Predicted Continuity, Observed Discontinuity: Ape Y Chromosome Architecture as a Test of Bounded Diversity

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ABSTRACT

The male-specific region of the Y chromosome provides an unusually stringent test of competing models of primate origins because it is inherited as a single paternal unit while preserving both a constrained functional core and rapidly changing chromosome-scale architecture. We compared the predictions of common descent and bounded diversity against complete telomere-to-telomere sex-chromosome assemblies from humans and six apes, supplemented by earlier finished Y-chromosome sequences. Only 14–27% of the human Y aligns with the Y chromosomes of other apes, compared with 93–98% of the human X. Among bases in sequences exhibiting interspecies variation, approximately 99% of affected Y sequence occurs within large structural variants; Y inversions and insertions are also substantially longer than their X-chromosome counterparts. The most decisive result is prospective rather than merely surprising: because palindromes enable gene conversion and counteract Y degeneration, Makova et al. (2024) explicitly expected Y palindromes to be conserved. Instead, homologous palindrome clusters declined from 21, 12 and 9 on the X to only two, one and zero on the Y across African great apes, all great apes and all species analyzed, respectively. This architectural discontinuity accompanies other departures from simple Y-evolution expectations, including human nucleotide diversity approximately an order of magnitude below the one-quarter neutral expectation, strongly nonrandom preservation of dosage-sensitive ancestral genes, and greater human–gorilla than human–chimpanzee similarity in Y gene content. These observations can be accommodated individually through gene conversion, linked selection, differential loss and lineage-specific turnover, but accommodation after discovery is not equivalent to prospective success. We also confront the dataset's strongest evidence for descent: the conserved single-copy core recovers the accepted species topology, and structural-variant abundance tracks phylogenetic branch length. We argue that these findings are compatible with genuine descent within created kinds and hierarchical template reuse between them, whereas the concentration of functional continuity in a small conserved core surrounded by sharply lineage-specific architecture is predicted more directly by bounded diversity. We conclude with falsifiable tests requiring future Y assemblies to distinguish boundary-associated discontinuity from variation explained solely by time, demography and reproductive biology.

Keywords: *Y chromosome, male-specific region, palindromes, ampliconic regions, telomere-to-telomere assembly, structural variants, evolution, baraminology, bounded diversity, created kinds, hierarchical template reuse, comparative genomics*

1. Introduction

The Y chromosome occupies a peculiar and valuable position in comparative genomics. Because most of its length does not recombine, it is inherited as a single linked block down the paternal line, which makes its structure an unusually direct record of what has happened to a lineage over time. For the same reason it has proven difficult to sequence, and until recently its most repetitive regions were routinely omitted from the reference assemblies on which comparative claims were built. That gap has now closed. The finished chimpanzee male-specific region (Hughes et al., 2010), the complete telomere-to-telomere human Y chromosome (Rhie et al., 2023), and, most comprehensively, the gapless telomere-to-telomere assemblies of the X and Y chromosomes of five great apes and one lesser ape (Makova et al., 2024) allow the male-specific region to be compared across species at complete resolution for the first time. The internal architecture of that region, its discrete sequence classes, its massive palindromes, and its ampliconic gene families, was first mapped in the finished human sequence by Skaletsky et al. (2003), and it is against that architecture that the new cross-species comparisons are measured.

This paper asks a simple question of those data. Under the hypothesis that humans and the great apes descend from a common ancestor within the last several million years, what should the Y chromosome look like, and does it look that way? We argue that the prediction is clear, that the observations depart from it sharply and in a consistent direction, and that the pattern of the departure, discontinuity between groups with continuity inside them, is what a model of bounded diversity within created kinds would anticipate. We are careful throughout to keep two questions apart: which observations are merely compatible with a model, and which observations actually discriminate between the two models on offer. Compatibility is cheap, because a sufficiently flexible framework can absorb almost anything after the fact. Discrimination is what a serious test requires, and it is the standard we hold both models to here.

2. The Standard Expectation

The mammalian sex chromosomes are thought to have arisen from an ordinary autosomal pair, with the Y progressively losing the ability to recombine with the X and, over long spans of time, contracting and shedding genes (Graves, 2006). On this account the human Y and the chimpanzee Y are two lightly modified copies of a single ancestral Y that existed in a shared ancestor roughly six to seven million years ago. The expectation that follows is straightforward. The autosomes and the X chromosome of humans and chimpanzees align across essentially their whole lengths and differ at only about one percent of aligned nucleotide positions. A Y chromosome inherited from the same recent ancestor should, on the same reasoning, be highly alignable, should preserve the same running order of its sequence classes, and should retain the palindromes that the theory itself invokes as a conservation mechanism.

If divergence time alone dominated structural conservation, the much greater architectural disruption of the Y relative to the X would be unexpected. Because the Y differs substantially from the X in recombination, repeat content, and selective dynamics, however, the relevant question is not merely whether the Y is free to diverge faster, but whether known Y-specific processes quantitatively account for the observed magnitude and pattern of that divergence. That is the question the completed assemblies now let us press, and it is the question we hold the standard account to in Section 4.

Palindromes are long inverted repeats whose two arms undergo gene conversion, a process understood to protect the non-recombining Y from mutational decay by allowing one arm to correct the other (Rozen et al., 2003). A structure actively maintained by selection over tens of millions of years is, by hypothesis, exactly the kind of feature one expects to find conserved across closely related species. A further and more general expectation is nested hierarchy: common descent predicts that similarity should be distributed in a tree-like pattern, with the Y chromosomes of more closely related species resembling one another more than either resembles a more distant relative, and with that pattern agreeing across independent regions of the chromosome. These are the benchmarks against which the completed assemblies can now be measured.

3. What the Complete Assemblies Revealed

Four features of the finished assemblies bear directly on the expectations set out above. In each case we give the mainstream measurement and the mainstream description, then return in later sections to what the pattern means.

3.1 Size instability and low alignability

Across the six apes sequenced by Makova et al. (2024), the Y chromosome ranged in size from 30 Mb in siamang to 68 Mb in the Sumatran orangutan, and differed by as much as 19 Mb between the two orangutan species and 11 Mb between bonobo and chimpanzee. The X chromosome, over the same set of species, ranged only from 154 Mb to 178 Mb and differed by just 1.5 Mb between the two orangutans and 6.3 Mb between bonobo and chimpanzee.

The contrast in alignability is sharper still. Only 14 to 27 percent of the human Y chromosome was covered by alignments to the Y chromosomes of the other apes, whereas 93 to 98 percent of the human X chromosome aligned to the other ape X chromosomes. Even between closely related species the pattern held: 60 to 87 percent of the Y aligned, against more than 95 percent of the X. The chromosome inherited as a single unbroken block down the male line is the one that has become almost unalignable between genera.

3.2 Structural saturation

Where sequence did align between species, the Y was found to be structurally reorganized almost in its entirety, and the precise denominator matters. Among the Y bases located in sequences that exhibit interspecies variation, roughly 99 percent were affected by large-scale structural variants, compared with 83 to 86 percent on the X. This is not a claim that 99 percent of the whole aligned Y has been rearranged; it is a statement about the sequences carrying interspecies variation, and stated that way it is unassailable. Inversions and insertions were about eightfold and threefold longer on the Y than on the X, and structural variants accumulated at 15.8 per Mb per million years on the Y against 6.1 on the X. The nucleotide-level divergence between human and chimpanzee was 2.68 percent on the Y and 0.97 percent on the X, with an eleven percent acceleration of substitution in the *Pan* lineage and a roughly nine percent slowdown in the *Pongo* lineage. Segmental duplications made up 22.8 to 55.9 percent of the non-human ape Y chromosomes but only 4.0 to 7.2 percent of the X chromosomes, and repetitive elements filled 71 to 85 percent of the Y against 53 percent of the human autosomes. The earlier chimpanzee assembly had already signaled the trend: the chimpanzee male-specific region carries roughly twice as many massive palindromes as the human, its ampliconic regions are about 44 percent larger, and it has lost large fractions of the protein-coding genes and gene families that the standard account assigns to the last common ancestor (Hughes et al., 2010).

3.3 Non-conservation of palindromes and ampliconic regions

This is the observation that speaks most directly to the standard expectation, because here, and here almost alone, the evolutionary theory made a specific prediction in advance. Palindromes on the X chromosome behaved as conservation theory expects: 21, 12, and 9 homologous palindrome clusters were shared among the African great apes, among all great apes, and among all species analyzed, respectively. Palindromes on the Y chromosome did the opposite. The corresponding counts were 2, 1, and 0. Ampliconic homology on the Y could be detected only between pairs of closely related species, and even those shared regions differed in organization. The authors state the result against their own prior expectation without hedging: they expected the Y palindromes to be conserved and instead found many of them to be lineage-specific. A structure whose entire theoretical rationale is long-term maintenance by gene conversion turns out, on the Y, not to be maintained across the tree at all.

The prior expectation was not vague. Rozen et al. (2003) had shown by comparative sequencing in the great apes that at least six of the human male-specific palindromes predate the divergence of the human and chimpanzee lineages, and Cechova et al. (2020), in their analysis of great ape Y chromosomes, inferred that the great-ape ancestor already carried substantial multi-copy sequence homologous to many present human and chimpanzee palindromes. The forecast that followed was therefore concrete: a shared, conserved palindrome architecture should be recoverable across the apes, maintained by the very gene-conversion mechanism the theory names. The strict, complete-assembly analysis of Makova et al. (2024) recovers very few conserved complete palindrome clusters. Earlier work inferred homologous ancestral sequence associated with multiple palindromes; the finished data find almost none conserved across the tree. That is not a softening of the result but a sharpening of it: the expectation was stated, it was specific, and the complete sequences overturned it. It takes its place in a growing list of forecasts the standard account has had to absorb after the event rather than anticipate.

3.4 Centromere discontinuity

The centromere told a parallel story. The X chromosome centromere holds a stable chromosomal position across primates and is flanked by ordered vestigial layers, the degraded remnants of older centromeres, in every ape examined. The Y chromosome centromere shifts position between lineages and is, in the authors' own word, naked, lacking those flanking layers. In human and *Pan* the Y centromere is built from an older alpha-satellite family than the one active on the X, a lagging arrangement not seen in the other apes, and it lacks the protein-binding motifs present in, for example, the gorilla Y centromere. The most conserved landmark of the X has no stable counterpart on the Y.

4. Description, Mechanism, and the Limits of the Standard Account

The standard account supplies genuine mechanisms to account for such discrepancies, including probable loss of recombination leading to mutational decay, genetic hitchhiking in the absence of crossing over, ectopic recombination within the male-specific region, male mutation bias, and selection driven by sperm competition, and it attaches quantities to several of them, including the structural-variant accumulation rates and substitution rates cited above. Although these mechanisms are independently documented as operating on the Y chromosome, no study has ever combined them into a rate-constrained model that reproduces the specific architecture observed, and comparable studies of other rapidly diverging non-recombining chromosomes report the same gap between documented mechanism and demonstrated sufficiency.

A further caution belongs precisely here. The figure most often cited for the pace of that architectural change, 15.8 structural variants per megabase per million years, is not a directly observed, per-generation mutation rate measured through real-time transmission. It is calculated from inferred evolutionary branch lengths and assumed divergence times, so it already presupposes the chronology under examination rather than measuring change independently of it. Quoting it as though it were a measured Y-chromosome mutation rate mistakes an evolutionary inference for an observation.

The mechanisms above, loss of recombination, hitchhiking, ectopic recombination, mutation bias, and sperm competition, were for the most part available to explain rapid divergence, greater or smaller gene loss, more or fewer palindromes, and either conservation or non-conservation, depending on what the data turned out to be. The distinction between accommodation and prediction is what matters here. A model earns credit when it forecasts a result in advance and the result arrives; it earns much less when it supplies, after the fact, a set of processes flexible enough to absorb whatever was found. We do not claim that every evolutionary explanation is post hoc; some predictions are made and confirmed. But most of the mechanisms marshalled for the Y are of the accommodating kind, and the one place the framework did commit itself in advance, the expectation that gene-converting palindromes would be conserved across related species, is the place where Section 3.3 shows it was wrong. That failure is not isolated. Like most evolutionary predictions that fail, it is quietly folded into the model as one more thing the theory can, in retrospect, accommodate, and it is added to a lengthening list. When the successful part of an account is largely retrodictive and its clearest advance commitment fails, the honest verdict is not that the account explains the data but that it has been fitted to them.

5. Why a Design Model Expects Both Similarity and Discontinuity

A reading that accounted only for discontinuity would be as incomplete as one that accounted only for similarity. The bounded-diversity model advanced here predicts both, and it predicts them from a single principle: sequence should be shared in proportion to shared function. Structures that carry out the same primary task are expected to be built from the same or closely similar sequence, while sequence should diverge where the secondary tasks, the ones that distinguish one kind from another, diverge.

This is not a recent or improvised claim. Before genome sequencing existed, Henry Morris argued that a common designer would reuse similar structures for similar functions and supply different structures for different functions, so that living things would be found to share pervasive similarity in their underlying code (Morris, 1975). That expectation extended an older tradition. Linnaeus held that the biblical kinds would fall into natural, bounded groups (Linnaeus, 1758), a boundary that sits naturally within a creation framework. Richard Owen attributed the shared vertebrate blueprint to a common archetype rather than to descent, and framed anatomical resemblance as similarity due to common design (Owen, 1849), a phrase Darwin later recast as similarity due to common descent. The nested pattern that both models now claim as their own was therefore predicted first on design grounds, in the underlying code by Morris and in comparative anatomy by Owen, before it was read into an ancestral narrative. We develop that historical priority, and score it formally against the evolutionary record, in a companion study (Nailor and Budinsky, 2026). It is on that basis that we are prepared to write, for the observations that follow, that the pattern favors bounded diversity over common descent rather than merely tolerating it.

Read through this principle, the widely cited figure of roughly ninety-nine percent identity between the human and chimpanzee genomes is not an embarrassment to be folded into an ancestral narrative but a direct prediction of common functional design. That figure refers to nucleotide identity within alignable orthologous sequence, not to whole-genome identity once every structural insertion, deletion, duplication, and unalignable region is included. Understood correctly, it says that where the same biology is being specified, the same sequence specifies it, which is exactly what shared function predicts. Two organisms that share most of their biology should share most of their code, because that code is doing most of the same work in both. The sharper half of the test is the case in which similarity of form runs against the molecular tree, because the resemblance cannot be a straightforward record of ancestry. A striking recent example comes from outside the primates. Another shocking find for the evolutionary community was that amphipods have genes also found in silkworms. Brittany Cummings of the Florida Museum of Natural History, has pieced together a family tree revealing that this group all must have developed silk independently multiple times. Siena McKim of the University of California, Santa Barbara, discovered that at least one amphipod species produces this fiber with some of the same genes as silkworms. Even silk biologists who attended McKim's talk were surprised. *"I didn't know that crustaceans were capable of making silk,"* says Angela Alicea-Serrano, a University of Akron postdoc who studies spider silk, McKim focused on just the silk producers, comparing the active genes in the one or two sets of their legs that make silk with their many pairs without silk glands. Two active genes from the silkmaking amphipod legs are found in silkworms, she reported. The finding *"leads us to believe they are using very similar genes as the moths,"* she said at the meeting. But why and how those similar genes arose, it's unlikely they date back to a common ancestor, "is what keeps me up at night" (Pennisi, 2024). In cases of this kind similarity of form is decoupled from the molecular hierarchy, which is a genuine difficulty for the assumption that similarity of structure is a record of ancestry. The discontinuity half of the prediction is carried by the other side of Morris's statement, different structures for different functions. If kinds are bounded, each should carry features and sequences that serve requirements unique to it, and these should appear as sharp, unbridged distinctions rather than as gradients. The genome supplies exactly this in the form of taxonomically restricted genes, often called orphan genes, which have no detectable counterpart outside a given group and resist derivation from any shared ancestral sequence. Human biology adds a lengthening catalog of lineage-restricted features, from regulatory change concentrated in the promoters of neural and nutritional genes (Haygood et al., 2007) onward. These are the observations a bounded-diversity model leads one to seek, and their steady accumulation is the discontinuity counterpart to the shared functional core. The Y chromosome, the subject of this paper, is this same logic carried to its extreme. Its conserved single-copy genes are the shared functional core, retained because they perform the same essential work across the apes, while its lineage-specific ampliconic and palindromic architecture is the divergent, kind-distinguishing component built out to species-appropriate designs. The two-part signature documented in Section 3, a conserved core inside a structurally discontinuous chromosome, is the whole design principle in miniature, which is the interpretation we now set out directly.

6. A Bounded-Diversity Interpretation

The completed assemblies carry a two-part signature that is easy to state. Between genera, the Y chromosome is discontinuous to the point of near non-alignability, saturated with structural change, and stripped of shared architecture. Within a genus, by contrast, the Y is orderly: chimpanzee and bonobo, or the two orangutans, share higher-order centromeric repeats, share some palindromes, and align across most of their length. Continuity is tight inside groups and collapses between them.

This is the signature that a model of bounded diversity within created kinds leads one to expect. On that model, variation within a kind is real, sometimes rapid, and often substantial, while the boundaries between kinds are genuine discontinuities rather than gradients waiting to be filled by better sampling. The Y chromosome is precisely where such boundaries should show most starkly, because it does not recombine and is transmitted as a single linked block, so that whatever distinguishes one kind from another is preserved on it without being averaged away. Read this way, the within-genus order reflects diversification inside a kind, and the between-genus discontinuity reflects a boundary that was there from the start. The functional multi-copy families that dominate the ampliconic regions, most of them dedicated to spermatogenesis, appear as purpose-built systems arranged in species-appropriate architectures, and the conserved single-copy toolkit appears as shared design for shared male physiology rather than as inherited residue.

7. The Strongest Common-Descent Evidence in the Same Dataset

A paper that pressed only the anomalies and hid its own difficulty would not be worth publishing. So before we defend our reading, we state the opposing case at its strongest, drawn not from a rival study but from the very dataset we have been citing. Five results in Makova et al. (2024) and its antecedents make up the most serious evidence for common descent on the Y chromosome, and we set them out without softening.

First, a phylogenetic analysis of the multi-species Y-chromosome alignments recovers the expected ape species topology, as the parallel analysis of the X chromosome does. The surviving alignable Y sequence, in other words, reconstructs the standard tree.

Second, the abundance of structural variants correlates positively with phylogenetic branch length. The Y accumulates them far faster than the X, at 15.8 against 6.1 per megabase per million years, but the accumulation still tracks the branches of the accepted tree rather than scattering at random.

Third, closely related species share more Y architecture than distant ones. Chimpanzee and bonobo, and the two orangutans, share palindromes, ampliconic organization, and higher-order centromeric repeats that are not shared across genera. Similarity falls off with phylogenetic distance, which is what descent predicts.

Fourth, ten single-copy ancestral Y genes are present across all the apes studied, and nine of the thirteen ancestral genes tested show signatures of purifying selection (Makova et al., 2024). A conserved, selected, single-copy toolkit persists on an otherwise volatile chromosome.

Fifth, earlier comparative work inferred that the great-ape ancestor already possessed multi-copy sequence homologous to many present human and chimpanzee palindromes (Rozen et al., 2003; Cechova et al., 2020), which is the pattern a single inherited ancestral Y would produce.

Stated together, these are not trivial. The conserved core does look tree-like, and its branching order is the single strongest line of evidence of common descent musters on this chromosome. A design reading expected this prior based on common design but with one caveat, genetic boundaries between kinds. What bounded diversity predicts differently is not the absence of this signal but its confinement. To read more about where these boundaries fall specifically, be sure to read the papers titled: One Ancestral Hominin Lineage Across Modern and Archaic Homo: A Creation-Model Test of a Recent Bottleneck and a companion study titled: Backward Through the Family Tree: Echoes of Creation (Nailor M., 2026).

In our model the tree-like signal should be real and strong exactly where function is shared and sequence is conserved and linked, and it should fail more to extend into the surrounding architecture, which is precisely what the same dataset shows: a small, constrained, completely linked core that recovers the tree, embedded in a chromosome that is otherwise the least alignable and least architecturally conserved yet sequenced. Common descent expects the tree-like signal and the shared architecture to reconcile, in the end, to one history. Yet conflicting trees are obtained when different regions are compared and when homology is added it gets even worse. Bounded diversity expects the conserved core to be tree-like and the architecture to remain discontinuous no matter how densely the tree is sampled. The dataset already leans the second way. Section 8 states the mechanism by which a design model produces a tree-like conserved core in the first place, so that this evidence is answered rather than merely absorbed.

8. What a Design Reading Must Itself Explain

The bounded-diversity interpretation carries a genuine explanatory debt, and it lies in the conserved, alignable Y-chromosome core documented in Section 3. Nucleotide differences within that core can reproduce the accepted ape hierarchy, including differences at positions that are not obviously constrained by protein function. Common functional design explains why the same indispensable genes are present, but the mere statement that organisms share a function does not, by itself, explain why weakly constrained sequence differences fall into a particular nested order. Neither does degradation over time. Degradation can explain the accumulation of differences, gene loss, pseudogenization, and architectural breakdown; by itself, it does not explain why those differences should be ordered as (((*Pan*, *Homo*), *Gorilla*), *Pongo*). The distinction must be stated plainly: **degradation explains change after origin; it does not specify the relationships among the starting designs.**

An important methodological qualification must first be made. The chromosome-wide analysis reported by Makova et al. (2024) was not a topology-blind discovery of the ape tree. For their seven-species whole-chromosome alignments, the investigators explicitly supplied the aligner Cactus with a guide tree of the accepted ape topology, grouping bonobo with chimpanzee, then human, then gorilla, then the two orangutans, with the gibbon as outgroup, after which Phylofit was used to estimate substitution rates from alignment blocks containing all seven species. Supplying a guide tree is a legitimate and conventional procedure when the purpose is alignment and branch-length estimation. It does mean, however, that the resulting figure cannot simultaneously be treated as an independent discovery of the topology that the analysis was given. The correct conclusion is narrower: the surviving multi-species-alignable Y sequence is compatible with the accepted topology and permits branch lengths to be fitted upon it. Separate, unconstrained gene-tree analyses remain relevant evidence, but they must not be conflated with an analysis conditioned on a prespecified guide tree.

A second qualification concerns statistical independence. Outside the pseudoautosomal regions, the Y chromosome is transmitted as one largely non-recombining paternal unit. Consequently, its nucleotide positions are not thousands of independent genealogical witnesses; they are linked characters carried on substantially the same paternal genealogy. Wilson Sayres et al. (2014) emphasized that because recombination is absent across most of the Y, selection acting at one site can influence linked neutral variation elsewhere on the chromosome. A topology recovered from many linked sites can be strongly supported as a Y-chromosome gene tree, but it is still one linked genealogical history rather than thousands of independent histories. Agreement between that paternal tree and the accepted species tree is real evidence for common descent, but its evidential weight should not be inflated by counting every linked nucleotide as a separate confirmation.

The distinction between a gene tree and a species tree is not a creationist invention. Mainstream great-ape genomics already recognizes that different genomic regions need not reproduce the same species topology. Scally et al. (2012), for example, found that in approximately 30 percent of the gorilla genome, the gorilla sequence is closer to either human or chimpanzee than human and chimpanzee are to one another, as expected under incomplete lineage sorting. More recent primate-wide work has found still higher proportions of discordant local genealogies at some ancestral nodes.

Makova et al. (2024) found ten ancestral Y genes in all the apes studied and evidence of purifying selection in nine of the thirteen ancestral genes tested. Bellott et al. (2014) independently identified the persistent mammalian Y genes as widely expressed, dosage-sensitive regulators. Moreover, the chromosome-wide substitution analysis necessarily used multi-species alignment blocks containing all seven taxa. This procedure conditions the analysis on the minority of Y sequences conserved sufficiently to remain alignable while excluding most of the lineage-specific, repetitive, and structurally transformed chromosome. Some positions within those blocks may indeed be nearly neutral, and selection cannot explain the particular identity of every such base. Nevertheless, these sites are embedded within a highly constrained, completely linked functional core; they are neither an independent sample of the whole Y chromosome nor representative of its overwhelmingly lineage-restricted architecture.

8.1 The Direct Created-Design Explanation

The created-design model advanced here requires three distinct historical components: **descent within created boundaries, hierarchical reuse between created boundaries, and post-origin mutation within every lineage.** Collapsing all three into a single undifferentiated appeal to degradation is the mistake this account is built to avoid.

First, bounded diversity does not deny descent. It predicts genuine descent, mutation, segregation, selection, and lineage sorting within a created kind. Under the provisional boundaries examined in this paper, the close neutral-site grouping of chimpanzee with bonobo and of the two orangutans is therefore expected to represent actual inherited history within *Pan* and *Pongo*. These are not cases in which common design must imitate genealogy; they are genealogies within bounded groups.

Second, the deeper cross-genus hierarchy is attributed to **hierarchical template reuse** rather than to independent convergence of thousands of mutations. On this model, the ancestral single-copy Y modules were instantiated as related sequence families across separately bounded designs. Reuse of a genomic module would transmit not only its indispensable amino-acid residues but also its regulatory context, synonymous positions, intronic organization, and incidental sequence features. A designed system does not require every nucleotide to have been independently optimized or assigned an individual function. When an entire module is reused, functionally indifferent details can be carried with it as properties of that module. Thus, a shared nearly neutral state need not be explained as the same mutation occurring independently in multiple lineages; it may instead be part of the shared starting template from which those lineages began.

This proposal directly predicts hierarchical similarity in the conserved functional core. Taxa sharing more of the foundational organismal plan should receive more closely related versions of the same core modules, whereas secondary reproductive architecture can be kind-specific. A tree-building algorithm measures nested covariance among characters; it does not identify the historical cause of that covariance. The same mathematical hierarchy can therefore summarize either material transmission through an ancestral population or hierarchical transmission from reused design templates. Sequence similarity alone does not bear a label declaring which of those two histories produced it.

Third, post-origin mutation, selection, gene conversion, loss, and degradation operate upon those starting templates. They explain terminal substitutions, lineage-specific accelerations, pseudogenization, copy-number change, and the progressive destruction or reconstruction of Y architecture. This avoids the false claim that degradation somehow generates the deeper topology. **The initial template hierarchy explains the ordering; subsequent descent and degradation explain the accumulating branch-specific differences.**

Common descent retains a genuine parsimony advantage for confidently identified neutral synapomorphies: one mutation inherited from a biological ancestor is ordinarily a simpler explanation than independently assigning the same state to several created genomes.

That evidence should be acknowledged rather than concealed. But parsimony must be applied to the entire chromosome, not only to the fraction most favorable to descent. Only 14 to 27 percent of the human Y aligns with the Y chromosomes of the other apes; among sequences exhibiting interspecies variation, approximately 99 percent of Y bases are affected by large structural variants; Y ampliconic homology is largely restricted to close species pairs; and no palindrome cluster was shared across all seven species examined. Common descent gains evidential credit from the conserved nucleotide core, but it simultaneously assumes the burden of producing the enormous architectural discontinuity surrounding that core within its proposed divergence times. It cannot count the core topology as decisive evidence and then exempt the majority of the chromosome from the same historical scrutiny by applying the label rapid evolution.

8.2 A Testable Distinction

Hierarchical design must not be used as an unlimited rescue device. Created-boundary assignments must be specified independently of the Y-chromosome result, and the two models should be tested across different character classes without supplying the expected topology in advance. Topology-blind analyses should separately examine conserved coding sequence, introns, putatively neutral intergenic sequence, shared insertional characters, gene content, palindromes, ampliconic organization, satellites, centromeres, and large structural variants.

The bounded-diversity model predicts strong genealogical continuity within proposed kinds but a persistent dissociation between the cross-kind conserved core and the surrounding architecture. Increased sampling within *Pan* and *Pongo* should reveal intermediates and shared organization, whereas additional genera should not progressively fill the between-genus architectural gaps. By contrast, abundant, confidently neutral, orthologous cross-kind characters that independently recover the same topology across numerous unlinked partitions, especially if accompanied by a rate-constrained series of intermediate structural states, would weigh against the bounded-design interpretation. Persistent confinement of the shared topology to a small, functionally constrained, linked core, combined with saturating discontinuity in the rest of the chromosome, would favor the model advanced here.

The result is not that the neutral-site hierarchy has been explained away. It is that its proper evidential scope has been defined and a direct design mechanism has been stated. The conserved core is positive evidence for common descent, but it is neither topology-blind in every cited analysis, statistically independent across its linked sites, nor representative of the entire Y chromosome. The created-design account answers it through real descent within kinds and hierarchical template reuse between kinds, with degradation confined to its proper role as a cause of later divergence.

The standard model explains the tree naturally but must quantify the architectural catastrophe; the design model explains the architectural boundaries naturally but must test its proposed template hierarchy. The decisive model will be the one that explains both without protecting its weakest evidence from prospective testing.

9. A Model-Comparison Framework

The preceding sections make a claim that is easy to assert and easy to abuse, namely that the data favor one model over the other. To keep that claim honest, we set the two frameworks side by side on each observation and ask, of each, not merely whether it is compatible with a model but whether it discriminates between them. Compatibility is weak currency, since a flexible framework can accommodate almost anything after the event. Discrimination is what decides questions.

The table below separates the two.

Observation	Prediction under common descent / Y evolution	Prediction under bounded diversity	Observed	Discriminating?
Y alignability	Declines with divergence; lower than X	High within kind, sharp fall across boundary	14 to 27 percent (human to other ape)	Potentially, but needs time correction
Y palindrome conservation	Some preservation expected from gene conversion	Architecture may be kind-specific	Much lower than expected	Discriminating: Yes.
Y topology	Expected species topology	Expected topology within kinds	Expected topology recovered	Discriminating: Yes. Favors design unless explained
Long-term Y-chromosome trajectory	Prevailing models predicted that gene loss would slow and ancient Y chromosomes would approach gene-poor evolutionary stasis	Distinct Y chromosomes may retain essential function while exhibiting sharp structural and gene-content discontinuities across the human–ape boundary	Human and chimpanzee Y chromosomes differ radically in structure and gene content; the chimpanzee Y contains twice as many massive palindromes and has lost large fractions of ancestral protein-coding genes and gene families (Hughes et al., 2010)	Contradicts the former evolutionary stasis model and predictions made. It is consistent with bounded discontinuity of the creation model but retrofitted into the evolutionary model. Favored design unless explained.
Close-relative ampliconic sharing	Expected	Expected within kind	Observed	Non-discriminating
Conserved Y ancestral genes	Expected	Expected shared function	Observed	Weakly discriminating
Age inferred from palindrome identity	Approximately 99.97% identity between palindrome arms was interpreted by molecular-clock reasoning as evidence that they originated only about 100,000–200,000 years ago	High identity could persist through a maintenance or homogenization mechanism and therefore need not indicate recent duplication	At least six palindromes were subsequently found to predate the proposed human–chimpanzee divergence; recurrent Y–Y gene conversion maintains their identity (Rozen et al., 2003)	Directly falsifies the original molecular-clock inference, but gene conversion is invoked to explain the result within evolutionary theory, another retrodiction and failed prediction. Discriminating - Yes
Human Y nucleotide diversity	A simple neutral model with equal male and female effective population sizes predicts Y diversity equal to one-quarter of autosomal diversity	Recent paternal ancestry, bottlenecks and strong functional constraint predict unusually low human Y diversity	Normalized Y diversity was approximately an order of magnitude below the one-quarter neutral expectation; demography alone could not explain it (Wilson Sayres et al., 2014)	Discriminating: Yes. Rejects the original simple neutral prediction; evolutionary models now invoke chromosome-wide linked selection can explain it.
Survival of ancestral Y genes	Mathematical degeneration models commonly treated ancestral Y genes as approximately equally likely to survive	Functionally indispensable, dosage-sensitive genes should be preferentially preserved	Survival was strongly nonrandom: retained genes are disproportionately broadly expressed, dosage-sensitive regulators of transcription, translation and protein stability (Bellott et al., 2014)	Weakly discriminating: Rejects random-survival decay models; consistent with both functional constraint under evolution and a function-centered bounded model.
Y gene-content hierarchy	Under a simple vertical-descent expectation, human Y gene content should resemble chimpanzee more than gorilla because humans and chimpanzees share the more recent inferred ancestor	Different lineages need not form the same nested hierarchy for every structural or gene-content character. Hierarchy is formed based on gene function.	Human Y gene content is more similar to gorilla than to chimpanzee; accelerated gene loss in the chimpanzee–bonobo lineage produced the discordance (Cechova et al., 2020)	Weakly discriminating: contradicts the simple gene-content hierarchy, but differential gene loss explains it under common descent

Read down the final column, the observations sort into three classes, and the sorting is the argument. Two of the rows are effectively non-discriminating. The conserved single-copy ancestral genes and the sharing of ampliconic architecture between close relatives are expected under both models, because both a shared designer working from a shared functional toolkit and a shared ancestor transmitting one predict that the same essential genes will be present and that near relatives will resemble one another. These rows are real data, but they do not decide anything, and a model-comparison that leaned on them would be leaning on weight that both pans of the balance already carry.

Two of the rows presently favor common descent, and we say so plainly. The recovery of the expected species topology by the conserved core, and the positive relationship between structural-variant abundance and branch length, are what an inherited single ancestral Y would produce. These are the rows a design reading must answer rather than dismiss, and Section 8 answers them: the topology is recovered from a small, completely linked, functionally constrained core rather than from thousands of independent partitions; in the chromosome-wide analysis it was recovered under a supplied guide tree rather than discovered blind; and hierarchical template reuse produces a tree-like conserved core without a single material ancestor, while confining that signal to exactly the region where the data confine it. The favorable rows are therefore favorable conditionally, unless explained, and the explanation is on the table.

One row, the decisive one, favors bounded diversity, and it does so because it is the single place the standard framework staked a prediction in advance and lost. Gene conversion was expected to conserve the Y palindromes across the apes; the finished assemblies found them overwhelmingly lineage-specific, with the shared-cluster counts collapsing from 21, 12, and 9 on the X to 2, 1, and 0 on the Y. A model is tested where it commits, not where it accommodates, and on the one Y-chromosome observation where the standard account committed, it was wrong in the direction bounded diversity anticipates. The remaining row, alignability, points the same way, sharp continuity within groups and collapse between them, but its full evidential force awaits a correction for divergence time, which is why we mark it discriminating in principle rather than settled.

The framework yields a clear reading. The observations that discriminate do not divide evenly. The pro-descent rows are conditional and answerable, and their strongest member rests on a topology supplied to the analysis rather than discovered by it. The pro-design row rests on a failed advance prediction, which is the strongest kind of evidence there is. That is why we are willing to write, without overstatement, that the Y chromosome as a whole is read more naturally as bounded diversity within created kinds than as the graded residue of common ancestry.

10. Predictions and Discriminating Tests

The two frameworks make divergent forecasts that further data can adjudicate, and we state ours so that they can be held against the record as more genomes are finished.

First, on sampling. A bounded-diversity model predicts that adding more species within a genus will leave within-genus Y comparisons highly alignable and architecture-sharing, while adding more genera will leave between-genus comparisons saturated no matter how densely the tree is sampled. Common descent predicts that improved sampling should begin to fill the structural gap with intermediates. The direction of change as the ape Y catalog grows is therefore a live test.

Second, on reconstruction. If the human and chimpanzee Y descend from a single ancestral Y, it should be possible to reconstruct a plausible ancestral hominin Y and a stepwise mutational path from it to each descendant that preserves male fertility at every intermediate stage. Producing such a reconstruction, with the gene-content changes and structural rearrangements ordered and rate-constrained, would materially strengthen the descent account. Its continued absence, given finished assemblies on both ends, is itself informative.

Third, on concordance. A design reading predicts a specific dissociation: the functionally constrained single-copy core should look tree-like, because it is a shared toolkit, while the unconstrained architecture, palindromes, ampliconic layout, satellite content, and centromere structure, should not resolve to one consistent history. Descent predicts that both should ultimately reconcile to a single tree. Measuring topological concordance between the conserved core and the structural component, region by region and across unlinked partitions, is a test that current assemblies already make possible.

11. Conclusion

Common descent predicts that the Y chromosome, inherited from a recent shared ancestor, should be broadly alignable, architecturally conserved, and tree-like across independent regions. The finished assemblies show a chromosome that is nearly unalignable between genera, saturated with structural change, and stripped of the very palindromes the theory named as its conservation mechanism. That last point is the hinge of the paper. In the one place the standard framework committed itself in advance, expecting gene conversion to conserve the Y palindromes across related species, the data overturned the prediction outright, and the shared-palindrome counts fell from 21, 12, and 9 on the X to 2, 1, and 0 on the Y. Within genera, by contrast, the Y chromosome is orderly and shared. Most Y palindromes were species-specific or confined to the closest relatives. This is not an expectation imposed on the study by its critics; it is the expectation stated by the investigators themselves and overturned by their own results. This two-part signature, discontinuity between groups with continuity inside them, is the signature that bounded diversity within created kinds anticipates, and the non-recombining Y is exactly where it should appear most sharply. Makova et al. (2024) explicitly stated that they expected Y palindromes to be conserved. The completed assemblies produced the opposite result, giving evolution another failed prediction and falsification of the theory that never results in anything, validating that evolution theory is unfalsifiable on every level. Significantly, the same analysis reported no evidence of species-specific positive selection on the Y ampliconic gene families that would directly account for the unexpected palindrome distribution.

The broader record reinforces this pattern of failed simple expectations followed by model revision. Continuing gene attrition was once extrapolated to predict the disappearance of the human Y within approximately 5–10 million years, whereas other accounts expected ancient Y chromosomes to settle into gene-poor stasis. Comparative sequencing supported neither universal trajectory. Gene loss in the older human Y strata evidently ceased more than 25 million evolutionary years ago, and the rhesus Y lost no older ancestral genes during the same inferred interval; yet the chimpanzee Y underwent extensive structural renovation and lost large fractions of ancestral protein-coding genes and gene families. Likewise, 99.97% identity between palindrome arms was initially interpreted through molecular-clock reasoning as evidence of duplication only 100,000–200,000 years ago, but comparative sequencing showed that at least six of those palindromes predated the proposed human–chimpanzee divergence. Gene conversion was then required to explain why molecular-clock identity had produced the wrong age.

Human Y diversity supplies another failed quantitative expectation. Under the simple neutral model, Y nucleotide diversity should equal approximately one-quarter of autosomal diversity. Instead, normalized Y diversity was approximately an order of magnitude below that expectation, and sex-biased demography alone could not reproduce the complete genomic pattern. Chromosome-wide linked selection was required. The surviving ancestral genes were also not the approximately random remnants assumed by some mathematical degeneration models. They proved to be a strongly nonrandom set enriched for broadly expressed, dosage-sensitive regulators of transcription, translation and protein stability. Even gene-content similarity did not reproduce the simplest species-tree expectation: human Y gene content is more similar to gorilla than to chimpanzee, despite the proposed more recent human–chimpanzee common ancestor. Differential loss in the chimpanzee–bonobo lineage can explain that discordance, but once again the explanation followed an unexpected result.

The bounded diversity offers a unified interpretation of the complete pattern: preservation of an indispensable functional core, strong purifying constraint on dosage-sensitive genes, very low diversity within the human paternal lineage, relative architectural continuity among the closest groups and abrupt loss of alignability, palindrome homology and ampliconic organization across larger boundaries. Under this reading, shared genes reflect shared biological requirements, while the chromosome-scale systems surrounding them are lineage-specific implementations. The conserved core and the discontinuous architecture are therefore not competing facts requiring opposite explanations; they are the two complementary components the model expects—shared function and bounded structural realization.

The decisive issue is not whether common descent can be expanded to accommodate every observation. With invoking combinations of different mechanisms evolution can explain anything, but that is not good science anymore. Anyone can retrofit the data after it comes in, its predictions that matter. The decisive issue is which model exposes itself to risky prediction before the next assemblies are examined. Bounded diversity predicts that additional sampling will continue to reveal substantially greater Y alignability and architectural sharing within independently specified biological boundaries than across them, even after divergence time, mutation rate, effective population size and mating system are controlled. It further predicts that essential single-copy functions will remain conserved while palindrome and ampliconic architectures remain sharply lineage-specific. Conversely, if additional complete Y chromosomes produce a smooth relationship between structural divergence and elapsed time, recover the same nested hierarchy across independently defined neutral and functional compartments, and erase the proposed within-boundary versus between-boundary discontinuity, the bounded model will be weakened or falsified.

The present evidence therefore does more than reveal that the Y chromosome varies rapidly. It reveals where continuity resides and where it stops. The standard framework successfully anticipated the conserved topology of the alignable core, but its explicit expectation of cross-species Y-palindrome conservation failed in the very dataset capable of testing it. Bounded diversity accommodates both the conserved core and the architectural discontinuity as parts of the same biological pattern based on function. When explanatory flexibility is separated from prospective success, the model presently offering the more coherent account of the complete Y chromosome is the biblical creation bounded diversity model.

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