown hominin from southern Siberia**

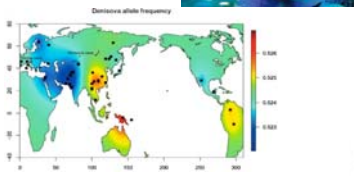


NATURE | Vol 464 | 8 April 2010

This replica of a tiny finger bone from Denisova Cave yielded an entire genome. *Photo: Max Planck Institute for Evolutionary Anthropology*

## A Crystal-Clear View Of an Extinct Girl's Genome





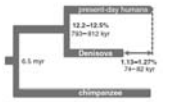




Fig. 2. Average sequence divergence and branch length differences between the Denisovan genome and 11 present-day humans represented as a tree. Divergence is reported as fraction of the branch leading from human to the common ancestor with chimpanzee, and in years, if one assumes a human-chimpanzee divergence of 6.5 million years ago.

Science AAAS

**A High-Coverage Genome Sequence from an Archaic Denisovan Individual**
Matthias Meyer *et al.*
*Science* **338**, 222 (2012);
DOI: 10.1126/science.1224344

Location of the Middle Pleistocene site of **Sima de los Huesos** (yellow) as well as Late Pleistocene sites that have yielded **Neanderthal** DNA (red) and **Denisovan** DNA (blue).

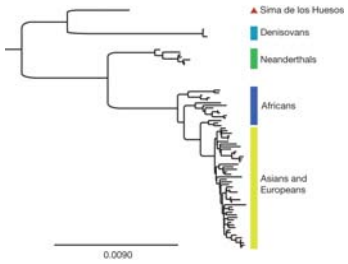

Svante Paabo

**A mitochondrial genome sequence of a hominin from Sima de los Huesos**

nature

M Meyer *et al. Nature* **000**, 1-4 (2013) doi:10.1038/nature12788

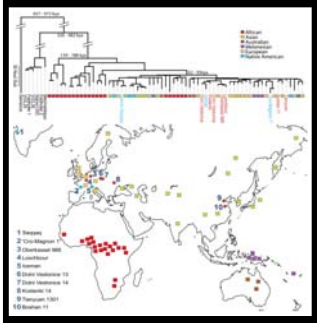
Bayesian phylogenetic tree of hominin mitochondrial relationships based on the Sima de los Huesos mtDNA sequence determined using the inclusive filtering criteria.




nature

M Meyer *et al. Nature* **000**, 1-4 (2013) doi:10.1038/nature12788

**A Revised Timescale for Human Evolution Based on Ancient Mitochondrial Genomes**
Fu et al.

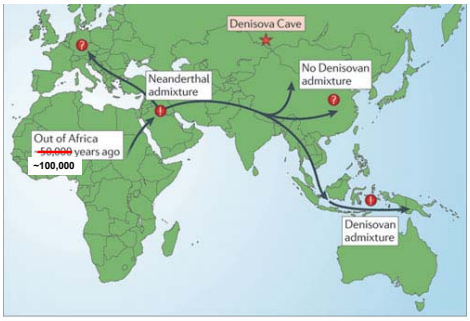


| | |
|---|---|
| Denisova | 657 – 973 kya |
| Neanderthal | 326 – 482 kya |
| Modern Humans | 134 – 188 kya |
| Out-of-Africa | 62 – 95 kya |

Cell Press



**Learning about human population history from ancient and modern genomes**
Mark Stoneking & Johannes Krause



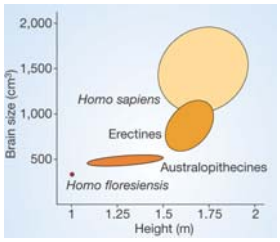

*Nature Reviews Genetics* **12, 603-614 (September 2011)**

Nature Reviews | Genetics

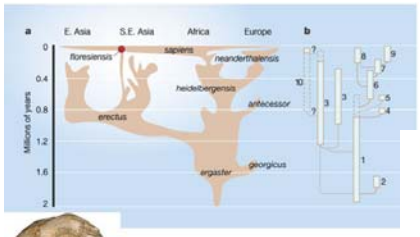
**Palaeoanthropology: Human evolution writ small**

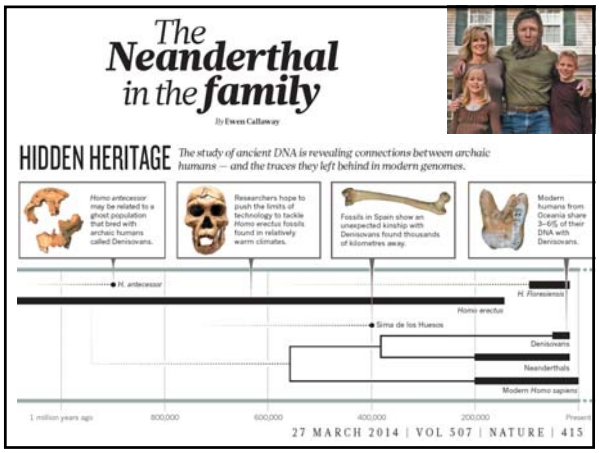
**We are the only living species of the genus *Homo*. Given the startling results of a cave excavation in Southeast Asia, it seems that we coexisted with another species until much more recently than had been thought.**

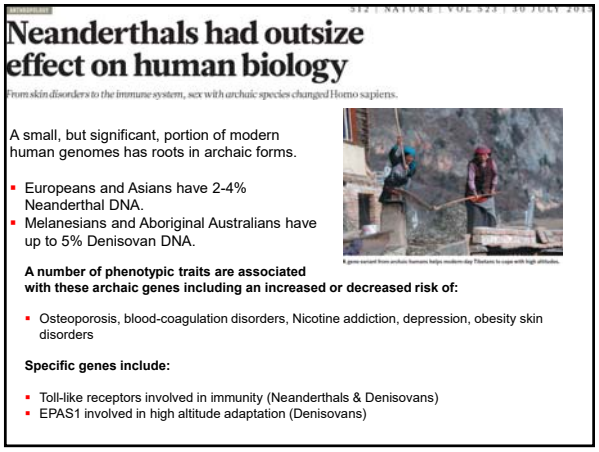

Tools associated with
*H. floresiensis*

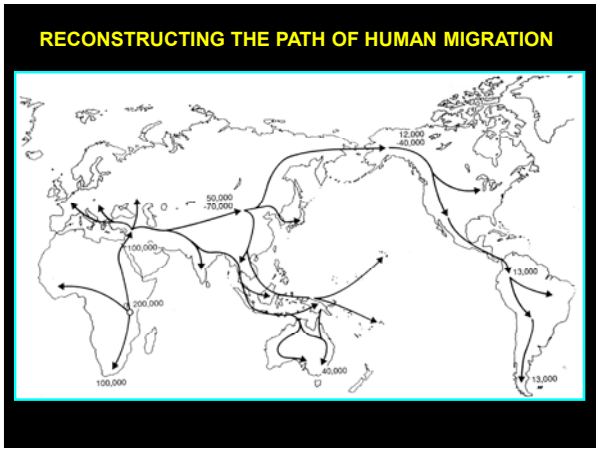



**Co-occurrence of *H. sapiens* and *H. erectus* as recently as 19,000 years ago?**





The Neanderthal in the family
By Ewen Callaway
HIDDEN HERITAGE The study of ancient DNA is revealing connections between archaic humans — and the traces they left behind in modern genomes.
Homo antecessor may be related to a ghost population that bred with archaic humans called Denisovans.
Researchers hope to push the limits of technology to tackle Homo erectus fossils found in relatively warm climates.
Fossils in Spain show an unexpected kinship with Denisovans found thousands of kilometres away.
Modern humans from Oceania share 3–6% of their DNA with Denisovans.
H. antecessor
H. floresiensis
Homo erectus
Sima de los Huesos
Denisovans
Neanderthals
Modern Homo sapiens
1 million years ago
800,000
600,000
400,000
200,000
Present
27 MARCH 2014 | VOL 507 | NATURE | 415

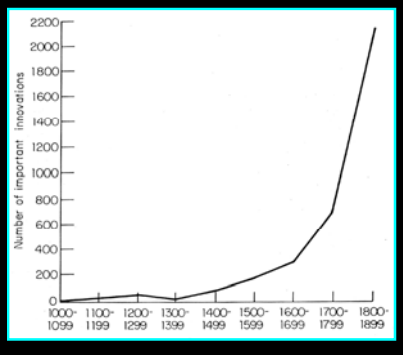

512 | NATURE | VOL 523 | 30 JULY 2015
Neanderthals had outsize effect on human biology
From skin disorders to the immune system, sex with archaic species changed Homo sapiens.
A small, but significant, portion of modern human genomes has roots in archaic forms.
Europeans and Asians have 2-4% Neanderthal DNA.
Melanesians and Aboriginal Australians have up to 5% Denisovan DNA.
A gene variant from archaic humans helps modern-day Tibetans to cope with high altitudes.
A number of phenotypic traits are associated with these archaic genes including an increased or decreased risk of:
Osteoporosis, blood-coagulation disorders, Nicotine addiction, depression, obesity skin disorders
Specific genes include:
Toll-like receptors involved in immunity (Neanderthals & Denisovans)
EPAS1 involved in high altitude adaptation (Denisovans)


RECONSTRUCTING THE PATH OF HUMAN MIGRATION
12,000
-40,000
50,000
-70,000
100,000
200,000
100,000
40,000
13,000
13,000


35,000 year-old statues

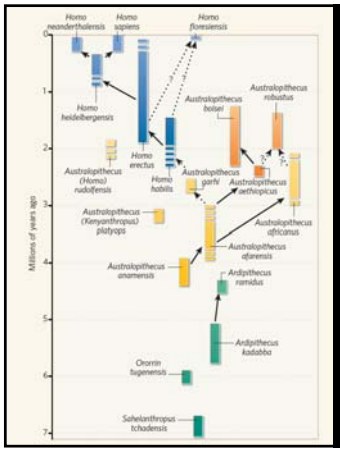
More….

## RAPID INCREASE IN TECHNOLOGY, ART, AND MUSIC DEMONSTRATES CULTURAL EVOLUTION IN MODERN HUMANS.




## HUMANS ARE UNIQUE IN THEIR EXTREMELY HIGH RATE OF CULTURAL EVOLUTION

- To what extent is an interaction between cultural evolution and phenotypic evolution possible?




- *H. floresiensis* ~18,000
- Denisova ~40,000
- H. neanderthalensis ~30,000

Possibly 4 separate lineages as recently as 40,000 years ago

Co-occurrence Late

NATURE|Vol 459|7 May 2009