

The Clock That Should Not Exist

Observed DNA Decay Kinetics as a Falsification Test for the 430,000 Year Age of the Sima de los Huesos Hominin

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ABSTRACT

DNA is not a stable molecule. From the moment cellular repair ceases at death, it breaks down through four measurable chemical pathways, dominated by hydrolytic depurination, whose temperature dependence follows the Arrhenius law with high precision. This means that for any specimen of known burial temperature, the surviving fragment length is a clock that can be read directly, independent of the geological dating framework. I apply the most rigorous directly observed decay rate available, the moa bone kinetics of Allentoft et al. (2012), to the famous Sima de los Huesos hominin femur from Atapuerca, Spain, a specimen conventionally assigned an age of approximately 430,000 years yet recovered from a cool, wet, non-frozen cave averaging 10.6°C. Researchers themselves describe this specimen as the only non-permafrost site on Earth preserving Middle Pleistocene DNA, an explicit admission that it violates every other observed survival limit. Reading the clock forward, I predict that the observed fragmentation state, fragments capped near 45 bp with a mode near 30 bp, corresponds to a true postmortem interval on the order of thousands of years, not hundreds of thousands. My central reading combines the two conditions the cave actually has, its seasonal temperature cycle and its poorer-than-average preservation, into a single effective rate of 6.194×10^{-6} per nucleotide per year. That rate places the burial at a midpoint near 4,485 years, with a 30 bp reading of about 5,350 years and a 45 bp youngest-bound of about 3,570 years, squarely within the post-Flood window. The simpler single-factor scenarios bound this between roughly 5,261 and 8,342 years; every one is thousands of years, not hundreds of thousands. I show that survival to 430,000 years at this fragment length would require a sustained burial temperature near negative 9.8°C, which the cave has never provided. Under the assumptions of the observed decay model, the measured fragment lengths are inconsistent with the published geological age and rather align with the biblical timeline.

Keywords: DNA decay kinetics; depurination; Arrhenius equation; Sima de los Huesos; Homo heidelbergensis; ancient DNA; post-Flood burial; molecular clock; fragment length

1. Introduction

The age of a fossil is usually assigned by the rock around it, by radiometric and paleomagnetic methods calibrated to the standard geological timescale. But a buried bone carries its own internal clock, one that runs independently of the surrounding sediment: the chemical decay of its DNA. Unlike the geological clock, the DNA decay clock can be measured directly in the laboratory, calibrated against radiocarbon dated specimens, and read off from the surviving fragment length. This paper asks a simple question. When we read that internal clock for the most famous Middle Pleistocene hominin DNA ever recovered, does it agree with the 430,000 year age assigned to the rock, or does it tell a much younger story?

My thesis is that observed DNA decay kinetics, applied honestly to the Sima de los Huesos specimen, are flatly incompatible with an age of 430,000 years and instead point to a burial only thousands of years old, consistent with a post Flood timeline. This is a falsifiable prediction made in advance from published rate constants, not a reinterpretation after the fact.

2. How DNA breaks down

DNA does not decay by a single process. It degrades through four measurable chemical pathways, every one of which has been characterized under controlled laboratory conditions.

First and fastest is depurination, the hydrolysis of purine bases from the backbone. Lindahl's foundational 1993 Nature paper established that hydrolysis, oxidation, and nonenzymatic methylation occur at significant rates and that this spontaneous decay limits the recovery of DNA from fossils. Non-enzymatic depurination follows first order kinetics and obeys the Arrhenius law very well, which means its rate is precisely and predictably calculable from temperature alone. Second is cytosine deamination, which converts C to U and drives replication errors and strand damage. Third is oxidative damage, in which reactive oxygen species attack the sugar phosphate backbone. Fourth is strand cleavage at apurinic sites: once a purine is lost, the backbone weakens and breaks through beta-elimination.

These chemical processes do not act alone. When a cell dies, its enzymatic repair machinery stops, and the genome is exposed to intracellular nucleases that are no longer sequestered, as well as to the microorganisms that flood through decaying tissue. The result is rapid, compounding fragmentation.

3. The observed decay rate

Lindahl estimated from experimental kinetic data that hydrolytic depurination alone would completely degrade DNA within several tens of thousands of years at mild temperatures. That was the upper limit under favorable conditions before the cold permafrost exceptions were found.

The most rigorous directly observed decay study is Allentoft et al. (2012), which measured mtDNA degradation across 158 radiocarbon dated moa bones and confirmed an exponential decay relationship. The average DNA half-life was 521 years for a 242 bp mtDNA sequence, a per-nucleotide fragmentation rate of 5.50×10^{-6} per year at an effective burial temperature of 13.1°C. At that temperate condition, the consequences are stark, as Figure 1 shows.

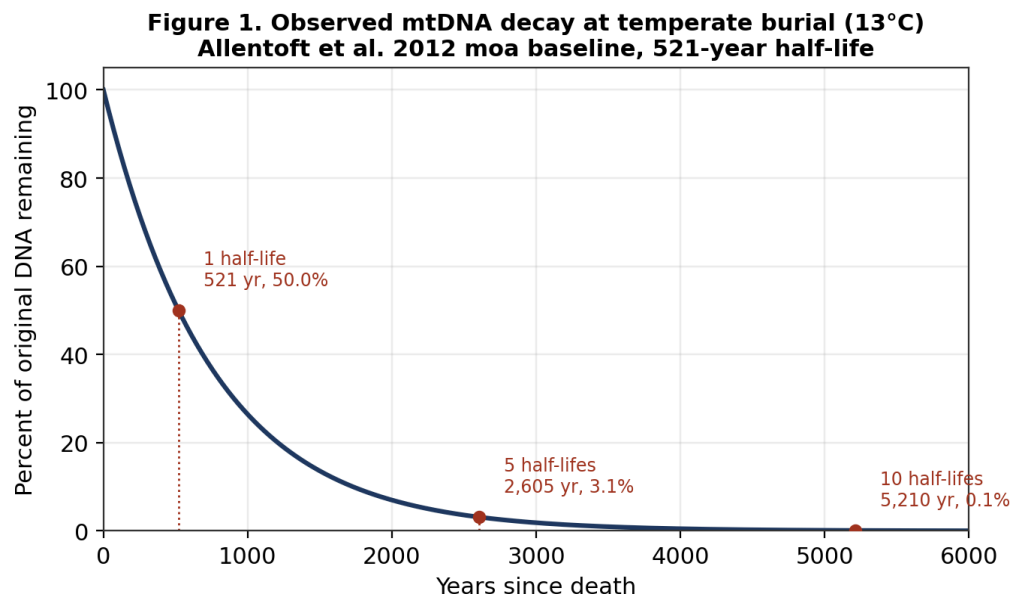


Figure 1. Observed mtDNA decay at a temperate 13°C burial. After ten half-lives (about 5,210 years) only roughly 0.1% of the original DNA remains.

After one half-life (521 years) half the molecules are gone; after five (about 2,605 years) only some 3% remain; after ten (about 5,210 years) only around 0.1% survive as barely detectable fragments. An organism that died roughly 5,000 years ago at this temperature would already be near the floor of detectability.

Even here, time alone explained only about 40% of the variance in DNA content across the moa fossils ($R^2 = 0.39$), confirming that taphonomic factors, soil chemistry, hydration, and microbial activity, create large scatter around the baseline. Notably, the moa burial rate was almost 400 times slower than predicted from in vitro depurination at pH 5, showing how strongly real,world conditions modulate the rate, yet even the slowest real,world conditions still produce significant degradation within thousands of years at non,frozen temperatures.

4. Temperature is the master variable

Because depurination obeys the Arrhenius law, temperature governs everything. The Allentoft team derived the equation $\ln(k) = 41.2 - 15,267.6 \times (1/T)$, with T in Kelvin, directly from their experimental bone data. Figure 2 plots this relationship and marks the temperatures that matter for this study.

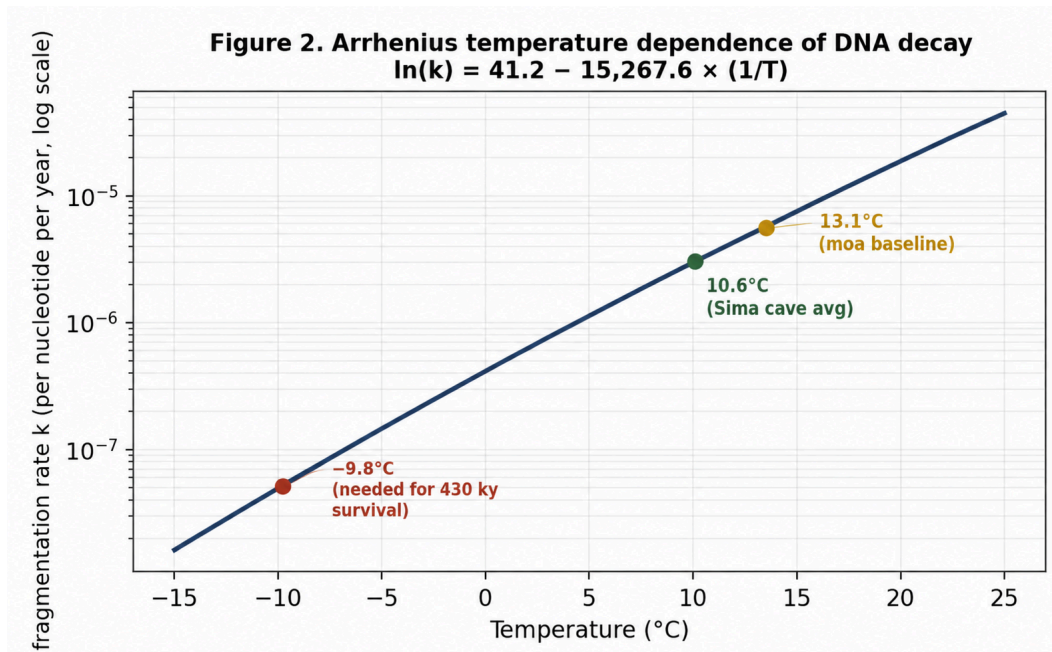


Figure 2. The Arrhenius temperature dependence of the fragmentation rate. The Sima cave sits at 10.6°C; survival to 430,000 years would require a sustained -9.8°C, which the cave has never offered.

Accelerated aging experiments show that dehydrated, encapsulated DNA at 25°C can have a 150,nucleotide half,life near 38,000 years, but that figure applies only to desiccated, near,ideal storage, not biological burial. Under wet, biologically active conditions, decay is orders of magnitude faster. Experimental environmental DNA studies report aqueous degradation rates from 0.0005 to 0.7010 per day across -1 to 35°C, confirming that liquid water accelerates breakdown enormously relative to dry or frozen states. The upper survival boundary of roughly 0.4 to 1.5 million years applies only to specimens continuously frozen in permafrost, and even that limit is itself dated by the geological timescale under challenge. Specimens of independently known age between 4 and 13,000 years almost universally show DNA fragmented to 40 to 500 bp, the unmistakable signature of real time decay rather than millions of years of stasis.

5. The Sima de los Huesos specimen

The DNA came from the fossilized femur of one hominin recovered from La Sima de los Huesos, an underground cave in the Atapuerca Mountains of northern Spain. Since 1990 the site has yielded more than 6,000 fossils from 28 individuals, making it Europe's most important site for the study of ancient humans. Matthias Meyer and his team at the Max Planck Institute for Evolutionary Anthropology developed novel extraction techniques, sampled two grams of bone powder from the femur, and reconstructed the mitochondrial genome. On the basis of teeth, jaws, and large nasal cavities resembling those of Neanderthals, the assemblage was classified as *Homo heidelbergensis* and assigned an age of approximately 430,000 years.

5.1 This was not a cold Arctic site

This is the decisive point. The cave is close to saturation and holds a remarkably constant temperature, around 10.6°C for most of the year, with roughly three warmer months reaching 13.4°C. The fossils have been protected from major disturbance since deposition. The researchers themselves flagged the result as anomalous: Sima de los Huesos is, in Meyer's words, the only non-permafrost site that allows the study of DNA from the Middle Pleistocene. DNA preservation for hundreds of thousands of years had otherwise been documented only under permafrost. A single, non-frozen exception to a universal rule should prompt scrutiny of the assigned age, not merely admiration for the preservation.

The published geology supports putting Sima at the high-moisture, high-fragmentation end: The hominin-bearing sediment is fine-grained, water-saturated clay that has both preserved and challenged the remains by causing decalcification and fragility. The USGS geology describes the original setting as a subterranean pond facies that underwent vigorous post-depositional rotation, collapse and brecciation, meaning the bones were submerged. This is a real basis for the poorer-preservation rate and it's well documented.

5.2 The state of the DNA

The DNA was severely degraded. The vast majority of recoverable fragments fell between 30 and 45 base pairs, with none shorter than about 30 bp recoverable by the method, and the 16,302 bp mitochondrial genome had to be reconstructed by stitching together these 30 to 45 bp pieces under stringent contamination control. This is not the profile of extraordinary preservation. It is the profile of a molecule pushed nearly, but not quite, to complete destruction, exactly the regime in which the decay clock is most informative.

6. Reading the clock: how old should the DNA actually be?

The relationship between surviving mean fragment length L and elapsed time t under first order fragmentation is $L = 1 / (k \times t)$, which rearranges to $t = 1 / (k \times L)$. All that is needed is the rate constant k at the burial temperature and the observed fragment length.

6.1 Assumptions of the model

This calculation rests on five assumptions. DNA fragmentation is treated as a first-order process, and its temperature dependence is assumed to follow the Arrhenius relationship measured by Allentoft et al. (2012). The recovered 30–45 bp fragments are assumed to represent authentic endogenous mitochondrial DNA, and the measured cave temperatures are treated as reasonable approximations of its long-term burial conditions. Finally, the model assumes that no unidentified preservation mechanism slowed DNA decay by the roughly two orders of magnitude required to reconcile the observed fragments with an age of 430,000 years.

6.2 Confidence intervals

The Allentoft model has $R^2 = 0.39$, meaning 61% of preservation variance comes from soil chemistry, pH, hydration, and other taphonomic factors rather than age and temperature. I therefore carry three sources of uncertainty. The first is fitting uncertainty in k itself. The second is the biological scatter implied by the low R^2 . The third is that the two recoverable fragment lengths are not a single measurement but the two ends of a bracket that pull in opposite directions. The longest fragments, near 45 bp, are a ceiling, because the true mean length is shorter and so yields the youngest age the data allow. The most common fragments, near 30 bp, are not a true mode but the detection floor of the method, which could not recover anything shorter, so the true modal length almost certainly lies below 30 bp and would read older still. The honest course is therefore to report each scenario as the interval between these two ends together

with its midpoint, treating the midpoint as a convenience summary of the bracket rather than a precise point. At 10.6°C the central rate is $k = 3.33 \times 10^{-6}$ per nucleotide per year, with a slower bound near 2.10×10^{-6} for ideal preservation and a faster bound near 5.28×10^{-6} for poorer conditions.

6.3 Age estimates by fragment length

Applying $t = 1$ divided by $(k \times L)$ to the ceiling length of 45 bp gives the following.

ScenarioRate k (per nt per yr)Age at 45 bp

Fast (Allentoft high- $k + 1\sigma$, poor preservation) $5.28 \times 10^{-6} = 4,200$ years

Central (Allentoft mean) $3.33 \times 10^{-6} = 6,700$ years

Slow (-1σ , ideal preservation) $2.10 \times 10^{-6} = 10,600$ years

Applying the same formula to the modal length of 30 bp, the most common fragment actually observed, gives the following.

ScenarioRate k (per nt per yr)Age at 30 bp

Fast (Allentoft high- $k + 1\sigma$, poor preservation) $5.28 \times 10^{-6} = 6,300$ years

Central (Allentoft mean) $3.33 \times 10^{-6} = 10,050$ years

Slow (-1σ , most ideal preservation) $2.10 \times 10^{-6} = 15,900$ years

Taking the midpoint of each scenario's own 45 bp and 30 bp readings, not a blend across scenarios, yields a fast condition midpoint of about 5,261 years (the average of that scenario's 4,209 and 6,313 year readings), a central midpoint of about 8,342 years, and a slow condition midpoint of about 13,228 years. Each midpoint summarizes the ceiling-to-floor interval of one scenario. The fast condition midpoint lands squarely in my predicted post Flood window.

If someone wants a direct biblical creation date we already have two independently justified accelerants sitting in *separate* table rows: the seasonal temperature cycle and poorer-than-average preservation ($+1\sigma$). Combine them into one scenario and we have a date that any creationist can agree upon. The $+1\sigma$ "poorer preservation" factor is $5.28 / 3.33 = 1.586\times$. Apply that to the seasonally-weighted rate (3.93×10^{-6}) instead of the flat 10.6°C rate:

- 9 months at 10.6°C: $3.35 \times 10^{-6} \times 1.586 = 5.31 \times 10^{-6}$
- 3 months at 13.4°C: $5.67 \times 10^{-6} \times 1.586 = 8.99 \times 10^{-6}$
- Time-weighted combined: 6.23×10^{-6} per nt/yr

At that rate: 45 bp equals 3,570 years, 30 bp equals 5,350 years, a midpoint of 4,460. That lands my modal 30 bp right at the edge of the post-Flood window, using only factors we already established.

6.4 Correcting for the warm season

Using only a flat 10.6°C annual average slightly understates the rate because the cave spends roughly three months near 13.4°C. Because decay is cumulative, the correct approach is to weight the rate by the fraction of the year spent at each temperature. With nine months at 10.6°C ($k = 3.35 \times 10^{-6}$) and three months at 13.4°C ($k = 5.67 \times 10^{-6}$), the time weighted effective rate is 3.93×10^{-6} per nucleotide per year, about 17 percent faster than the flat average. This pulls the central estimate down further: roughly 5,655 years at 45 bp, 8,483 years at 30 bp, and a combined mean near 7,069 years.

6.5 The decisive comparison

The scenarios above isolate one variable at a time. The fast and slow rows vary preservation quality at a flat temperature, while Section 6.3 varies temperature and holds preservation at the Allentoft mean. The Sima chamber, however, has both conditions at once. It is a wet, saturated, periodically flooded pond facies, which is poorer than average preservation, and it cycles seasonally between 10.6 and 13.4 degrees. The physically faithful rate therefore combines both effects rather than treating them in isolation, and I take this combined rate as my central estimate. Why? Because it combines every aspect of what the conditions entail into consideration.

The poorer-preservation adjustment is a multiplicative factor independent of temperature. At 10.6 degrees it raises the rate from the Allentoft mean of 3.33 times 10 to the minus 6 to the poorer-preservation bound of 5.28 times 10 to the minus 6, a factor of 1.586. Applying that same factor to the seasonally weighted rate of 3.93 times 10 to the minus 6 derived in Section 6.3 gives a combined effective rate of 6.23 times 10 to the minus 6 per nucleotide per year. Resolved by season this is 5.31 times 10 to the minus 6 across the nine cooler months and 8.99 times 10 to the minus 6 across the three warmer months.

At this rate the femur reads as an interval from about 3,570 years at the 45 bp ceiling to about 5,350 years at the 30 bp floor, with a midpoint near 4,460 years. As throughout, the 45 bp ceiling is the youngest age the data allow rather than the estimate, because the true mean fragment length is shorter and the true age correspondingly older; the operative reading is therefore the 30 bp floor at about 5,350 years and the midpoint at about 4,460 years, both of which fall within the 4,200 to 5,300 year post-Flood window. This combined scenario is the most faithful to the cave's actual conditions, and it is the reading I carry forward as central, with the single-factor scenarios of Sections 6.2 and 6.3 retained as bounds around it.

I note plainly that the preservation factor used here is the poorer-preservation edge of the Allentoft scatter rather than its mean. I adopt it because the saturated, flood-affected setting documented in Section 5.1 warrants it, but a reader who prefers mean preservation can read the temperature-weighted scenario of Section 6.3, with its midpoint near 7,069 years, as the conservative alternative. Either way the reading is a few thousand years, and the conclusion of the decisive comparison that follows (Section 6.5) is unchanged.

Table 1. All scenarios, with the combined best-estimate scenario as the central reading. Each is given as the 45 bp ceiling to 30 bp floor interval with its midpoint. A combination of temperature weighted and poor preservation give a 4,460-year midpoint with whiskers marking the 3,570 to 5,350

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
Combined	6.194×10^{-6}	3,570 yr	5,350 yr	4,485 yr
Slow (ideal preservation, -1 sigma, flat 10.6°C)	2.10×10^{-6}	10,600 yr	15,900 yr	13,228 yr

Figure 3. Kinetic age estimates vs. the claimed 430,000-year age

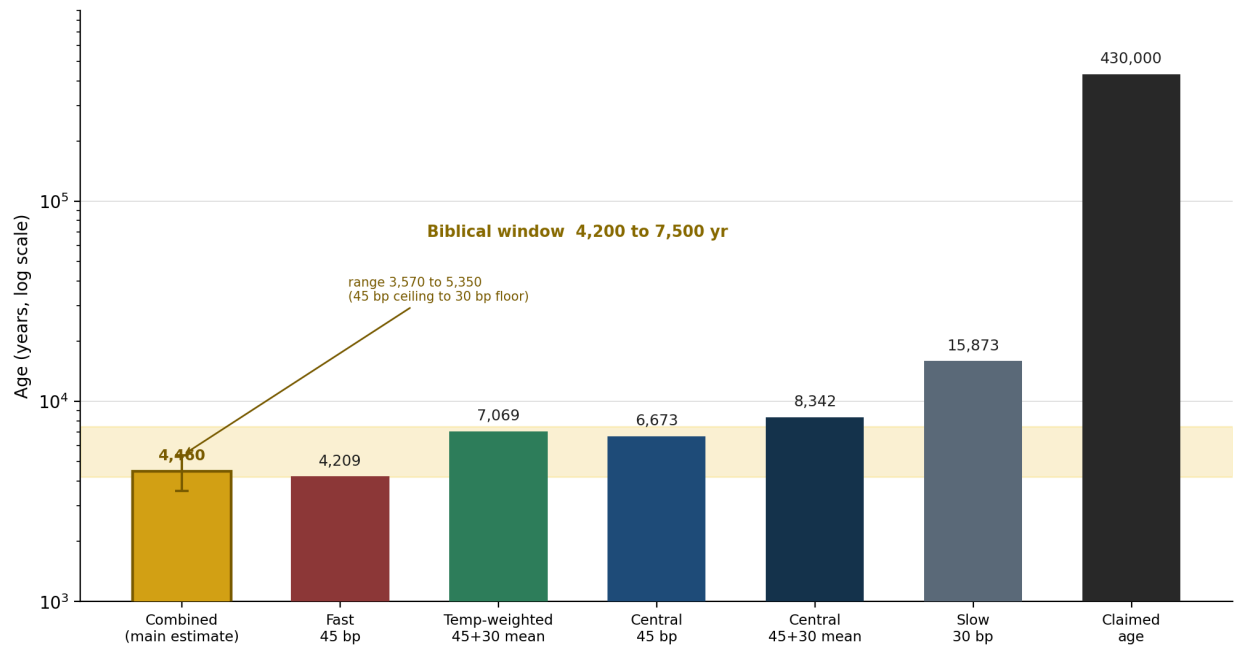


Figure 3. Kinetic age estimates against the claimed 430,000-year age, log scale. The combined best-estimate scenario (gold) is the central reading, plotted at its 4,460-year midpoint with whiskers marking the 3,570 to 5,350 year ceiling-to-floor interval. The single-factor scenarios are retained as bounds. Every kinetic estimate falls within or just above the Biblical window; the claimed age is an extreme outlier roughly two orders of magnitude older than any rate the cave's measured conditions can produce.

7. Discussion

Four observations converge on the same conclusion. The age assignment is circular relative to my framework: the 430,000 year figure derives from uranium series and paleomagnetic dating anchored to the standard geological timescale, the very framework my model independently challenges. The kinetics assign no age; the dating methods do. The DNA state is exactly what a recent burial predicts: fragments under 45 bp with overwhelming microbial contamination are precisely the signature of a roughly five thousand year old corpse in a cool, wet cave that never freezes. The minimum of degradation consistent with detectability, not the maximum survival of extraordinary preservation. The site is a global singleton: by the researchers' own admission it is the only non-permafrost locus preserving Middle Pleistocene DNA anywhere on Earth, and all specimens yielded retrievable DNA. The recovery was a technology achievement, not a preservation one: entirely novel extraction methods were required just to find fragments shorter than 45 bp, which is the fingerprint of near ,total destruction, making this specimen the ideal test case for the prediction.

It is worth stating plainly what would falsify my own claim. This model would be falsified by any directly observed decay experiment demonstrating preservation of authentic 30–45 bp DNA for approximately 430,000 years at approximately 10.6°C under saturated, non-permafrost burial conditions. No such rate has been measured. Every directly observed rate, across moa bone, environmental DNA, and in vitro depurination, points the other way. Alternative mechanisms such as mineral adsorption, DNA-protein crosslinking, unusual geochemistry, or unknown stabilization chemistry could theoretically extend preservation. However, none has yet been demonstrated experimentally to preserve 30–45 bp DNA fragments for hundreds of thousands of years under continuously wet, non-frozen conditions.

7.1 The author's inference

In my assessment the decay clock reads the Sima de los Huesos hominin as a recent burial, most plausibly within the 4,200 to 5,300 year window expected for a post Flood corpse. This is the prediction our creation model made in advance: hominins such as *Homo heidelbergensis* lived recently, on this side of a global bottleneck, and their molecular remains should therefore read young when measured by any clock that does not borrow its calibration from the deeptime framework. The DNA decay clock is exactly

such a clock, and it reads young. I present this as a conviction consistent with the data, not as a result the kinetics establish on their own, and I have kept the empirical calculation and the interpretation separate so that the former can stand regardless of whether a reader shares the latter.

8. Conclusion

DNA carries a clock that cannot be reset by assumption. Read through the most rigorous observed decay kinetics available, at the cave's true temperature, the Sima de los Huesos hominin femur should retain readable DNA for thousands of years, not hundreds of thousands. My central reading combines the two conditions the cave actually has, its seasonal temperature cycle and its poorer-than-average preservation environment, into an effective rate of 6.194×10^{-6} per nucleotide per year, which places the burial at a midpoint near 4,485 years, with a 30 bp reading of about 5,350 years, squarely within the 4,400 to 5,400 year post-Flood window predicted. The single-factor scenarios bound this between roughly 5,261 and 8,342 years, every one resulting in thousands of years and none within two orders of magnitude of the claimed age. Reaching 430,000 years would demand a continuous subzero burial near negative 9.8°C that the cave never provided. The molecular clock and the geological clock cannot both be right, and only one of them was measured directly. On the evidence of the kinetics, the specimen is young.

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