

Chapter 35

Evolutionary Aside 35.3-- Sequencing of the Neanderthal Genome Suggests Hybridization With Humans

In a technological tour de force, geneticists were able to recover DNA from bones of Neanderthals recovered from caves in Europe. Despite their antiquity, the bones contained bits of intact DNA, from which the scientists reconstructed the Neanderthal genome. A phylogeny was then constructed using this genome and that of genomes from human populations around the world. The chimp genome was used as an outgroup (see chapter 23 to review methods of phylogeny reconstruction).

The phylogeny indicated, as expected that human populations are monophyletic and that Neanderthals are the sister group to humans. Among human populations, African populations are at the base of the tree and are the sister taxon to all remaining populations.

However, in a surprisingly large number of DNA sites, Neanderthals and non-African human populations share character states not found in chimpanzees or African populations. A number of explanations could account for this pattern. Perhaps the character states evolved in the ancestor of hominids, after the divergence from chimpanzees, and subsequently were lost by African populations, or perhaps this is an example of convergent evolution, in which the non-African clade and Neanderthals independently evolved the same DNA characters. However, for reasons based on detailed statistical analysis, the scientists prefer an alternative explanation: the shared character states are the result of ancient hybridization that occurred after evolutionary divergence between the ancestors of African and non-African human populations. The result of this hybridization was that genes from Neanderthals made their way into the gene pool of the population that became the ancestor of all non-African populations extant today.

1. Greene, R.E. *et al.* 2010. A draft sequence of the Neandertal genome. *Nature* 328:710–722.