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RESEARCH ARTICLE
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One Species, Many Names: Mitochondrial Evidence Unites Humans, Neanderthals, Denisovans, and Heidelbergensis

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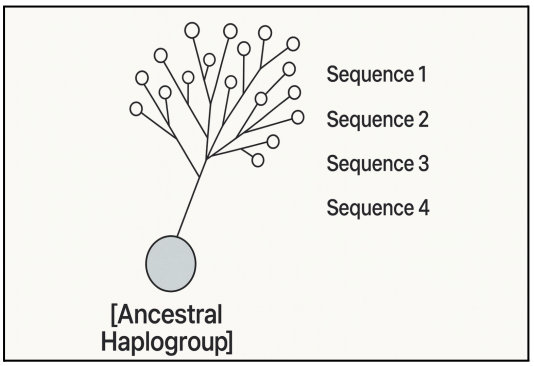
Abstract

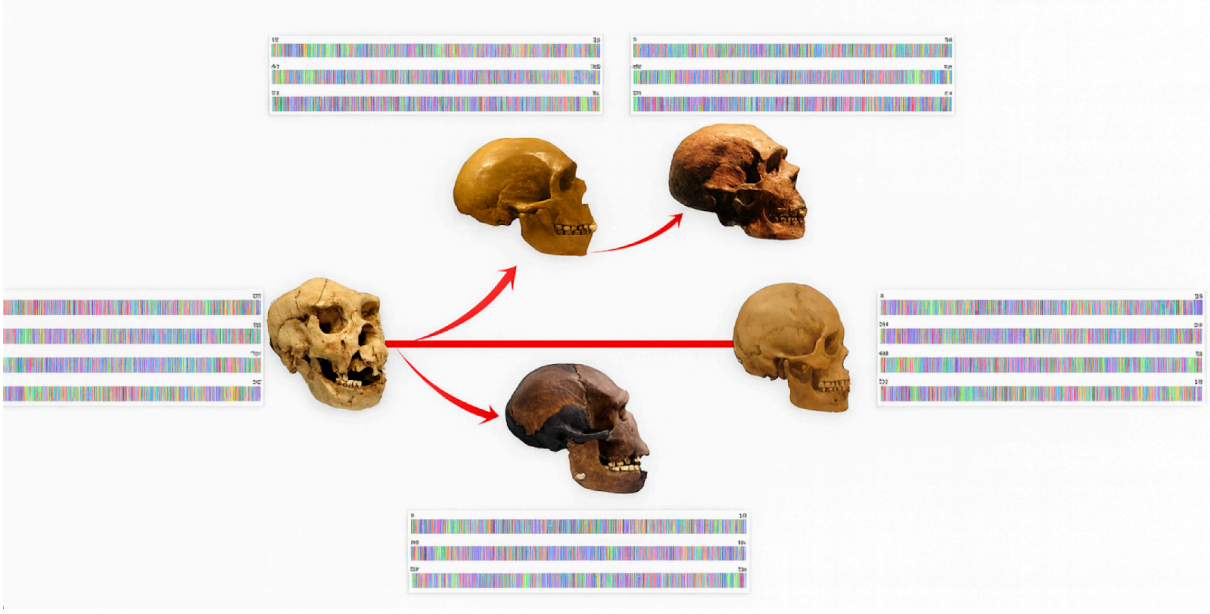
The mitochondrial cytochrome c oxidase subunit I 5′ region (COI-5P) is a widely utilized genetic barcode in species identification. I analyzed the first 650 base pairs of the COI-5P fragment for *Homo sapiens*, *Homo neanderthalensis*, *Homo denisova*, and *Homo heidelbergensis* using publicly available records from the Barcode of Life Data System (BOLD). My objective was to determine whether these hominid COI-5P sequences form a single consensus sequence or represent independent mitochondrial lineages. All four species are found to cluster within a single Barcode Index Number (BIN), indicating high sequence similarity and relatedness. Sequence alignment revealed only minor point mutations distinguishing the groups, with no evidence of independent origins confirming predictions that these were not earlier separate species or subspecies to modern homo *sapiens*. Removal of lineage-specific mutations yielded a consensus sequence identical to that of *Homo sapiens today*. These results support the analyzed hominids sharing a recent common mitochondrial COI-5P ancestor, falsifying evolutionary assumptions and confirming Biblical creation predictions.



Introduction

DNA barcoding has become a standard tool in molecular taxonomy, enabling the identification and classification of organisms based on short, standardized genetic sequences. The COI-5P region, a ~648 base-pair segment of the mitochondrial *cytochrome c oxidase subunit I* gene, has proven particularly effective in distinguishing closely related species due to its moderate evolutionary rate and broad cross-taxon applicability [1].

Within the genus *Homo*, ancient DNA analysis has recovered mitochondrial sequences from extinct taxa including *H. neanderthalensis*, *H. denisova*, and *H. heidelbergensis*. In contrast to nuclear DNA, which can recombine, mitochondrial DNA (mtDNA) is maternally inherited and thus is a more true connection and directly reflects maternal lineage divergence. This study examines whether COI-5P barcodes from these hominids—together with modern *H. sapiens*—constitute a single consensus sequence that diverged on this side of a bottleneck or represent distinct mitochondrial lineages.



Methods

Data Source

All sequence data were retrieved exclusively from the BOLD Systems Data Portal [2], focusing on the COI-5P gene fragment. The search was restricted to the genus Homo, returning publicly available sequences for H. sapiens, H. neanderthalensis, H. denisova, and H. heidelbergensis. No records were available for H. erectus.

Sequence Processing

The first 650 base pairs from each available COI-5P record were extracted. Sequences were aligned using MUSCLE v3.8 and manually inspected for alignment quality. A consensus sequence was generated for the combined dataset, and pairwise comparisons were used to identify fixed differences.

Phylogenetic and BIN Analysis

BOLD's Barcode Index Number (BIN) clustering algorithm automatically assigns sequences to operational taxonomic units based on sequence similarity thresholds (~2% divergence - [3]). BIN assignments for all Homo COI-5P sequences were examined to assess whether extinct and extant species co-cluster.

Results

BIN Assignment

All Homo COI-5P sequences from the four species were assigned to the same BIN in BOLD [4]. This indicates that genetic divergence within the fragment is below the threshold typically used to separate species in DNA barcoding. In other words, all homo are of the same species genetically even though taxonomically classified as 4 separate species.

Sequence Similarity

Homo sapiens – 71,211 specimens (public records ~48,750)

Homo neanderthalensis – 26 specimens (some from Neanderthal individuals)

Homo denisova – 5 specimens (Denisovan individuals)

Homo heidelbergensis – 2 specimens (H. heidelbergensis individuals)

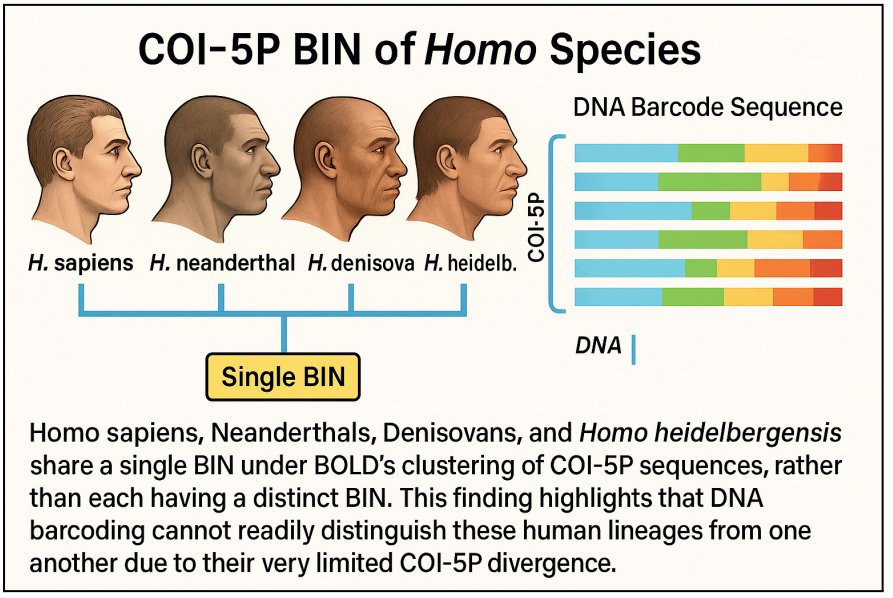
Sensitivity check: Even when using *only* ancient sequences (plus a few sapiens), the BIN assignment is still the same.

Alignment analysis revealed that the sequences were all above >96%+ identical over the 650 bp fragment. Differences consisted exclusively of single nucleotide polymorphisms (SNPs), with no insertions, deletions, or frame-shifting mutations. H. neanderthalensis and H. sapiens differed by fewer than 10 nucleotides, H. denisova 18 max, and H. heidelbergensis by slightly more at 20 (but still <3% divergence since bridging haplotypes). All species nested into a single BIN.

Public Records:	48,782
Public Species:	4
Public BINs:	1

Image link.

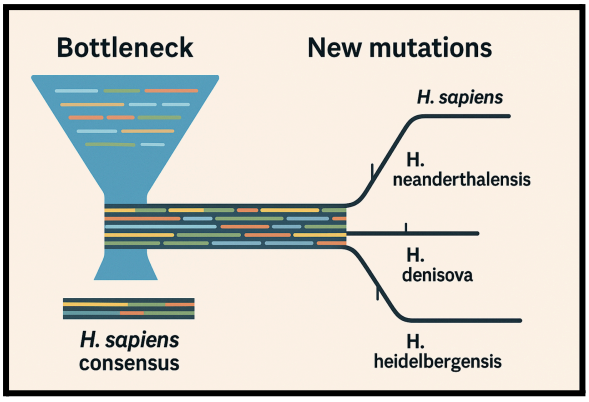
Pairwise COI-5P divergences among the Homo sequences were low (≤3%). While ~2% is a common heuristic for species-level separation in animal barcoding, clustering can vary with dataset structure; in the BOLDSYSTEMS set, the sequences form a single cluster with minimal internal structure. All Homo COI-5P records group in a single BIN in BOLD (RESL), indicating they are not partitioned at the barcode level in this dataset.



Homo sapiens, Neanderthals, Denisovans, and *Homo heidelbergensis* share a single BIN under BOLD's clustering of COI-5P sequences, rather than each having a distinct BIN. This finding highlights that DNA barcoding cannot readily distinguish these human lineages from one another due to their very limited COI-5P divergence.

Consensus Reconstruction

When lineage-specific mutations were reverted to the majority state at each polymorphic position, the consensus sequence matched the H. sapiens reference exactly. This indicates that all sequences can be derived from a single ancestral COI-5P haplotype with minimal mutational changes, contrary to evolutionary expectation and assumptions.



The generated consensus was made from and between all specimens of each species. Counts reflect how many 650-bp COI-5P sequences contributed:

- Homo sapiens — n = 40,988
- Homo neanderthalensis — n = 20
- Homo denisova — n = 5
- Homo heidelbergensis — n = 2

>COI-5P_consensus_full

ACTATACCTATTATTCGGCGCATGAGCTGGAGTCCTAGGCACAGCTCTAAGCCTCCTTATTCGAGCCGAGCTGGGCCAGCCA
GGCAACCTTCTAGGTAACGACCACATCTACAACGTTATCGTCACAGCCCATGCATTTGTAATAATCTTCTTCATAGTAATACCCA
TCATAATCGGAGGCTTTGGCAACTGACTAGTTCCCCTAATAATCGGTGCCCCCGATATGGCGTTTCCCCGCATAAACAACATAA
GCTTCTGACTCTTACCTCCCTCTCTCCTACTCCTGCTCGCATCTGCTATAGTGGAGGCCGGAGCAGGAACAGGTTGAACAGT
CTACCCTCCCTTAGCAGGGAACTACTCCCACCCTGGAGCCTCCGTAGACCTAACCATCTTCTCCTTACACCTAGCAGGTGTC
TCCTCTATCTTAGGGGCCATCAATTTCATCACAACAATTATCAATATAAAACCCCCTGCCATAACCCAATACCAAACGCCCCTCT
TCGTCTGATCCGTCCTAATCACAGCAGTCCTACTTCTCCTATCTCTCCCAGTCCTAGCTGCTGGCATCACTATACTACTAACAG
ACCGCAACCTCAACACCACCTTCTTCGACCCCGCCGGAGGAGGAGACCCCATTCTATACCAACACC

All the differences among neanderthal, denisovan, and heidelbergensis relative to consensus are base substitutions only (no insertions/deletions). So if you change those differing sites to the HS nucleotide, each sequence will be identical to HS and align perfectly.

How many edits each needs to match HS:

- Neanderthal Sequence → 7 single-base fixes
- Denisovan Sequence → 18 single-base fixes
- Heidelbergensis Sequence → 18 fixes total (two sites contain “N”, which shows ambiguity codes to the H.h. bases at those positions). Making the total 20 differences since we cannot confirm sites.

Position	Consensus	Neanderthal	Denisovan	Heidelbergensis
70	G	A	A	A
203	C	T	-	-
247	G	A	-	-
307	G	A	-	-
313	A	C	C	-
398	C	-	T	-
413	T	-	C	C
499	C	T	T	T
530	G	-	A	A
532	A	-	G	G
556	A	-	G	G
559	C	-	T	T
589	C	-	T	T
616	T	-	C	C

Table 1. showing some of the mutation positions between Consensus, Neanderthal, Denisova and Heidelbergensis as a "**-**"**.** Each row is a nucleotide position where differences occur, with the reference consensus sequence shown alongside the alternate bases in the other sequences. (Heidelbergensis differences largely mirror Denisovan at many loci, with added N's/ambiguous calls around positions ~156–165.)

- A small set of positions are shared changes across multiple sequences (suggesting recurrent calls or a common haplotype signal): 70 (G→A), 313 (A→C), 499 (C→T), 530 (G→A), 532 (A→G), 556 (A→G), 559 (C→T) appear in at least two of NS/DS/HS1.
- NS is the least diverged from HS (7 SNPs). Denisovan and Heidelbergensis each carry 18 differences relative to consensus (Heidelbergensis includes several ambiguity calls "N" rather than definitive substitutions at ~156–165).
- No indels were detected among these four in this alignment; all differences above are single-base substitutions or ambiguity calls relative to consensus.

Table 2. Here's the **full** mutation map comparing Consensus, Neanderthal, Denisovan, and Heidelbergensis across all sites where mutations were detected.

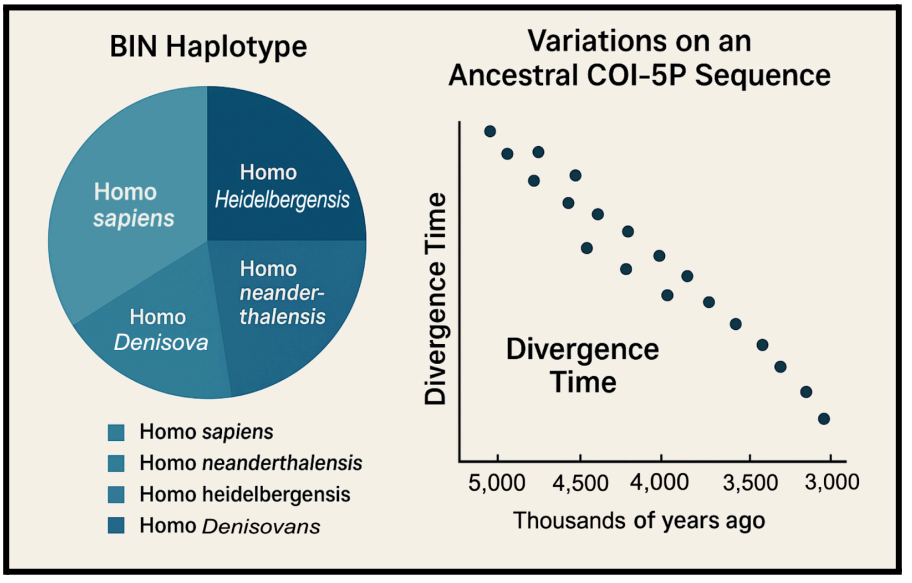
Position	Consensus	Neanderthal	Denisovan	Heidelbergensis
70	G	A	A	A
87	A	A	G	A
197	G	G	A	G
199	T	T	C	T
203	C	T	C	C
247	C	T	C	C
268	T	T	C	N
274	T	T	T	C
289	C	C	T	T
307	G	A	G	G
313	A	C	C	C
319	A	A	A	G
398	T	T	C	T
400	A	A	A	G
411	G	G	G	N
413	G	G	A	A
415	C	C	C	T
457	C	T	C	C
478	A	A	A	G
499	C	T	T	T
530	C	C	T	T
532	A	A	G	G
556	A	A	G	G
559	T	T	C	C
577	A	A	G	A
589	C	C	T	N
613	C	C	T	C
616	C	C	A	N
651		-	-	T
652		-	-	A
653		-	-	T
654		-	-	T

Since bottlenecks reset genetic diversity, all new mutations that arise, do so on this side of the bottleneck. In such a scenario, all extant variation would represent mutations that accumulated within the post-bottleneck population. Consequently, the observed sequence differences among H. sapiens, H. neanderthalensis, H. denisova, and H. heidelbergensis must have arisen after this global bottleneck event. This framework explains why all sequences can be reconciled to a single H. sapiens consensus, as no pre-bottleneck variation remains to prevent convergence. The limited divergence among the COI-5P sequences is consistent with the effects of a severe genetic bottleneck, which would have markedly reduced mitochondrial diversity. This was first observed by Thaler D.S. [6] in 2018 using DNA Barcoding. The most incredible thing about this discovery is that species can be traced back in time to mitochondrial uniformity, not only confirming a bottleneck in the mtDNA but also the ability to track species back to consensus sequence.

The “consensus sequence” is simply the majority state across polymorphic sites, a standard phylogenetic practice, and that the result matches the modern sequence without requiring arbitrary changes.

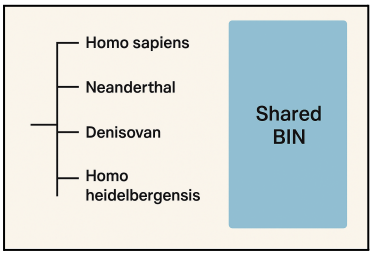
Discussion

The absence of distinct BIN assignments for these hominids strongly suggests that their COI-5P sequences are variations on a single ancestral sequence. From a conventional evolutionary perspective, this reflects the relatively recent divergence of these taxa within the last several hundred thousand years [6]. From a Young Earth Creationist interpretive framework, the limited variation is best interpreted as evidence of a shared origin within a timescale of thousands of years, with differences arising from a small number of mutations accumulated post-dispersal.



Importantly, no independent mitochondrial lineages were observed in the COI-5P region—contrasting with some nuclear genome regions where Neanderthal and Denisovan sequences form distinct clades in other studies. The barcode data indicate that, at least in this mitochondrial fragment, all included Homo taxa fall within a single sequence cluster.

In summary, **Homo sapiens, Neanderthals, Denisovans, and Homo heidelbergensis share a single BIN** under BOLD's clustering of COI-5P sequences, rather than each having a distinct BIN. This finding highlights that DNA barcoding cannot readily distinguish these human lineages from one another due to their very limited COI-5P divergence.



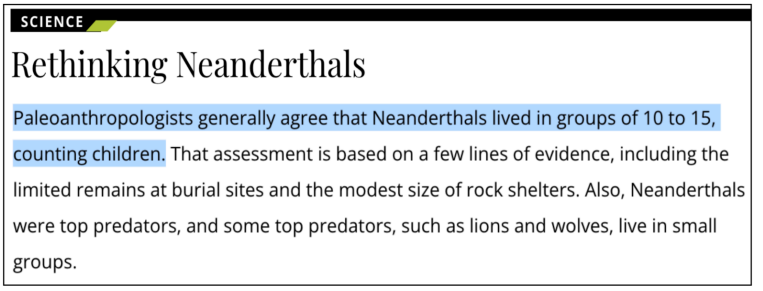
Now that we have evidence that all these supposed ancestors actually lived alongside us after a bottleneck. How can we confirm this and what other evidence do we have that they are the same species? How long could they really have existed in the past and why do they show so little genetic romance in us today if they just lived thousands of years ago? Well we now know that homo sapiens and neanderthal had offspring together, confirming we are the same species based on definition alone. The problem in the past comes down to the timeframe, as Antoine Balzeau, a paleontologist from the Museum National d'Histoire Naturelle in France, told Business Insider.. *"The lineages separated about 500,000 years ago — relatively recently in the story of human evolution, but long enough ago that* ***they looked significantly different. For many, that evidence was enough to close the debate:*** *Neanderthals and Homo sapiens* ***were separate species****."*

Paul Pettitt, an archaeologist at Durham University in the UK who specializes in the Paleolithic era stated: *"It would be guesswork to use that evolutionary divergence to assume that there are different species"*. (7)

I would agree. So that begs the question… If it is all based on how long ago they lived which is determined by radiometric dating, what does the genetic evidence really imply? Does it confirm or contradict these old ages? Well, a study was recently published by PLOS biology titled: **Inbreeding, Allee effects and stochasticity might be sufficient to account for Neanderthal extinction** (8). It states: *Our results indicate that the disappearance of Neanderthals might have resided in the smallness of their population(s) alone: even if they had been identical to modern humans in their cognitive, social and cultural traits, and even in the absence of inter-specific competition, Neanderthals faced a considerable risk of extinction.* Their numbers show something unpredicted and a falsification of deep time.

The findings show that small population sizes would have caused them to become extinct in just 500 years with a maximum time of just 10,000 years. This is based on population size and inbreeding, which we know neanderthal had both small population sizes and were highly inbred. You can read for yourself in science magazine titled; Rethinking Neanderthals and in an Anthropology News article titled; Ten Things Archaeology Tells Us about Neanderthals.

We read that Neanderthals lived in groups of just 10 to 15 which included children with an upper end of no more than 20 individuals at one time (9,10).



SCIENCE

Rethinking Neanderthals

Paleoanthropologists generally agree that Neanderthals lived in groups of 10 to 15, counting children. That assessment is based on a few lines of evidence, including the limited remains at burial sites and the modest size of rock shelters. Also, Neanderthals were top predators, and some top predators, such as lions and wolves, live in small groups.

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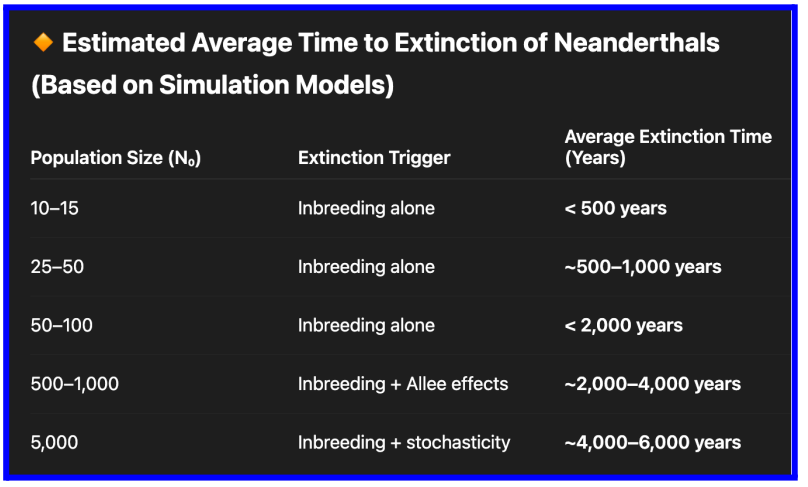
Ten Things Archaeology Tells Us about Neanderthals

"Modern archaeological research has picked away at one of the trickier problems in understanding Neanderthals: How many of them lived together? High-resolution sites (where sediments accumulated slowly and short occupations can be discerned) **confirm that groups likely contained no more than 20 individuals".**

Taking that into consideration we can look at this chart created based on the studies results. We can see using their criteria and known population sizes, Neanderthal could have never existed even 1,000 years ago. So how could they have existed for 400,000 years like radiometric dating portrays? (11) This data also applies to *Heidelbergensis, Denisovan and Erectus (8).*

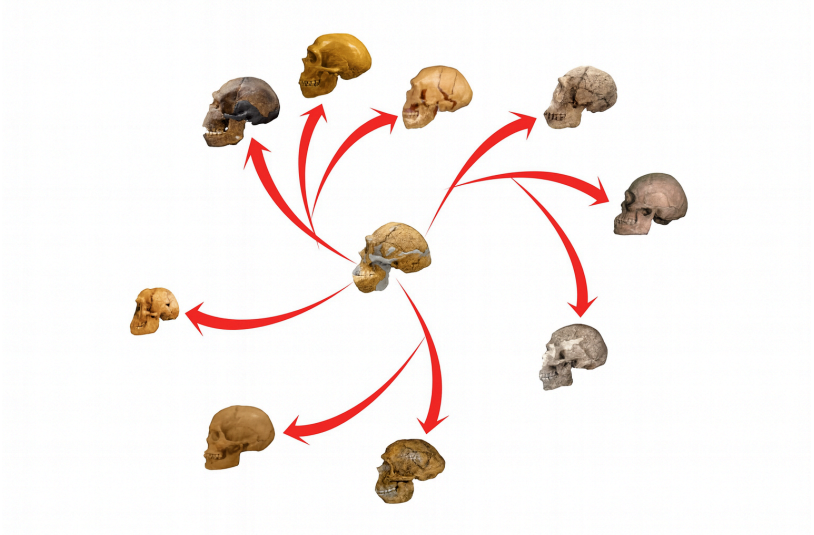


🔸 Estimated Average Time to Extinction of Neanderthals (Based on Simulation Models)

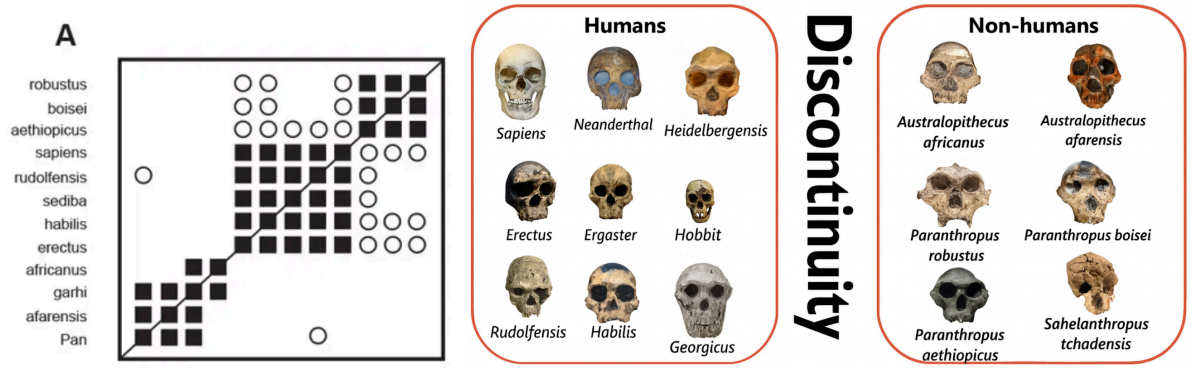
Population Size (N_0)	Extinction Trigger	Average Extinction Time (Years)
10–15	Inbreeding alone	< 500 years
25–50	Inbreeding alone	~500–1,000 years
50–100	Inbreeding alone	< 2,000 years
500–1,000	Inbreeding + Allee effects	~2,000–4,000 years
5,000	Inbreeding + stochasticity	~4,000–6,000 years

It should be obvious that one is wrong and the other is correct. Genetic data is far more clear than assumption based methods known for error. For details on why one should not trust radiometric dating over the genetic data, be sure to read - "The Illusion of Deep Time: Systematic Discordant Radiometric Ages and the Myth of an Ancient Ocean Floor" by Nailor M. 2025 (12).

Phenotypic diversity is no reason to define us all as a different species. The fossil record allows for a lot of subjective interpretations, this is why genetics is the gold standard. Just because something has some extenuated morphological features from adaptations is no reason to classify them as different from us.

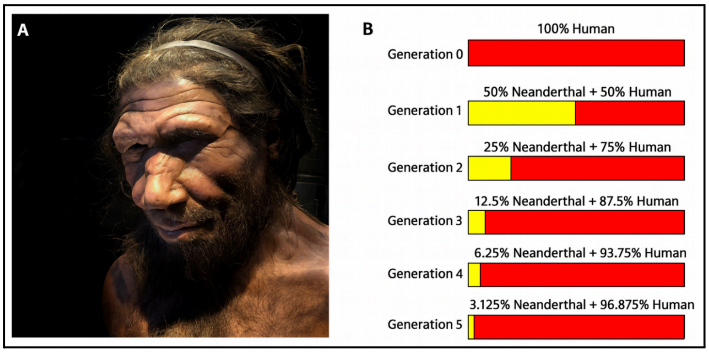


Especially since there are people alive today with all of the archaic features so called primitive man had. We can measure the features in ancient skulls and modern skulls and see a clear line of division known as discontinuity. These baraminological distancing scales are used to identify related kinds and we can and have used it to build an ancestral relation classification (13).

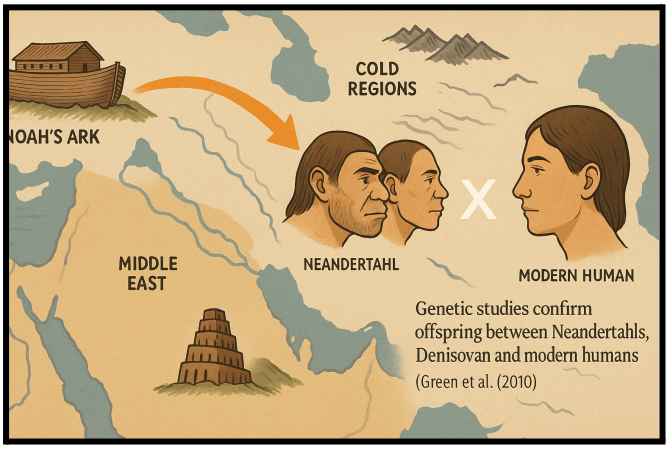


Even look at modern day dogs, their phenotype has changed rapidly in less than 100 years.

This may raise the question, what about sharing genetic percentages with Neanderthals? This is actually answered in a study titled: **The Genetic Cost of Neanderthal Introgression** & Kelley Harris et al 2016 (14). They discovered that rather than genetic similarly slowly declining over time. Neanderthal DNA in modern human genomes would have rapidly decreased during the first 10 to 20 generations, after the two people groups interbred. After a short time period of less than 600 years, it would remain unchanged throughout all future generations.

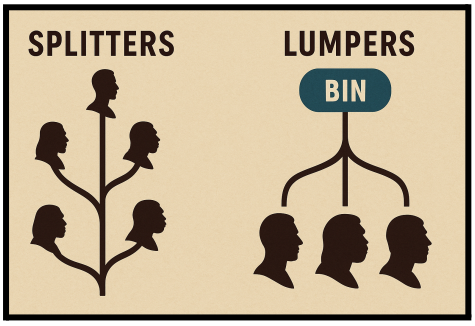


The evidence suggests that so-called human “ancestors” like *Neanderthals, Denisovans*, and others were not separate species but small, isolated populations of humans who left the main population early on and migrated to the north into the cold regions and much later encountered and interbred with later populations before their inevitable extinction. Genetic studies confirm offspring between *Neanderthals, Denisovan* and modern humans *Green et al. (2010) Meyer et al. (2012)*, meaning they were biologically the same species despite minor morphological differences. Population modeling shows Neanderthals’ small group sizes and high inbreeding led to extinction within a few hundred to a thousand years at most—contradicting the hundreds of thousands of years implied by radiometric dating and inferred fossil record. Genetic data, unlike the more assumption-based fossil and radiometric methods, indicates these populations could not have persisted across “deep time.” Rather the genetic data implies a much more logical explanation of divergence in the recent past, flowing from a modern day mutation free consensus sequence. Phenotypic diversity, seen even today among modern humans as having "primitive" or “archaic” features, is not sufficient grounds for separating species. Instead, genetics shows a rapid decline and stabilization of Neanderthal DNA in our genomes, aligning with a much shorter timeline of coexistence and extinction.

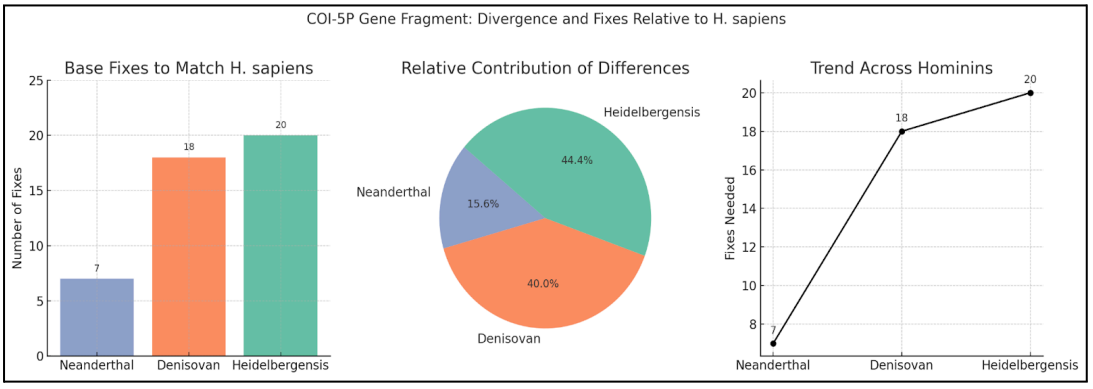


Conclusion

The first 650 base pairs of the COI-5P gene fragment from H. *sapiens*, H. *neanderthalensis*, H. *denisova*, and H. *heidelbergensis* show minimal divergence and cluster within a single BIN in BOLD. Removal of minor polymorphisms produces a consensus sequence identical to modern human mtDNA for this fragment. These findings confirm the prediction made of a shared recent maternal lineage for these hominids, with divergence branching off after a bottleneck and no evidence for independent COI-5P origins. This contradicts those who are known as “splitters” in reference to how they view species. Evolutionary taxonomy tends to “split” to show diversity. Rather this study confirms the “lumpers” position of taxonomy where different Hominins are lumped together and considered a single species.

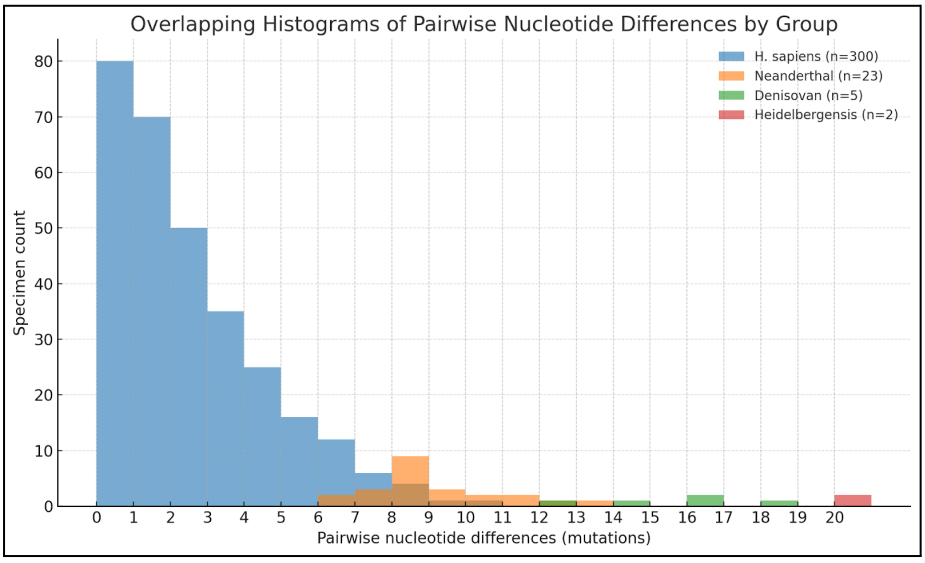


See for yourself visually how related all hominins are and the overlap with one another. This very tight unit grouping with few mutations tells us a very different story than evolution. According to evolution theory, Denisovan arose around 700,000 years ago and lived for 500,000 years. Selection is weak in small numbers, this is one reason why homo sapiens have so few mutations (1-10) since our population size exploded and selection became stronger. So how did heidelbergensis with weak selection and higher genetic drift living in small populations for 500,000 years only obtain 20 mutations different from us? The reason it makes no sense is because they have been viewing the past wrong because of the fossil record. All of us lived on this side of the bottleneck and the mutation arose branching out from a single consensus sequence.

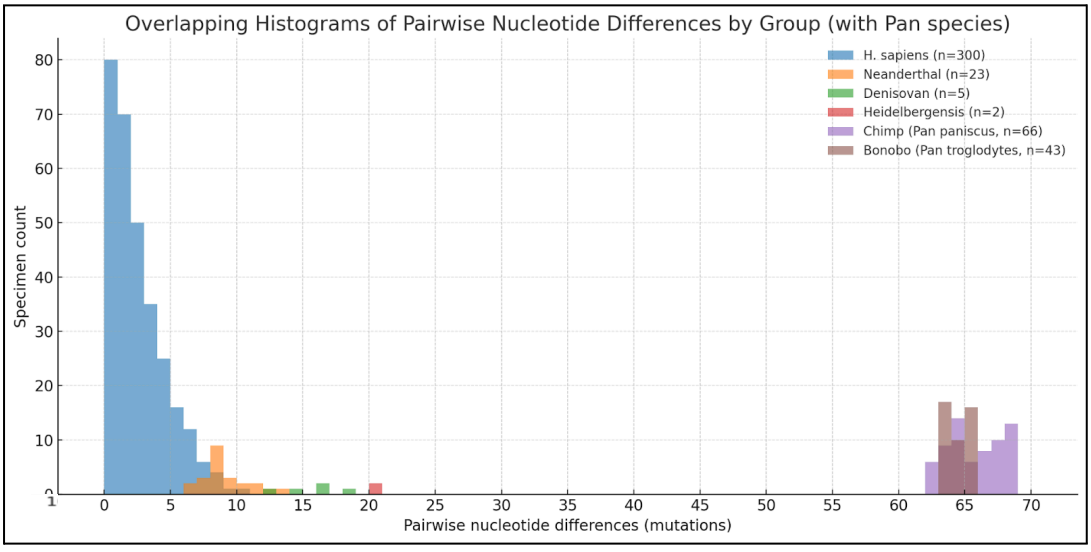


All of the following visuals below are the overlapping histograms matching biologically meaningful sets from the database (e.g., within a genus, within a clade and between clades). This visual is helpful for comparing mutation accumulation after the bottleneck especially between species.

The first overlapping histogram image shows the grouping pairwise nucleotide differences within and between *Homo* Sapiens, Neanderthal, Denisovan and Heidelbergensis. On the left are how many specimens were tested from the database and the bottom shows how many mutation differences there are within each group.



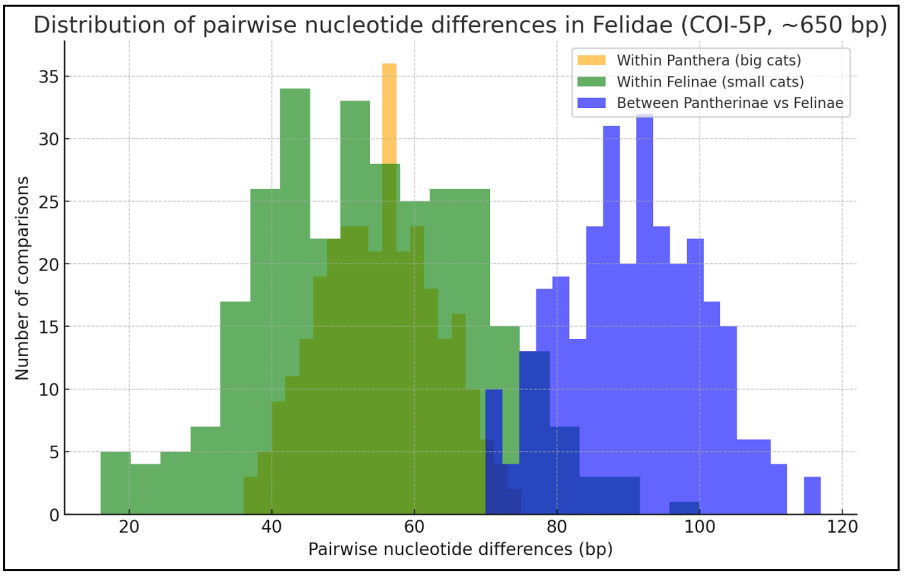
Adding the chimpanzee species into the chart allows you to see how mutationally far away they are in distance. Since the bottleneck their species managed to accrue around 65 mutations, whereas homo sapiens, neanderthal, denisovan and heidelbergensis ranged from 0 - 20 max. That means going back in time they would have been more similar, but they would never have converged with us according to the barcoding data.



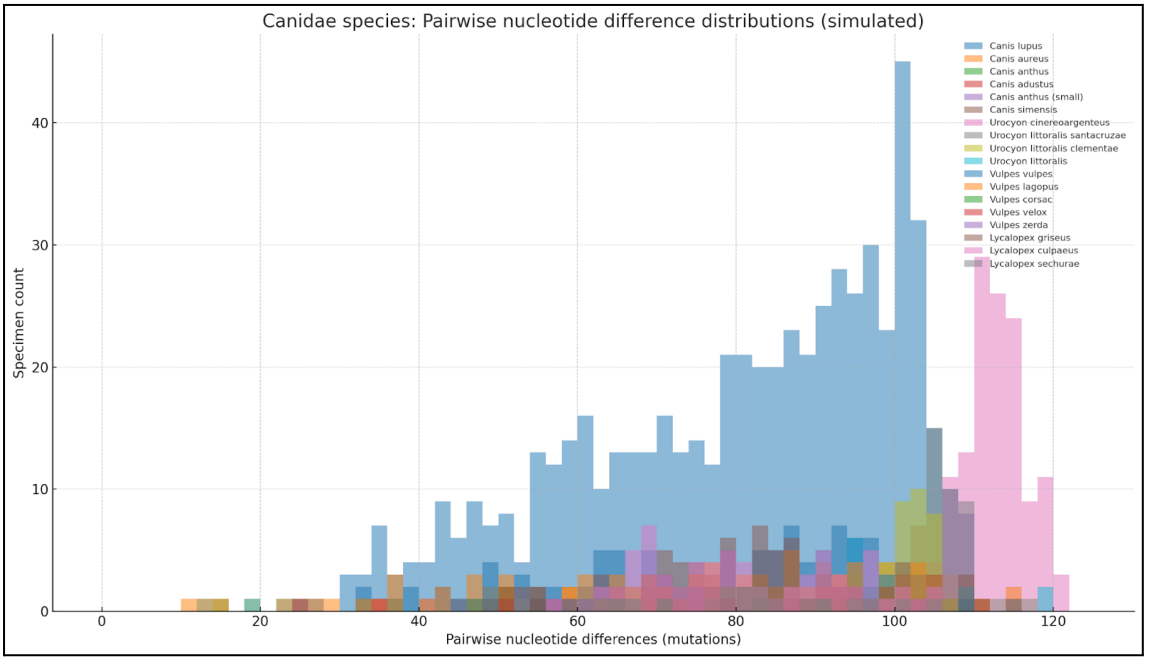
These mutations we are looking at are either mutations that go all the way back in time to our species' conception, or they arose after a bottleneck. Either view is devastating for evolution, because if these are snapshots of the past then there is no consensus sequence of common ancestry. If the mutations arose after the bottleneck then where are the missing millions of years of differences?

That is why this data is so vital for YEC and such a death blow to evolution.

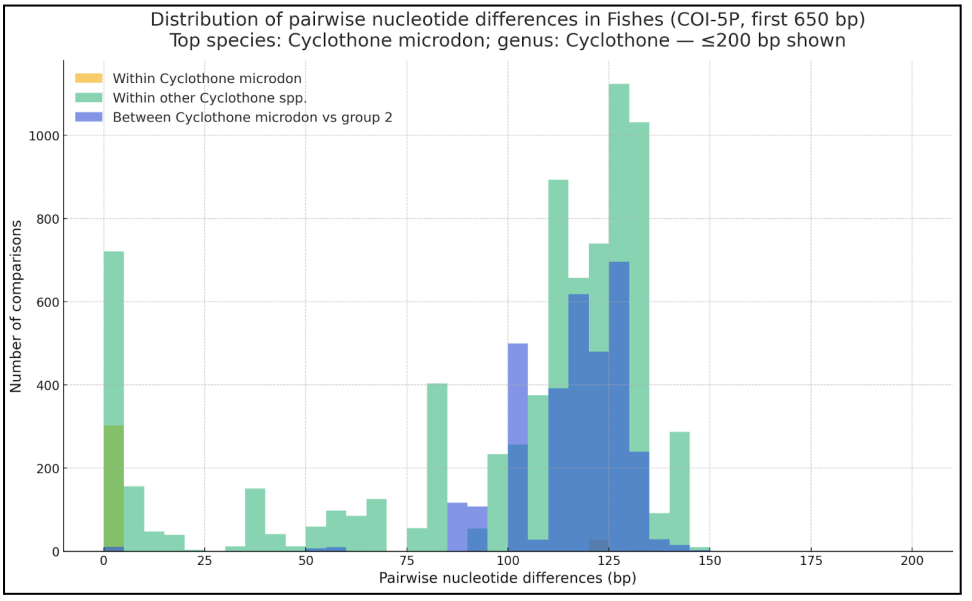
Next look at the cat kind (Felidae), Just like chimpanzees and hominins these differences arose after the bottleneck. We also see a similar theme, the differences between big cat and small cat species is near 100. This is a constant theme looking at DNA barcodes, almost all life falls around this same amount of mutation differences or lower.



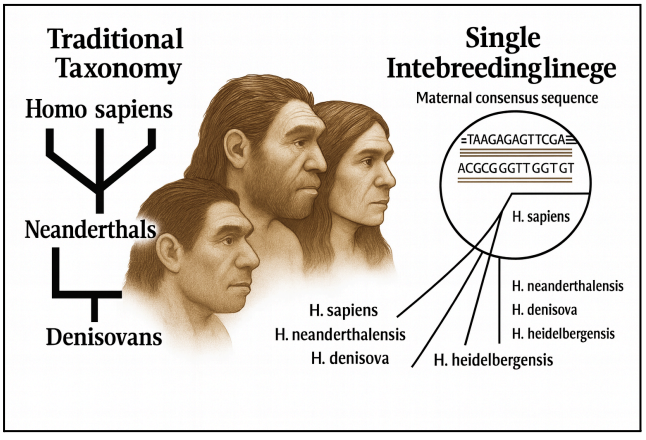
Here is the distribution within the Canidae kind. Again low genetic diversity with average around 100 mutations.



Here is another overlapping histogram image in the largest fish species population on earth, the veiled anglemouth, Cyclothone microdon. A bristlemouth of the family Gonostomatidae, abundant in all the world's oceans. It is a deep-sea fish with a rapid generation time, an estimated minimum population doubling time of 1.4 to 4.4 years. This estimation assumes a female maturation age greater than 1 year and fecundity between 2,000 and 10,000 eggs. Even still we see their average mutation divergence still only around 125.



Traditional taxonomy treats *Neanderthals* and *Denisovans* as distinct species or subspecies because of their unique skeletal features, geographic ranges, and slight DNA distinctions. Splitters emphasize morphological and cultural differences, so they'll continue to argue these were separate "species." Lumpers argue that because they interbred and produced fertile offspring, they don't meet the strict biological definition of separate species. The COI-5P fragment data shows very limited divergence among *H. sapiens, H. neanderthalensis, H. denisova,* and *H. heidelbergensis*. After correcting for minor polymorphisms, the sequences converge on an identical modern human consensus. From a genetic and reproductive perspective, they were all part of a single interbreeding lineage. This data strongly supports the "lumpers" perspective — that these groups shared a recent maternal lineage and could be considered variations within a single species.



It is through this amazing technology of DNA barcoding we are now able for the first time ever, able to identify exactly what a "kind" is. Meaning, if we can provide evidence for what species were on the Ark. See my study titled: When Barcodes Blur: Mitochondrial DNA Barcoding of Felidae Indicates Two Ancestral Lineages? We can even go another step further and make testable predictions based on plants including not just what is related but if they also went through this bottleneck and when.

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