

# Recent evidence in human evolution

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*Our understanding of the evolution and range expansion of *Homo sapiens* is improving rapidly, but information as yet undiscovered will alter our current model and improve the story.*

Evidence for our origins comes from studying old bones and the DNA of living people. The bones of those who died thousands of years ago provide information about their anatomy and DNA. Some hominin lineages we know only from their bones, such as *Homo floresiensis* in Indonesia and *Homo luzonensis* in the Philippines, and some we know best from DNA, such as Denisovans.

Bone discoveries enable theories from anthropology and population genetics to be tested against each other. However, biologists in different fields can have different criteria for how they recognise a group as distinct enough to be named as a separate species. This is important when assigning fossils into species, and interpreting interbreeding between distinct populations.

## Common ancestor

Fossil and genetic evidence both suggest that modern populations of *Homo sapiens* share a common ancestor about 300,000 to 200,000 years ago. This ancestral population must have lived somewhere in Africa. Re-dating of a Moroccan fossil in 2017\* places our ancestors in north Africa about 300,000 years ago, and in east Africa more recently, about 200,000 to 150,000 years ago. The east African fossils have most of the key features associated with *Homo sapiens* that we use to classify different species.

Modern populations of *Homo sapiens* vary widely in skin colour and body size, but all share four important traits: A large globular braincase; small teeth with reduced jaw architecture (the shape and structure of the bones and muscles of the mouth, which is closely associated with what food is eaten, and eating behaviour); a narrow pelvis; and distinct anatomy of the middle and inner ears.

The east African fossils have most of the features that we associate with *Homo sapiens*. Interestingly, the older fossils from Morocco have some traits of modern humans, such as reduced jaw architecture, but not others such as the typical braincase shape. Deciding which sections of a lineage that has evolved through

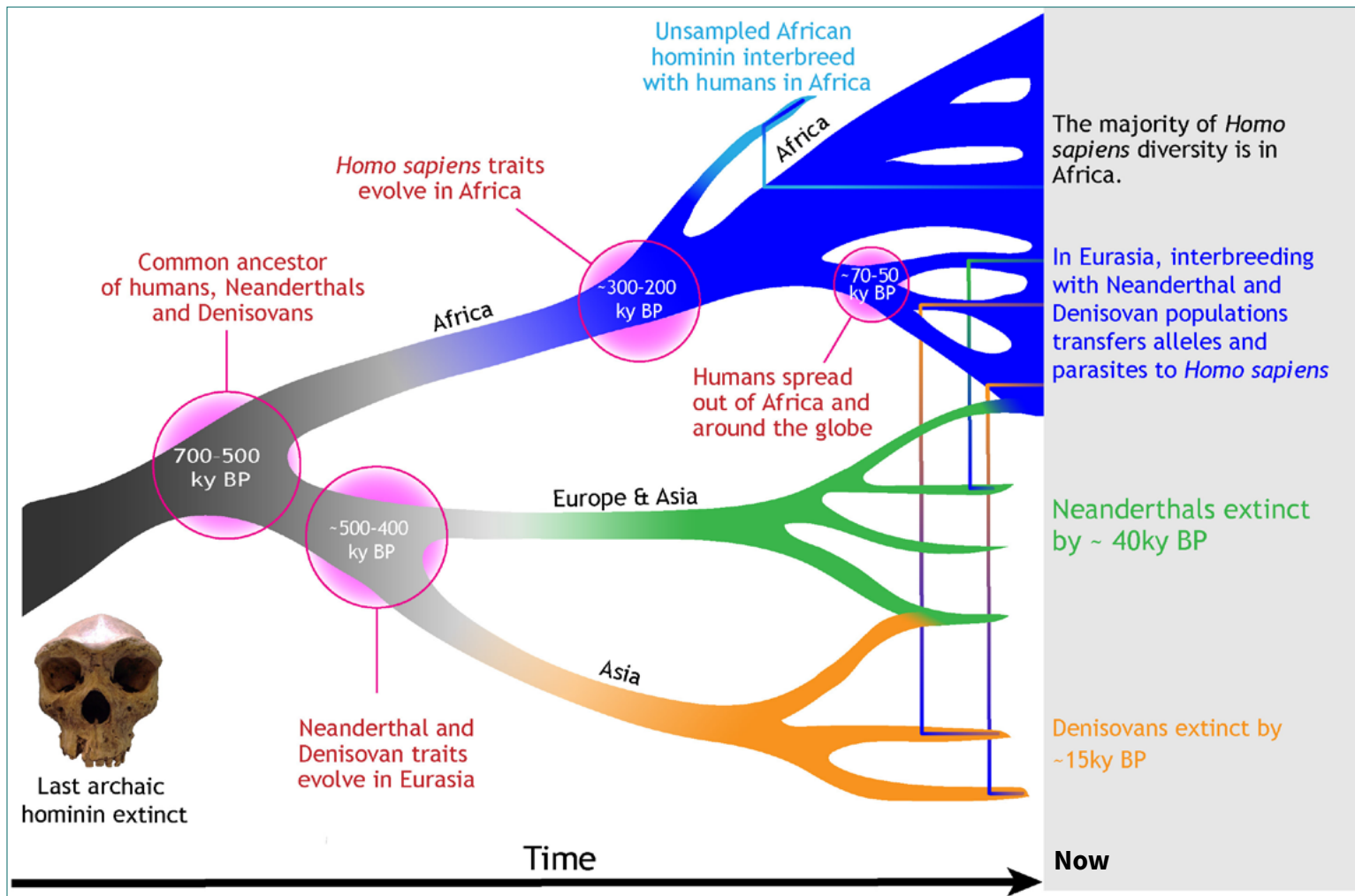
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**Figure 1. Successive dispersals from Africa;** *Homo erectus* (yellow), *Homo neanderthalensis* (ochre) and *Homo sapiens* (red). Wikipedia Commons.

\* Hublin, J.-J., Ben-Ncer, A., Bailey, S. E., Freidline, S. E., Neubauer, S., & Skinner, M. M. (2017). New fossils from Jebel Irhoud, Morocco and the pan-African origin of *Homo sapiens*. *Nature*, 546 (7657). DOI: 10.1038/nature22336





**Figure 2. Hypothesis of range expansion and interbreeding in hominin evolution.**

Vertical lines represent interbreeding between different hominin lineages, which enabled the transfer of distinct alleles and parasites.

time are separate species is very difficult.

Analyses of fossil anatomy and DNA sequences from archaic hominins suggest multiple waves of dispersal from Africa (Figure 1). Two groups arrived in Eurasia about 700,000 to 400,000 years ago and led to the establishment of the Neanderthals and the Denisovans, while another group of humans expanded their range from Africa into Eurasia at least 50,000 years ago (Figure 2).

## Interbreeding

Our previous theories of hominin speciation have been upset by new evidence that members of *Homo sapiens* successfully interbred, at various times and places, with a number of related lineages that are usually considered separate species. (Remember, usually separate species do not successfully interbreed, but the boundaries of species are often not clear.) This interbreeding produced

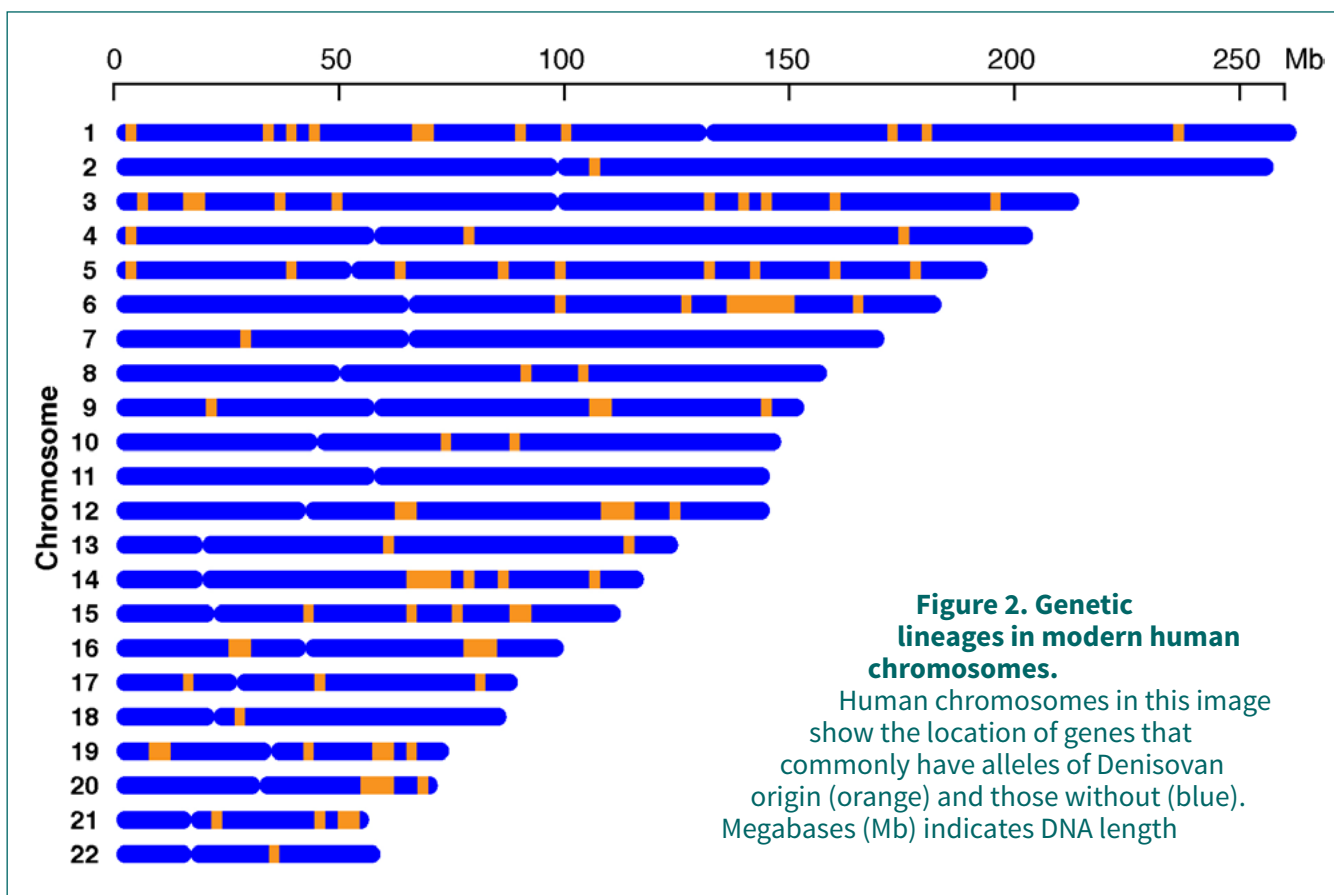
children with a mix of traits from both parents.

In Africa there is genetic evidence of older *Homo* lineages interbreeding with our own. When *Homo sapiens* expanded their range into Eurasia, they interbred with Neanderthals (usually classified as *Homo neanderthalensis*) (Figure 2). A third lineage in Asia, Denisovans, also interbred with both humans and Neanderthals.

These periods of interbreeding resulted in our DNA being a mix of different lineages (Figure 3). For example, modern Pacific populations have more archaic hominin ancestry than anyone else in the world.

It is not uncommon for archaic alleles, about half Neanderthal and half Denisovan, to make up five to eight percent of some modern human genomes - several hundred genes scattered across the chromosomes (Figure 3).

Many of these genes resulted in differences in structure, function or behaviour, such as alleles associated with hair colour or



susceptibility to depression. For example, you might be able to fight off a virus because of the Neanderthal versions of immune genes that you carry.

There are two alternative theories explaining why our genome contains only a small proportion of widely scattered, archaic alleles. The first theory is that interbreeding resulted in offspring with low fertility, so that few alleles were passed on. The second theory suggests that the populations of Neanderthals were small compared with humans, explaining why the proportion of archaic alleles is small. This theory argues that the offspring of the interbreeding were healthy and fertile, and that the different populations merged.

Geneticists are investigating the exact scenario of interbreeding between populations of Homo lineages in Europe and Asia, using larger and larger DNA sequence datasets from living populations and more sophisticated mathematical and population models. Population interactions were also likely to have also involved the spread of new parasites and diseases.

## Evidence from parasites

Modern human head lice, *Pediculus humanus*, right, are composed of at least six lineages. Our best estimates are that this diversity is about one million years old, suggesting that human populations may have acquired lice populations that evolved in association with archaic hominin hosts. For example, interbreeding between humans and Neanderthals might have resulted in an exchange of parasites.

One of our six lice lineages is common, and contains genetic diversity that formed while humans were leaving Africa (100,000 to 50,000 years ago), showing that the population of head lice grew at the same time. This suggests that lice travelled with humans out of Africa, and that interbreeding between archaic hominins resulted in the addition of new head lice lineages to our existing parasites.

A range of commensals (unrelated species living together without harming or benefiting each other) and parasites that travelled and evolved with humans shows that their



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population history (inferred from genetic diversity) often matches their host (human) population history. Examples include the stomach microbe *Helicobacter pylori* and malaria *Plasmodium falciparum*.

Interestingly, a new type of louse has also evolved since humans began wearing clothes – the human body-louse is adapted to living in clothes and almost never reproduces with head-lice, even on the same human host.

## Adaptation in Eurasia

Interbreeding among archaic hominins might have benefited populations moving from Africa into new environments in Eurasia. Expanding populations usually have low genetic diversity, which would leave the population less able to adapt to challenging new environments. It is possible that mating with locals added to the gene pool alleles for a warmer covering of hair, or protection from diseases with improved immune responses.

A few alleles, known to have been in the genomes of Denisovans or Neanderthals, have been found to be common in particular human populations, suggesting they provide a selective advantage in particular environments. For example, an allele of the *EPAS1* gene that confers resistance to hypoxia at high elevation is very common in the modern Tibetan population. The allele provides a selective advantage to people living at high elevation where air pressure reduces the available oxygen. This particular allele of the *EPAS1* gene seems to have



*Neanderthal child by Alberto Álvarez Marsal, CC BY-SA, Wikimedia Commons.*

originated with a Denisovan population and been introduced into human populations via interbreeding.

## Open access links

- Blaxland, B. (2018). Hominid and hominin – what's the difference? <https://australianmuseum.net.au/learn/science/human-evolution/hominid-and-hominin-whats-the-difference/>
- Danneman M., Kelso, J. (2017). The contribution of Neanderthals to phenotype variation in modern humans. *The American Journal of Human Genetics* 101: 578–589. <https://doi.org/10.1016/j.ajhg.2017.09.010>
- Wei-Haas, M. (2019). Multiple lines of mysterious ancient humans interbred with us. <https://www.nationalgeographic.com/science/2019/04/enigmatic-human-relative-outlived-neanderthals/>

### Ngā Kupu

**Hanumi** – Interbreeding

**Huakita taupiri** – Commensal bacteria

**Huinga ira** – Genome

**Kukuwhatanga** – Evolution

**Pirinoa** – Parasite

**Pītau ira** – DNA

**Pūira** – Chromosome

**Urutaunga whaiaroaro** – Functional or physiological adaptation

**Whakapapa** – Lineage

From *Paekupu and Te Aka Dictionary*



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