Predictions on Trial

Comparing Creation and Evolutionary Predictions Across Biology and Development

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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. 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 prediction test, the prediction must predate the relevant observation, be traceable to a named source where possible, and specify an observable outcome capable of distinguishing competing expectations. A failed historical prediction is treated as a failure of that stated expectation rather than automatically as a falsification of every subsequent formulation of the broader framework. Because several comparisons draw upon related evidence streams, the scorecard is descriptive and the individual comparisons are not assumed to be 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*.

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

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.

Genome Level DNA Similarity and Common Design

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* 1974/1975 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, 1975).*

The first complete DNA genome sequenced was the tiny 5,375-base genome of bacteriophage φX174, 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.* 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. 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. 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 called 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 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 therefore 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. Therefore 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.

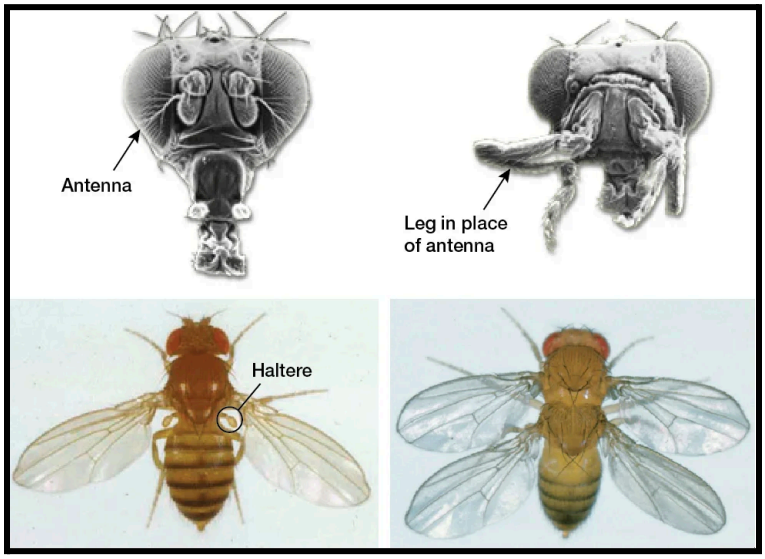


Figure 1. *shows (top) a leg growing out of the face where an antenna belongs and (bottom) shows an extra set of wings growing where halteres should be. Halteres are special sensory organs at the base that detect changes in body position and rotation. Halteres act like gyroscopes and help the fly balance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

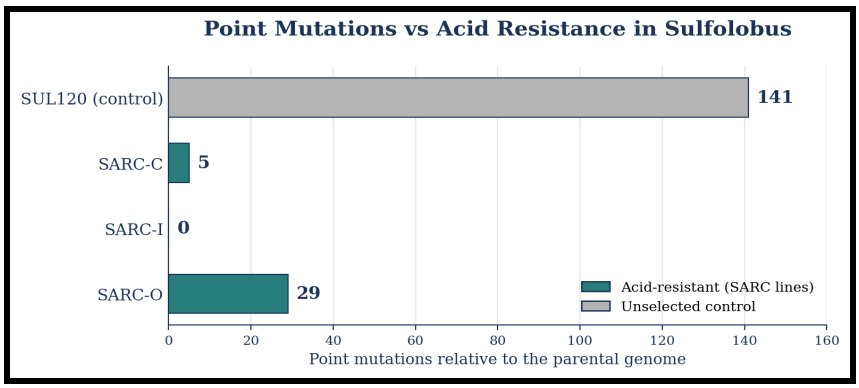


Figure 2*. Point mutations in the experimentally evolved Sulfolobus solfataricus lineages. The three acid resistant SARC lines acquired the trait with 0 to 29 point mutations, SARC-I with none, whereas the unselected control line SUL120 accumulated 141 mutations without becoming acid resistant. Adaptation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

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. 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..

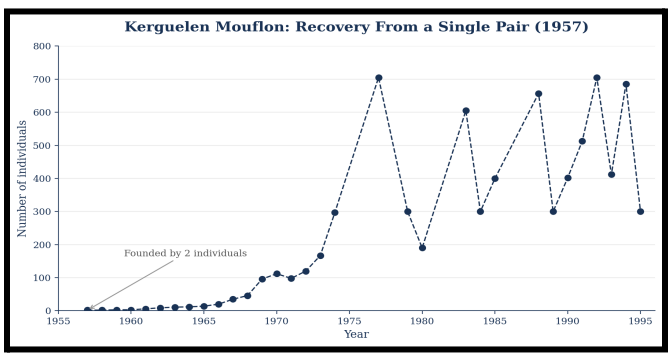


Figure 3. *The Kerguelen mouflon population, founded by a single pair in 1957, climbed to roughly 700 by 1977 and then cycled between about 200 and 700. Heterozygosity, measured over 46 years, rose rather than declined, exceeding the range predicted by neutral models. Redrawn from Kaeuffer et al. (2007).*

Rapid Speciation Versus Gradualism

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.

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 1957, and again in his 1975 Doorway Papers, 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 therefore 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 Neandertal 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).

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, 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**.

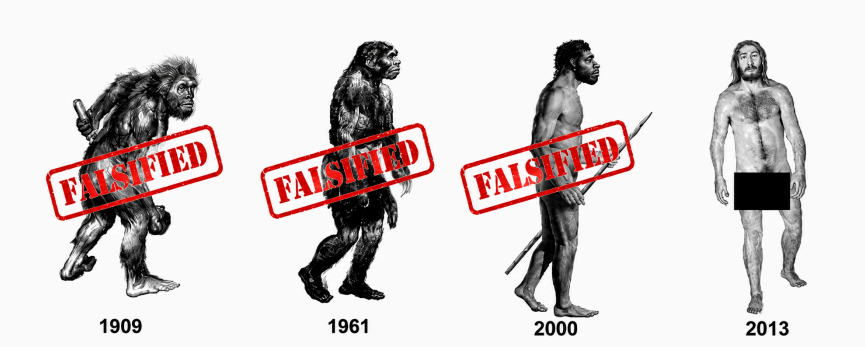


Image 1. Neanderthal depictions over the century.

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.

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 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 therefore opposite to the previously published preservation expectation. 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 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 times 10 to the minus 6) and three months near 13.4 degrees (k = 5.67 x 10-^{6}) give a time-weighted effective rate of 3.93 times 10 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×. 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 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.

This is further corroborated with *Fu et al.* (2013) 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 is again yet another than lands solely on the side of Biblical creation and nowhere near the expected evolutionary timeframe.

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. 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. Rev. Walter Lang, in material first published in 1973 and revised in 1982 as Genesis and Science. Lang argued that modern genetics made it reasonable that God placed the full potential for human diversity inside Adam and Eve. His key claim was that the genetic *"coding for all people"* was already present in Adam and Eve, and that their genes contained the potential for all later races/peoples and that this genetic data would one day confirm this and that they lived recently. 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 ~2.6 × 10^{-7}/p/gener-ation. In contrast, the results in table 2 yield a mutation frequency of ~5.2 × 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. 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 that was confirmed by science that even to this day the pedigree / phylogeny paradox still exists. The phylogenetic mutation rate and observed measurable pedigree mutation rates are an order of magnitude different from one another and no known mechanism can close the gap.

The Sapient Paradox and the Onset of Documented History

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 5,300 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 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, 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.

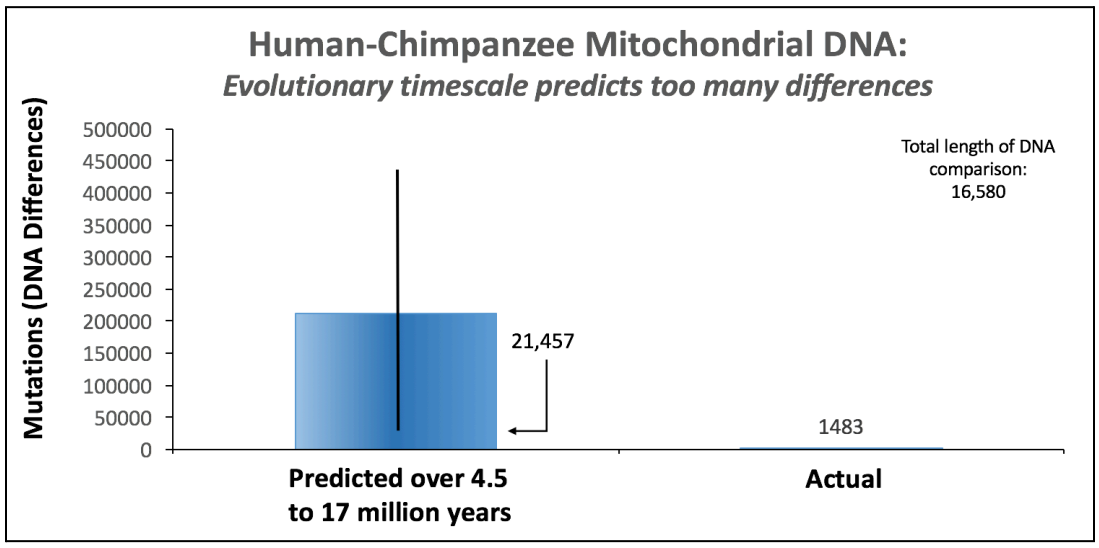


***Figure** 4. Mutation saturation chart showing predicted amount versus observed amount.*

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 at Noah, since only he and his sons were the only male lineages to survive the flood. So to test this prediction he 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.

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.

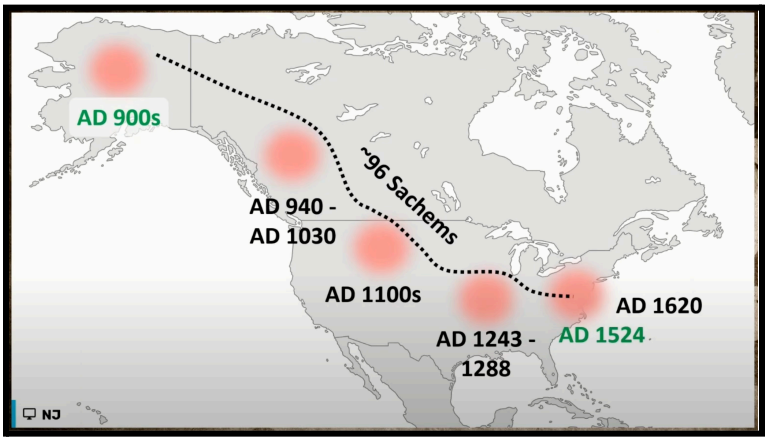


Figure 5. *Migration map of native Americans documenting their travels through Sachems (the time a chief ruled) documented in the Red Record.*

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. Dr. Jeanson predicted 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 Maretty 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).

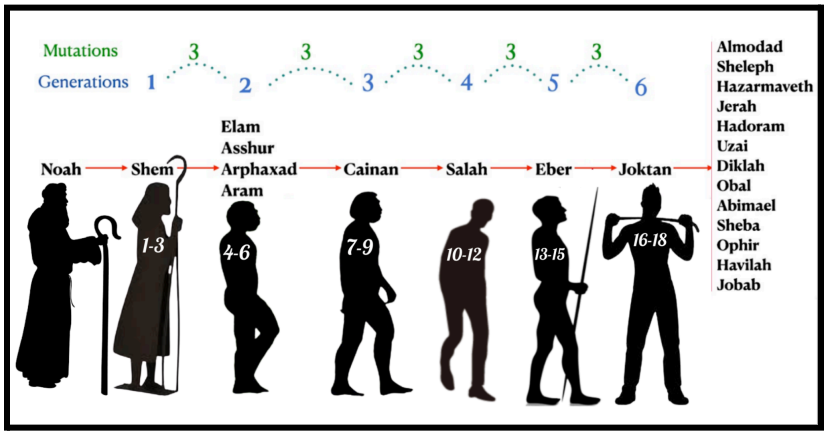
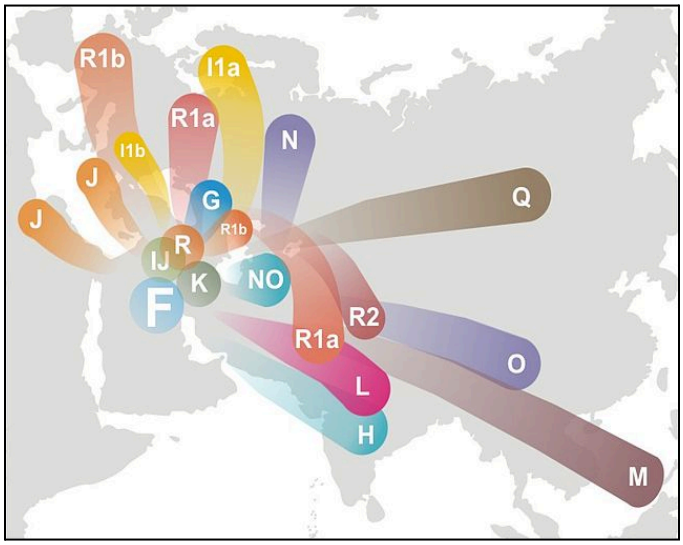
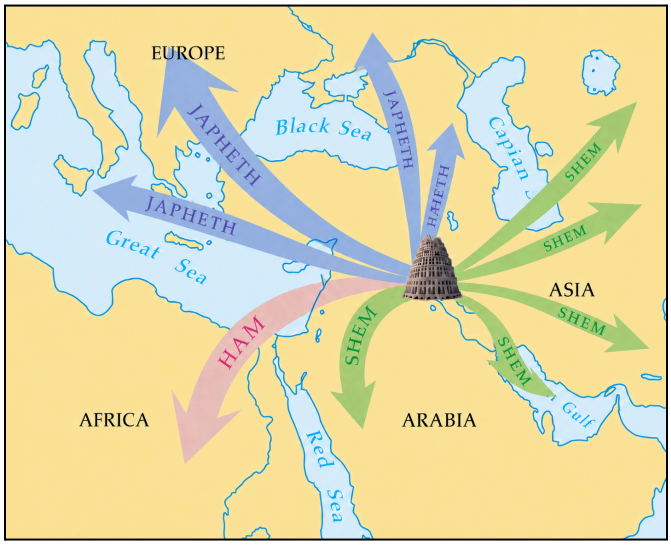


Figure 6. *Shows that following 3 mutations per generation lands on the expanding population which aligns with the secular consensus of when these haplogroups formed (figure 6) and also where they formed (Middle East).*





Figures 7 & 8: *Figure 7 on the left shows the conventional haplogroup formation location and migration pattern (M. Zlojutro, 2008). Figure 8 on the right shows the biblical location and story of babel dispersion. The close match is undeniable and exactly what the Bible describes.*

The Genealogical Convergence of All Living Humans

Creationist Henry M. Morris predicted that not just evidence in genetics would confirm the biblical model of the babel account but also even evidence for Adam and Eve. In his article "World Population and Bible Chronology," Morris argued that population statistics fit a recent biblical history better than a long evolutionary history. He built formulas before existing evidence from population genetics ever existed using starting population, family size, generation length, and lifespan, and concluded that biblical chronology was "completely realistic," while million-year human history led to absurd population implications.

In 2010 Dr Robert Carter argued that genetic evidence points to descent from Adam and Eve, a severe population crash at Noah's Flood, and a single post-Babel dispersal. He explicitly wrote that the single dispersal, Middle East route, three major mitochondrial lineages, and small migrating groups are *"directly predicted by the Tower of Babel account."* In 2011 he also said he hoped enough genetic data would eventually allow creationists to backtrack human history to Adam and Eve. This evidence eventually made its way in the form of advanced population genetics simulations.

Rohde, Olson, and Chang (2004) used multiple mathematical computer simulations to model the genealogical ancestry of all living people under realistic assumptions about migration and population substructure. They made three different mathematical simulations and ran them individually explicitly calculating genealogical ancestry through all parental lines, and they distinguish it from mtDNA and Y-chromosome genetic ancestry. They obtained a constant theme and found that the most recent common genealogical ancestor of everyone alive today, the most recent person from whom all of us descend through some ancestral line, likely lived just a few thousand years ago, on the order of 1500 BC or 3,525 years ago, and that the identical-ancestors point, the still earlier moment beyond which every then-living person who left descendants is an ancestor of every person now alive (Identical Ancestors Point), fell at around 5,353 BC or 7,378 years ago in all of their models.

That window coincides with the mitochondrial and demographic estimates above matching the biblical Septuagint timeline with creation being around 7,600 years ago and a global bottleneck around a few thousand 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 therefore 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 therefore 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, thereby stabilizing and increasing expression of TAL1, a major regulator of 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 therefore unusually 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 therefore 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.

Biological Wheels and Magnets: Haldane's 1949 Prediction

An unusually explicit evolutionary limitation was stated by one of the founders of modern population genetics, J. B. S. Haldane. During the 1949 debate *Is Evolution a Myth?*, Haldane considered the types of biological structures that would present serious difficulty for gradual evolution by mutation and natural selection. Among his examples were *"various mechanisms, such as the wheel and magnet, which would be useless till fairly perfect"* (Haldane, 1949). His reasoning was straightforward: natural selection can preserve successive useful intermediates, but a mechanism that produces no advantage until most of its components are already assembled would lack the selectable intermediate stages required by the theory. A biological wheel or magnetic mechanism was therefore offered as an example of the kind of system evolutionary processes should have difficulty producing.

The biological discoveries that followed were striking because they involved Haldane's own examples. In 1973, Howard Berg and Robert Anderson demonstrated that bacterial locomotion involves rotation of the flagellar filament rather than merely undulatory movement. The bacterial flagellum is driven at its base by a membrane-embedded rotary motor capable of turning the helical filament as a propeller (Berg & Anderson, 1973). Later work revealed another molecular rotary machine in ATP synthase. Noji et al. (1997) directly visualized rotation of the F1 portion of ATP synthase at the single-molecule level, demonstrating that the enzyme operates as a genuine nanoscale rotary motor.

Haldane's second example likewise appeared in living organisms. Richard Blakemore reported magnetotactic bacteria in 1975 and showed that their movement was oriented by the geomagnetic field (Blakemore, 1975). Subsequent work identified intracellular particles of magnetic minerals—magnetosomes—that allow the cells to align with magnetic-field lines. Thus both categories Haldane specifically chose as examples of mechanisms difficult to reach through gradual selection, **wheels and magnets**, were subsequently discovered as functioning components of living systems.

This result should again be stated precisely. The discovery of biological rotary motors or magnetosomes does not by itself demonstrate that no evolutionary pathway to those systems is possible; evolutionary biologists have subsequently proposed histories involving modification and co-option of component systems. What it does establish is that Haldane's **1949 empirical criterion did not survive discovery**. He selected wheel-like and magnetic mechanisms as examples of biological machinery whose existence would pose the kind of difficulty he regarded as especially serious for gradual evolutionary construction. Within several decades, both were experimentally documented in living organisms. As a historical prediction test, the observable outcome fell on the side Haldane had identified as problematic rather than on the side his expectation anticipated.

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. Becraft et al. 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. 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.

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. 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.

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 Bapteste (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. Bapteste 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

Across the **thirty prediction comparisons assembled in this study**, a striking and remarkably consistent pattern emerges. Again and again, observations that later became established features of modern biology were anticipated, at least in broad outline and often explicitly, by creation or design-based expectations before the relevant evidence was available. Conserved genes and developmental systems were found where deep divergence had been expected to erase recognizable homology. Biological similarity repeatedly reflected common structural and functional solutions. Organisms remained organized into recognizable taxonomic and genetic clusters rather than dissolving into an observable continuum. Speciation and adaptation proved capable of occurring with extraordinary speed. Severe population bottlenecks proved survivable. Genomic regions once dismissed as evolutionary debris acquired regulatory, developmental, or physiological functions. Pseudogenes once cited specifically as broken remnants were found participating in essential biological processes. Biological rotary machinery and magnetic systems appeared in nature despite having once been invoked as examples of mechanisms considered difficult for gradual evolutionary construction. Microbial genomes predicted to diverge dramatically instead displayed extraordinary long-term conservation. Biomolecules exceeded preservation limits that had previously been regarded as plausible boundaries. And the accumulating genetic, demographic, anatomical, and archaeological evidence concerning humanity repeatedly produced results far more compatible with recent, concentrated episodes of diversification and population expansion than earlier expectations had suggested.

The importance of this pattern is not that evolutionary biology possesses no mechanisms capable of accommodating these observations. Modern evolutionary theory can invoke conservation, stabilizing selection, developmental constraint, convergence, co-option, horizontal gene transfer, incomplete lineage sorting, regulatory evolution, evolutionary stasis, unusually efficient repair, exceptional molecular preservation, rapid selection, population expansion, and many other biological processes. The crucial question addressed in this paper however, is **not whether a theory can explain an observation after it has been discovered. The question is what each framework led investigators to expect beforehand.** Explanation after observation and prediction before observation are not epistemically equivalent. A model becomes scientifically impressive not merely because it can survive unexpected results, but because it repeatedly places risky expectations in front of the evidence and then watches those expectations succeed.

That distinction is the central issue raised by the record examined here. In numerous cases, the result eventually incorporated into evolutionary explanation was originally surprising precisely because the previous expectation had pointed elsewhere. Genes thought unlikely to remain recognizable across distant organisms turned out to be deeply conserved. A genome once expected to contain vast quantities of expendable sequence revealed layers of regulation and organization. “Broken” genomic elements proved functional. The simple universal Tree of Life became a forest of gene histories, networks, reticulations, and conflicting signals. Supposedly primitive humans increasingly acquired the anatomy, genetics, behavior, cognition, and interbreeding capacity expected of humanity. Mutation rates measured directly in families challenged rates inferred from phylogenetic timescales. Rapid biological change repeatedly appeared where gradual change had traditionally been emphasized. Even organisms supposedly separated for immense periods sometimes retained levels of genetic similarity that surprised the researchers studying them.

None of this means that every modern evolutionary explanation is thereby falsified, nor does every individual observation uniquely prove creation. That would demand more of the evidence than prediction testing can legitimately establish. What the evidence **does** permit us to ask is a simpler and more uncomfortable question: **Which framework repeatedly expected the direction in which the evidence actually moved?** Under the prediction criteria applied in this study; priority, specificity, falsifiability, and comparison with subsequently observed outcomes, the answer is difficult to ignore. Across the tests evaluated here, the scored outcomes repeatedly landed on the side of the creation/design expectation, while the competing historical evolutionary expectation was repeatedly modified, qualified, or replaced once the evidence became known.

This matters because successful prediction is one of the strongest currencies in science. A framework that makes no risky predictions can explain almost anything after the fact; a framework that repeatedly predicts unexpected observations before they are found has demonstrated something far more demanding. Popper's principle of falsifiability cannot be applied selectively. Creationist claims should be exposed to severe testing, but so should evolutionary claims. Failed predictions cannot cease to matter merely because a broader theory remains capable of incorporating their opposite. Likewise, successful predictions should not become scientifically invisible simply because they originated outside the prevailing paradigm.

The record presented here therefore challenges a common characterization of Biblical creation as a position incapable of generating scientific expectations. Whatever one's ultimate interpretation of the evidence, that characterization is no longer adequate to the historical record examined in this study. Creation and design thinkers made claims about biological boundaries, common structural plans, conserved genetic systems, rapid diversification, genomic function, bottleneck recovery, human origins, mutation rates, molecular preservation, and biological complexity **before many of the decisive observations were made**. Those claims were testable. They could have failed. In the cases assembled here, they did not.

The deeper lesson is methodological. Science advances when competing explanations are permitted to make predictions and then face the evidence on equal terms. A dominant framework should not receive unlimited explanatory flexibility while an alternative is dismissed before its predictions are even counted. If creation repeatedly predicts observations that later surprise the dominant model, then those successes deserve to be acknowledged, investigated, and subjected to further prospective testing. The proper response is not insulation from challenge, but more challenge: sharper predictions, cleaner experiments, larger datasets, and increasingly difficult opportunities for either model to fail.

That is precisely where this study ends and where the next one should begin.

Thirty tests were placed on the table. Thirty outcomes were compared with the expectations that preceded them. Under the scoring criteria of this study, every one landed on the creation/design side. That result should not be waved away because it is uncomfortable, nor accepted merely because it is provocative. It should be tested again.

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.**

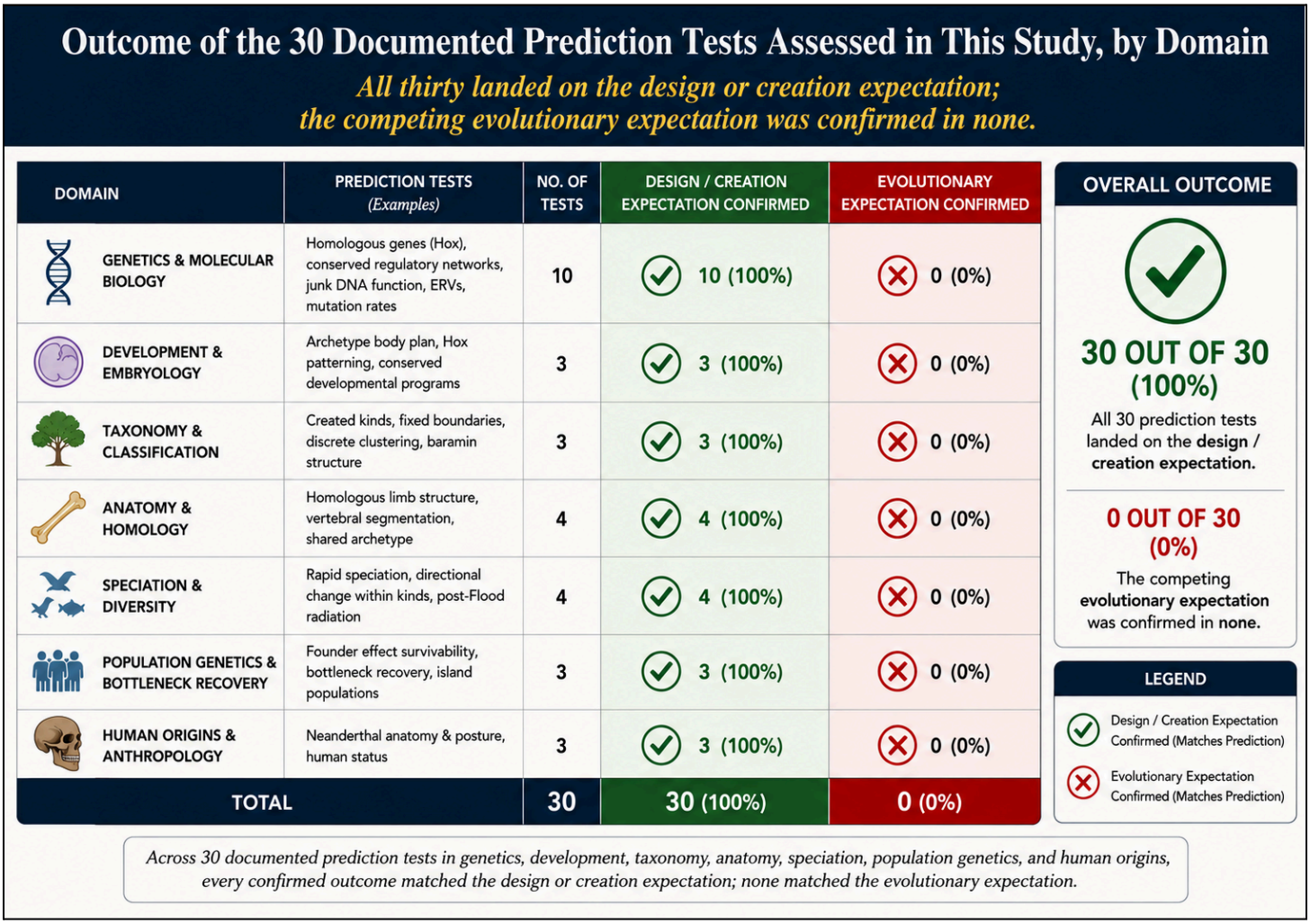


Figure 9. *Descriptive outcome of the 30 documented prediction comparisons assessed in this study, grouped by domain. The classifications summarize the historical comparisons developed in the text; because several comparisons involve related evidence streams, they should not be interpreted as statistically independent trials. See Table 2 below for the head-to-head comparison.*

Table 2. Head-to-Head Comparison of Predictions Chart Below

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Head-to-Head Comparison of Predictions

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

Design / Creation Confirmed: 30 / 30 | **Evolutionary Expectation Confirmed: 0 / 30**

#	PREDICTION TEST / DOMAIN	DESIGN / CREATION PREDICTION (Source & date)	EVOLUTIONARY EXPECTATION (Source & date)	SUBSEQUENT OUTCOME
1	Classification & created kinds	Carl Linnaeus, Systema Naturae (1735–1758): fixed natural groups; variation within kinds.	Evolutionary viewpoint / Darwinian continuum: no absolute created boundaries among organisms.	Discrete taxonomic clusters and bounded groups remain the working framework of biology.
2	Homology & archetype	Sir Richard Owen, 1830s–1849: vertebrates share a common structural blueprint/archetype.	Darwin, 1859: homologous structures explained by common ancestry rather than common design.	Shared vertebrate limb plans and developmental patterning confirmed the predicted blueprint.
3	Nested hierarchy	Owen, 1848: life forms a nested hierarchy of created kinds, not a seamless continuum.	Evolutionary viewpoint: branching continuity from universal common descent.	Biology recovered nested, conserved programs and clustering with limits.
4	Homologous genes / Hox system	Henry Morris, 1975: similar controlling genes across life reflect common functional design.	Ernst Mayr, 1963: homologous genes across distant organisms would be "quite futile" to seek except among close relatives.	Hox clusters and conserved developmental control genes were found across the animal kingdom.
5	Genome-level DNA similarity	Morris, 1975: broad DNA-level similarity would reflect a unified design pattern.	Evolutionary viewpoint: genome similarity would be interpreted as descent from common ancestors.	Widespread molecular similarity was found and then read through the ancestry framework.
6	Tree of life	Design-based systematics: expect clustering with limits and conflicting signals at boundaries.	Evolutionary theory: gene sequences should converge on a single universal tree of common descent.	Gene trees often conflict: molecular and morphological trees show incongruence and bush-like signals.
7	Genetic boundaries / DNA barcoding	H. W. Clark, 1940–1941; Marsh, 1941; Morris, 1974; Wood: bounded variation within created kinds.	Neutral/deep-time expectation: diversity should scale with population size and time, with continuity between forms.	Stoeckle & Thaler, 2018: low within-species diversity and clear genetic gaps/boundaries.
8	Multicellularity & endosymbiosis	Design viewpoint: observed clustering should reuse existing genes/machinery rather than generate new information.	Evolutionary viewpoint: major transitions, including multicellularity and endosymbiosis, arose by undirected processes.	Observed algae clustering used existing adhesion systems; key endosymbiotic steps remain unobserved.
9	Beneficial mutations: modification/loss	Creation expectation: mutations mainly modify, duplicate, or degrade existing systems, not create new anatomy.	Evolutionary expectation: mutation plus selection can build genuinely new structures/body plans.	Hox experiments, lizard valves, and microbial adaptation show alteration/plasticity/loss rather than new organs.
10	Founder effect & bottleneck recovery	Frank Lewis Marsh, 1940s: small created populations could pass through bottlenecks and recover.	Population-genetic expectation / 50–500 rule: a single pair cannot found a healthy long-term population.	Kerguelen mouchho began from one pair and rose to hundreds; heterozygosity increased beyond neutral-model expectations.
11	Rapid speciation vs gradualism	Creation / post-Flood radiation model: rapid, bounded diversification after a bottleneck.	Darwin, 1859; Benton, 2005; Gee, 2000: speciation requires slow change, often tens of thousands of years.	Finch lineage formed in about three generations; many taxa show rapid directional change in decades/centuries.
12	Junk DNA & ERVs	Linda Walkup, 2000; Todd Wood, 2002: transposable elements and ERVs would prove functional.	King & Jukes, 1969; Ohno, 1972: much DNA is junk; ERVs are genomic fossils.	Syncytin and many ERV-derived regulatory functions confirmed pervasive functionality.
13	Neanderthals as fully human	Custance, 1957/1975; Parker, 1980–1981; Morris & Parker, 1982; Lubenow, 1998; DeWitt/Skiner, 2000–2001: fully human/interbreeding.	Krings et al., 1997 / Cell headline: Neanderthals were not ancestors; often portrayed as subhuman and non-symbolic.	Green et al., 2010 confirmed interbreeding; later finds support cognition, symbolism, tools, language-related traits.
14	Neanderthal upright posture	Creation writers: Neanderthals were ordinary upright humans; apparent stoop due to age/disease.	Marcellin Boule, 1911–1913: stooped, bent-kneed, brutish reconstruction.	Boule's specimen had pathology; later reassessment found upright human posture and gait.
15	DNA decay & recent archaic hominins	Morris & Whitcomb, 1961: later creationists: archaic humans are recent post-Flood/post Babel branches.	Deep-time framework: Sima de los Huesos Homo heidelbergensis is about 430,000 years old.	Fragment-length decay calculations in the study read the Sima DNA in a few-thousand-year window.
16	Small archaic populations	Creation model: Neanderthals/Denisovans/erectus were short-lived, small, isolated human branches.	Evolutionary model: small effective populations persisted for tens or hundreds of thousands of years.	Vaesen et al., 2019: small population size, inbreeding, Allee effects, and stochasticity can explain extinction.
17	Recent protein-coding variation & expansion	Creation/Babel timeframe: recent post-bottleneck expansion a few thousand years ago.	Deep-time human history: variation accumulated across long prehistoric timescales; growth placed in a conventional Neolithic setting.	Fu et al., 2013: ~73% of coding SNVs and ~86% of deleterious coding SNVs arose in the last 5,000–10,000 years; growth onset ~5,115 years ago.
18	Population growth from a small founding number	Creation model: six post-Flood founders can reach today's population with modest average annual growth.	Deep-time model: 200,000+ years of humans requires near-zero net growth for most of prehistory.	Required 0.39–0.48% average annual growth is within ordinary historical ranges; no long stasis required.
19	Mitochondrial DNA & biblical Eve	Walter Lang, 1973/1982; Carl Wieland, 1998: genetics would fit a recent Eve within biblical expectations.	Evolutionary phylogenetic clock expectation: mtDNA Eve should fall far outside the biblical timescale.	Howell, 1996 and Parsons, 1997/1998 found rapid pedigree rates; reported MRCA estimates around 6,500/6,000 years.
20	Sapient paradox & documented history	Arthur Custance, 1957 onward: Genesis 10/Table of Nations records real post-Flood spread of peoples.	Deep-time archaeology: behaviorally modern humans existed 200,000–300,000 years before cities, writing, and states.	Documented civilization, writing, and continuous history appear abruptly in the last ~5,300–5,000 years.
21	Genealogical convergence of all living humans	Henry M. Morris, "World Population and Bible Chronology"; Robert Carter, 2010–2011: genetics/genealogy should converge toward Adam, Flood, and Babel.	Common intuition/deep-time framing: recent universal ancestry of all living humans seems implausible.	Rohde, Olson & Chang, 2004: universal genealogical MRCA likely only a few thousand years ago; identical ancestors point also recent.
22	Mutation saturation	Nathaniel Jeanson, 2015: deep-time mtDNA should show saturation; young history should remain far below saturation.	Human-chimp divergence model: millions of years should produce tens of thousands of mtDNA mutations and saturation.	Observed human mtDNA mutation count is presented as far below predicted saturation.
23	Y-chromosome mutation rates	Nathaniel Jeanson, 2019: Y-chromosome mutation rate should be fast, similar to mtDNA pedigree rates.	Older low-coverage pedigree studies, Xue 2009 and Helgason 2015: slower Y rates supporting older timelines.	High-coverage Karmin 2015 and Maretty 2017 data support a much faster rate, about 10–17× older estimates.
24	Peleg's generation of expansion	Jeanson, 2017/2022: Y-chromosome clock should locate expansion around Peleg's generation.	Conventional haplogroup chronology: expansion assigned to much older deep-time dates.	Using ~3 mutations/generation places key expansion in the Peleg/Babel window and Middle East region in the study's model.
25	Beneficial mutations & new kinds	Lee M. Spetner, 1968/1970: beneficial mutations do not build new biological information or new created kinds.	Neo-Darwinian expectation: beneficial mutations supply raw material for new organs, body plans, and kinds over time.	Reported beneficial mutations are framed as loss, trade-off, altered expression, or reduction of existing features.
26	Pseudogene function / HBBP1	John Woodmorappe, 2000: pseudogenes should not be assumed functionless; expect regulatory or other functions.	Kenneth Miller, 2005: the beta-globin pseudogene HBBP1 is broken and nonfunctional.	HBBP1 showed functional constraint and was experimentally shown essential in erythropoiesis / red-blood-cell development (2013, 2021).
27	Biological wheels	Design viewpoint: engineered rotary systems are fully compatible with common design.	J. B. S. Haldane, 1949: a wheel would be useless till fairly perfect and should not evolve.	Bacterial flagellum and ATP synthase were discovered to be genuine rotary molecular machines.
28	Biological magnets	Design viewpoint: purposeful biological engineering can include magnet-based systems.	J. B. S. Haldane, 1949: a magnet would be useless till fairly perfect and should not evolve.	Magnetotactic bacteria and magnetosome systems were discovered in living organisms.
29	Deep-subsurface microbial stasis	Creation viewpoint: bounded diversity and long-term stability can characterize microbial lineages.	Becraft et al., 2021: geographically separated CDA genomes should be genetically divergent and locally adapted.	>99.2% average nucleotide identity was found, revealing extraordinary genomic conservation / evolutionary stasis.
30	Biomolecular preservation limit	Recent-age / creation expectation: original biomolecules may persist in remains far younger than deep-time assignments suggest.	Schweitzer et al., 2007 summarizing prior literature: no original protein and/or DNA beyond ca. 100 kyr.	Authenticated environmental DNA reached ~2 Ma and proteins 21–24 Ma, overturning the proposed 100-kyr ceiling.

TOTAL: 30 documented prediction tests — Outcome claimed in study: 30 landed on design/creation expectation; 0 on competing evolutionary expectation.

Table 2. For each prediction, the named source and date on each side where the record allows, and the subsequent outcome. Where a specific attribution cannot be documented, the side is listed by viewpoint rather than by name.

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