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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

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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

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-lice 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

Ng Kupu

Hanumi – Interbreeding

Huakita taupiri – Commensal bacteria

Huinga ira – Genome

Kukuwhatanga – Evolution

Pirinoa – Parasite

P tau ira – DNA

P ira – Chromosome

Urutaunga whaiaroaro – Functional or physiological adaptation

Whakapapa – Lineage

Neanderthal child by Alberto Álvarez Marsal, CC BY-NC 4.0 International / <https://www.flickr.com/photos/14811470@N00/2411111111/>

Open access links

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