

# Neandertal sharing and gene flow haplotypes in modern humans

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Although Neanderthals share approximately 10% of genome with modern humans, including Africans, actual gene flow regions from Neandertal to modern humans account for only < 0.5% of the genome. Interbreeding between Neanderthals and ancestors of Eurasians is manifested in over 100 gene flow regions. More than ten thousand shared haplotypes dates back to around one million years ago; thus there have been at least two different deep lineages present at these loci, when one of the shared homologs was brought along by the Neanderthals when they left Africa about 400,000 years ago. Both ancient haplotypes had also remained and evolved continuously in Africa, until the last wave of “Out Of Africa” around 100, 000 years ago. Our newly identified, fine resolution dense Neandertal-Eurasian haplotypes provide unusual detailed interaction history between modern humans and Neandertal.

By scanning the Neandertal draft genome with six diverse modern human genome copies, the total Neandertal sharing regions on the whole genome is ranging from 3% (South African) to 7% (Papuan New Guinea). In addition, we have observed two types of gene flow haplotypes from Neandertal: (1) Most of the newly identified gene flow regions are formed by accumulation of Neandertal mutations on top of the ancient sharing haplotype during the 400,000 years while Neanderthals were outside Africa. Then Neandertal interbred with the ancestors of Eurasians ~100,000 years ago, passing back the newly assembled long range haplotype. (2) The second gene flow haplotype is the deep Neandertal lineage unique to Eurasians, in which the Eurasian gene tree is older than the African one. These regions are generally great than 1.5 million-year-old, and do not contain the above ancient sharing haplotypes with modern Africans.

