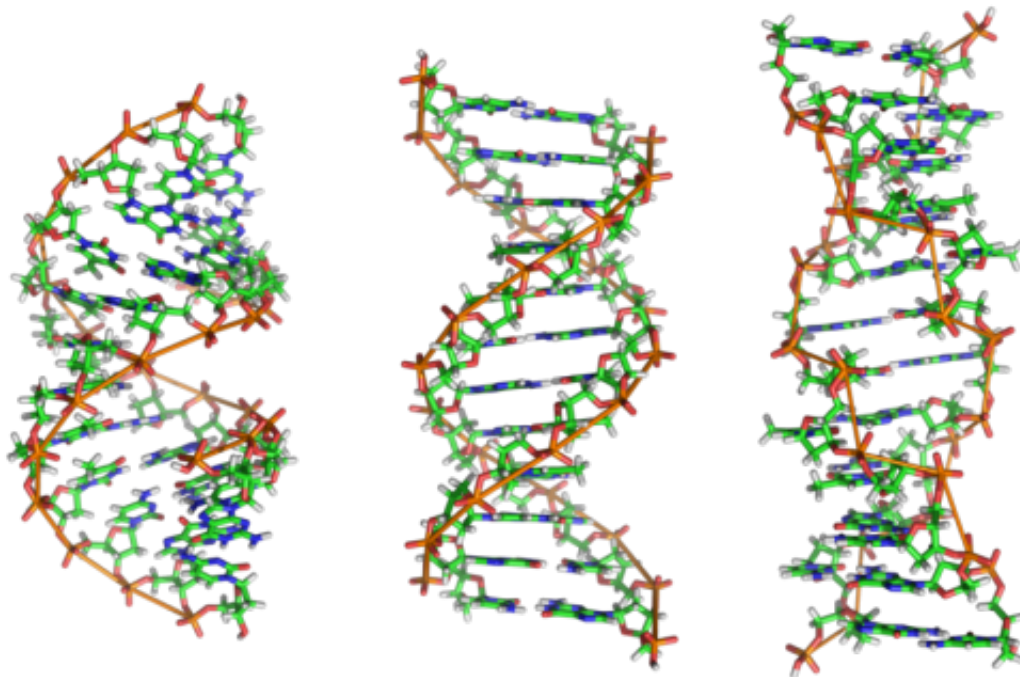


# DNA from an ancient, unidentified ancestor was passed down to humans living today

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From left to right, the structures of A-, B- and Z-DNA. Credit: Wikipedia

A new analysis of ancient genomes suggests that different branches of the human family tree interbred multiple times, and that some humans carry DNA from an archaic, unknown ancestor. Melissa Hubisz and Amy Williams of Cornell University and Adam Siepel of Cold Spring Harbor Laboratory report these findings in a study published 6th August in *PLOS Genetics*.

Roughly 50,000 years ago, a group of humans migrated out of Africa and interbred with Neanderthals in Eurasia. But that's not the only time that our ancient human ancestors and their relatives swapped DNA. The sequencing of genomes from Neanderthals and a less well-known ancient group, the Denisovans, has yielded many new insights into these interbreeding events and into the movement of ancient human populations. In the new paper, the researchers developed an algorithm for analyzing genomes that can identify segments of DNA that came from other species, even if that [gene flow](#) occurred thousands of years ago and came from an unknown source. They used the algorithm to look at genomes from two Neanderthals, a Denisovan and two African humans. The researchers found evidence that 3 percent of the Neanderthal genome came from ancient humans, and estimate that the interbreeding occurred between 200,000 and 300,000 years ago. Furthermore, 1 percent of the Denisovan [genome](#) likely came from an unknown and more distant relative, possibly Homo erectus, and about 15% of these "super-archaic" regions may have been passed down to [modern humans](#) who are alive today.

The new findings confirm previously reported cases of gene flow between ancient humans and their relatives, and also point to new instances of interbreeding. Given the number of these events, the researchers say that genetic exchange was likely whenever two groups overlapped in time and space. Their [new algorithm](#) solves the challenging problem of identifying tiny remnants of gene flow that occurred hundreds of thousands of years ago, when only a handful of ancient genomes are available. This algorithm may also be useful for studying gene flow in other species where interbreeding occurred, such as in wolves and dogs.

"What I think is exciting about this work is that it demonstrates what you can learn about deep [human](#) history by jointly reconstructing the full evolutionary history of a collection of sequences from both modern

humans and archaic hominins," said author Adam Siepel. "This new [algorithm](#) that Melissa has developed, ARGweaver-D, is able to reach back further in time than any other computational method I've seen. It seems to be especially powerful for detecting ancient introgression."

**More information:** Hubisz MJ, Williams AL, Siepel A (2020) Mapping gene flow between ancient hominins through demography-aware inference of the ancestral recombination graph. *PLoS Genet* 16(8): e1008895. [doi.org/10.1371/journal.pgen.1008895](https://doi.org/10.1371/journal.pgen.1008895)

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