

LEGACY FROM NEANDERTHAL/DENISOVA

Non-African humans carry a legacy of ancient interbreeding, with 1 to 4 percent of their genome tracing back to Neanderthals and Denisovans. That fraction is markedly higher in Papua New Guinean populations, who carry roughly twice as much archaic ancestry as other non-African groups.

Until recently, most of what we knew about this inheritance came from single-nucleotide variants. The availability of telomere-to-telomere (T2T) human genome assemblies, together with the first high-quality long-read sequencing of Papuan genomes, allowed Evan Eichler's group (1) to extend the analysis to structural variants: insertions, deletions, inversions and duplications that short-read sequencing struggles to resolve, especially in complex, repetitive regions of the genome.

The resulting map of archaic structural variation, built from Papuan and other pangenome assemblies, shows that these introgressed segments aren't randomly distributed: they sit near genes more often than expected, and a subset of them carries clear signatures of positive selection, having risen in frequency well after the initial admixture. Because Papuans carry so much more archaic DNA, their genomes offered the clearest view of this pattern, but the conclusion likely applies more broadly: what survived of our archaic inheritance tends to be what was useful.

1. <https://www.science.org/doi/10.1126/science.adz7518>