

Predictions Under Trial

A Comparative Analysis of Creation and Evolutionary Predictions and Expectations

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ABSTRACT

The ability to generate accurate, risky, and falsifiable predictions is a central test of a scientific framework. This study compares documented predictions made within Biblical creation and design models with historical evolutionary expectations and evaluates each against observations obtained after the predictions were made. To qualify as a prediction test, an expectation was required to predate the relevant evidence, identify an observable outcome, and, where possible, be traceable to a named source. Multiple prediction comparisons spanning genetics and molecular biology, development and embryology, taxonomy and classification, anatomy and homology, speciation and diversity, population genetics, and human origins spanning decades were assessed. These include predictions concerning conserved genes and developmental systems, genome-level similarity, nested biological organization, genetic boundaries, rapid and bounded diversification, multicellular adaptation through pre-existing biological systems, the functional character of genomic elements formerly classified as junk, recovery from severe population bottlenecks, Neanderthal humanity and anatomy, recent human genetic expansion, mitochondrial and Y-chromosome mutation rates, mutation saturation, and the recoverability of a universal Tree of Life. Across the comparisons examined, the subsequent observations were classified as consistent with the prior creation/design expectation in all cases, whereas the competing evolutionary expectation identified in each comparison was confirmed in none. Several evolutionary predictions were subsequently revised or replaced as contrary evidence accumulated. The historical pattern assembled here demonstrates that Biblical creation and design models have generated specific, testable predictions that preceded later discoveries. This review compares historical creation/design and evolutionary claims with biological observations, distinguishing documented advance predictions from broader model expectations and retrospective interpretations. Agreement between an expectation and an observation is evaluated separately from whether that observation discriminates between competing explanations. These results challenge the characterization of creation as inherently non-predictive and support its continued evaluation as a competing predictive framework in origins research.

Keywords: *Biblical creation model; evolutionary theory; scientific prediction; falsifiability; common design; genetic boundaries; DNA barcoding; mitochondrial DNA; Y-chromosome mutation rates; mutation saturation*

Introduction

Genetic and anatomical similarity across organisms is routinely presented as a prediction of evolution. Historically, however, it was creation and design thinkers who predicted the patterns that were later found, and leading evolutionists who predicted the reverse. In 1963 Ernst Mayr expected conserved genes to be undetectable across distant taxa; the discovery of Hox clusters and deeply conserved regulatory networks contradicted that expectation and was then folded back into the evolutionary account. This is the recurring pattern examined here: when a surprising result falsifies an evolutionary prediction, it is retrofitted into the theory rather than treated as evidence for an alternative. Retrofitting after the fact is not prediction. My aim is not to rehearse old debates but to line up, across many disciplines, the predictions each framework actually made in advance and to compare them with what was found. We proceed in time across genetics and biology, taxonomy, cladistics and homology, and we close with a scorecard and a head to head table. Throughout, we name the person who made each prediction and the date wherever the record allows, and where a specific attribution cannot be documented we state only that the result was expected on a given view.

For a comparison to count as a documented advance prediction test, the expectation must be stated in a dated, attributable source before the relevant testing evidence became known and must specify an observable outcome sufficiently clear for evidence to count for or against it. This review places particular emphasis on historical predictive priority: who first documented the relevant expectation before its confirmation. A successful prediction need not be exclusive to one framework; competing models may independently predict the same outcome. Earlier documentation establishes historical predictive priority, a central focus of this review. Comparative superiority requires additional evidence that the successful prediction distinguishes the originating model from its competitors. Whether the evidence distinguishes competing models is assessed separately from predictive accuracy and priority.

For this paper, a testable prediction is a specified observable consequence of an identified model or hypothesis, stated under conditions that allow evidence to count against it. A prediction may be qualitative or quantitative; an exact numerical forecast is not required, but the expected outcome must be sufficiently specific to distinguish agreement from disagreement. To qualify as a documented advance prediction, a dated, attributable statement must precede knowledge of the particular evidence used to test it. That evidence must not merely repeat observations used to formulate the expectation. A successful test requires agreement with the original stated expectation, without revising its meaning after the result becomes known.

Predictive accuracy and discriminatory power are assessed separately. An observation may fulfill a genuine advance prediction while also being expected under a competing model. Such an outcome supports the accuracy of the stated expectation but does not, by itself, establish the superiority of its originating framework. A diagnostic comparison additionally requires identifying an outcome that the competing models predict differently under their stated assumptions.

Accordingly, this review distinguishes documented advance predictions, broader model expectations for which specific predictive priority has not been established, and retrospective interpretations of existing evidence. Only documented advance predictions are eligible to be counted as successful advance predictions. The same criteria apply to creation/design and evolutionary claims. Failure of an individual historical expectation does not automatically falsify the broader framework, and comparisons drawing on overlapping evidence are not treated as statistically independent.

Classification and Created Kinds

Carl Linnaeus (*Systema Naturae*, 1735 to 1758), the father of taxonomy, worked from a creationist framework and predicted that organisms would fall into fixed, natural, hierarchical groups because they were created according to their kinds (Genesis 1). He held that variation occurs within kinds but that real boundaries separate them: "*Species are the works of nature, varieties are the works of time*" (10th ed., 1758). He also classed humans among the primates anatomically while regarding mankind as set apart with no relation between the two. Evolutionary theory, by contrast, requires an open continuum with no absolute barriers.

The Linnaean categories remain the indispensable framework of biology precisely because the bounded groups Linnaeus predicted are real. Comparative anatomy under Owen, and later baraminology and whole genome sequencing (for example, Thaler et al., 2018), confirmed discrete clustering rather than a seamless continuum, leaving evolution with a standing taxonomic boundary paradox. Then again later but still in the pre-Darwinian "*common plan/design*" concept was clearly stated by **William Paley (1802)**, *Natural Theology*, comparing organisms to human-engineered machines built on a shared plan with variations, "*a general plan pursued, yet with such variations as are required by the particular exigency.*"

Homology, Convergence and the Archetype

Sir Richard Owen, a creationist anatomist, proposed in the 1830s and 1840s that all vertebrates share a common structural blueprint, an archetype, and predicted homologous bones across every vertebrate limb, one upper bone, two lower bones, wrist or ankle bones, and digits, even where reduced or modified (On the Nature of Limbs, 1849). He attributed this unity to common design. Embryology and, in 1978, the discovery of Hox genes controlling limb patterning confirmed a shared developmental plan. Darwin adopted Owen's homology but relabeled the common phrase at the time "*similarity due to common **design***" as "*similarity due to common **ancestry***," changing the interpretation while keeping the pattern. Owen's prediction of a segmented, vertebra based body plan was even confirmed and corroborated in 2012, when a multi segmented spine, previously thought exclusive to land animals, was reported in a fish. **Frank Lewis Marsh** (*Fundamental Biology*, 1941; *Evolution, Creation, and Science*, 1944) emphasized the *discontinuity* between created kinds (the gaps); we now see these gaps not just in structure, but also taxonomy and genetics. "*One general plan, modified as each particular use requires*" (the Arkwright's-mill analogy) is a hub-and-spokes picture: a central design radiating out into variants sorted by *function*. That explains similarity-with-modification, and more importantly the organizing criteria is purpose. He was the first to predict a convergence view as well. He stated that if similar function yields similar structure by design, you expect the same solution to show up in unrelated creatures whenever the functional need recurs, which is *convergence*.

Vestigial Structures as a Historical Test

1. **Charles Darwin**, 1874: human appendix. In the second edition of *The Descent of Man*, Darwin described the vermiform appendix categorically: "*Not only is it useless, but it is sometimes the cause of death*" (Darwin 1874, 21).
2. **Ernst Haeckel**, 1879: human coccyx. Haeckel called the coccyx "*a useless rudimentary organ, retaining no physiological significance either in Man or in the Tail-less Apes or Anthropoids*" (Haeckel 1879, 282).
3. **W. E. Dixon and W. D. Halliburton**, 1909: pineal gland. These investigators reported that it had been "*generally assumed that the pineal gland in mammals is a functionless, vestigial organ*" (Dixon and Halliburton 1909, 283).
4. **Robert Wiedersheim**, 1895 In *The Structure of Man: An Index to His Past History*, Wiedersheim classified numerous human structures as: "*Organs having become wholly or in part functionless... For the greater part Organs which may be rightly termed Vestigial.*" classification B, p. 200.

The strict definition remained explicit in later evolutionary literature. Harvard zoologist George Howard Parker opened his 1928 treatment with the statement, "*Vestigial organs are those that are quite useless.*" He added that classification required demonstrating that the organ was "*without function*" (Parker 1928, 34). Consequently, the historical association between vestigiality and complete uselessness was real and common.

On the opposite side we have creationist who predicted the exact opposite.

Alexander Patterson, 1903 Presbyterian minister and explicit advocate of special creation. Patterson predicted that "*there is not the slightest doubt ... that there is use for these peculiar embryonic features*" (Patterson 1903, 69). A genuine prediction concerning alleged human "relics," especially the so-called embryonic gill slits. This was a caution against arguments from ignorance based on evolutionary assumptions of lack of function.

A closely related methodological warning appeared in Jesuit author John Gerard's *The Old Riddle and the Newest Answer*, first published in 1904. Gerard considered it "*the wiser part to refrain from basing any vital conclusions upon these organs*" until biological knowledge was adequate (Gerard, verified in the 1907 fourth edition, 192).

George McCready Price, 1924 Seventh-day Adventist creationist. Concerning the appendix, Price predicted that *“we may well suppose that it has a useful function to perform, though it is not well understood just what its function really is”* (Price 1924, 160).

George Barry O’Toole, 1925 Benedictine priest, professor of animal biology, and anti-evolutionary author. O’Toole observed that *“this list of ‘useless organs’ is being rapidly depleted, so that the scientific days of the rudimentary organ appear to be numbered”* (O’Toole 1925, 291).

The vermiform appendix

Darwin’s assertion of complete uselessness is contradicted by subsequent evidence. The appendix contains abundant gut-associated lymphoid tissue and participates in interactions between mucosal immunity and intestinal microorganisms. Bollinger and colleagues proposed in 2007 that its anatomy and biofilms make it suitable as a protected reservoir - or “safe house”, for commensal bacteria capable of reseeding the colon following severe gastrointestinal disturbance (Bollinger et al. 2007). A later review summarized evidence for immunological and microbiome-associated roles while also emphasizing the appendix’s involvement in inflammatory disease (Kooij et al. 2016).

Price’s 1924 forecast was correct at the qualitative level: the appendix is not biologically functionless. Today we now know it does far more, it also has been found to harbor killer B cells, similar to how the thymus produces killer T cells.

The coccyx

Modern clinical anatomy identifies the coccyx as an attachment site for the levator ani, coccygeus, gluteus maximus, ligaments, tendons, and components of the pelvic floor. These attachments contribute to pelvic-floor support and voluntary bowel control. The coccyx also forms part of the weight-bearing tripod used in a seated position (Lirette et al. 2014).

This evidence contradicts Haeckel’s assertion that the coccyx possessed no physiological significance. O’Toole identified its muscular-attachment role in 1925. The historical error was Haeckel’s movement from “functionless as a tail” to “physiologically functionless altogether.”

The pineal gland

The pineal gland is now recognized as a neuroendocrine organ whose principal systemic product is melatonin. Melatonin was isolated from pineal tissue by Lerner and colleagues in 1958 (Lerner et al. 1958). Modern physiology shows that pineal melatonin conveys information about the environmental light-dark cycle and participates in circadian and seasonal timing (Arendt and Aulinas 2022). Creationist O’Toole had asserted in 1925 that the pineal was an endocrine rather than a functionless organ, anticipating the general direction of later research. His treatment is best classified as a partial pre-melatonin anticipation, not an independent prediction of modern pineal physiology. Patterson’s broader example also merits notice. The alleged human *“gill slits”* are more accurately described as parts of the embryonic pharyngeal apparatus. The pharyngeal arches, pouches, clefts, and associated tissues contribute to the jaws, muscles and bones of the face and neck, the external and middle ear, the palatine tonsils, thymus, parathyroid glands, and major blood vessels (Casale et al. 2023). Patterson’s expectation of developmental utility was therefore correct. Because portions of this developmental anatomy were already under investigation in 1903.

What the historical comparison establishes

These cases establish that categorical declarations of complete uselessness were hazardous and, in the appendix, coccyx, and pineal cases, empirically mistaken. Meanwhile the creationist oriented authors adopted a productive heuristic: an organ whose utility was unknown should remain a target for functional investigation rather than be treated as functionless by default. The discovery of present function consequently falsifies a strict claim of total uselessness as early evolutionists claimed.

A 2016 peer-reviewed review concluded that the idea of the appendix as a vestigial organ should be discarded. Kooij et al., *Clinical and Experimental Immunology*. The fact they admit this concept should be removed tells us everything we need to know. Another prediction in the creationists favor and another failed evolutionary prediction that not only set back science but medicine as well. Countless lives have been lost from removing perfectly good organs for no other reason other than an evolutionary mindset. Today, the definition for vestigial has undergone evolution itself, and it currently means "*lost its primary function*". Like many other failed evolutionary predictions, people who do not know history never notice the slight of hand moves that keep the theory unfalsifiable no matter how many times its falsified or how many predictions it gets wrong.

The Nested Hierarchy

Owen further predicted that life would form a nested hierarchy, the outworking of creation after their kind, rather than a branching continuity (Owen, 1848). Molecular and developmental biology in the 1960s and 1970s revealed exactly such a conserved, nested genetic program. What is claimed as evidence for descent is equally, and on the design view more naturally, read as evidence of a common designer. Later in his work (Louis Agassiz's *Essay on Classification*, 1857) he argued homology reflects a divine plan and Louis Agassiz (1850s–1860s), who framed the "*unity of plan*" across life as a thought in the mind of the Creator. Each level keyed to an aspect of the structural plan:

"Branches or types are characterized by the plan of their structure; Classes, by the manner in which that plan is executed; Orders, by the degrees of complication of that structure; Families, by their form; Genera, by the details of the execution in special parts; and Species, by the relations of individuals to one another and to the world in which they live."

That is clearly a nested hierarchy, and Agassiz insisted the categories were real, not human conveniences, and that "*all differences observed among finite beings are ordained by the action of the Supreme Intellect, and not determined by physical causes*", published in *Contributions to the Natural History of the United States*, Vol. I, 1857. So he affirmed the nested pattern and read it as the structure of the Creator's thought. He described it as *several* nested hierarchies leading back to a mosaic (*one per archetype*) than a single nested tree back to one root, but the prediction still lands in our court. The nested *pattern* was catalogued and interpreted as design by creationist naturalists before Darwin (Linnaeus, Cuvier, Agassiz).

Homologous Genes and the Hox System

The historical question is whether creationist authors articulated expectations concerning molecular similarity before the particular discoveries used to test them. Frair (1967, p. 18) explicitly anticipated that further investigation of DNA and proteins would reveal molecular homologies within a creationist interpretation of biological organization. Morris subsequently argued that common design provides a basis for expecting biological similarities. These statements document a broader expectation of molecular and structural correspondence while evolution had predicted the exact opposite.

In 1963 Ernst Mayr predicted that the search for homologous genes across distant organisms would be “*quite futile except in very close relatives,*” since deep time and random change would obscure them. In 1975 the creationist Henry Morris predicted the opposite: that the same controlling genes would be found across most of life, reflecting common functional design rather than common ancestry, he said; “*The creative process would have designed similar structures for similar functions and different structures for different functions..*” “*..In the creation model, the same similarities are predicted on the basis of a common purposive designer.*” (The Troubled Waters of Evolution - 1974/1975 First Edition).

Building on earlier creation predictions of a shared structural plan, Owen’s homology (1843 onward) and Linnaeus’s fixed taxonomy (1745), Morris reasoned that a common purposive designer would reuse similar structures for similar functions across otherwise unrelated kinds. The data vindicated him. In 1978 Edward Lewis showed Hox genes arranged in expression ordered clusters in *Drosophila*, and the same Hox system was then found across the animal kingdom. Sean Carroll later conceded that “not even the most ardent advocate of fruit fly research predicted the universal distribution and importance of Hox genes” (2005), and that biologists “*had long assumed*” different animal groups were built by entirely different means (2013).

The surprise fell on the evolutionary side; the confirmation fell on the creation side. Sean Carroll emphasized the significance of the discovery: “*It was inescapable. Clusters of Hox genes shaped the development of animals as different as flies and mice, and now we know that includes just about every animal in the kingdom, including humans and elephants. Not even the most ardent advocate of fruit fly research predicted the universal distribution and importance of Hox genes*”. (Carroll, 2005, p. 64). Carroll further observed: “*The implications were stunning. Disparate animals were built using not just the same kinds of tools, but indeed, the very same genes... No biologist had even the foggiest notion that such similarities could exist between genes of such different animals*” (Carroll, 2005, pp. 64–65). In a later reflection, he noted that this represented a failure of evolutionary expectations: “*Comparative and evolutionary biologists had long assumed that different groups of animals, separated by vast amounts of evolutionary time, were constructed and had evolved by entirely different means*” (Carroll, 2013). These acknowledgments illustrate the unexpected nature of Hox gene conservation across animal phyla and highlight the challenge such findings posed to prior evolutionary assumptions. For this review, the case is classified as a prior model expectation from multiple creationists consistent with later developmental discoveries while the evolutionary expectations and predictions turned out to be the exact opposite. These findings can be compared with the earlier creationist expectation of molecular similarity.

Genome Level DNA Similarity and Common Design

The broader question of molecular similarity requires distinguishing a documented design expectation from a specific forecast of future sequencing results. Frair’s 1967 discussion explicitly addressed DNA and proteins as subjects of comparative investigation. Creationist Dr Henry Morris’s 1974 prediction extended beyond developmental control genes to the genome as a whole and specifically DNA. Before detailed DNA sequencing existed, he argued that living organisms would be found to share similar underlying DNA-level properties, reflecting a unified pattern of functional design, and that such similarity would point to a common designer and to relatively little elapsed time since creation rather than to descent from a common ancestor. He stated in his book *The Troubled Waters of Evolution* 1974 First Edition: “*It may yet be demonstrated that all living organisms exhibit similar underlying DNA-level properties reflecting a unified pattern of functional design. Such findings would be consistent with the hypothesis of a common designer and suggest that relatively little time has elapsed since creation*”. (Morris, 1974-First edition). Frair anticipated that further characterization of biological macromolecules would reveal molecular homologies within a creationist understanding of biological organization (Frair, 1967, p. 18). This documents a creationist research expectation and prediction concerning molecular similarity before the later discoveries discussed here.

Morris's subsequent common-design arguments likewise establish a more direct DNA expectation of biological similarity rather than a documented forecast of the same developmental control genes across distant animal groups.

The first complete DNA genome sequenced was the tiny 5,375-base genome of bacteriophage ϕ X174, published in 1977 by Frederick Sanger's three years after Morris' prediction. This new tech finally made it possible to directly read the genetic code, allowing scientists to compare genes, not just proteins (Dayhoff 1960s) across species. This breakthrough opened the door to modern genomics and provided the tools that confirmed Morris's prediction of underlying DNA-level similarities across life. By contrast, evolutionary theorists like Motoo Kimura, writing around the same time, assumed any such similarity as the product of random genetic drift rather than purposeful design. In effect, Kimura predicted the exact opposite of Morris: *that shared DNA sequences reflected chance processes, not functional patterns driven by mutation pressure and random genetic drift rather than Darwinian natural selection*. Today, the evidence is clear: genetic sequences are not random strings, but carry functional purposes.

In fact, one of the primary tools of modern genomics is to predict a gene's role by comparing its sequence to known genes across species. This very principle, that DNA similarity reflects purposeful design and functional patterns, was anticipated by Morris in 1975 and is now routine in biology. Far from being a surprise to creationists, the discovery that genes are conserved, ordered, and functionally significant stands as a striking confirmation of the creationist predictions over time. Despite the unexpected nature of these findings and lack of direct prior predictions, the majority of evolutionary interpretations have continued to incorporate genetic similarities, junk DNA, homology, hierarchical patterns and Hox gene conservation as evidence supporting common ancestry rather than reconsidering the alternative view that keeps obtaining and confirming their prior predictions outside the evolutionary framework. Instead of viewing the data as falsified by earlier failed predictions, the results simply get reinterpreted within the existing evolutionary framework regardless. This illustrates a broader pattern in which anomalous or surprising discoveries are accommodated by theoretical adjustment. Evolutionary theory today presents overall genetic similarity as a signature of shared ancestry and the best evidence for evolution there is in genetics. Contrary to their earlier predictions, and when the molecular data arrived however, the predicted widespread DNA similarity was indeed found across most of life, and it was read into the ancestry framework after the fact. This is the recurring pattern of this study: the same similarity Morris predicted on design grounds in advance was, once discovered, retrofitted into evolutionary theory treated as confirmation of common descent. Since "*design*" necessarily implies agency, and agency remains the best inference from the evidence, design is the most compelling conclusion. The strong predictive power of the Biblical Creation framework serves as the tool that demonstrates why design is not only an inference, but the best explanation and the superior model.

Genetic Boundaries and DNA Barcoding

Harold W. Clark, in 1940, with his book *Genes and Genesis*. Clark was arguing that the new science of genetics supported creation rather than evolution. In a 1941 article explaining the book, he said the genetic evidence led him to a creationist model of "*multiple creation*" in which each created group could "*vary within itself*," and he claimed that the new genetic discoveries showed "*the scientific evidence is on our side*." later Carl Linnaeus taxonomic boundaries along with. Frank Lewis Marsh, who coined the term baramin (1941), and Henry Morris (Scientific Creationism, 1974) who predicted that DNA-level similarity would be found within created kinds and that life was created recently. Then in December 2013, Jeanson published a technical creationist model of mitochondrial diversity in *Answers Research Journal*. He argued that, under a young-earth timescale, within-group mitochondrial diversity should remain comparatively limited and that his equations could make testable quantitative estimates of genetic diversity "*across the entire animal kingdom*." He explicitly called the section "A predictive young-earth model." He made the qualitative prediction even more plainly in an ICR

article dated March 31, 2014: “If their origins trace back only 6,000 years, then **they should be more genetically homogeneous.**” Immediately before that, he contrasted this with the expectation that kinds existing for millions of years “**should be quite genetically diverse.**” He then stated that measured mitochondrial mutation rates could be used to **predict genetic diversity**. All of these set hard bottleneck boundaries from creation and the flood. This means species would have similar levels of genetic diversity and all low levels of diversity since not a lot of time has passed. DNA barcoding confirmed this. July 2, 2014 Stoeckle & Thaler: report uniformly low intraspecific mitochondrial variation in a large bird dataset. Then later when analyzing the COI gene across roughly 100,000 species, Stoeckle and Thaler (2018) found that most species show similarly low, recent intraspecific diversity, what they then renamed low average pairwise differences (APD) and were separated by clear genetic gaps they called “*genetic boundaries*” with little in between, and that. Thaler reported, “*I fought against it as hard as I could.*” The same data set undercuts two long-standing puzzles, Lewontin’s paradox (diversity does not scale with population size) and the genetic equidistance pattern, both resolved by a recent common bottleneck followed by limited time for divergence.

Low, uniform diversity across animals that differ a hundredfold in generation time matches a recent global bottleneck, not the neutral theory expectation that diversity scales with population size and time. The conventional 200,000 year date for this uniformity has no corresponding event in the fossil record (Weaver, 2012, citing Brauer, 2008), whereas a recent global bottleneck does. Todd Wood’s prediction that statistical baraminology would recover sharp discontinuities between kinds, with bounded variation within them, has been borne out across data types. Harold W. Clark’s prediction all the way back in 1940 and Jensen’s 2013 predictions regarding created boundaries with genetically homogeneous diversity would be found came true in 2018 when genetics confirmed these genetic boundaries leading back to what creationists refer to as independent ancestry.

Multicellularity: A Prospective Creation-Model Prediction

Unlike a retrospective explanation constructed after an experiment has been performed, a useful scientific prediction must be stated in advance. In this case, a creation-model expectation concerning microbial adaptation was explicitly published before several of the most prominent experimental demonstrations of rapidly arising multicellularity. In 2008, creationist researchers Georgia Purdom and Kevin Anderson developed a model of biological adaptation in microorganisms. They argued that a creation model predicts microorganisms capable of rapid and versatile adaptation, while also predicting that such change would ordinarily remain limited and would frequently proceed through alteration, reduction, activation, or loss of pre-existing cellular systems, rather than through the origin of entirely new biological machinery. Significantly, after discussing bacteria they stated that the same general principle also applies to other unicellular organisms, specifically mentioning yeast and protists (Purdom & Anderson, 2008). Thus, before the major experimental multicellularity studies discussed below, the creation model had already generated a prospective mechanistic expectation: dramatic adaptive phenotypes in unicellular organisms could arise rapidly, but examination of their genetic basis should reveal extensive dependence upon pre-existing biological machinery rather than the de novo construction of the systems producing the phenotype.

A striking test came several years later. Ratcliff et al. (2012) subjected initially unicellular *Saccharomyces cerevisiae* to selection favoring rapid settling and obtained heritable multicellular “snowflake” clusters. The result was widely presented as an experimental model for an evolutionary transition from unicellularity to multicellularity. Subsequent genetic analysis, however, revealed an especially simple mechanism. Snowflake yeast can arise through disruption of the transcription factor ACE2. Loss of normal ACE2 activity prevents the usual separation of daughter cells from their mothers following cell division, causing descendants to remain physically attached and thereby producing branching multicellular clusters (Ratcliff et al., 2015). The multicellular phenotype did not initially require the construction of a novel cell-adhesion system; it emerged

through disruption of an existing regulatory program controlling cell separation. The result became more significant when the experiment was effectively repeated in another budding yeast. Wang et al. (2024) subjected *Kluyveromyces lactis* to settling selection and again obtained rapidly appearing snowflake multicellularity. Whole-genome analysis showed remarkable convergence: multicellular phenotypes were produced by loss-of-function mutations in either ACE2 or AIM44, both regulators associated with cell division. ACE2 mutations occurred in every experimental lineage, and most involved stop codons or frameshifts expected to truncate the protein. Experimental knockout of ACE2 in the ancestral strain was itself sufficient to generate the snowflake phenotype. The investigators concluded that the multicellular forms arose through failure of normal mother-daughter cell separation rather than through construction of a new adhesion mechanism. This sequence is important because the creation-model statement preceded the experiments. The prior creationist prediction was testable: rapid adaptive change in unicellular organisms such as yeast should be possible, yet dramatic phenotypic novelty should often arise through modification or loss of pre-existing biological systems rather than through the observed construction of new cellular machinery.

The subsequent snowflake-yeast experiments produced exactly this class of outcome. The accurate creationist prediction has now been replicated across distinct yeast species. Selection generated a conspicuous new multicellular phenotype rapidly, yet its initial genetic basis repeatedly involved loss or disruption of existing regulatory functions controlling cell separation. This does not demonstrate that evolutionary mechanisms can never generate unique adaptations, nor does simple snowflake multicellularity represent the full complexity of animals, plants, or other highly differentiated multicellular organisms. It does, however, constitute a legitimate prospective success for the narrower Biblical creation model prediction made beforehand: large adaptive changes in phenotype can occur rapidly while remaining mechanistically dependent upon alteration of biological systems that already exist.

Beneficial Mutations: Modification and Loss, Not New Structures

Creationist have long held to the view that God created different “kinds” of animals, birds, fish and species. Thus universal common ancestry is off the table and that natural selection, by itself, does not introduce new genetic variants; meaning Natural selection takes evolution nowhere, on its own - rather, it acts upon variation already present in a population by increasing or decreasing the frequency of specific alleles. The real new variation in the evolutionary models requires mutation, which provides the raw material upon which selection may act. As stated by Evolutionary Naturalist Jean-Baptiste Lamarck, *"Nature, by its own means, has successively produced all species of animals, beginning with the simplest and ending with the most complex."*

On the opposite side of this debate is creationist Dr. Lee M. Spetner, who was probably the strongest early creationist to make the genetic / information-based prediction that beneficial mutations would not build new kinds of animals. Spetner's argument was: *Beneficial mutations may help survival, but they usually do so by damaging, disabling, reducing, or altering existing genetic systems, not by creating the new biological information required to build new body plans or new created kinds.*

He developed this argument technically in the 1960s, with papers on natural selection and information, including a 1968 paper titled “Information Transmission in Evolution” in *IEEE Transactions on Information Theory*, and a 1970 *Nature* paper titled “Natural Selection versus Gene Uniqueness.

Since that time empirical studies raise nothing but questions and doubts about the capacity of mutations to generate entirely new novel anatomical structures in the linear, branching manner represented in textbook diagrams of evolution. For example, experimental work focusing on Hox genes (master regulators of body-plan development) has demonstrated that mutational changes can alter or disrupt existing developmental pathways, but

such alterations have not been observed to produce entirely new, beneficially functional anatomical features as expected which again is required to validate the evolutionary narrative. Instead, the results frequently involve loss of function, duplications, or deformations, consistent with modification of existing genetic information rather than the origination of novel structures (see Carroll, 2005; Carroll et al., 2013).

To date, we have the entire genome sequenced of...

- Fruit fly (*Drosophila melanogaster*) – genome completed in 2000 (published in *Science*, part of a big international collaboration with Celera Genomics).
- Nematode worm (*Caenorhabditis elegans*) – first multicellular organism to have its genome sequenced, completed in 1998 (published in *Science*).
- House mouse (*Mus musculus*) – genome draft completed in 2002 (published in *Nature*; it was the second mammalian genome after humans).
- Yeast (*Saccharomyces cerevisiae*) – first eukaryote to have its genome fully sequenced (1996).
- Plants – *Arabidopsis thaliana* (a small flowering plant, model for genetics) completed in 2000.

Experimental manipulations of Hox gene regions in the above organisms are often presented as demonstrations of evolutionary mechanisms in school text books. Yet, the outcomes of these targeted alterations consistently result in developmental abnormalities, not the emergence of genuinely novel anatomical structures.

For instance, forced mutations in the Hox gene in fruit flies producing additional wings or legs do not represent **new** traits but rather the misexpression of pre-existing structures. In such cases, the extra wings were non-functional and impaired flight, while legs that developed in place of antennae were malformed and non-adaptive (Lewis, 1978; Carroll, 2005).

These results highlight a key limitation: mutations in Hox regulatory regions can reorganize or duplicate existing features but have not been shown to generate entirely new, functional traits. Thus, while these experiments underscore the pivotal role of Hox genes in developmental patterning, they stop short of providing direct evidence for the evolutionary origin of novel new body parts slowly arising.

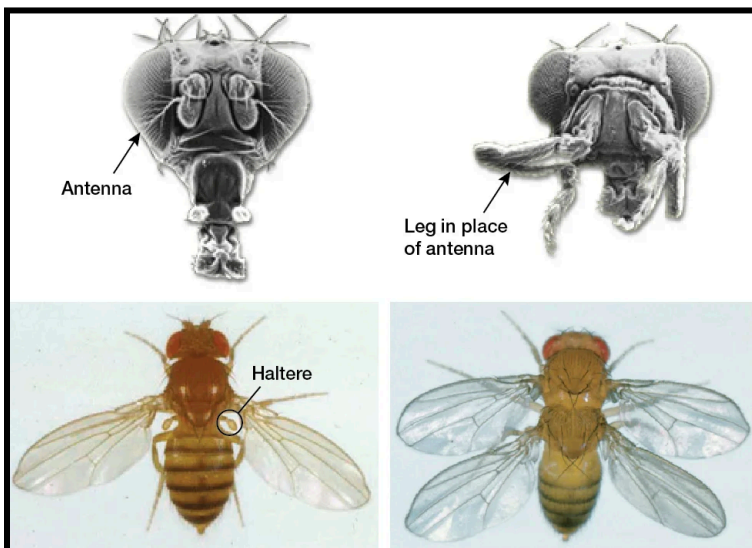


Figure 1. shows (top) a leg growing out of the face where an antenna belongs and (bottom) shows an extra set of wings growing where halteres should be. Halteres are special sensory organs at the base that detect changes in body position and rotation. Halteres act like gyroscopes and help the fly balance as it flies.

As of 2026 creationist Dr. Lee M. Spetner's prediction has only been confirmed. Reported cases of so-called 'beneficial mutations' do not demonstrate the origin of new novel anatomical features as predicted by creationists. Rather, they involve altered expression of existing traits, often accompanied by trade-offs, or the loss of previously present structures. Examples include the reduction or **loss** of wisdom teeth, the **loss** of the palmaris longus tendon in humans, wing **loss** in beetles, vision **loss** in cave fish, **loss** of flight in certain birds, tail **loss** in dogs, feather **loss** in chickens, and the emergence of tuskless elephants.

While such changes may confer situational advantages, they represent modifications or reductions of pre-existing features rather than the origination of entirely new ones. Since evolution requires innumerable transitions from mutation that add anatomical features slowly over time, one would expect such evidence to exist today or even be replicated in a lab. No such examples exist, as creationists predicted.

Evolution requires mutation to build genuinely new anatomy. The record instead shows modification, duplication, or loss. Forced Hox mutations in fruit flies produce misplaced or extra structures, legs where antennae belong, nonfunctional second wings, not new functional organs (Lewis, 1978; Carroll, 2005). The Italian wall lizards moved to Pod Mrcaru developed cecal valves within about thirty generations (Herrel et al., 2008), once cited as a new structure, but the valves reverse within weeks on an insect diet (Vervust et al., 2010), appear across related herbivorous lizards (Sagonas et al., 2015), and represent enlargement of existing musculature (Menton, 2008): plasticity and latent capacity, not novelty.

In archaea, three *Sulfolobus solfataricus* lineages independently evolved for extreme acid resistance acquired the heritable trait with few or no point mutations, the SARC-I lineage with none, while an unselected control line accumulated 141 mutations without ever becoming acid resistant (Payne et al., 2018); the adapted strains in fact showed reduced mutation and transposition rates, so the trait runs opposite to point mutation count (Figure 1).

In long term *E. coli* and yeast experiments, beneficial mutations are overwhelmingly loss or degradation of function (Chen and Zhang, 2020), and destructive changes occur an estimated 100 to 1,000 times faster than constructive ones. After decades of study there is still no catalogue of thousands of clearly new organs or physical features slowly arising by mutation; there is one ambiguous lizard case, easily explained without it.

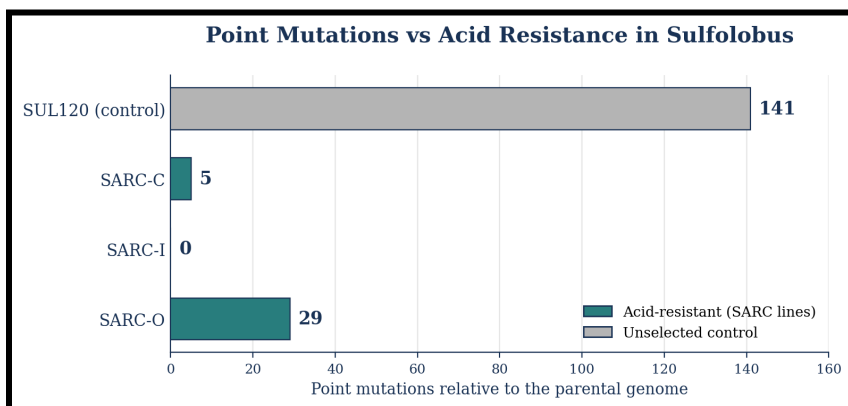


Figure 2. Point mutations in the experimentally evolved *Sulfolobus solfataricus* lineages. The three acid resistant SARC lines acquired the trait with 0 to 29 point mutations, SARC-I with none, whereas the unselected control line SUL120 accumulated 141 mutations without becoming acid resistant. Adaptation is decoupled from, and runs opposite to, point mutation count. Data from Payne et al. (2018).

Conserved homologous genes/proteins

Frair (1967). Creationist biologist Wayne Frair argued that the emerging fields of protein and DNA analysis should reveal an underlying “*creative pattern*” in living organisms. At a time when only a small number of protein structures had ever been characterized and direct DNA sequence comparison was not yet practicable, Frair predicted that improved molecular methods would permit increasingly detailed comparisons among organisms and would reveal molecular “homologies” or “essential similarity.” He explicitly anticipated that, as protein-sequencing techniques improved, investigators would be able to compare proteins throughout living organisms and reconstruct their molecular groupings. Meanwhile in 1963, leading evolutionary biologist Ernst Mayr wrote: “*the search for homologous genes is quite futile except in very close relatives. If there is only one efficient solution for a certain functional demand, very different gene complexes will come up with the same solution, no matter how different the pathway by which it is achieved. The saying “Many roads lead to Rome” is as true in evolution as in daily affairs.*” Mayr reasoned that long evolutionary separation should make recognizable homologous genes difficult to find across distantly related organisms. Henry Morris later stated in 1975 that a creation model predicts similarities because of a “common purposive designer.” Then in 1973, researchers had 5S-rRNA sequences from widely different organisms including *E. coli*, *Pseudomonas*, yeast, human cells, and *Xenopus*. Researchers were comparing them explicitly for conserved and variable regions. By 1975, Fox and Woese performed an extensive comparative analysis of 5S rRNA and identified a highly conserved segment of more than 30 nucleotides in prokaryotic 5S rRNA. Then finally came the big news, On March 29, 1984, McGinnis and colleagues reported a conserved DNA sequence in several *Drosophila* developmental genes, the sequence that became known as the **homeobox**. So before the later discovery of deeply conserved developmental genes and proteins across widely separated animal groups, a creationist molecular framework had already anticipated that improved molecular biology would uncover extensive underlying biological similarity rather than erase it. The evolutionary prediction was the exact opposite and was essentially falsified and the data was again re-interpreted and retrofitted back into the model.

The Founder Effect and Bottleneck Recovery

Creationist Frank Lewis Marsh implied that a small number of kinds could survive a genetic bottleneck, Noah’s Flood, and then recovered. He predicted that future studies would confirm this is possible, while modern genetics of his day said that populations require a minimum population size in the hundreds. Ernst Mayr first fully outlined the founder principle in his seminal 1942 work, *Systematics and the Origin of Species*, utilizing Sewall Wright's earlier mathematical models of genetic drift. It was not until the late 1970s and 1980s, biologists began to quantify this threshold into concrete numbers (the famous 50/500 rule). 50 being minimum to survive inbreeding and 500 for survival and maintain long-term evolutionary potential. So population genetics has long held that a single pair cannot find and hold a healthy population. Yet we now have multiple examples from diverse species worldwide that confirmed Marsh's prediction. In 2002, creationist Todd Wood explicitly developed a creationist model requiring rapid diversification from small post-Flood founding populations, including a proposed single ancestral pair for modern cats. This establishes a dated small-founder model. Pedigree mutation rate studies have since confirmed recent population bottlenecks throughout the animal kingdom, sealing Marsh’s predictions in both genetics and fossils. The best examples are that of island populations because they can be observed and catalogued easier than other populations. Our primary example for this section is that of a single pair of mouflon sheep introduced to the sub Antarctic Kerguelen archipelago in 1957 grew to 700 by 1977, and heterozygosity, measured over 46 years, increased and “*exceeds the range predicted by neutral genetic models and stochastic simulations*” (Kaeuffer et al., 2007, in a paper titled **Unexpected heterozygosity in an island mouflon population founded by a single pair of individuals**). The same recovery from severe bottlenecks is documented in insects (BBC, 2016), birds (Grant & Grant, 2002), deer (YLE, 2018), rabbits (CNN, 2022), fish (National Geographic, 2008), bison (National Geographic, 2020), wolves (Vilà et al., 2003; Viluma et al.,



2022), whales (*Marcos Suarez Menendez et al 2023*), lizards (Herrel et al., 2008), and yes, even humans (Soodyall et al., 2003; Macgregor et al., 2009). The creationist prediction, that recovery is possible given a single generation bottleneck and rapid growth, from a single pair is confirmed (*Figure 3*) contrary to evolutionary expectations..

Figure 3. *The Kerguelen mouflon population, founded by a single pair in 1957, climbed to roughly 700 by 1977 and then cycled between about 200 and 700. Heterozygosity, measured over 46 years, rose rather than declined, exceeding the range predicted by neutral models. Redrawn from Kaeuffer et al. (2007).*

Rapid Speciation Versus Gradualism

In 1997, Carl Wieland explicitly argued that the creationist post-Flood model requires rapid speciation within created kinds. This establishes a documented model expectation before the 2017 finch report discussed here. Darwin predicted slow change: natural selection “will always act very slowly” (*Origin of Species*, 1st ed.). Standard texts echoed this. Benton’s *Vertebrate Palaeontology* (2005, p. 49) states that speciation “*typically requires tens of thousands of years,*” and Henry Gee placed the emergence of new species across “*tens of thousands of years*” (*In Search of Deep Time*, 2000, p. 44).

Observation has overturned this. A new Darwin’s finch lineage on Daphne Major was established in about three generations (Lamichhaney et al., 2017), which the authors noted can occur where hundreds of generations were assumed necessary. Trinidadian guppies adapted at rates “*some 10,000 to 10 million times faster than the average rates determined from the fossil record*”; anole lizards, *Drosophila*, sockeye salmon, London Underground mosquitoes, Madeira house mice, and Australian cane toads (Hudson et al., 2020) all show rapid, directional change within decades to a few centuries. Rapid, bounded radiation is precisely the creation expectation for a post Flood world, and it is a falsification of strict gradualism.

Junk DNA and Endogenous Retroviruses

In 1969 King and Jukes asserted that “*99 percent of mammalian DNA is not true genetic material,*” and in 1972 Susumu Ohno popularized the view that most of the genome is nonfunctional junk. Evolutionary theory placed endogenous retroviruses (ERVs) in this junk category and cited them as evidence of common descent. Creation and design thinkers predicted the opposite. In 2000 Linda Walkup argued that transposable elements, including ERVs, were designed to enable variation within kinds and would prove to have functional aspects (*CEN Journal of Creation* 14(2)). Her article contains a section titled “*The AGEing theory and diversification.*” She explicitly attributes the hypothesis to Wood and cites his unpublished Baraminology Conference 1999 paper.

That same year (2000) the first clear ERV function was confirmed: syncytin, an ERV derived protein essential for placental cell fusion. Since then, ERV derived sequences have been shown to provide promoters for over a fifth of human genes (Conley et al., 2008), to regulate immunity (MER41; Buttler and Chuong, 2022), to demarcate chromatin domains in stem cells (Zhang et al., 2019), and to function across embryogenesis and antiviral defense.

Since this time, only a small fraction of ERV loci have been individually tested for function, realistically well under one percent of the hundreds of thousands of ERV-derived elements in the human genome. Yet nearly every element examined has yielded evidence of some biochemical or regulatory role, from promoters and enhancers to immune and developmental functions.

What was once dismissed wholesale as junk is, wherever it has actually been probed, turning out to do something. The junk-DNA paradigm for ERVs, offered as a specific evolutionary expectation, has not survived that scrutiny, and even nomenclature reviews now state that ERVs are not, "*as was once believed*," mere junk DNA (Gifford et al., 2018).

If that is not amazing enough, it gets better. Todd Wood in Baraminology 99, Liberty University, August 5–7, 1999. The presentation was titled approximately: "*The AGEing Process: Post-Flood Intrabaraminic Diversification Caused by Altruistic Genetic Elements (AGEs)*". In it he said that we would also find unique ERV's specific within related "*kinds*". He proposed calling them "*Altruistic Genetic Elements*," abbreviated AGEs and proposed a mechanism he called the "*AGEing process*".

Since that time they have confirmed related ERV's such as:

- BERVs — bovine endogenous retroviruses. Xiao et al. 2008; Nakaya et al. 2010 (J Virol)
- OERVs — ovine endogenous retroviruses. Palmarini et al. 2000–01; Klymiuk et al. 2003
- RELIK — rabbit endogenous lentivirus type K, in the European rabbit (later hares). Katzourakis, Tristem, Pybus & Gifford 2007 (PNAS 104:6261).
- PSIV — prosimian immunodeficiency virus, in the gray mouse lemur and other Malagasy lemurs. Gifford et al. 2008 (PNAS 105:20362); Gilbert et al. 2009 (PLoS Genetics 5:e1000425).
- MELV — mustelid endogenous lentivirus, in the weasel family. Han & Worobey 2012 (Mol Biol Evol 29:2905).
- DELV — dermopteran endogenous lentivirus, in the colugo. Han & Worobey 2015 (Mol Biol Evol 32:211).
- SpELV — springhare endogenous lentivirus, in the springhare (rodent). 2022 (genome-mining study).
- KoRV — koala retrovirus, in the koala. Hanger et al. 2000 (J Virol 74:4264).
- CfERVs — canine endogenous retroviruses (Fc1 lineage), in the dog. Martínez Barrio et al. 2011 (PLoS ONE 6:e19832).
- EqERV-β1 — equine endogenous beta-retrovirus 1, in the horse. van der Kuyl 2011 (Viruses 3:620).
- ERV-DC — endogenous retrovirus of the domestic cat, in the cat. Anai et al. 2013 (Journal of General Virology 94(7):1587-1596).

Shared ERVs, by themselves, do not decide between the models; both expect them. What would actually discriminate is the pattern the design side has long pointed to: ERVs sitting at non-orthologous sites, and ERV distributions that violate the standard evolutionary tree. PtERV1 is exactly that. Roughly 95.8% of its integrations fall at non-orthologous positions between even closely related species, and it is present across the African apes and Old World monkeys while being wholly absent from humans, a pattern that badly strains any single-ancestral-infection account (Yohn et al., 2005, PLoS Biology 3:e110).

PtERV1 is not a lone curiosity. It sits on top of a fact that the standard evolutionary argument tends to pass over and ignore quietly: retroviral integration is not random. Retroviruses and their integrase machinery show strong, reproducible preferences for particular chromatin states, transcription start sites, and specific DNA structures, and genuine integration "hotspots" exist where the same locus is targeted again and again by independent insertions (Desfarges & Ciuffi, 2010; Kirk et al., 2023). This matters, because the entire force of the "*shared ERV proves common ancestry*" argument rests on an unstated premise, that integration is so random that two lineages could never independently acquire an insertion in the same place. Once integration is known to be targeted rather than random, that premise extremely weakens, and independent insertion at the same site stops being unthinkable and starts being expected at some rate. PtERV1 is what that looks like in practice: 287 integrations mapped, roughly 95.8% of them at non-orthologous positions between even closely related species, present across the African apes and Old World monkeys yet absent from humans, a distribution the discoverers

themselves could only explain as multiple independent invasions of the germline rather than inheritance from one common ancestor (Yohn et al., 2005).

The second line of evidence is, if anything, harder to fit into a single tree. The syncytins are envelope genes captured from endogenous retroviruses and put to work as the fusion proteins that build the placenta, and they are indispensable, knock them out and the embryo dies. If these captures were rare accidents inherited from one ancestral event, we would expect one syncytin, shared by descent. Instead, biologists have now found syncytins captured independently, from entirely unrelated retroviruses, over and over across the mammals: syncytin-1 and -2 in primates, syncytin-A and -B in mice and their kin, syncytin-Ory1 in rabbits, syncytin-Car1 in carnivores, syncytin-Rum1 in ruminants, syncytin-Mar1 in squirrel-related rodents, and still others in tenrecs (Lavialle et al., 2013; Cornelis et al., 2012, 2013). The same functional solution, the same class of tool built for the same purpose, acquired again and again from separate sources in separate lineages.

A parallel case has been documented in the envelope genes independently domesticated in the even-toed ungulates and the carnivores from one ancient source (Fématrin and its relatives; PLOS Genetics, 2022). Repeated, independent arrival at the same functional answer is the signature of design constraint and functional requirement, not the signature of a single random inherited accident. Just as predicted by creationists, while entirely ignored by the naturalistic view.

The situation is that ERV distributions carry signal for more than one history at once. But that is exactly the point this chapter has pressed from the beginning. We invoke created design diversity and when integration is targeted rather than random, when shared locations turn out to be independent invasions, and when the most essential ERV-derived genes in all of biology were captured not once but a dozen separate times, the confident claim that endogenous retroviruses are simply inherited viral debris tracing a single tree is no longer the only reading of the data, nor the most natural one. Todd Wood predicted, before these genomes were sequenced, that we would find ERVs distributed within related kinds and serving the organisms that carry them. Two decades of sequencing have delivered exactly that: retroviral elements that are taxonomically bounded, functionally essential, repeatedly and independently acquired, and woven into the deepest machinery of life. The evidence that was supposed to be the clinching proof of universal common ancestry turns out, read without that prior commitment, to speak just as clearly of design, function, and purpose.

Interestingly, this design-based interpretation is also compatible with one of the major scientific hypotheses for viral origins: the escape or progressive hypothesis. This hypothesis proposes some viruses if not all originated from cellular mobile genetic elements that acquired the machinery necessary for transmission between cells. Retroviruses are particularly relevant because phylogenetic and genomic studies place them close to LTR retrotransposons, and one proposed pathway derives retroviruses from Ty3/Gypsy-like retroelements following acquisition of an envelope gene. Thus, the observation that retroviral-like elements can participate in normal genomic function is not inherently inconsistent with the possibility that the cellular element preceded the infectious virus. This does not establish the escape hypothesis, but it demonstrates that the common assumption “virus first, useful host function later” is not the only biologically plausible direction of causation.

Neanderthal Upright Posture

A particularly clear historical comparison concerns Neanderthal posture. Marcellin Boule's influential 1911–1913 reconstruction of the La Chapelle-aux-Saints skeleton depicted Neanderthals as incompletely erect, helping establish the familiar stooped and bent-kneed image. 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 *Monkeyshines: Fakes, Fables, Facts Concerning Evolution* in 1926. Rimmer specifically attacked the inaccurate Neanderthal reconstructions 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.” He was right.

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, creationist 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.

The complete historical walkthrough of the evolutionary failed predictions

1911–1913: Marcellin Boule: Boule's scientific study of La Chapelle-aux-Saints produced the famous reconstruction of a Neanderthal with an incompletely erect posture. His monograph appeared in *Annales de Paléontologie*.

1926: Harry Rimmer, creationist: Rimmer explicitly says the reconstructions do **not** represent the skeleton correctly and declares Neanderthal a “true man.”

1950s / 1957: scientific reappraisal: The old reconstruction is anatomically reassessed; Straus & Cave publish *Pathology and the Posture of Neanderthal Man*.

1985: Trinkaus: Trinkaus confirms that the incompletely erect depiction derived primarily from Boule, states that its inaccurate aspects were corrected in the 1950s, and concludes that Boule's mistaken posture interpretation reflected anatomical misinterpretation combined with evolutionary preconceptions.

2019: Haeusler et al., PNAS: Modern reconstruction again finds human-like lumbar and cervical curvature and concludes that Neanderthals possessed a **fully upright human axial posture**.

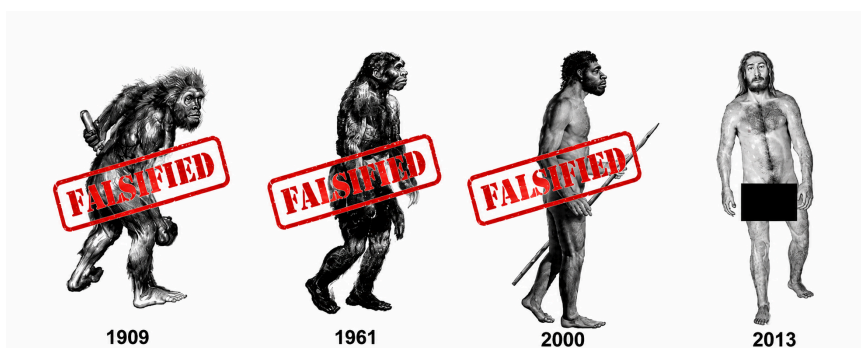


Image 1. Neanderthal depictions over the century.

Boule's specimen was later recognized to have suffered from severe osteoarthritis, and reassessment showed Neanderthal posture and gait were fully upright and essentially modern. The prediction of upright human posture was eventually confirmed, and the brutish stoop was an artifact of a diseased individual, not a feature of the kind. The images that adorned textbooks changed yet again.

Neanderthals as Fully Human

When the first Neanderthal DNA was sequenced, the 1997 paper made the cover of *Cell* under the headline "*Neanderthals were not our ancestors*" (Krings et al., 1997), and Neanderthals were long portrayed as subhuman, non symbolic, and incapable of language. The creation side had predicted the reverse, and had done so for decades. As early as 1926, and again in his 1975 *Doorway Papers*, creationist Arthur C. Custance argued that Neanderthals were not ape men, that their robust skull traits fit human variation and environment, and that as tool makers they were truly human.

Gary Parker, writing for the Institute for Creation Research around 1980 and 1981, held that Neanderthals were fully human people rather than subhuman links, and Henry Morris and Parker reaffirmed in 1982 (*What Is Creation Science?*) that they were ordinary humans whose unusual features reflected pathology or environment. After the 1997 mtDNA study placed Neanderthals outside the modern range, John D. Morris maintained they were as human as we are and may have interbred with other people, and in 1998 Marvin Lubenow (*Recovery of Neanderthal mtDNA: An Evaluation*) argued specifically that a single mtDNA sequence could not exclude Neanderthals from humanity, predicting they were fully human and ancestral to at least some living people. The same year Jack Cuozzo (*Buried Alive*) proposed they were post Flood, long lived humans whose anatomy reflected development and longevity rather than subhuman evolution. In 2000 Dave Phillips (*Neanderthals Are Still Human!*) marshaled language anatomy, brain size, the hyoid bone, burial, and mtDNA overlap to the same conclusion.

Working from the premise that Neanderthals were descendants of Adam and Eve, David DeWitt, with W. Skinner, made the most explicit genetic prediction in 2000 and 2001: that a base by base comparison would show Neanderthals differing from modern humans mostly at sites where modern humans already differ from one another, the signature of genetically similar humans sharing a recent common gene pool, directly counter to the 1997 secular conclusion (DeWitt, 2014). Through 2003 and 2004 Sarfati, Lubenow, and other creation writers continued to treat Neanderthals and modern humans as one human kind capable of interbreeding. The prediction held. The Neanderthal genome confirmed interbreeding and shared variation (Green et al., 2010), and DeWitt noted that the result confirmed a Bible based prediction that ran counter to the secular consensus. Answers in Genesis summarized the position in 2018: Neanderthals were fully human ancestors of some modern humans. The reversal on the evolutionary side was not limited to ancestry; nearly every behavioral and cognitive claim made about Neanderthals has since been overturned. Once dismissed as dim witted brutes, Neanderthals are now regarded as cognitively indistinguishable from modern humans, sharing symbolic thinking, on the evidence of cave art (Zilhao and colleagues, reported by the Max Planck Society, 2018). Long described as scavengers too dull and clumsy to organize a hunt or fashion efficient tools, they are now credited with planned hunting, artful carved objects, and possibly language (Smithsonian, 2003). Claims that they were incapable of language or symbolic thought, and that they lacked the intelligence to adapt across ecological zones or to develop functional tools, have likewise been abandoned as the record showed them to be accomplished across varied environments.

They are now credited with art, ornaments, tools, musical instruments, cosmetics, burial of their dead, and the language associated with the FOXP2 gene, and are classified as *Homo sapiens*. Genetic work has further found Neanderthals carrying immune gene variants that were not weaker but in some cases better functioning, contributing beneficial immune alleles to living people (Phys.org, 2020). Even a supposedly diagnostic

anatomical signature, distinct internal nasal features said to have evolved for cold, dry Ice Age air, did not survive testing (PNAS, 2025). Each of these was a confident expectation on the evolutionary side, and each was reversed toward the human status the creation side had predicted. This convergence is the subject of my study uniting humans, Neanderthals, Denisovans, and Heidelbergensis as one species (Nailor, 2025).

DNA Decay and Recent Archaic Hominins

Henry Morris and John Whitcomb's *The Genesis Flood* (1961) helped launch the modern creation-science movement by defending Genesis 1–11 as literal history, including creation, Noah's Flood, and the dispersion at Babel using science. This was not yet a DNA argument, but it established the modern creationist expectation that science and history should align with Adam, Noah, Babel, and a recent human past. Later creationists applied that expectation to archaic hominins, arguing that Neanderthals, Denisovans, and Heidelbergensis were not pre-human ape-men, but early post-Flood human populations living within the biblical window, often in small, isolated groups subject to inbreeding and decline.

Ancient DNA now provides a confirmation of that prediction with a direct biochemical test of that claim. Tomas Lindahl's influential 1993 review of spontaneous DNA degradation concluded that hydrolysis, depurination, deamination, oxidation, and strand breakage impose severe chemical limits on the long-term survival of DNA (Lindahl, 1993). Subsequent studies of fossil biomolecules likewise emphasized the rapid degradation and chemical alteration expected with increasing age (Bada et al., 1999; Briggs et al., 2000).

The prevailing expectation was summarized unusually clearly by Mary Schweitzer, Jennifer Wittmeyer, and John Horner in 2007. Reviewing the earlier preservation literature, they wrote that it had been proposed that *“no original protein and/or DNA fragments can be recovered beyond ca. 100 kyr”* (Schweitzer et al., 2007).

In 2005, creationist Carl Wieland interpreted reported soft-tissue preservation in dinosaur remains as supporting a young-earth chronology. In 2022, environmental DNA approximately two million years old was recovered and authenticated from the Kap København Formation in Greenland, exceeding the proposed 100-kyr boundary by approximately twentyfold. More dramatically, advances in palaeoproteomics have extended authenticated protein sequence recovery into the Miocene. Paterson et al. (2025) recovered partial sequences of seven enamel proteins from a rhinocerotid conventionally dated to approximately 21–24 million years, more than two hundred times the proposed 100,000-year limit.

The historical dinosaur discoveries remain striking as well. Claims of endogenous dinosaur proteins have generated substantial debate over contamination, chemical alteration, and preservation mechanisms, so they should not be treated as the sole demonstration that the old 100-kyr limit failed. The fact is, before these discoveries, prominent biomolecular literature proposed that original protein or DNA would not remain recoverable beyond approximately 100,000 years.

Subsequent empirical work pushed authenticated DNA into the million-year range and proteins beyond twenty million years. The direction of the discovery was opposite to the previously published preservation expectations based on evolution. This is a clear failed prediction by the evolutionary camp, regardless of the rescue device inserted.

If there is one thing we know it is that DNA is not stable after death. It fragments through measurable chemical pathways, especially hydrolytic depurination, and its decay rate follows temperature-dependent kinetics (Lindahl, 1993). Allentoft et al. (2012) calibrated this decay clock using 158 radiocarbon-dated moa bones,

finding an exponential decay rate with a 242 bp mitochondrial DNA half-life of about 521 years at 13.1°C and an Arrhenius relation for temperature correction.

Under first-order fragmentation, mean surviving fragment length is expressed as $L = 1/(kt)$, so age can be read from fragment length by $t = 1/(kL)$. The Sima de los Huesos Homo heidelbergensis femur is an ideal test case because it is conventionally dated to about 430,000 years, yet it comes from a non-permafrost cave with a measured mild temperature regime: about 10.6°C most of the year and about 13.4°C for roughly three months. The recovered DNA is extremely degraded, with fragments mostly around 30 to 45 bp. Using the cave’s seasonal temperature cycle gives a temperature-weighted rate of about 3.93×10^{-6} per nucleotide per year, yielding an age bracket of roughly 5,655 to 8,483 years, with a midpoint near 7,069 years.

Using the combined seasonal and poorer-preservation rate of 6.23×10^{-6} gives a bracket of about 3,570 to 5,350 years, with a midpoint near 4,485 years.

Applying $t = 1$ divided by $(k \text{ times } L)$ at the 45 bp ceiling and the 30 bp floor gives the intervals and midpoints.

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 (best preservation, -1 sigma, flat 10.6°C)	2.10×10^{-6}	10,600 yr	15,900 yr	13,228 yr

Table 1. Kinetic age readings for the Sima de los Huesos femur at the cave's measured temperature,for the three preservation scenarios that fit a wet, temperature-cycling cave: a fast poorer-preservation rate, a temperature-weighted seasonal rate, and the two combined.. Each scenario is given as an interval from the 45 bp ceiling (younger bound) to the 30 bp detection floor (older bound), with the midpoint reported as a summary of that bracket.

The temperature-weighted rate is obtained from the cave's seasonal cycle: nine months near 10.6 degrees ($k = 3.35 \text{ times } 10 \text{ to the minus } 6$) and three months near 13.4 degrees ($k = 5.67 \times 10^{-6}$) give a time-weighted effective rate of $3.93 \text{ times } 10 \text{ to the minus } 6$ per nucleotide per year, about 17 percent faster than the flat average. Read at the cave's own temperature, the femur dates to a midpoint of about 5,261 years under the faster, poorer-preservation rate that a wet, saturated cave warrants, and to about 7,069 years under a conservative temperature-weighted only rate, *with the full ceiling-to-floor brackets shown in Table 1*. We can also combine the two into one scenario: the seasonal temperature cycle and poorer-than-average preservation (+1σ).

The +1σ "poorer preservation" factor is $5.28 / 3.35 = 1.586\times$. 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: $3.35\times10^{-6} \times 1.586 = 5.31\times10^{-6}$. 3 months at 13.4°C: $5.67\times10^{-6} \times 1.586 = 8.99\times10^{-6}$. Time-weighted combined: $k = 6.194 \times 10^{-6}$ per nt/yr. At that rate: 45 bp equals 3,588 years at 45 bp, 5,381 years at 30 bp, **midpoint 4,485 years**.

We take this scenario's true rate reading as it takes not only the cave's natural conditions into account but also takes the cave’s temperature into account as well. Both results are just a few thousand years, and both leave the claimed 430,000 year age an extreme outlier, more than sixty times. 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 based

on 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.

When the Sima DNA is read by a biochemical decay clock rather than by the geological date assigned to the surrounding context, it falls in a few-thousand-year window, not a 430,000-year window. Run in reverse, the survival of 30 to 45 bp fragments for 430,000 years would require decay conditions far colder than the actual cave environment. The cave was never a freezer.

This supports the creationist prediction that archaic hominins lived recently, on this side of the Flood and Babel, and that their molecular remains should read young when tested by a clock independent of deep-time calibration. DNA decay therefore functions as a biochemical stress test on the assigned radiometric age and confirms another creationist prediction while challenging the deep-time framework. For an even more detailed study see; *The clock that should not exist* by Nailor, M. (2026).

So not only have the predictions failed the evolutionary model, but the results from these studies actually land within the biblical timeline instead.

Small Population Size and Existence

Biblical creationists have long argued that archaic humans were not separate pre-human species living across vast evolutionary ages, but early post-Flood human populations that branched off after a severe bottleneck and then lived in small, isolated groups. In 1966, Henry M. Morris published a mathematical population-growth argument relating a small founding population to biblical chronology. The argument examined whether specified reproductive and generational assumptions could produce a large population within that chronology. It is therefore a dated feasibility argument that he said one day future work would either confirm or falsify, making this a clear population genetics prediction.

In this model, the original bottleneck was brief and followed by rapid population growth, avoiding a long-term inbreeding collapse for the main human population. The archaic groups that failed to thrive, including Neanderthals, Denisovans, Heidelbergensis, and erectus, are explained as small, fragmented populations that declined through isolation, inbreeding, drift, and demographic instability. The evolutionary model faces the harder burden. It places these same archaic populations in small effective population sizes for tens or hundreds of thousands of years, often with long periods of near-zero net growth. But small populations cannot be stretched indefinitely without serious demographic consequences. Vaesen et al. (2019), in *"Inbreeding, Allee Effects and Stochasticity Might Be Sufficient to Account for Neanderthal Extinction,"* modeled Neanderthal extinction and found that small population size alone could explain their disappearance. In their simulations, inbreeding, mate-finding difficulty, and random demographic fluctuations were sufficient to drive extinction, especially in very small groups. They modeled population sizes of 50, 100, and 1,000 individuals. The smaller population sizes were at a much greater risk, and that is what we are going to take a look at.

The results fit the creationist expectation far better than the deep-time expectation. In their study the simulation that ran population size of 50 individuals showed it is not a stable platform for survival across 10,000 years, much less across the 400,000-plus years assigned to Neanderthals in the conventional framework. If they cannot even survive for 10,000 years how were they supposed to have lived for 400,000 years? This is called the Neanderthal Extinction Dilemma (Thomas, 2019) and it has never been solved. Once we add *homo Erectus* who supposedly lived for 2 million and *homo heidelbergensis* who lived for approximately 900,000 years when the same population size problems existed, tells us that the entire

evolutionary story falls apart. In Science Magazine titled; Rethinking Neanderthals, we read *"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."*

This is further corroborated in Anthropology News March 2021: *"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**".* This was confirmed the following year by Skov et al 2022. In regards to the Vaesen et al data, this means they would not be able to survive to 10,000 years becomes even far less probable. This is telling us something very important, if a population size of 50 cannot survive 10,000 years, imagine population sizes of only 10 - 20. The smaller the more problems and the less survivability. The creation model predicts short-lived, post-bottleneck branches of mankind; the deep-time model requires fragile populations to persist for implausibly long periods.

Creationists Dr. Jeanson and Lisle's honed the older creation model into the created heterozygosity model, developed within Answers in Genesis, provides a mechanism for this broader framework: created genetic diversity, followed by mutation, recombination, gene conversion, selection, and rapid population growth after a bottleneck. Their 2016 model made testable predictions about how diversity could arise quickly within a young-creation timescale. Vaesen et al. (2019) independently confirmed the key demographic point: small archaic populations are expected to disappear, not persist for hundreds of thousands of years. The evidence therefore supports and confirms the biblical creationist view and predictions that archaic humans were recent, isolated branches of mankind, not ancient evolutionary side branches enduring through deep time.

The Recent Origin of Human Protein-coding Variation, and the Onset of Expansion

Creationist using scripture predicted the timeframe of early dispersal from Babal, saying it occurred a few hundred years after the flood bottleneck which occurred either around 4,500 or 5,500 years ago depending on the version of scripture you read (*Masoretic / Septuagint*). Compilations of the connected genealogical chains that descend from these accounts trace named lineages across this same span. For example; we have unbroken chains of genealogies in different places around the world, one such example is the lineage compilations maintained at the royal genealogical charts found on *The British Monarchy's Official Web Site* and on displayed at the British Kings list on display at Hatfield House in Hertfordshire, England). These examples are just textual and traditional evidence, however the added line of evidence from another outside corroborating source that matches the data pool cannot be ignored. We include it because the framework this paper tests is the Biblical one, and the chronology internal to that framework places the relevant founding and bottleneck events squarely inside the window where the genetic and demographic lines independently converge. The agreement between an internal textual chronology and externally measured pedigree is the kind of correspondence a true chronology would be expected to produce and a false one would not. In 2010, Robert W. Carter presented a creationist demographic framework involving a recent founding population, a Flood bottleneck, subsequent dispersal, and rapid population growth. This establishes a dated broad demographic expectation. This is later confirmed by Fu et al. (2013) who resequenced 15,336 genes in 6,515 individuals of European American and African American ancestry and dated 1,146,401 autosomal single-nucleotide variants. They estimated that roughly 73 percent of all protein-coding SNVs, and roughly 86 percent of those predicted to be deleterious, arose within the past 5,000 to 10,000 years. The deleterious class is the more telling of the two, because harmful variants are precisely the ones purifying selection removes fastest, so a

large standing load of them is the signature of a population that expanded so recently that selection has not yet had time to clear it. The same study went further and dated the expansion itself. From a demographic analysis of 1,351 European Americans and 1,088 African Americans, *Tennessen et al.* (2012) placed the maximum-likelihood onset of accelerated population growth at 5,115 years ago while *M. Zlojutro*, 2008 independently reported a D2 coalescence estimate of approximately 5,247 years. This does not date the origin of humanity, and we do not claim that it does. It dates the beginning of a rapid demographic expansion, and it lands within our biblical timeframe directly from the Greek Septuagint. This is precisely the event our model predicts: a recent spreading-out of an already-founded population following the post-Flood bottleneck and the dispersal from Babel. The mainstream reading places this same expansion in the Neolithic; the data point, an explosive growth episode beginning around 5,115 years ago. What differs is whether the preceding thousands of years of supposed near-stasis existed at all that they assume. Our model needs no such preceding interval: the expansion follows directly from the founding, and the 5,000 year *Fue et al.*, rise of deleterious SNVs and *Tennessen et al.*, and *M. Zlojutro* date of 5,115 - 5,247 years of maximum-likelihood onset of accelerated population growth both falls squarely on the post-bottleneck dispersal our chronology already requires. This prediction by *Carter* is again yet another than lands as expected on the side of biblical creation timeframe and nowhere near the expected evolutionary dates.

Population Growth from a Small Founding Number

Creationist also predicted that population growth rates would also confirm the Biblical window of Noah's flood and expansion. Morris (1966) argued that a large human population could develop from a small founding population within biblical chronology. He predicted that from just a small group of 8 people (Noah and his family), that the entire world's population of today would be confirmed through future demographic population growth rates of diverse people groups around the world in the future. With the founding number our model supplies after the Flood bottleneck: three couples, or six individuals. (*The Biblical account documents Noah and his wife but no additional children, so the eight total aboard the Ark reduces to six maternal lineages post-Flood*). To reach today's world population of roughly 8.2 billion in the 4,400 to 5,400 years our chronology allows requires an average annual growth rate of only about 0.39 to 0.48 percent. Rates in that range are unremarkable. They sit well below the global growth rates recorded through much of the twentieth century, which exceeded 1 percent per year for decades and peaked above 2 percent, and growth rates within this range have been observed in a variety of historical human populations, including some tribal and frontier populations during periods of sustained expansion. Growth certainly fluctuated, with famine, disease, and war pulling it down for stretches, but the long-run average the model requires is modest by any historical standard. What is notable is the reverse calculation. If anatomically modern humans had been present for 200,000 years or more and had sustained even a very small positive average growth rate, the cumulative population, and the cumulative number of burials, would vastly exceed anything the demographic or skeletal record contains. This tension is long recognized and is known as the hominin fossil gap paradox. Mainstream demography holds that pre-modern growth was not modestly positive but very near net-zero for almost all of prehistory: high fertility was balanced by high mortality under Malthusian constraints, with sustained growth beginning only at the Neolithic and accelerating agriculture on that account, the absence of an enormous ancient population is expected rather than anomalous. We do not claim that growth arithmetic refutes deep time; the near-zero-growth model can absorb it even if there is no evidence for it. We include it because the recent-origin model reaches the observed modern population from a small recent founding number using ordinary, observed growth rates and no extended epoch of stasis, while the standard model must posit that stasis as a separate condition and that it occurred throughout most of history. The recent-origin account is again the more direct, and the growth onset it requires coincides with the Biblical flood 5,400 years ago and the independent dates of 5,115 - 5,247 expansion signals above.

Mitochondrial DNA and biblical Eve

Creationist predicted genetic evidence would confirm Biblical Eve who lived recently. Morris (1966) argued that a large human population could develop from a small founding population within biblical chronology. He predicted exactly when all living people would share a genealogical ancestor using scripture. Henry Morris generally worked within the traditional Ussher chronology, placing the creation of Adam and Eve at approximately 4004 BC, while acknowledging some uncertainty in the biblical genealogical chronology. So he believed Eve would have lived between 6,000 - 8,000 years ago and Noah around 4,400 - 5,600 years ago. The creationist expectation of a younger mitochondrial chronology was documented before the pedigree findings discussed here. Wieland (1991) explicitly argued that the mitochondrial clock required revision toward a substantially more recent maternal ancestor. Beasley (1992, p. 43) further stated that inflated calibration dates would imply substantially higher mitochondrial divergence rates. These statements establish a prior qualitative expectation, rather than an interpretation first introduced after the first 1996–1997 results. The historical claim is very specific: earlier creationist arguments anticipated a younger chronology and, conditionally, faster rates. They did not forecast the exact pedigree result, and the measurement alone does not establish a particular biblical date.

The first genetic discovery of when mitochondrial Eve may have lived came in 1996 by Howell et al who found a rapid substitution rate in a deep rooted 12 generation deep pedigree study. His study directly states: *“A divergence rate of 2%/Myr extrapolates to a mutation frequency of $\sim 2.6 \times 10^{-7}$ /p/generation. In contrast, the results in table 2 yield a mutation frequency of $\sim 5.2 \times 10^{-5}$, a 200 fold higher rate.”*

This shocked the scientific community. A year later ran the largest pedigree study possible using the FBI database bloodbank. *Parsons et al* in 1997 confirmed that mutation rates were indeed fast and landed on a MRCA for Eve living just 6,500 years ago. They concluded: *“Our observation of the substitution rate, 2.5/site/Myr, is roughly 20-fold higher than would be predicted from phylogenetic analyses.”* (Parsons et al., 1997). A study the following year (Jazlin et al 1998) pooled data which landed Eve on 6,000 years. If these dates were not an issue for evolution they would not make such comments as science writer and secular journalist Ann Gibbons (1998) noted in Science, in an article titled Calibrating the Mitochondrial Clock:

- *“But solving the mystery of the Romanov's remains raised another puzzle that **first troubled forensics experts and is now worrying evolutionists.**”*
- *“It could also **complicate the lives of evolutionary scientists** who use the mtDNA mutation rate as a clock to date such key events as when human ancestors spread around the globe.”*
- *“**Evolutionists have assumed** that the clock is constant, ticking off mutations every 6000 to 12,000 years or so.”*
- *“Regardless of the cause, **evolutionists are most concerned about the effect of a faster mutation rate.** For example, researchers have calculated that ‘mitochondrial Eve’ the woman whose mtDNA was ancestral to that in all living people - lived 100,000 to 200,000 years ago in Africa. Using the New Clock, she would be A MERE 6,000 YEARS OLD.”*

You can clearly see in her writing that evolution is in trouble regarding this data. It has not gotten any better for them over the decades either. On Ann Gibbons' report regarding the 6,000 year date: we read that when they discovered this date, that... *“No one thinks that's the case,...”*. This is very telling. They got direct results that landed on the biblical timeline but that no one thinks this data is true. Why? Because of

evolutionary mindsets. It is no wonder she wrote an entire article talking about how desperate evolutionists were regarding these new observed rates landing on the Biblical timeline of Adam and Eve. But let's keep reading: "...but at what point should models switch from one mtDNA time zone to the other?... What would they need to do to avoid these biblical dates? You guessed it, adjust them and alter what was observed to what was not observed. *"Recalibrating the mtDNA clock would narrow the difference (Science, 28 February 1997, p. 1256)"*. You see that? They begrudgingly admitted via question, at what point can you ignore the observational mtDNA data and make it work in another model aka the evolutionary one? Today the data over three decades of time has shown that they cannot, hence the paradox problem they cannot solve.

Creationist Carl Wieland's 1998 article *"A Shrinking Date for Eve"* exposed that the measured mtDNA mutation rates discovery made mitochondrial Eve perfectly compatible and in line with the biblical Eve and when scripture says she lived confirming Morris (1966) prediction. CMI later summarized his argument by saying creationists welcomed the mitochondrial Eve hypothesis because it fit biblical expectations, Carl Wieland in a 2006 article about the subject states: *"I explained how the mitochondrial Eve findings were in line with biblically based expectations. While not proving the biblical Eve, they were consistent with her reality, and were not predicted by evolutionary theory."* Regarding Neanderthals, he also said: *"In addition, I explained that these real-time findings also seriously weaken the case from mitochondrial DNA, which argues (erroneously) that Neandertals are not true humans"* So we have another powerful prediction by creationists that was confirmed later by science that even to this day, the pedigree / phylogeny paradox still exists for evolution but not for creationists. Dr. Henry Morris 1966 prediction came true in the 90's and has been confirmed through pedigree studies for all the decades following.

The Sapient Paradox and the Onset of Documented History

Arthur C. Custance's essay *Primitive Cultures*, first published in 1960. Custance described humanity as possessing language and cultural capabilities from its beginning, followed by rapid cultural development within a short chronology. Under this model, a prolonged interval separating the emergence of fully capable humans from substantial cultural development is not expected. This position predates Renfrew's formulation of the sapient paradox in 1996. A recent-human-creation model avoids the long chronological interval by proposing a shorter human history and Custance's position directly predates the sapient paradox and addresses its shortcomings by giving a better predictive model of ancestry.

The paradox goes like this. Anatomically modern humans are conventionally dated to roughly 200,000 - 300,000 years ago, yet settled communities, agriculture, monumental construction, the city, the state, and writing all appear only within the last few thousand years or so years, and continuous documentary history within roughly the last 5,000. Colin Renfrew named this the sapient paradox: the puzzle of why behaviorally modern humans, if they existed for so long, left no record of the cumulative, documented culture they began producing in such density once they started. Mainstream prehistory answers with a combination of climatic triggers, demographic thresholds, and cultural-ratchet effects that supposedly held for tens of millennia and then released.

We note, again carefully, that the term itself is framed from within a deep-time chronology; it is a paradox only on the assumption of the long preceding interval. That is exactly our point. On a recent-origin chronology there is no paradox to resolve, because there is no long silent interval to explain: documented history begins shortly after the founding population because the founding population is recent. The data, the abrupt and recent onset of the cumulative record, are agreed by everyone. What differs is whether one must additionally posit a cultural and cognitive ratchet that stayed locked for the preceding ninety-five percent of

our species' supposed existence without direct historical evidence. The recent-origin model requires no such additional assumption, and here Occam's razor does real work, this is why our prediction based on Babel explains the arrival of writing systems, math, astronomy, medicine, civilizations, etc all formed right after this time in the same location the bible talks about and not in Africa as evolution expected and predicted to find. Arthur C. Custance was one of the first to write down this prediction in print; His *Doorway Papers* began in 1957, and *Noah's Three Sons* argued that Genesis 10 records the origins and spread of the present world population from Noah's sons. His work explicitly treated the Table of Nations as a real historical-genealogical map of mankind after the Flood.

Mutation Saturation

Another prediction from creationists comes in the form of mutation saturation predictions. Jeanson (2015) reasoned that if deep times had really passed that mutation saturation would surely have affected most, if not all species alive today. He made a prediction on humans first, and since we know the assumed evolutionary date of divergence and also have the human genome scanned and sequenced for the required testing. According to evolution, humans had diverged from a primate ancestor with chimpanzees seven million years ago, the accumulation of mitochondrial DNA (mtDNA) mutations should have long since reached saturation, and all new mutations would simply overwrite existing ones in the same nucleotide positions, obscuring further diversity. Based on expected rates, he ran a simulation to test his prediction and found that approximately 21,457 mutations minimum should have arisen over that time with a maximum of 450,000 occurring. Saturation occurs at around 12,000 mutations, yet empirical data show only 1,483 mutations, far below saturation. See figure 4 below to see side by side comparison of what was expected next to what was actually observed. This prediction is published in his book *Replacing Darwin*.

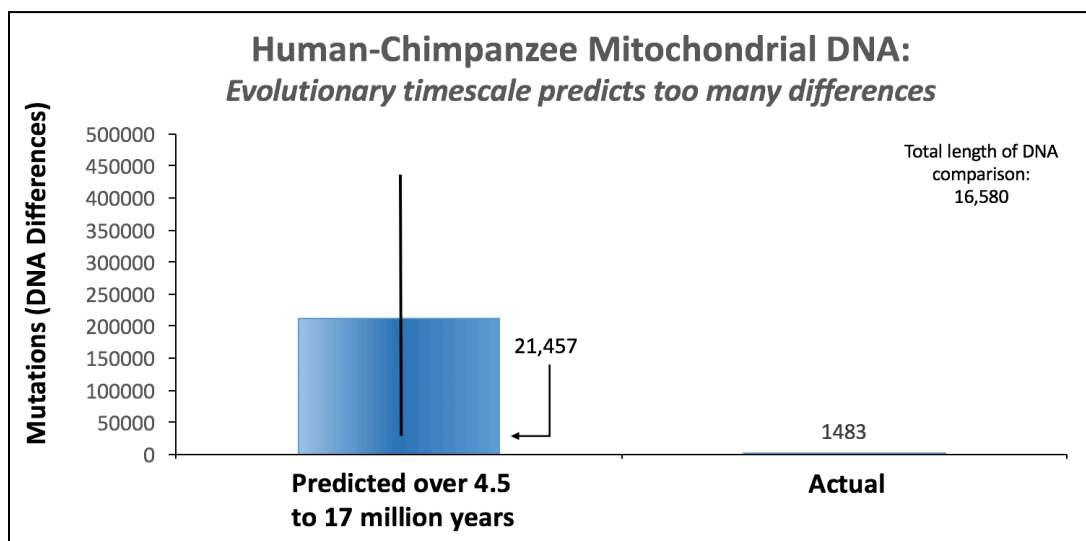


Figure 4. Mutation saturation chart showing predicted amount versus observed amount.

This disparity confirms Jeanson's prediction that mtDNA diversity has accumulated over only a few thousand years, consistent with a recent origin of humanity as described in Scripture. This same lack of mutation saturation is observed across the animal kingdom, providing further evidence that places a young-earth timestamp on the origin of life. Taken together, these results raise a fundamental problem for evolutionary theory: if its foundation rests on mutation and selection, yet it cannot reliably model or predict mutation rates, the framework is undermined. Indeed, evolutionary theorists themselves have acknowledged the inability to make accurate predictions of mutation rates within their paradigm.

Y Chromosome Mutation Rates

Dr. Nathaniel Jeanson's first AiG/Answers Research Journal observation of fast Y-chromosome mutation rates was published December 4, 2019. Dr Jeanson had predicted that the Y chromosome mutation rate was fast, similar to mtDNA but even much faster since Noah lived more recently than Eve and the Y chromosome would bottleneck actually be Noah, since only he and his sons were the only male lineages to survive the flood in 2013. In his ICR article "**Does 'Y-Chromosome Adam' Refute Genesis?**", Jeanson laid out the Y-chromosome clock argument and explicitly identified the paternal MRCA with **Noah rather than Adam**. He wrote: "*Therefore, finding 'Y-chromosome Adam' is, effectively, finding 'Y-chromosome Noah.'*"

Jeanson then described exactly how this hypothesis should be tested: count modern Y-chromosome differences, measure the mutation rate occurring today, and use that measured rate to calculate when the clock began. Since his model placed that paternal bottleneck at Noah only about 4,000–4,500 years ago, the model necessarily predicted that an adequately measured Y-chromosome rate would have to be fast enough to generate the observed diversity within that short interval.

So to test this prediction, in 2019 Jeanson and Ashley Holland formally published the quantitative result. They went to the most recent studies using high-coverage Y-chromosome data from Karmin et al. 2015 and Maretty et al. 2017, which revealed as he predicated, a high mutation rate about 10–17 times faster than the older low-coverage pedigree studies by Xue 2009 and Helgason 2015. To future test this prediction Jeanson (2020) applied his Y-chromosome molecular clock to Amerindian population history, suggesting a major migration into the Americas around 800 AD, with potential links to eastward expansions from the Roman world into China. His prediction was consistent with approximately 4,500 years of paternal ancestry.

More recently, Jeanson (2022) expanded on this work in *Traced: Human DNA's Big Surprise*, integrating Native American historical sources such as the Red Record, containing genealogies, migration accounts, and time units based on sachem reigns, alongside archaeological, linguistic, and haplogroup data to support a recent origin and diversification of human Y-chromosome lineages.

By tracing genealogies recorded in the Red Record and counting the reigns of Indian chiefs documented as "sachems", Jeanson (2022) calculated a timeline consistent with a crossing of the Bering Strait region into the Seward Peninsula, Alaska, around 900 AD. Using a mutation rate of three per generation, this estimate closely aligns with his earlier prediction that Native Americans migrated into the region around 800 AD (Jeanson, 2020).

In the historical sciences, including archaeology, genetics, and geology, dating methods rarely achieve precise single-year accuracy, often carrying margins of error spanning decades or even centuries. Thus, a result within a century of the predicted value supports rather than falsifies the model.

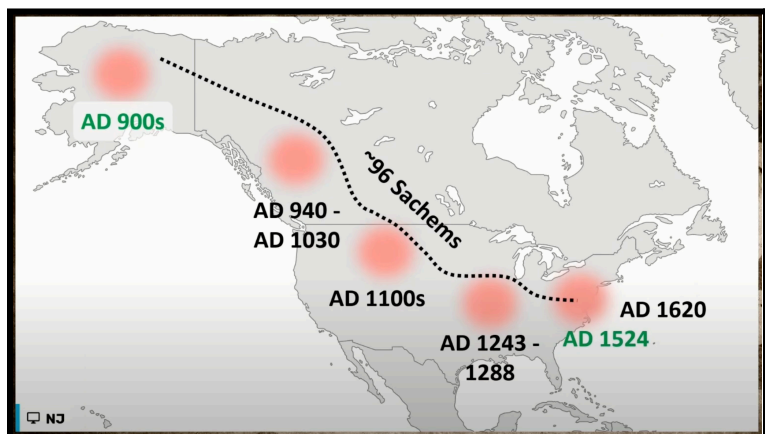


Figure 5. Migration map of native Americans documenting their travels through Sachems (the time a chief ruled) documented in the Red Record.

Had the prediction been entirely incorrect, such as if the migration had taken place thousands of years earlier as evolution poses, the model would not be supported and the prediction failed. Instead, the proximity of the calculated result to the prediction demonstrates explanatory power within the expected range of historical uncertainty. This data aligns with mtDNA pedigree rates, population growth and expansion, mathematical simulations and more.

Peleg's Generation of Expansion

Based on scripture, the genealogies tell us that it was in the generation of Peleg that the population expanded and diversified. Before the later high-coverage Y-chromosome datasets, creationist geneticist Robert Carter in 2010 explicitly associated the Babel dispersal with the generation of Peleg and argued that the biblical division of peoples according to paternal ancestry should leave a corresponding genetic signature: geographically structured Y-chromosome lineages. Carter estimated a rapidly expanding population of approximately 1,000–10,000 people by the Peleg/Babel period and stated that, if the biblical account were historically accurate, evidence for the Table of Nations should ultimately be recoverable from genetic data. Later high-coverage Y-chromosome datasets provided substantially improved branch resolution and pedigree mutation-rate estimates with which this previously stated Peleg/Babel paternal-dispersal expectation could be tested. Dr. Jeanson then predicted in 2013 that since the Y chromosome mutation rate is much more clear than mtDNA that it can be used to test what generation diversity expands from. Using the rate of 3 mutations per generation obtained from Karmin et al. 2015 and Marett et al. 2017, the cumulative total from Noah's lineage corresponds to the generation of Peleg. In the biblical record, Peleg's lifetime is associated with the division and expansion of human populations from the Middle East (Genesis 10:25). The alignment of genetic calculations with this specific generational marker is another confirmed prediction by creationist and further support for the concordance between pedigree-based mutation rates and the biblical timeline (Jeanson, 2017, 2022).

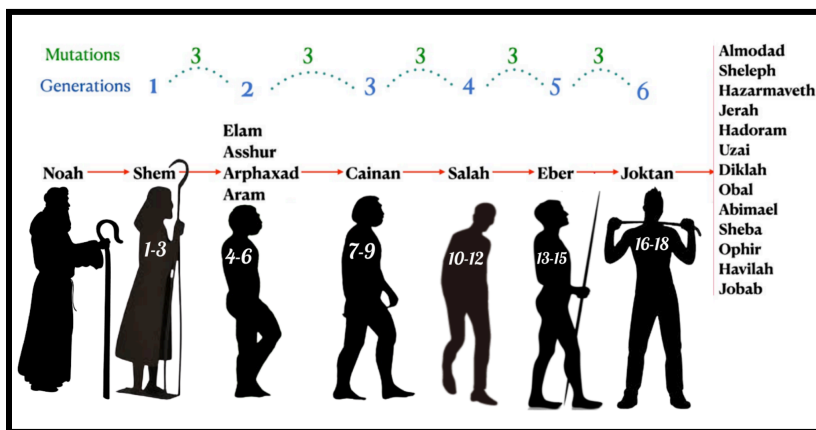


Figure 6. Shows that following 3 mutations per generation lands on the expanding population which aligns with the secular consensus of when these haplogroups formed (figure 6) and also where they formed (Middle East).

years later. We present Rohde et al. as another, independent source that confirms the list of other pieces of evidence listed throughout this study.

First, it shows that recent universal common ancestry of all living humans is not a creationist claim but a mathematical expectation, which removes one common intuitive objection to a recent shared origin.

Second, the recent-origin model is the one in which the genealogical and the genetic convergence coincide, rather than being separated by two orders of magnitude; this makes the model more parsimonious.

A later creationist review by Robert Carter and Chris Hardy says this directly about Morris and his prediction and outcome: “*Morris was the earliest reference we could find for someone who attempted an algebraic solution.*” We conclude yet another accurate testable prediction made way prior by creationists.

Pseudogene Function: The β -Globin HBBP1 Test

Pseudogenes provide an unusually clear historical test because a creation/design expectation concerning their possible function was stated before one of the strongest later experimental examples was discovered. In December 2000, creationist John Woodmorappe published *Are Pseudogenes “Shared Mistakes” Between Primate Genomes?* in the *Journal of Creation*. Woodmorappe challenged the widespread practice of treating pseudogenes as functionless simply because they no longer encoded an intact protein. He noted that evidence for pseudogene function was already beginning to accumulate and argued that the absence of a protein product did not establish the absence of biological function. His expectation was prospective: as pseudogenes were investigated more closely, additional functions and non-random biological roles should continue to be discovered rather than the class proving to consist simply of useless evolutionary debris (Woodmorappe, 2000).

A particularly striking opposing claim was subsequently made concerning the human β -globin pseudogene, now designated HBBP1. During his testimony in *Kitzmiller v. Dover Area School District* in September 2005, evolutionary biologist Kenneth R. Miller used this pseudogene as evidence for common ancestry. Miller described the locus as “broken,” stated that its molecular errors rendered it “*non-functional*,” and argued that the errors had “*no functional purpose*.” His reasoning was that because the same supposedly purposeless defects were shared among primates, inheritance from a common ancestor provided the best explanation. This supplies a named, dated and testable claim concerning a specific pseudogene: the β -globin pseudogene was a disabled gene without biological function.

Subsequent genomic research overturned the nonfunction premise. Moleirinho et al. (2013) analyzed variation throughout the human β -globin cluster and found that both HBD and its neighboring pseudogene HBBP1 showed signatures of purifying selection. Rather than evolving freely as unconstrained genetic debris, HBBP1 displayed evidence of functional constraint. The authors concluded that the pattern was most consistent with a regulatory role associated with the developmental switching of globin-gene expression. Thus, less than a decade after HBBP1 had been presented publicly as a broken and functionless sequence, population-genetic evidence indicated that natural selection was preserving it.

The decisive experimental result arrived in 2021. Ma et al., publishing in *Developmental Cell*, carried out genome-wide analyses followed by extensive functional experiments and demonstrated that HBBP1 is essential for human erythropoiesis, the process by which red blood cells are produced. HBBP1 functions as a noncoding RNA and binds the RNA-binding protein HNRNPA1, stabilizing and increasing expression of TAL1 for erythropoiesis. The investigators further found that the HBBP1/TAL1 interaction was associated with

milder symptoms in β -thalassemia patients. Far from having “no functional purpose,” the pseudogene participates directly in the regulatory machinery of human red-blood-cell development (Ma et al., 2021).

Chronologically, the comparison is very strong. Woodmorappe's creation/design expectation was published in 2000; Miller's explicit claim that this particular β -globin pseudogene was nonfunctional followed in 2005; evidence of functional constraint appeared in 2013; and direct experimental demonstration of an essential regulatory function followed in 2021. The result does not by itself falsify common ancestry, since an evolutionary model can accommodate a pseudogene that retains or acquires a regulatory role. It does, however, falsify the specific historical premise that HBBP1 was biologically nonfunctional and that its sequence alterations possessed no functional purpose. For the purposes of a prediction comparison, the significant point is that the creation/design side had explicitly warned beforehand that pseudogene nonfunction should not be assumed and expected additional functions to emerge as the genome was investigated. In the HBBP1 case, that expectation was subsequently confirmed in unusually direct experimental fashion.

Extreme Genomic Conservation in *Candidatus Desulforudis audaxviator*

One of the cleanest prediction tests in this comparison comes from a 2021 genomic investigation of the deep-subsurface bacterium *Candidatus Desulforudis audaxviator* (CDA). Unlike retrospective statements about what evolutionary theory might have been expected to predict, the researchers themselves explicitly recorded their expectation before presenting the genomic result. Creation microbiologists had explicitly proposed before the relevant genomic test that microbes inhabiting stable environments should exhibit stasis rather than unrestricted change. Francis and Purdom (2009) stated that “morphological stasis” in microbes should be expected in static ecosystems, while Bartlett (2009) described the creation model as predicting “dynamic stasis,” in which basic biological patterns are preserved while limited variation occurs. Carter (2012) further argued that the relatively low mutation rates and periods of dormancy characteristic of bacteria could preserve older, less-mutated genomes over the long term, and Truman (2015) specifically maintained that bacterial genomes are “constrained to permit valuable, but not unlimited, variability.” These statements collectively yield a testable creation-model expectation: geographically isolated microbial populations inhabiting stable environments may accumulate limited variation while retaining substantial genomic conservation rather than undergoing unrestricted divergence.

Becraft et al. (2021) compared CDA populations recovered from geographically isolated deep-subsurface environments in Africa, North America, and Eurasia. Because the populations were separated by enormous geographic distances, they stated: “*we hypothesized that CDA genomes should be genetically divergent.*” Because the habitats also differed physically and chemically, they further anticipated divergent local adaptations, predicting evolutionary trajectories analogous to those observed among Darwin's finches (Becraft et al., 2021).

The genomic evidence produced the opposite result. Across 126 single-amplified genomes, additional metagenome-assembled genomes, and a cultured Eurasian isolate, the geographically separated CDA populations shared greater than 99.2% average nucleotide identity, exhibited very low frequencies of single-nucleotide polymorphisms, and possessed remarkably conserved prophage and CRISPR sequences. The authors described this degree of genomic similarity as unexpected and tested several possible explanations, rejecting laboratory cross-contamination, recent natural dispersal, and unusually strong purifying selection as sufficient explanations.

The result is particularly striking within the chronology adopted by the authors themselves. Geological reconstruction led them to regard the populations as potentially isolated since continental separation was associated with the breakup of Pangaea, placing possible separation between approximately 165 and 55 million years ago. Yet the genomes exhibited only minimal change. Becraft and colleagues therefore concluded that the populations had undergone remarkably little evolution since their physical separation and proposed unusually high-fidelity DNA replication and repair as the most plausible explanation for the observed stability. Significantly, however, this was an explanation introduced after the unexpectedly conserved genomes had been observed; the prediction stated at the beginning of the investigation had been genetic divergence and divergent adaptation.

The investigators themselves acknowledged the broader importance of the discrepancy. They described CDA as a stark contrast to conventional microbial model organisms, which can develop adaptive genomic changes over vastly shorter periods, and concluded that their results call for a re-evaluation of explicit and implicit assumptions about microbial evolution. They further noted that long periods of previously unrecognized evolutionary stasis could affect molecular-clock scaling, inferred phylogenetic relationships, and divergence thresholds used in microbial taxonomy.

This example therefore meets an unusually stringent definition of a failed prediction by evolution. The investigators were named, the expectation was stated explicitly in advance of the reported result, and the observable outcome was clear: populations separated geographically and environmentally were predicted to possess divergent genomes and divergent adaptations. Instead, the researchers found greater than 99.2% nucleotide identity and extraordinary conservation. This does not falsify all evolutionary change, the authors themselves interpreted the result as an exceptional case of evolutionary stasis, but it directly falsified the particular evolutionary hypothesis they set out to test. Under the prediction criteria used in the present study, that makes the CDA experiment one of the clearest documented examples of observation producing the opposite result from the stated evolutionary expectation. In 2023, creationist Don Batten cited the genomic conservation reported by Becraft and colleagues in 2021 as a challenge to evolutionary expectations in *40 failed predictions of evolution* by Creation Ministries International where he shows the creationist predictions win yet again.

The Tree of Life Problem: When Anatomy, Genes, and Genes Themselves Disagree

One of the clearest predictions associated with universal common ancestry was that living organisms should ultimately be recoverable as branches of a coherent historical tree. Different sources of biological evidence might initially contain noise, but as anatomical characters gave way to genes and then to whole genomes, the expectation was that increasing amounts of independent information would progressively converge upon the same underlying branching history. That expectation is important because a historical tree is not directly observed. It is inferred from similarities and differences among living and fossil organisms. The strength of the inference therefore depends in part upon whether independent characters repeatedly recover the same relationships.

In layman's terms, the test is straightforward. Imagine six members of a known family and suppose we reconstructed their family tree independently from hundreds of different inherited markers. Individual markers might occasionally be misleading, but if they all came through one branching genealogy, we would expect a strong common signal eventually to emerge. If one set repeatedly grouped A with B, another grouped A with C, another grouped B with D, and the disagreement became more extensive rather than disappearing as additional data were collected, the individual markers could no longer simply be treated as interchangeable records of one obvious tree. That is the problem phylogenetics encountered as molecular data multiplied.

The difficulty predates modern genomics. Creationists Patterson, Williams, and Humphries (1993), reviewing molecular and morphological phylogenies, reported that “*Congruence between molecular phylogenies is as elusive as it is in morphology.*” The hoped-for molecular solution did not simply cause independently derived trees to collapse onto one topology. Michael Lynch (1999), discussing relationships among the major animal phyla, likewise observed that different genes, and even different analyses using the same genes, could yield a diversity of phylogenetic trees. These were not creationist criticisms of evolutionary biology; they were statements appearing within the mainstream phylogenetic literature itself. In 2000, Pierre Jerlström interpreted disagreements among molecular evolutionary trees as consistent with a creationist “orchard” of separately originating groups. The creationist “orchard of life” concept traces its historical roots back to 18th-century taxonomy and modern creation science starting in 1941 (Frank Marsh). The following is confirmation of this prediction.

The genomic era magnified rather than eliminated the problem. Galtier and Daubin (2008) summarized the situation bluntly: “*Incongruence between gene trees is the main challenge faced by phylogeneticists in the genomic era.*” Their wording is important. A gene tree is the history inferred from one stretch of DNA. A species tree is the proposed historical relationship among the organisms themselves. The two are not automatically the same. Different genes can produce genuinely different genealogies, and phylogeneticists must then decide how those conflicting genealogies are to be reconciled into a proposed species history.

This problem is not confined to bacteria. Rokas and Carroll (2006) noted that genome analyses of several important animal radiations had produced “*bushes and not resolved trees.*” They explained that rapid successive divergences combined with homoplasy, characters appearing independently in separate lineages, can make ancient branching orders extremely difficult to recover. Particularly significant was their warning that some histories might not be resolved even by enormous increases in ordinary sequence data. The problem therefore cannot always be dismissed simply by saying that more genes will eventually reveal the tree.

A second problem is that anatomical similarity itself can point toward a different tree from molecular sequence data. In 2022, Oyston, Wilkinson, Ruta, and Wills directly compared 48 pairs of morphological and molecular phylogenies and tested them against biogeographic information. Molecular phylogenies showed the better average agreement with geography. Matthew Wills summarized the result in the University of Bath release: “*It turns out that we’ve got lots of our evolutionary trees wrong.*” The authors concluded that convergent evolution, unrelated organisms independently acquiring similar-looking characteristics, is more common than had often been appreciated.

This finding needs to be stated carefully. It does not mean that anatomical homology is useless or that every anatomical similarity is convergence. It means something narrower and more relevant to the present prediction test: similarity of form does not uniquely identify ancestry. Organisms can resemble one another strongly enough to be placed together morphologically and yet be placed elsewhere when their molecular data are analyzed. A character interpreted as inherited similarity can later be reclassified as convergence. Thus the pattern used to infer ancestry is not itself immune from alternative explanation.

The difficulty becomes considerably greater when the proposed tree is expanded from animals to all cellular life. Horizontal gene transfer allows genetic material to move laterally between microbial lineages rather than exclusively downward from parent to descendant. A simple branching tree assumes vertical inheritance: one lineage splits into two, those split again, and branches do not later exchange large amounts of genetic material. Extensive horizontal transfer produces something fundamentally different, a network.

W. Ford Doolittle recognized this problem early in the genomic era. In 1999 he concluded that “*the history of life cannot properly be represented as a tree.*” His point was not that branching descent never occurs, but that there need not be one recoverable universal genealogy represented by all genes. Different genes inside the same organism can have different historical trajectories.

Dagan and Martin (2006) made the same point in their aptly titled paper *The Tree of One Percent*. They emphasized that lateral gene transfer among prokaryotes and endosymbiotic gene transfer in eukaryotes are fundamentally non-tree-like processes. A genome is therefore not necessarily a single historical document. It can be a mosaic whose components followed different routes.

Doolittle and Baptiste (2007) subsequently challenged the stronger assumption directly. They argued that the idea of a universal Tree of Life assumes that the natural order of all organisms is one inclusive hierarchy and observed that incorporating prokaryotic genomes into such a universal structure is particularly problematic. Their proposed alternative was “*pattern pluralism*”: different portions of biological history may require different representations rather than one universal branching diagram.

The debate became even more explicit in 2009. Baptiste and ten colleagues wrote that it had been much easier to defend a universal Tree of Life before genome data were available. They concluded that the monistic concept of one universal tree appeared increasingly obsolete in the face of microbial genomic data. Their paper also provides an important qualification: they explicitly stated that multicellular eukaryotic evolution remains predominantly tree-like. The strongest Tree-of-Life problem therefore concerns the attempt to place all life and all genes onto one universal bifurcating structure, not the ordinary observation that many animal and plant lineages exhibit branching descent.

That distinction makes the argument stronger rather than weaker. A claim does not have to be exaggerated to be important. Darwin's tree was historically used as a universal picture of the history of life. Modern genomic evidence requires that picture to be supplemented by horizontal transfer, hybridization, lineage merger, incomplete lineage sorting, gene duplication and loss, and convergent evolution. The result is no longer one simple genealogical object from which every biological character should recover the same topology.

Perhaps the most revealing empirical demonstration was published by Puigbò, Wolf, and Koonin (2009). Instead of choosing a handful of genes, they examined 6,901 individual gene trees from 100 prokaryotes. The result was not one uniformly congruent Tree of Life but what they called a “*forest of life.*” They detected a statistical central tendency, particularly among a restricted class of nearly universal genes, but inconsistency increased markedly with phylogenetic depth. Deep relationships were especially difficult to resolve, and the authors concluded that the strong version of the Tree of Life, in which most genes should tell the same evolutionary story, had been overthrown. They nevertheless retained the possibility of a weaker statistical tree representing a central trend.

O'Malley and Koonin (2011) subsequently stated the conclusion with unusual clarity: “*The original TOL hypothesis has failed.*” They did not conclude that evolution itself had failed. Instead, they proposed replacing the strong historical Tree of Life with a weaker “*statistical Tree of Life,*” a pattern extracted from a forest of partially conflicting gene histories. This distinction is central. The original prediction was one recoverable universal hierarchy. The replacement model accepts widespread disagreement among individual genetic histories and allows for discontinuity and even further unfalsifiability.

The 2009 *New Scientist* feature *Why Darwin Was Wrong About the Tree of Life* brought this controversy into public view. Discussing attempts to reconstruct organismal relationships from different genes, the article

summarized the difficulty simply: “*different genes told contradictory evolutionary stories.*” Evolutionary biologist Michael Rose was quoted even more dramatically: “*The tree of life is being politely buried—we all know that.*” The article's title was intentionally provocative, and many evolutionary biologists rejected the implication that common descent itself had been overturned. The substantive issue underneath the headline, however, was real and remains so: biological history is considerably less describable by one universal bifurcating tree than nineteenth- and much twentieth-century representations implied.

Modern evolutionary biology has developed several explanations for these conflicts. Incomplete lineage sorting can cause genes to retain histories older than the species divisions in which they occur. Hybridization and introgression can move genes between related lineages after they diverge. Horizontal gene transfer does the same on a much larger scale among microorganisms. Gene duplication and loss can make related genes appear to have different histories. Convergent evolution can make unrelated organisms resemble one another anatomically. Finally, model misspecification, inadequate sampling, long-branch attraction and other analytical artifacts can lead the same underlying data to different inferred trees.

These mechanisms are real biological processes, so gene-tree disagreement cannot simply be declared a falsification of common ancestry. That would overstate what the evidence establishes. The relevant prediction test is narrower and stronger: did increasing molecular and genomic data reveal the simple, universal, uniquely recoverable branching hierarchy that the classical Tree of Life picture led researchers to expect?

The answer from the literature is no. The field itself moved from a single universal tree toward gene trees, species trees, networks, forests, statistical trees and explicitly reticulate evolutionary models because the incoming data demanded those distinctions.

This matters for the creation/design comparison developed in this paper. A model beginning with separately founded biological groups does not require every anatomical character or every gene to resolve into one universal genealogy. It can accommodate recurrent structural solutions, bounded clustering, and different historical patterns at different levels without expecting all similarity to trace through one ancestral branch. The evolutionary framework can force accommodate discordance, but it does so begrudgingly since it goes against predictions and by adding processes that separate the history of individual genes from the history of species and, in the microbial world, by replacing the strict tree itself with network-like models. Gene histories conflict, anatomy and molecules can conflict, similar structures require research to invoke convergence for the reason that unrelated species might imitate inherited genetic similarity, and horizontal genetic exchange can make entire portions of biological history intrinsically network-like.

The most important point is the direction in which the theory had to move once the data arrived. More sequence information did not simply sharpen one universal tree. It revealed why different genes may contain different histories and why no individual gene tree can automatically be equated with the history of the organism carrying it. The classical tree became a forest of gene trees, and in some domains a network. What remains is a statistical or local tree where a sufficiently strong vertical signal exists.

For a prediction-based comparison, this is the result that should be scored. Creation and design models had long emphasized discontinuity, bounded groups, repeated structural solutions, and the possibility that similarity need not uniquely imply ancestry. The classical universal-tree expectation anticipated convergence toward one recoverable branching history. The genomic data instead revealed pervasive incongruence and forced the tree concept itself to become conditional: robust in some portions of life, statistical in others, and inadequate where reticulate processes dominate. That is a much more defensible result than simply announcing that “*the Tree of*

Life collapsed,” and it places the burden of explanation precisely where the modern literature places it, on why independent biological characters so often refuse to tell one simple historical story.

Conclusion

This paper examines thirty selected historical comparisons to assess the predictive record of Biblical creation/design arguments alongside particular evolutionary expectations. Its central argument is that creation/design claims deserve evaluation through their documented timing, specificity, and empirical performance. The comparisons differ in evidential status: some are presented as documented advance predictions, others as broader expectations, and others as retrospective tests of consistency. Those categories must remain distinct when interpreting the results.

The strongest comparisons are those in which an attributable statement preceded the relevant testing evidence, specified an outcome that could have failed, and subsequently agreed with the observation. Where an explicitly conflicting historical expectation was also documented, the result supplies comparative support for the successful claim over that particular alternative. Where both frameworks expected the observation, the result establishes predictive accuracy and superiority of a model.

The case for creation is strongest where its claims withstand that scrutiny. Critics should address the original statement, its date, the evidence available when it was made, the outcome used to test it, and the competing expectation. Advocates must answer those challenges with sources and reproducible analysis. Future work should extend this approach through predictions published before testing, with explicit conditions for success and failure. The decisive issue is the demonstrated performance of the claims themselves.

Because in science, the question is ultimately not which explanation can be rewritten to accommodate what we already know. **The question is which model had the courage to tell us what we would find before we found it.** And on the record examined here, **creation did.**

The case advanced here is that creation/design deserves recognition as a serious predictive framework, and its strongest comparisons must be judged on their evidential merits. Where a documented creation/design prediction preceded the testing evidence, specified an outcome that could have failed, and succeeded against an explicitly conflicting historical expectation, that result provides comparative support for the creation/design claim over that particular alternative. Later accommodation does not erase an earlier predictive failure, just as earlier authorship alone does not establish scientific superiority. Shared successes establish predictive accuracy; genuinely discriminating successes carry the argument for comparative superiority.

This paper grounds its case for creation in the comparisons that meet those stronger requirements, rather than treating all thirty entries as pure equivalent victories. The challenge to critics is concrete: identify an error in the documented prediction, its timing, the competing expectation, or the claimed empirical result. Dismissing creation as inherently incapable of prediction does not answer that evidence.

So we leave you with this. After the last two visuals in our paper, you can find even more novel future testable predictions made by us. Further advancing the biblical model of ancestry.

Summary of the Historical Comparisons

DOMAIN	PREDICTION TESTS <i>(Examples)</i>	NO. OF TESTS	DESIGN / CREATION EXPECTATION CONFIRMED	EVOLUTIONARY EXPECTATION CONFIRMED	OVERALL OUTCOME
 GENETICS & MOLECULAR BIOLOGY	Homologous genes (Hox), conserved regulatory networks, junk DNA function, ERVs, mutation rates	10	✔ 10 (100%)	✘ 0 (0%)	✔ 30 OUT OF 30 (100%) All 30 prediction tests landed on the design / creation expectation. 0 OUT OF 30 (0%) The competing evolutionary expectation was confirmed in none. LEGEND ✔ Design / Creation Expectation Confirmed (Matches Prediction) ✘ Evolutionary Expectation Confirmed (Matches Prediction)
 DEVELOPMENT & EMBRYOLOGY	Archetype body plan, Hox patterning, conserved developmental programs	3	✔ 3 (100%)	✘ 0 (0%)	
 TAXONOMY & CLASSIFICATION	Created kinds, fixed boundaries, discrete clustering, baramin structure	3	✔ 3 (100%)	✘ 0 (0%)	
 ANATOMY & HOMOLOGY	Homologous limb structure, vertebral segmentation, shared archetype	4	✔ 4 (100%)	✘ 0 (0%)	
 SPECIATION & DIVERSITY	Rapid speciation, directional change within kinds, post-Flood radiation	4	✔ 4 (100%)	✘ 0 (0%)	
 POPULATION GENETICS & BOTTLENECK RECOVERY	Founder effect survivability, bottleneck recovery, island populations	3	✔ 3 (100%)	✘ 0 (0%)	
 HUMAN ORIGINS & ANTHROPOLOGY	Neanderthal anatomy & posture, human status	3	✔ 3 (100%)	✘ 0 (0%)	
TOTAL		30	30 (100%)	0 (0%)	

Figure 9. Descriptive outcome of the 30 documented comparisons assessed in this study, grouped by domain. The classifications summarize the historical comparisons developed in the text; because several comparisons involve related evidence streams, they should not be interpreted as statistically independent trials.

Table 2. Summary of the Thirty Historical Comparison Categories

This study evaluates 30 selected head-to-head comparison categories encompassing more than 30 individual historical predictions and model expectations. Because several categories contain multiple related predictions or empirical tests, the number of individual claims examined exceeds the 30 comparison units summarized in Table 2.

Head-to-Head Comparison of Expectations

Table 2: named source and date where the record allows, with subsequent outcome

Design / Creation Expectation Confirmed: 30 / 30

Evolutionary Expectation Confirmed: 0 / 30

#	COMPARISON TEST / DOMAIN	DESIGN / CREATION EXPECTATION (Source & date)	EVOLUTIONARY EXPECTATION (Source & date)	SUBSEQUENT OUTCOME
1	Classification & created kinds	Linnaeus, 1735–1758: fixed natural groups; variation within kinds.	Darwinian continuum: no absolute created boundaries.	Discrete taxonomic and genetic clusters persist; bounded groups remain the framework.
2	Homology & archetype	Owen, 1830s–1849: common structural blueprint.	Darwin, 1859: homologous structures from common ancestry.	Shared vertebrate limb plans and developmental patterning confirm a common blueprint.
3	Nested hierarchy	Owen, 1848: nested hierarchy of created groups.	Universal common descent should recover one branching pattern.	Clustering and hierarchy recovered, with limits, conflicts, and incongruence.
4	Deep molecular homology / conserved developmental genes	Frair, 1967: molecular homologies and common design.	Mayr, 1963: finding homologous genes across distant taxa largely futile.	Conserved rRNA sequences, homeobox/homeobox-related sequences, and conserved developmental-control genes were found across distant taxa.
5	Genome-level DNA similarity	Morris, 1975: broad DNA similarity reflects unified design.	Common ancestry should explain genome-wide similarity.	Widespread molecular similarity, with patterns hard to read through simple ancestry.
6	Tree of Life	Design-based systematics: clustering with limits, not one tree.	Darwin, 1859: sequences should converge on one Tree of Life.	Gene trees often conflict; incongruence and bush-like signals.
7	Genetic boundaries / DNA barcoding	Jeanson, 2013: kinds remain bounded and comparatively homogeneous.	Neutral/deep-time: diversity scales with time and population size.	Stoeckle & Thaler 2014/2018: low within-species COI diversity, clear barcode gaps.
8	Multicellularity & endosymbiosis	Purdum & Anderson, 2009: reuse existing systems, not build new.	Major transitions arose through undirected processes.	Experimental examples reused existing systems; key problems unresolved.
9	Beneficial mutations: modification / loss	Purdum & Anderson, 2009: mainly modify, duplicate, or degrade.	Mutation plus selection can build new structures and body plans.	Adaptational mostly involved loss, altered regulation, or reuse of existing features.
10	Founder effect & bottleneck recovery	Marsh, 1940s: small populations could survive and recover.	50–500 rule: a single pair should not sustain long-term population.	Mouflon, wolves, and others recovered from severe bottlenecks.
11	Rapid speciation vs gradualism	Marsh; Wieland, 1997: rapid, bounded diversification.	Darwin, 1859; Benton, 2005; Gee, 2000: requires gradual change.	Finches, island lizards, and many taxa showed rapid change or speciation.
12	Junk DNA & ERVs	Walkup, 2000; Woodmorappe, 2000: noncoding DNA/ERVs have function.	King & Jukes, 1969; Ohno, 1972: much DNA is junk; ERVs are fossils.	Synctin, regulatory ERV functions, topological roles, and many noncoding functions.
13	Neanderthals as fully human	Custance et al., 1926–2001: fully human and likely interbred.	Krings et al., 1997: not our ancestors; behaviorally inferior.	Interbreeding, symbolism, cognition, tools, and language support fully human status.
14	Neanderthal upright posture	Creation writers: ordinary upright humans.	Boule, 1911–1913: stooped, bent-kneed, brutish reconstruction.	Pathology explained specimen: later found upright human posture and gait.
15	DNA decay & recent archaic hominins	Morris & Whitcomb, 1961: recent post-Flood humans.	Deep-time: Sima de los Huesos hundreds of thousands of years.	Fragment-length decay calculations yield only thousands of years.
16	Small archaic populations	Creation model: short-lived, small, isolated human groups.	Deep-time: small populations persisted for very long periods.	Inbreeding, Allee effects, and stochasticity explain Neanderthal decline.
17	Recent protein-coding variation & expansion	Carter, 2010: recent founding population and rapid expansion.	Deep-time: much coding variation over long timescales.	Fu et al. 2013; Tennessen et al. 2012: most rare variants and growth less than 10 kyr.
18	Population growth from a small founding number	Morris, 1966: post-Flood founders could reach today's population.	Deep-time: ~200,000 years with near-zero net growth.	Required long-term growth is within ordinary historical ranges.
19	Mitochondrial DNA & biblical Eve	Lang, 1973/1982; Wieland, 1998: recent biblical Eve / MRCA.	Phylogenetic-clock: mtDNA Eve far outside biblical timescale.	Howell 1996; Parsons 1997: rapid rates and MRCA in few-thousand-year range.
20	Sapient paradox & documented history	Custance, 1960: fully capable humans from the start.	Renfrew, 1996: modern humans long predating civilization.	Civilization, monumental culture, and writing appear within last few millennia.
21	Genealogical convergence of all living humans	Morris, 1966; Carter, 2010: recent convergence after Adam, Flood, Babel.	Deep-time: expectation: recent universal ancestry implausible.	Rohde et al., 2004: recent MRCA and IAP about 7.4 kyr ago.
22	Mutation saturation	Jeanson, 2015: recent history far below mtDNA saturation.	Deep-time: far more mtDNA accumulation and saturation.	Observed human mtDNA counts far below saturation; tight population clusters.
23	Y-chromosome mutation rates	Jeanson, 2013/2019: fast, near pedigree scale, trace to Noah.	Xue 2009; Helgason 2015: slower Y rates, older timescales.	Karmin 2015; Maretty 2017: much faster Y-chromosome rates.
24	Peleg's generation of expansion	Carter, 2010: Babel occurred in/near Peleg's generation; paternal dispersal should leave geographically structured Y-chromosome lineages.	Conventional chronology assigns much older deep-time dates.	~3 mutations per generation places expansion in Peleg / Babel window.
25	Beneficial mutations & new kinds	Spetner, 1968/1970: do not build new information or kinds.	Neo-Darwinian: beneficial mutations supply raw material.	Reported beneficial mutations mainly loss, trade-off, or reduced features.
26	Pseudogene function / HBBP1	Woodmorappe, 2000: pseudogenes can have regulatory functions.	Miller, 2005: HBBP1 is broken and nonfunctional.	HBBP1 under purifying selection and experimentally essential (2013; 2021).
27	Biological wheels	Design viewpoint: rotary systems are compatible with design.	Haldane, 1949: a wheel useless until nearly perfect.	Bacterial flagella and ATP synthase recognized as rotary molecular machines.
28	Biological magnets	Design viewpoint: purposeful engineering can include magnets.	Haldane, 1949: a magnet useless until fairly perfect.	Magnetotactic bacteria and magnetosome systems discovered.
29	Deep-subsurface microbial stasis	Francis & Purdom, 2009; Bartlett, 2009; Truman, 2015: long-term stasis.	Becraft et al., 2021: separated CDA genomes should be divergent.	>99.2% average nucleotide identity and genomic conservation in CDA.
30	Biomolecular preservation limit	Wieland, 2005: original biomolecules may persist much younger.	Schweitzer, Wittmeyer & Horner, 2007: no originals beyond 100 kyr.	Environmental DNA near 2 Ma and proteins 21–24 Ma exceed 100-kyr limit.

TOTAL: 30 comparison tests

Outcome claimed in study: 30 landed on the design / creation expectation; 0 on the competing evolutionary expectation.

Appendix A. Future Tests and Research Directions

The following proposals extend the creation/design framework examined in this review. They are presented for further investigation and are not included in the historical scorecard as successful predictions. Each proposal should identify the observations already used in its formulation, the additional evidence required for testing, and the outcomes that would support or weaken it. Claims of predictive priority require a dated statement preceding access to the relevant testing results; analyses of already-known findings should be identified as retrospective.

Echoes of Creation - This prediction assumes that all archaic homo are not ancient, thus not closer to the common ancestor than ancient homo sapiens. Thus we should find an inconsistent pattern, and not modern humans being the least similar to Pan or the ancestral reconstructed sequence. Rather we will find the opposite pattern evolution expects with archaic homo even less similar than we are, since they diverged after the flood like us.

One Ancestral Hominin Lineage Across Modern and Archaic Homo. This prediction will show that we all nest into the same DNA barcoding bin making us all extremely related, even more related than the classification of different species.

Missing Diversity Prediction: The Barcode Paradox - This prediction states that there should have been over 2,275 mutational differences over the 7 million year split between humans and chimpanzees. Yet, only 65 differences are observed. We also predict that there would be no convergence on an ancestral sequence between homo and pan.

The Not So Old - Oldest Tree. We predict that the true mutation rate of Pando will match the YEC timeline, regardless of radiometric dating results.

The Clocks That Should Not Exist - Collagen decay rates in unfrozen samples from archaic homo and dinosaurs will yield YEC dates and timelines. We predict that when we obtain results from these soft tissues we can use their decay rates as a clock and use them as a secondary model for testing timeframes.

Fossilization - Mineralization rates - We predict that we will discover this process to be fast in experiments that show pre-mineralization timeframes. Case studies will confirm that this same rapid rate we find in wood, will roll over to bone.

Predicted Radiocarbon Dating Dinosaur Fossils Based on Pre-flood world

With baseline production normalized to a 100 pMC equilibrium, we model radiocarbon accumulation from an initial concentration of 0.1 pMC. For this chronological sensitivity calculation, we adopt a 1,500-year pre-Flood interval with a magnetic field several times stronger than today's (Snelling 2011) and *Baumgardner et al.*, 2003 ratio who claims around 20% lower C14 production under an assumed strong magnetic field. This is followed by 4,500 years of additional decay.

This calculation yields approximately **7.74 pMC today**.

To explore the possible influence of stronger pre-Flood magnetic shielding, we apply an illustrative 20% reduction in radiocarbon production throughout the accumulation interval. Within the assumed fixed carbon reservoir, this reduces the equilibrium concentration from 100 pMC to 80 pMC.

Under these assumptions, radiocarbon increases from 0.1 pMC at Creation to approximately 13.36 pMC at the Flood. After 4,500 years of subsequent ordinary radioactive decay, the calculated remaining concentration is approximately 7.75 pMC.

The 20% production reduction is a sensitivity assumption rather than an independently established estimate of pre-Flood conditions. Although stronger magnetic shielding can reduce radiocarbon production, describing a

magnetic field as “several times stronger” does not establish a specific production reduction without a separate physical calculation.

The calculation assumes a fixed, uniformly mixed carbon reservoir during accumulation and preservation of the sampled carbon without subsequent exchange after incorporation. The baseline normalization is a simplified modeling assumption rather than a directly observed reconstruction of pre-Flood radiocarbon buildup.

This scenario provides a conditional prediction that can be evaluated using securely identified original carbon from materials whose chronological placement and preservation history are independently constrained. Such testing requires suitable pretreatment, process blanks, and assessment of environmental or conservation-derived carbon.

Under the stated assumptions, carbon incorporated at the end of the pre-Flood interval would retain approximately **7.75 pMC today**. A reproducible intrinsic concentration substantially exceeding this value, beyond analytical and model uncertainty, would contradict this particular combination of initial concentration, chronology, production history, reservoir behavior, and closed-system preservation.

Concentrations below this boundary would satisfy an upper-bound constraint but would not, by themselves, establish the proposed accumulation history. The model assumptions must be specified independently of the measurements used to evaluate them.

Carbon incorporated earlier and subsequently isolated from exchange would retain less radiocarbon today. For organisms living until the same mortality event, however, the relevant starting concentration would depend on their carbon sources and tissue turnover near death.

Radiocarbon accumulation with reduced production.

Let f represent the fraction of baseline production retained. A 20% reduction gives $f = 0.80$, corresponding to an assumed equilibrium concentration of 80 pMC.

The accumulation equation is:

$$\text{pMC}(t) = (100 \times f) + [\text{initial pMC} - (100 \times f)] \times 2^{(-t / 5730)}.$$

Here, initial pMC = 0.1, $f = 0.80$, and $t = 1,500$ years. Ordinary radioactive decay occurs throughout this accumulation interval.

Concentration at the Flood.

$$\text{Flood pMC} = 80 + (0.1 - 80) \times 2^{(-1500 / 5730)}.$$

$$\text{Flood pMC} = 80 - 79.9 \times 2^{(-1500 / 5730)}.$$

$$\text{Flood pMC} = \text{approximately } 13.3588 \text{ pMC}.$$

Ordinary radioactive decay after the Flood.

$$\text{Present pMC} = \text{Flood pMC} \times 2^{(-4500 / 5730)}.$$

$$\text{Present pMC} = 13.3588 \times 2^{(-4500 / 5730)}.$$

$$\text{Present pMC} = \text{approximately } \mathbf{7.75 \text{ pMC}}.$$

The modeled sequence is: 0.1 pMC at Creation → approximately 13.36 pMC after 1,500 years of accumulation with 20% reduced production → approximately 7.75 pMC after 4,500 years of ordinary radioactive decay. Therefore when we test dinosaur fossils we should not find any specimens above 7.75 pMC. Any fossils found above that concentration that cannot be proven contamination would falsify our model and predictions.

Chromosome 2 fusion confusion prediction

We predicted that the head-to-head arrangement of interstitial telomeric repeats associated with the proposed chromosome 2 fusion site at 2q13 will also be found elsewhere in the human genome, including at loci without an independently established history of chromosome fusion. Under the model proposed here, such arrangements are potentially recurring genomic structures rather than configurations restricted to a single ancestral fusion junction. This prediction goes beyond the familiar observation that telomeric repeats occur inside chromosomes: it specifically requires oppositely oriented repeat arrays meeting at a junction when read along the same DNA strand. Merely detecting TTAGGG on one strand and its reverse complement, CCCTAA, on the opposite strand would not satisfy the prediction. A rigorous test requires a genome-wide search using explicit criteria for repeat length, orientation, sequence identity, and junction spacing, followed by publication of assembly identifiers, exact coordinates, and flanking sequences for independent verification. The chromosome 9 candidate reported in this study represents a potential positive result because it is described as containing adjacent, oppositely oriented telomeric arrays with a comparatively uninterrupted junction. If independently confirmed under the same structural criteria applied to 2q13, this finding would falsify the absolute claim that the head-to-head configuration occurs only at the chromosome 2 site. Failure to recover another qualifying site in a sufficiently comprehensive search would count against the prediction. The significance of a confirmed counterexample would be specific: the orientation alone could no longer establish the uniqueness of 2q13, and its historical interpretation would require additional contextual evidence. However, the absence of a proposed fusion at chromosome 9 would not itself establish that no ancient rearrangement occurred there, and a similar repeat arrangement would not independently demonstrate shared function or a common mechanism of origin. The prediction consequently tests the claimed exclusivity of the sequence configuration; it does not, by itself, resolve the chromosome 2 fusion hypothesis, which also incorporates chromosome-wide correspondence with ape chromosomes and evidence concerning an ancestral centromere.

The Recent Biosphere Prediction - Substitution Rate Predictions

We believe that the observed rates of change in pedigree germline studies are the true rates and while over time they may slow down a bit, it has no bearing on our model since our model runs over just a few hundred generations. We predict that all observable rates can explain the diversity of life in our model. We call this the Hidden Clock of Humanity Prediction. While for now this prediction is just limited to humans, we believe it will roll over to all animal species and even so called living fossils as well. This would be added confirmation of our model and an even more rich falsification of deep time.

Greater Functional Integration Among Fixed ERV Loci Prediction. The proposed model predicts that ERV-derived loci fixed within a species will, on average, show a higher frequency of reproducible contributions to host gene regulation and cellular function than comparable insertionally polymorphic loci. This expectation concerns a difference between groups rather than a claim that every fixed element is functional or every variable element is dispensable. A rigorous comparison would classify loci by population frequency before examining their functional effects, then compare representative sets matched for sequence length, ERV family, genomic context, and technical accessibility. Targeted perturbation would measure effects on gene expression, development, or cellular responses under predefined conditions. A higher proportion of functionally consequential fixed loci would support the predicted association, whereas equivalent or greater functional involvement among polymorphic loci would count against it. Fixation alone would remain insufficient evidence of function, and any observed enrichment would require comparison with evolutionary explanations involving selection and the retention of beneficial insertions.

Regulatory Function Persists After Loss of Viral Coding Capacity Prediction. We predict that additional solo LTRs and truncated ERV-derived sequences will prove capable of regulating host genes despite lacking the

internal sequences required to encode a complete retrovirus. More specifically, retained regulatory motifs and their genomic context should predict regulatory activity better than the presence of intact viral coding genes. This extends the paper's distinction between viral replication capacity and host regulatory function: an element may be incapable of producing a virus while still influencing when, where, or how strongly a nearby gene is expressed. Testing would compare previously uncharacterized fragments with and without candidate regulatory motifs and assess their effects at their native genomic locations. Precise disruption of those motifs should alter the relevant regulatory output, with restoration of the sequence recovering the effect where feasible. Failure to detect reproducible contributions across an adequately powered, representative screen would weaken the prediction. Positive findings would establish functions for the tested fragments without implying that every solo LTR is active or necessary.

Additional ERV Functions Will Emerge Under Specific Biological Conditions. We predict that a subset of ERV-derived sequences showing little or no measurable contribution under baseline laboratory conditions will reveal regulatory functions during immune stimulation, cellular differentiation, or defined developmental transitions. The proposed explanation is that some elements contribute to conditional responses rather than continuously active processes, making their effects difficult to detect in a single cell type or unstimulated state. The paper's examples involving interferon signaling, pluripotency, and development provide a basis for extending this prediction to uncharacterized loci. A direct test would compare the effects of the same targeted perturbations across predefined baseline and stimulated conditions, measuring both gene-expression changes and relevant cellular outcomes. Support would require reproducible effects that depend on the tested condition and can be attributed specifically to the disrupted sequence. An adequately powered study finding no increase in detectable effects across the nominated conditions would count against this expectation. Conditions and outcome measures should be specified before testing so that the hypothesis does not depend on indefinitely invoking an untested context.

Repeated Use of ERV-Derived Regulatory Elements at Corresponding Genes Prediction. Building on the paper's discussion of B3GALT5 and NAIP, we predict that comparative functional studies will identify additional corresponding genes in different mammalian species whose expression is regulated by ERV-derived elements, including cases in which different ERV families contribute to regulation of the same gene. The testable expectation is that this repeated regulatory involvement will occur more frequently than in appropriately matched comparison genes. Testing would require identification of corresponding host genes, confirmation of the locations and ancestry of the associated elements, and independent demonstration that each element contributes to gene regulation in its native species. Sequence proximity or transcription alone would not establish the predicted relationship. Support would consist of statistically supported enrichment accompanied by reproducible functional effects; absence of enrichment or failure of the candidate elements to influence their proposed targets would weaken the hypothesis. Such findings would document repeated use of ERV-derived regulatory sequences, while distinguishing common design from evolutionary recruitment would require additional predictions that differ between those explanations.

Missing Orphan Genes Prediction - I predict that the highest genetically diverse people groups in Africa will have fewer orphan genes than other people. Why? Studies have shown that orphan genes can be bred out of a population using adolescent females to produce offspring. Since it is predicted that Africans have a younger generation time and that is why they have more mutations in them, then this should be reflected in their total amount of orphan genes. If this prediction turns out to be true, this will answer two major conflicts between the models. It will tell us that Africans really have had consecutive younger generations and that they are the same age as every other people group on earth regardless of having more mutations. This will also validate that all people did not evolve in Africa or from Africans. It will show us that Africans are just another people group like any other who inhabited their own lands and isolated themselves there.

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