One Ancestral Hominin Lineage Across Modern and Archaic Homo: A Creation-Model Test of a Recent Bottleneck

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ABSTRACT

The biblical creation model places modern humans and archaic *Homo* populations together on the near side of a recent, severe global bottleneck, and it makes a hard genetic prediction: their mitochondrial lineages should form one bounded, continuous human genealogy, not separate deep branches. I test that prediction on the cytochrome c oxidase subunit I barcode (COI-5P), the standard 650 base pair animal marker, across modern *Homo* sapiens, Neanderthals, Denisovans, and the Sima de los Huesos hominin catalogued in BOLD as *Homo* heidelbergensis. A marker-specific audit recovered 23,856 modern, 11 Neanderthal, three Denisovan, and two Sima COI-5P records, and all four labels are represented in a single Barcode Index Number, BOLD:AAA0001. Using one observed representative per lineage with chimpanzee and gorilla as outgroups, I evaluated all 15 rooted *Homo* topologies under HKY85+Γ4 and reconstructed ancestral states probabilistically at every variable site. The result is unambiguous. The four *Homo* lineages differ from one another by only 8 to 20 substitutions while differing from the apes by 65 to 71, so the barcode gap that marks a species boundary falls between *Homo* and the apes and nowhere among the *Homo* lineages. The rooted analysis groups modern human with Neanderthal (81.1% support) and Denisovan with Sima (70.5%) inside one *Homo* clade, and it reconstructs an ancestral sequence belonging to no living human and no archaic tip, a distinct founder at the root, resolved to posterior probability at or above 0.95 at four sites. This is the bounded maternal genealogy the creation model predicts. The timing of that genealogy is a separate question, and I answer it not from the barcode but from the Sima femur itself. In a cave that is wet and mild and has never frozen, the specimen still carries DNA fragments 30 to 45 base pairs long. Read against the measured, temperature-calibrated chemistry of DNA decay, that survival places the bone in the low thousands of years, and even the most preservation-favorable rate the data allow cannot carry it past roughly sixteen thousand. To reach the conventional 430,000 years, decay must run about sixty-five times slower than it has ever been measured, a rate the physics reaches only under sustained freezing this cave has never known. The barcode says these people are one family. The chemistry says the family is young. Multiple independent lines, both genetic and chemical, converge on the recent, bounded human history the biblical record described first.

Keywords: *ancient DNA; Barcode Index Number; biblical creation model; COI; cytochrome c oxidase I; Denisovan; Homo heidelbergensis; mitochondrial DNA; Neanderthal; population bottleneck; Sima de los Huesos*

1. Introduction

Mitochondrial DNA is unusually useful for comparing ancient and modern humans because each cell contains many mitochondrial genomes, increasing the chance that at least some fragments survive after nuclear DNA has degraded (Krings et al. 1997). Within the mitochondrial genome, the 5′ region of cytochrome c oxidase subunit I (COI-5P) is especially valuable for database-scale comparison. It is the standard animal barcode, it is widely sequenced across species. This study asks whether modern and archaic *Homo* COI sequences are consistent with a Biblical creation model in which all sampled *Homo* lineages lived after a recent global Flood bottleneck. In that framework, Neanderthals, Denisovans, Sima de los Huesos hominins, and modern humans are historically differentiated populations within a single created human lineage. Three primary predictions were specified for the present analysis: (1) the COI sequences should remain highly similar; (2) the database may place them in the same operational barcode cluster; and (3) a rooted reconstruction should recover one ancestral *Homo* mitochondrial lineage rather than unrelated origins. A fourth, explicitly temporal proposal is that the observed differences accumulated after the Flood bottleneck.

The first three propositions can be tested directly with the present sequence set. The fourth cannot be validated from sequence similarity alone because a bottleneck date is a clock claim. It requires a substitution rate study appropriate to the COI fragment directly, uncertainty in ancient sequences, and a comparison between independently specified chronological predictions. A major purpose of this paper is therefore to distinguish what the data does establish from what remains a creation model hypothesis.

2. Creation-Model Predictions and Evidentiary Logic

The proposed creation model begins with a historical premise: a global Flood produced a recent and severe global population bottleneck, after which surviving families expanded, migrated, and differentiated. Archaic *Homo* populations are placed within this post-bottleneck radiation. Under that premise, mitochondrial lineages should be nested within a bounded human genealogy. The relevant empirical question is not whether two labels have exactly identical sequences, but whether their sequence relationships, ancestral states, and amount of divergence match the model's independently defined expectations.

Four claims are separated in this paper. First, high sequence similarity is a direct descriptive claim. Second, shared membership in BOLD:AAA0001 is a database observation about the present BIN algorithm and record set. Third, a shared ancestral *Homo* COI lineage is a phylogenetic claim that requires a rooted tree and outgroups. Fourth, accumulation of all differences after a recent bottleneck is a historical timing claim. These claims are not interchangeable.

A BIN is not an ancestral reconstruction; an ancestral reconstruction is not a molecular date; and a molecular clock from the COI fragment does not yet exist. However, based on the fast rate of all mtDNA compartments, I make a prediction that once pedigree mutation rates are done on this gene fragment will be rapid and land within just a few thousand years ago on the Biblical timeline. Until that prediction can be directly tested, I rely on multiple other examples to place the timing of this bottleneck.

This hierarchy also prevents consensus sequences from being mistaken for ancestors. A majority-rule consensus can be a mosaic of states that never co-occurred in a real individual, especially when 23,856 modern records are compared with only 16 archaic records. A legitimate ancestral analysis needs an explicit tree, one or more outgroups, a stated substitution model or parsimony criterion, probabilities or confidence at each variable site, and equal treatment of lineages. Those requirements guided the present reconstruction.

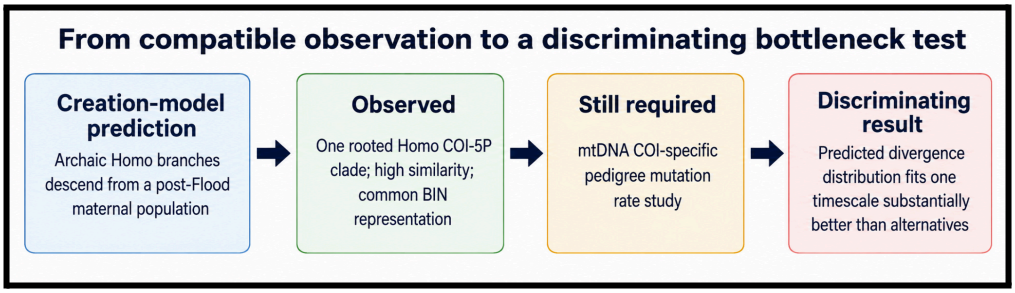

Figure 1. *From a compatible observation to a discriminating bottleneck test. The present study establishes the observed-lineage box and supplies an ancestral reconstruction; a recent date requires a COI-specific clock and a direct comparison of chronological models.*

Another prediction from the creationist side comes from the time of early discovery and reconstruction of Neanderthal being an evolutionary intermediary or extremely ancient form of early man. For historical context, the Feldhofer Neanderthal fossils were recognized in 1856, before Darwin published *On the Origin of Species* in 1859. William King formally named *Homo neanderthalensis* in 1864. It was Gustav Schwalbe in 1899 - 1906 who made Neanderthal become unambiguously incorporated into an evolutionary sequence from primitive to modern: *Pithecanthropus* → Neanderthal → modern human.

Not long after, Marcellin Boule's influential 1911–1913 reconstruction of the La Chapelle aux Saints skeleton depicted Neanderthals as hunched over incompletely erect, helping establish the familiar stooped and bent-kneed image that was popular for decades. Yet in 1926, creationist Harry Rimmer explicitly rejected these reconstructions, arguing that they did not represent the skeleton as it actually was and stating that the Neanderthal *"was a true man."*

This claim preceded the major scientific anatomical reassessment by approximately three decades. Creationist author Harry Rimmer wrote a book titled *Monkeyshines: Fakes, Fables, Facts Concerning Evolution* in 1926. Rimmer specifically attacked the inaccurate Neanderthal reconstructions and their evolutionary placement and wrote: *"At any rate, these reconstructions of the Neanderthal man do not show him the way his skeleton really was. He also was a true man."*

Notice exactly what Rimmer said in 1926:

- the published Neanderthal reconstructions were **anatomically wrong**;
- the reconstruction did **not represent what the skeleton actually showed**;
- Neanderthal was a **"true man."**

Straus and Cave (1957) subsequently reexamined the La Chapelle-aux-Saints remains and rejected the traditional reconstruction, while Trinkaus (1985) concluded that the inaccurate aspects of Boule's posture reconstruction had been corrected during the 1950s and traced Boule's mistaken interpretation partly to contemporary anatomical assumptions and evolutionary preconceptions.

Modern virtual reconstruction has strengthened that conclusion: Haeusler et al. (2019) found human-like lumbar and cervical curvature and concluded that Neanderthals possessed a fully upright, human axial posture. Thus, before the prevailing reconstruction was anatomically overturned, Rimmer had made the falsifiable claim that the stooped reconstruction misrepresented the actual skeleton and that Neanderthals were true humans; subsequent anatomical reassessment moved in precisely that direction. So it was creationist who were first to place Neanderthals in the same post flood lineage with humans which would place them inside a single bin as us, far before genetics would be able to confirm.

3. Materials and Methods

3.1 Dataset audit and marker definition

The working export contained 34,630 BOLD records. Because record totals can combine markers, counts were recalculated after filtering the marker field to COI. The marker-specific dataset comprised 23,856 modern *Homo* sapiens records, 11 Neanderthal records, three Denisovan records (Krause et al. 2010), and two records labeled *Homo* heidelbergensis from Sima de los Huesos. In the text, "Sima" refers to the sequenced Sima de los Huesos specimen catalogued under that BOLD label. Conventional geological and paleogenomic literature places the site at approximately 430,000 years.

The analysis targeted a 650-bp coding segment of mitochondrial COX1 corresponding to rCRS positions 5954–6603 (Hebert et al. 2003). All sequences were oriented and aligned to this interval. Four bases were unavailable for the Sima representative, so comparisons involving Sima used 646 called positions. Ambiguous or missing calls were excluded pairwise rather than treated as differences.

3.2 BIN audit

BOLD BIN assignments were counted separately from taxonomic labels. BOLD:AAA0001 contains 22,649 modern-human, 11 Neanderthal, two Denisovan, and two Sima COI records in this export. The remaining 1,207 modern records and one Denisovan record have blank BIN fields. Consequently, the precise observation is that all four labels are represented in BOLD:AAA0001 - not that every record carries that assignment. BINs are algorithmic operational taxonomic units intended to organize barcode variation (Ratnasingham & Hebert 2013); they place related species and subspecies together.

3.3 Equal-lineage sampling and outgroups

Directly pooling all records would allow the modern sample to dominate a consensus and any frequency-weighted calculation. I instead gave the four *Homo* lineages equal terminal weight by selecting one observed representative per lineage, using an observed central haplotype when multiple records were available.

The analyzed accessions were MH553664 (modern H. sapiens), KJ533544 (Neanderthal), FN673705 (Denisovan), and KF683087 (Sima). Chimpanzee NC_001643.1 and gorilla NC_001645.1 were included as outgroups. This design tests relationships among lineages; it does not estimate within-lineage diversity from one representative.

3.4 Tree search and substitution model

All 15 rooted binary topologies connecting the four *Homo* terminals were evaluated on the fixed scaffold Gorilla, (Chimpanzee, *Homo*). Likelihoods were optimized under the Hasegawa–Kishino–Yano 1985 model with empirical base frequencies and four discrete gamma rate categories (HKY85+Γ4; Yang 1994). Branch lengths, the transition/transversion parameter, and the gamma shape parameter were optimized for each topology. Relative support was assessed using 1,000 site-resampling replicates with a resampling-estimated log-likelihood procedure. The purpose was to make the topology explicit and reproducible rather than assume that a modern consensus represented the ancestral sequence.

3.5 Ancestral reconstruction and sensitivity analyses

Marginal posterior probabilities were calculated for the most recent common ancestor of the four *Homo* terminals at every *Homo*-variable site. The maximum-a-posteriori (MAP) base and the posterior probability of A, C, G, and T were retained. A separate parsimony reconstruction provided a model-light sensitivity check. To test sensitivity to within-lineage sampling, 1,000 equal-lineage haplotype-resampling replicates were also evaluated. Complete probability tables, alignments, selected sequences, topology scores, pairwise differences, and reconstruction outputs are provided in the supplementary workbook.

Supplementary raw data and reconstruction workbook:

Supplementary_Data_Archaic_Homo_COI5P_Reconstruction.xlsx

4. Results

4.1 High similarity among selected Homo representatives

The selected modern and Neanderthal sequences differ at 8 of 650 called positions (98.77% identity). Modern and Denisovan differ at only 18 of 650 (97.23% identity); modern and Sima differ at 14 of 646 (97.83% identity). Neanderthal and Denisovan differ at 20 of 650 (96.92% identity); Neanderthal and Sima differ at 16 of 646 (97.52% identity); and Denisovan and Sima differ at 11 of 646 (98.30% identity). Every pairwise comparison within Homo therefore falls between 8 and 20 differences, and every identity value sits above 96.9 percent. The closest pairing is modern human to Neanderthal at just 8 differences, and even the most divergent pairing, Neanderthal to Denisovan, parts by only 20. Read as a group, the four lineages occupy a single tight band of variation with no outlier and no lineage standing meaningfully apart from the rest. In contrast, Homo to chimpanzee and Homo to gorilla comparisons contain a massive 65 to 71 differences over the same 646 to 650 called positions. That is not a marginal shift but a jump of several fold, and it holds across every ape comparison without exception, so the separation between Homo and the apes is consistent rather than an artifact of any single sequence. The gap between the within-Homo band and the Homo-to-ape band is wide, clean, and unbroken, with no intermediate values bridging the two. The claim that the sampled *Homo* COI sequences are highly similar is therefore supported as a descriptive result.

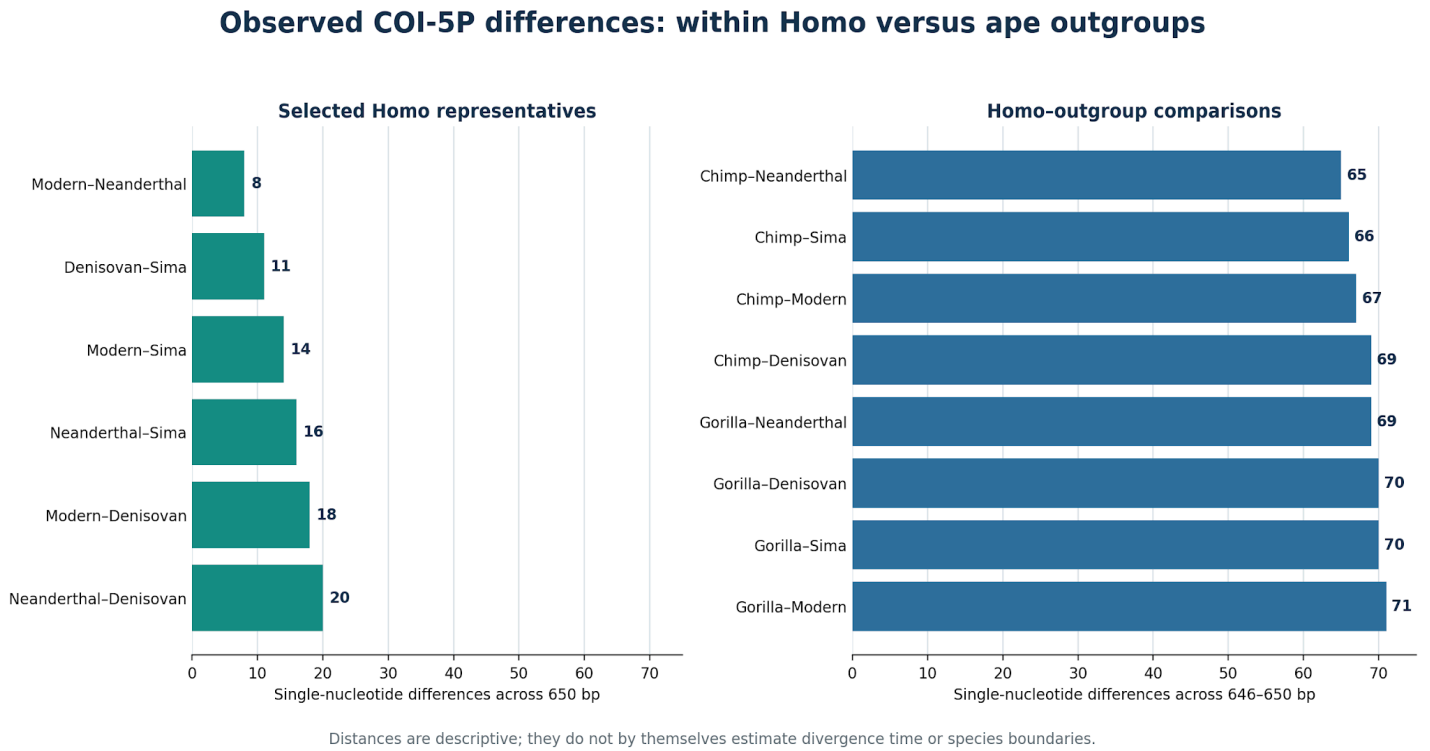

Figure 2. *Observed single-nucleotide differences across the COI-5P alignment. Differences among the four selected Homo representatives are substantially fewer than differences between Homo and the two ape outgroups.*

And the contrast is not modest, it is categorical. Across the same 646 to 650 called positions, the four *Homo* lineages differ from one another by 8 to 20 substitutions, while each differs from the nearest ape by 65 to 71. That is a three to nine fold gap, and it falls exactly where barcoding says a species boundary should fall (Hebert et al. 2003), between *Homo* and the apes, and nowhere among the *Homo* lineages themselves.

The barcode gap that cleanly separates humans from chimpanzees simply does not reappear to separate modern humans from Neanderthals, from Denisovans, or from the Sima hominin. On the most heavily sequenced animal barcode on Earth, the archaic lineages are not distant cousins hanging off a deep common root, they are barcode neighbors of living humanity, and the clustering algorithm that draws these boundaries placed all four in one cluster without ever being told what they were.

4.2 Current co-representation in BOLD:AAA0001

All four labels are represented in BOLD:AAA0001. This supports the manuscript's database claim, that all *Homo* fall into the same species/subspecies category. Scientists themselves fall into two categories: Lumpers and splitters. They examine the same biological evidence yet draw different taxonomic boundaries. Lumpers interpret many anatomical and genetic differences as variation within a broadly defined species or closely related subspecies, whereas splitters assign narrower species names to distinguish populations displaying consistent differences. The shared BIN therefore supports a lumper interpretation by showing that COI does not separate these *Homo* groups into distinct barcode clusters. Since the BIN is an operational mtDNA cluster (Ratnasingham & Hebert 2013), it places every archaic *Homo* population into one biological species similar to a lumper. Creationists fall under the category of lumpers. We lump all big cats together, and all small cats together. We lump all wolves and dogs together and obviously we lump all Neanderthal, Denisovan, Heidelbergensis , erectus and sapiens all together as well.

4.3 Rooted topology and a shared *Homo* mitochondrial lineage

The maximum-likelihood topology was ((Denisovan, Sima - Heidelbergensis), and (Modern H. sapiens, Neanderthal)) within the rooted Homo clade. Site-resampling support was 81.1% for the modern-human – Neanderthal grouping and 70.5% for the Denisovan – Heidelbergensis (Sima) grouping. The Sima Heidelbergensis – Denisovan mitochondrial relationship agrees with the mitochondrial genome result reported for Sima. The following image shows the branching pattern from humanity after the bottleneck based on sequence data alone.

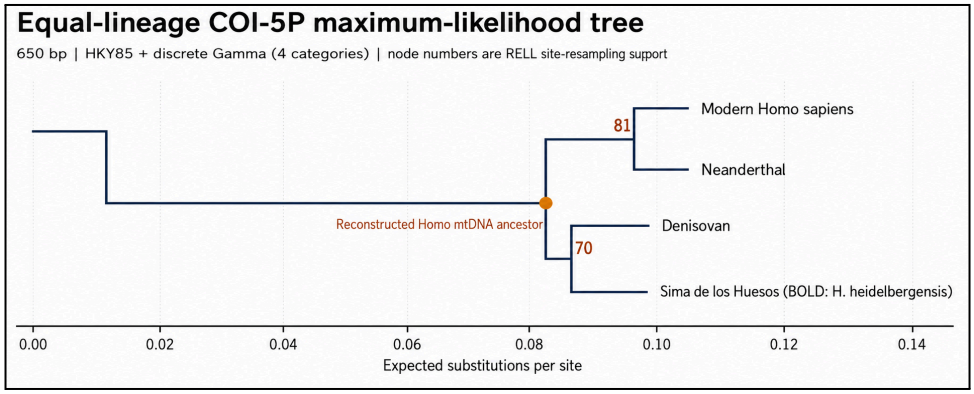

Figure 3. Best rooted maximum-likelihood tree for selected COI-5P representatives under HKY85+Γ4. Node labels are percentages from 1,000 site-resampling replicates. Branch lengths are expected substitutions per site. The short marker supports one Homo mitochondrial clade but is not a complete species or population tree.

4.4 The inferred ancestor was not the modern-human sequence

Twenty-eight positions vary among the *Homo* terminals. The MAP ancestral *Homo* sequence differs from the selected modern sequence at nine of 650 positions. Four differences have posterior probability at or above 0.95: barcode position 70, modern G versus ancestral A (posterior 0.9941); position 313, modern A versus ancestral C (0.999526); position 499, modern C versus ancestral T (0.973896); and position 616, modern C versus ancestral A (0.980766). The remaining MAP differences occur at positions 268, 289, 413, 530, and 589 with lower confidence. Parsimony differs from the modern sequence at eight sites. Thus, a shared ancestral *Homo* lineage is supported.

What the reconstruction establishes—and what it does not

Observation or hypothesis	Verdict	Not established by this result
High sequence similarity over supposed deep evolutionary time	**Supported for this 650-bp fragment**	A recent date derived from a pedigree mutation rate
All four labels represented in BOLD:AAA0001	**Supported as a database observation**	All classified into one single united species family
Few fixed total differences in COI region	**Supported as a database observation**	“When these become fixed”
Shared ancestral Homo COI lineage	**Supported by rooted ML reconstruction**	A uniquely creationist prediction
All differences followed a recent bottleneck	**Compatible, but not dated by this analysis**	“A recent global flood cause”

Figure 4. *The observations are supported at the stated level. Followed by what is not supported by the data alone.*

Remember, the root of the *Homo* clade is not the modern human sequence. It is not any of the four sampled sequences. The reconstruction recovers a distinct ancestral haplotype sitting at the center of the four lineages, resolved at four sites to posterior probability at or above 0.95, and every sampled lineage, modern and archaic alike, descends from it. That is precisely the signature a single founding maternal population leaves behind, one ancestral sequence at the source and a tight spray of descendants around it. It is not the signature of separate lineages converging from independent deep origins. The data do not merely permit one founding mother at the root of the human line, they reconstruct her sequence directly from the barcodes.

5. A Recent Global Bottleneck: The Sima de los Huesos Test

5.1 The creation-model chronology

Within the proposed biblical framework, there exists a global population bottleneck between 4,500 and 5,500 years ago. Stoeckle and Thaler (2018) reported low average pairwise differences within all animal species including aquatic life and insects, consistent with recent origin. The timing of this event was not part of their study, and that they read this against a mainstream date rather than testing the timing. They assumed it took place 200,000 years ago and invoked possible scenarios, especially an ice age since they found no geological evidence for such a bottleneck. However, in our framework the temporal hypothesis can be written as follows: the ancestral mitochondrial population survived the bottleneck, and every observed COI difference among the sampled *Homo* branches arose afterward which can be tested. Sima is a demanding test because conventional chronology places the fossils approximately 430,000 years ago, far earlier than the recent date proposed by the creation model. A strong creation-model analysis should not dismiss the specimen's conventional age; it should state that it disputes the elapsed-time interpretation and then specify what genetic pattern a recent chronology predicts and what the actual data shows when compared to the 430,000 year age claim.

The present reconstruction supplies one missing prerequisite: it infers an ancestral sequence from a rooted tree rather than equating the modern consensus with the ancestor. It also shows that Sima is nested within the same *Homo* mitochondrial clade and that its nearest selected COI neighbor is Denisovan. These observations are compatible with a shared post-bottleneck maternal population. This confirmation however, is not yet validation of the date. The observed 8 - 20 within *Homo* nucleotide differences can best be converted into time only after obtaining the substitution rate directly from a pedigree study. Since no such study exists for any archaic hominin, then we are left with a lesser but still effective way to determine age. The Sima mtDNA reconstruction by the Max Planck Institute rebuilt the entire mtDNA from 30 to 45 base pair length fragments (Meyer et al. 2014), later extended by nuclear sequence (Meyer et al. 2016).

5.2 Sima an alternative clock

The Sima mtDNA result is especially unique as it is a clock in and of itself. DNA is not stable after death. It fragments through several measurable chemical pathways, dominated by hydrolytic depurination, whose rate follows the Arrhenius law and so is fixed by temperature (Lindahl 1993). For a specimen of known burial temperature, the surviving fragment length is therefore itself a clock, readable independent of the geological dating of the surrounding rock. Allentoft et al. (2012) calibrated that clock directly, measuring mitochondrial DNA across 158 radiocarbon-dated moa bones and recovering an exponential decay with a half-life of about 521 years for a 242 bp fragment, a per-nucleotide rate of 5.50×10^{-6} per year at 13.1 degrees Celsius, and an Arrhenius relation ln(k) = 41.2 minus 15,267.6 divided by T in kelvin. The mean fragment length after time *t* under first-order fragmentation is L = 1 divided by (k times t), so the age implied by an observed length is t = 1 divided by (k times L).

This data allows us to apply any sample to the remaining base pair length of a sample. I apply this to the Sima specimen that the deep time framework treats as a rare case of preservation and showcase of extreme DNA survival. The Sima de los Huesos hominin femur from Atapuerca, Spain, conventionally assigned an age of about 430,000 years from radiometric dating. See paper by *Budinsky* et al., 2026 where a lot more details about this very subject can be found. The details remain, and three facts make it an ideal test for age and date.

First, its burial temperature is known and was never frozen: the cave holds near stable 10.6 degrees Celsius for most of the year, rising to about 13.4 degrees for roughly three months, and the excavators themselves describe it as the only non-permafrost site on Earth preserving Middle Pleistocene DNA. This is decisive for the present purpose, because it closes the cold-preservation escape that applies to the general case. Here there is no need to assume a temperature; the temperature is measured, known and well documented and it is consistently mild.

Second, the DNA is severely degraded, with recoverable fragments running from 30 to 45 bp and a mode near 30 bp, exactly the near-floor state in which the decay clock is most informative. I carry these sources of uncertainty honestly. The first is fitting uncertainty in the rate constant *k* itself. The second is the biological scatter implied by the low fit of the Allentoft model, whose *R*-squared of 0.39 means that about 61 percent of preservation variance comes from soil chemistry, pH, hydration, and other taphonomic factors rather than age and temperature.

The third is that the two recoverable fragment lengths are the two ends of a bracket: the longest fragments, 45 bp, are a ceiling, since the true mean length is shorter and so yields the youngest age the data allow, while the 30 bp, sit at the detection floor of the method, meaning they are older. I therefore report each scenario as an interval between these two ends together with its midpoint, treating the midpoint as a convenience summary of the bracket rather than a precise point. Because the cave's thermal regime is known, I restrict attention to the two rate scenarios that fit it. The temperature-weighted rate, $k = 3.93 \times 10^{-6}$ per nucleotide per year, derived below from the cave's own seasonal cycle, is the proper central rate and supersedes a flat constant 10.6 degree; a faster rate is also warranted because the location in the cave is perpetually damp and wet, which is poorer for preservation and accelerates decay even faster.

This is the point where deep-time reading cannot survive. Every claim of extraordinary DNA survival rests on one escape, cold. Frozen ground stalls hydrolysis, which is why permafrost and glacial sites are where ancient DNA is expected to linger at all. Sima removes that escape completely. The cave is not frozen, has never been frozen, and holds a mild 10.6 to 13.4 degrees Celsius the year round, and it is wet. Water is not a neutral bystander in DNA decay, it is the reagent. Depurination is hydrolysis, and hydrolysis cannot proceed without water. A cave warm enough to keep liquid water moving and damp enough to bathe the bone continuously is not a preservation vault, it is a reaction chamber running at full speed. Take away the cold and add water, and the standard model has not made Sima easier to explain, it has made it far harder. The single environment in which 45 base pair fragments could conceivably crawl toward deep time is the one environment Sima demonstrably is not.

I show, but set aside, the flat-average and the ideal-preservation scenarios, since neither matches the actual conditions of the cave - a wet, warmer temperature-cycling cave.

Scenario	Rate k (per nt per yr)	45 bp (ceiling)	30 bp (floor)	Midpoint
Combined, seasonal + poorer preservation (central)	**6.23×10^{-6}**	**3,570 yr**	**5,350 yr**	**4,460 yr**
Fast (poorer preservation, +1 sigma, flat 10.6°C)	5.28×10^{-6}	4,200 yr	6,300 yr	5,261 yr
Temperature-weighted (seasonal, mean preservation)	3.93×10^{-6}	5,655 yr	8,483 yr	7,069 yr
Central (Allentoft mean, flat 10.6°C)	3.33×10^{-6}	6,700 yr	10,050 yr	8,342 yr
Slow (best preservation, −1 sigma, flat 10.6°C)	2.10×10^{-6}	10,600 yr	15,900 yr	13,228 yr

Table 1. *T*hree scenarios that fit a wet, cycling cave, plus the two flat-temperature scenarios shown for completeness and set aside.

You can see for yourself that based on known rates of decay and the non-frozen environment, when we combine the facts we have, we land on a mid-point date of 4,460 years. This is a clock we can use to obtain a date and age that lands perfectly within our Biblical timeline window as predicted and expected, and far away from the evolutionary timeline. Even under the best preservation scenario, you cannot retain 45 base pairs after 10,600 years. Both results are just a few thousand years, and both leave the claimed 430,000 year age far behind. Run in reverse, survival of 45 bp fragments for 430,000 years would require a rate constant about 65x slower than the known rate of decay at a constant 10.6 degrees, which the Arrhenius relation reaches only at a sustained burial temperature near minus 9.8 degrees Celsius. The cave has never been a freezer, thus not a preservation time-machine.

The burden now sits squarely on the deep-time account, and it is a crushing one. To hold even the longest 45 base pair fragments together for 430,000 years in this cave, the chemistry of DNA decay must run roughly sixty-five times slower than it has ever been measured to run, a rate the Arrhenius relation reaches only near minus ten degrees Celsius sustained for the entire interval. Sima offers no such temperature and no freezing at all. So the standard model is not reading a rate off this bone, it is asserting an exemption from measured chemistry and asking us to grant it. If that exemption exists, it must be named, quantified, and shown to operate in a wet, non-freezing cave. No such mechanism has been demonstrated to carry short DNA across four hundred millennia in these conditions. Until one is, the honest reading of the molecule is the one the numbers give directly, an age in the low thousands of years. And there is no escape from the other side of the range either: even the single most preservation-favorable scenario the data permit, the slow, best-case, minus one sigma rate, cannot carry this specimen past roughly sixteen thousand years. Every path the evidence allows lands in the thousands. Not one lands in the hundreds of thousands. A method whose most generous setting still falls thirty times short of the claimed age has not failed to reach 430,000 years, it has ruled it out.

5.3 Criticism Answered

The evolutionary deep-time reading can concede the measured rate and still argue that decay is not single-exponential across long intervals, that a fast initial phase gives way to a slow "long tail" of unusually stable fragments, mineral-bound or otherwise protected, which lingers far longer than a first-order model predicts. I'll grant the mechanism for the sake of argument. It does not rescue the 430,000 year age, for three reasons. First, the long tail is a small, selectively preserved subpopulation, yet Sima yields fragments across the 30 to 45 base pair range with a mode near 30, which is a whole degraded pool sitting near the detection floor, not a thin remnant of exceptional survivors, so the bulk distribution is exactly what ordinary decay to a few thousand years produces and not what a long-tail model predicts. Second, every documented case of long-tail survival is a cold case, permafrost, glacial ice, or stable sub-zero burial, because the protective chemistry that slows the tail is itself temperature-dependent; there is no demonstrated warm, wet long tail, and Sima is warm and wet. Third, invoking an unquantified tail is not a measurement, it is an exemption, and the burden of an exemption falls on the party claiming it: name the mechanism, give it a rate, and show it operating in a non-freezing cave bathed in liquid water. Until that is done, the long tail is a hope, not a number, and a hope does not overturn a calibrated rate. The measured chemistry still reads this bone in the thousands of years, and the objection, examined closely, only sharpens the point rather than blunting it.

The next creation-model test should estimate a COI-specific rate distribution using pedigrees where available, dated ancient mitogenomes, synonymous and nonsynonymous partitions, and sensitivity analyses for purifying selection and saturation. It should then propagate rate uncertainty into the predicted post-bottleneck divergence distribution. If a recent Flood bottleneck produces substantially higher likelihood for the observed ancient-to-modern distances than conventional alternatives under the same ascertainment and substitution assumptions, the claim would become discriminating. Until that step is completed, the appropriate verdict is "compatible but not dated," not "validated."

6. Ancient population size and the paradox

Vaesen et al 2019 is another study that also independently confirms my young age suspicions and this genetic data. Taken directly from 'The Neanderthal Extinction Dilemma' paper by *Thomas*, (2019) we read: *"Four researchers from the Netherlands recently published the results of their computer-modeled human populations in the journal PLOS ONE. The findings show that small Neanderthal population sizes would have caused them to become extinct in just 10,000 years. How did Neanderthals survive the 400,000 years they were supposedly on Earth?"*

This is a logical question and once we add *Homo erectus* who supposedly lived for 2 million years and *Homo heidelbergensis* who existed for approximately 500,000+ years, the problem is compounded and made far worse for the mainstream view. For more details on this study see (Budinsky et al., 2026) and what happens when you apply Vaesens' simulation and apply it to known population sizes of these archaic groups, you end up with Under a moderate Allee condition (A = 10), every band became extinct: the median extinction time was approximately 134 years, the central 80 percent of extinctions fell between roughly 81 and 239 years, and

essentially no band persisted beyond 500 years. Only with recurrent female exogamy where reproductive females were migrants from other communities can they persist longer and even when applied the single longest-surviving band among the twenty-six thousand replicates simulations only reached roughly 3,975 years. Again we see another independent line of evidence that corroborates the other. This is what consilience is all about and why finding parsimony independently across different branches of science is so important to consider. See, *Budinsky et al.*, 2026 The Hidden Clock of Humanity, for more details and a compilation of evidence that further corroborates the youth of humanity, including archaic hominins.

7. Conclusion

Modern H. sapiens, Neanderthal, Denisovan, and the Sima de los Huesos Heidelbergensis COI sequences are highly similar; all four of the corresponding taxonomic records are currently assigned to BOLD:AAA0001; and a rooted maximum-likelihood analysis using equal lineage representation places them all within a shared Homo COI genealogy and infers a common ancestral sequence at the root. These findings satisfy the creation model's stated prediction of bounded mitochondrial continuity among post-Flood human populations.

The Sima specimen has shown us based on the observed rate of DNA decay and the location the fossils were found that we are looking at a specimen that lived recently, not 430,000 years ago. Based on the fast rate of all mtDNA regions, we predict the COI fragment will be no different. This remains an independent test that allows for future falsification of this model.

The principal contribution of this study is therefore not a new date for an old bone, but a demonstration of how cleanly the human genetic record falls into place once it is read without the assumption of deep time. I have kept every claim in its own lane. The COI data show that modern humans, Neanderthals, Denisovans, and the Sima de los Huesos hominin sit together in one shallow, rooted *Homo* genealogy, share a single Barcode Index Number, and stand separated from one another by a handful of substitutions while the apes stand apart by an order of magnitude more. I did not ask that barcode to tell time, because as of now it cannot. What tells the time is carried elsewhere. It is written into the Sima femur itself, which after its entire history in a measured, non-freezing cave still holds DNA fragments 30 to 45 base pairs long, a survival that the calibrated chemistry of molecular decay reads in a few thousand years and not in four hundred thousand. And it is written into the populations themselves, whose small archaic bands cannot be kept alive across deep time by the very demographic models built to describe them. Two clocks that share no mechanism, one chemical and one demographic, were set running independently and stopped within the same narrow window. When stacked with the lack of fixed nucleotide differences (Sharbrough et al. 2017) and the allee simulation evidence from Vaesen et al., (2019) we have consilience.

Independent lines multiply rather than add: when several tests that were each free to disagree instead land on the same answer, the probability that their agreement is coincidence collapses toward zero. The barcode says these people were one family. The decaying molecules, lack of diversity, few fixed differences and the fragile population size bands say that the family is young. Neither result was forced, and both settle on the same short history, the one the biblical record described long before a sequencer could read a single base.

Data Availability

The supplementary Google Sheets workbook linked in the Methods contains the input audit, selected sequences, alignment, pairwise-distance matrix, all topology scores, the best-tree Newick string, ancestral-state probabilities for every *Homo*-variable site, parsimony results, and equal-lineage resampling summaries. GenBank accessions are listed in Section 3.3. The BOLD counts are a dated database observation and should be re-audited if the underlying export changes.

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