

Are Lizards Observed Evolving Live Birth?

What Direct Observation Shows, What Historical Inference Adds, and Why the Evidence Favors Designed Adaptability

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ABSTRACT

The claim that lizards are being observed evolving live birth is stronger in rhetoric than it is in evidence. Direct observation establishes that living squamates display egg laying, live bearing, prolonged egg retention, reduced shells, placental exchange, hybrid phenotypes, and, in one exceptional *Saiphos equalis* pregnancy, both laid eggs and a live neonate. These facts are important. They do not constitute a witnessed historical transition in which an egg-laying population acquired the complete viviparous condition across generations. The history, direction, timing, and number of proposed origins are reconstructed from present organisms through phylogenetic and population models. The newest whole genome study of *Zootoca vivipara* makes the evolutionary case more precise while also removing several common overstatements. It supports one origin of viviparity in that species, extensive historical gene flow, a polygenic basis, and the gradual accumulation of regulatory variants across many genomic regions. It does not demonstrate the real time construction of a new organ class, and it reports no coding variants in the key concordant genes while expressly leaving structural variation, gene gain, gene loss, and newly evolved genes unresolved. The evidence therefore rules out a simplistic single switch account, but it also rules out the popular claim that macroevolution has simply been observed. A biblical creation model can affirm selection, mutation, recombination, regulatory change, and diversification within created lineages. Its decisive claim is that these processes operate through an already integrated amniote reproductive architecture. The repeated recruitment of homologous tissues and established networks for endocrine control, tissue remodeling, vascular development, immune modulation, transport, and alternative splicing fits that expectation. Complex skink placentation is the strongest objection and must be treated as a genuine integrated phenotype, not minimized. Even there, the demonstrated mechanism is coordinated modification of homologous membranes, uterine tissues, and standing molecular systems. The observed record is best described as adaptive reconfiguration within squamate reproductive architecture. Calling it direct observation of macroevolution confuses measured present mechanisms with an inferred history and grants the evolutionary narrative more than the data themselves provide.

Keywords: *viviparity, oviparity, squamate reptiles, reproductive mode, created kinds, designed adaptability, regulation, placentation*

Introduction

The transition from egg laying to live birth in lizards is frequently presented as evolution in action and, in popular treatments, as observable macroevolution. The phrase compresses several distinct claims into one memorable slogan. Living species with different reproductive modes are directly observed. Intermediate reproductive traits are directly measured. Historical transitions, ancestral states, the direction of change, the number of independent origins, and the time required are inferred from those present data. A careful review must keep those categories separate. Once that distinction is enforced, the flagship claim becomes far narrower than its rhetoric suggests.

Squamates are exceptionally valuable for studying reproduction because closely related lineages can differ in parity mode while retaining homologous reproductive tissues. Current studies commonly estimate many dozens to more than one hundred origins of viviparity across lizards and snakes, and global datasets place the viviparous share near one fifth of living squamates.

Those estimates deserve attention, but they are outputs of comparative reconstruction, not a series of witnessed origin events. Different taxon samples, confidence thresholds, trees, and ancestral state assumptions yield different counts. Recknagel, Kamenos, and Elmer reported estimates from 59 to 126 transitions depending on analytical settings, while other syntheses report more than one hundred. A range this wide is not an embarrassment. It is an honest reminder that the historical claim is model dependent.

The central question is not whether reproductive mode varies. It plainly does. Nor is the question whether natural selection can favor longer embryonic retention in particular climates. Strong evidence supports that mechanism. The disputed question is whether the observations demonstrate the origin of qualitatively new biological machinery through an unguided process, or whether they reveal selection acting on an already coherent, adaptable reproductive system. I argue that the latter interpretation is more faithful to what has actually been demonstrated.

Thesis: No study has directly observed an egg laying lizard population construct the complete viviparous condition across generations. The studies document present variation, selection, gene flow, regulatory divergence, and functional reuse within an existing amniote reproductive system. Those are real biological changes, but the label direct observation of macroevolution outruns the evidence.

Scope and Evidentiary Method

This paper is a critical synthesis of the primary literature on squamate reproductive mode, with special attention to the three best studied bimodal species, *Saiphos equalis*, *Lerista bougainvillii*, and *Zootoca vivipara*. It also evaluates comparative genomic, transcriptomic, placental, ecological, hybridization, and phylogenetic studies available through August 2026. The review is not presented as an exhaustive systematic meta analysis. Its purpose is narrower and sharper: to test the public claim of direct observation against the methods and results of the studies used to support it.

Evidence is ranked in four categories. First are observations of living animals and reproductive events. Second are experimental crosses, tissue studies, and manipulations that test function. Third are genomic and expression associations that identify molecular correlates and candidate mechanisms. Fourth are phylogenetic, demographic, and ecological reconstructions that estimate ancestral states and historical paths. All four categories are scientifically legitimate. They do not answer the same question, and only the first two directly observe a present event or causal response.

The Claim Must Be Defined Before It Is Defended

Macroevolution is used in at least two senses. In a taxonomic sense it can mean evolutionary change at or above the species level. In that weak sense, the term may describe lineage divergence by definition, but the definition does not establish the origin of a new body plan, organ class, or genetic system. In the stronger public sense, macroevolution refers to the creative origin of new and integrated biological machinery. That is the claim at issue. A change in parity mode can satisfy a taxonomic label without demonstrating the strong creative claim.

The phrase new biological information is also useless unless made operational. Here it means indispensable, sequence dependent functional machinery that cannot be reduced to altered timing, dosage, localization, splicing, or combination of homologous components already serving established functions. This definition does not assume that every regulatory change is trivial. It asks the decisive mechanistic question: did the change construct an unprecedented system, or did it redeploy an existing one?

What Is Observed, and What Is Reconstructed

Claim	Direct evidence	Inferential step	Warranted conclusion
Squamates use egg laying and live bearing	Births, eggs, shell traits, gestation, uterine tissues, and embryonic development are measured in living animals	None is needed to establish present reproductive diversity	Reproductive mode is variable and biologically real
Viviparity originated many times	Present traits and molecular sequences are observed	Trees, ancestral states, direction, and transition counts are modeled	Repeated origins are a strong historical inference, not witnessed events
Saiphos can express both modes	One female laid eggs and later produced a live neonate in the same pregnancy	Whether this event represents an ancestral stage or a derived retention is interpreted	The same animal can retain access to both outcomes
Zootoca viviparity arose once	Whole genomes, geography, gene expression, and present parity are measured	Gene trees and demographic histories reconstruct a single origin and later gene flow	The 2026 genomic model is strong, but it remains a historical reconstruction
Cold climates favor longer retention	Climate, physiology, behavior, and parity correlate, and process models predict gestation	Past selective histories are inferred from present patterns and modeled fitness	Cold climate selection is well supported as a driver, not an explanation for the origin of the toolkit

The Empirical Baseline

Oviparous squamates deposit an eggshell around the embryo and lay the egg before development is complete. Viviparous squamates retain embryos until birth. Between those endpoints lie prolonged retention, reduced shell deposition, abbreviated external incubation, and different degrees of maternal exchange. This range has been central to the literature for decades (Shine, 1985; Blackburn, 2006). The continuum is real, but the word continuum should not be allowed to do argumentative work by itself. A sequence of present conditions is not a filmed historical series. It becomes a proposed historical pathway only after ancestry and direction are assigned.

The transition is not merely a delay in laying. Successful viviparity requires coordinated changes in uterine retention, eggshell production, gas and water exchange, endocrine control, immune tolerance, tissue remodeling, parturition, and, in some lineages, nutrient transport. Gao and colleagues (2019) correctly emphasized this integrated suite. Van Dyke, Brandley, and Thompson (2014) also showed that every viviparous squamate forms a placenta in the broad anatomical sense, through apposition of maternal and embryonic tissues. Most viviparous squamates remain chiefly yolk nourished, but some skinks show substantial placentotrophy (Blackburn and Vitt, 2002). Any design argument that reduces the entire transition to a timing switch is too weak to survive review.

The stronger design argument is not that the phenotype is simple. It is that the complexity is produced through coordinated use of homologous tissues and established cellular systems. The uterus, embryonic membranes, shell glands, endocrine signals, vascular pathways, immune pathways, transport proteins, and developmental controls are already integrated parts of amniote reproduction. Viviparity changes their deployment and interaction. That is a major phenotypic reconfiguration, but it is not equivalent to demonstrating the de novo construction of reproductive architecture.

The Three Bimodal Species

Three species receive special attention because geographic populations differ in parity mode and because each system contains forms described as transitional. They are not one freely interbreeding population, and they should never be presented that way. Their populations are geographically structured, their histories differ, and contact between parity lineages can permit gene flow in one location while producing strong isolation in another. Precision strengthens the case because it prevents one overstated sentence from discrediting the entire analysis.

***Saiphos equalis*, Both Outcomes in One Pregnancy**

The three toed skink Saiphos equalis includes populations with oviparous, short incubation, and viviparous reproduction (Smith and Shine, 1997; Stewart et al., 2010). Laird, Thompson, and Whittington (2019) reported the decisive direct observation. One female from a normally viviparous population laid three eggs. One egg hatched, and 41 to 48 days after the first egg was laid the same female gave birth to a live neonate. This was the first documented case of both parity outcomes within one vertebrate pregnancy.

The egg coverings combined characteristics associated with oviparous and viviparous populations. The investigators concluded that coverings for retained embryos and laid eggs were produced by the same secretory machinery. This observation is powerful because it demonstrates retained functional overlap within one animal. It does not establish the historical direction of parity change, but it directly contradicts any portrayal of the two modes as requiring wholly separate reproductive apparatuses.

The design inference is straightforward. A reproductive system capable of producing both outcomes in a single pregnancy is functionally richer than a rigid either or mechanism. Doyle argued in 2011 that bimodal squamates could preserve remnants of an ancestrally broader reproductive capacity. The 2019 observation was not available when that proposal was made. It therefore counts as a genuine successful anticipation of the kind of flexibility the model expected. It is a prediction of creation & positive evidence that the live bearing condition can retain access to egg laying machinery.

***Lerista bougainvillii*, Geographic Variation and Prolonged Retention**

The Australian skink Lerista bougainvillii includes oviparous, viviparous, and prolonged retention populations. Qualls and colleagues (1995) documented the phylogenetic and reproductive pattern, while Qualls and Shine (1998) analyzed it as a case study of the transition. Viviparous populations occur in colder portions of the range, and transitional populations retain embryos longer and lay eggs with advanced embryos and short external incubation.

This species is strong evidence that retention length, shell condition, and parity can vary within a narrow lineage. It also supports selection in cold environments. What it does not supply is a longitudinal record in which a measured oviparous population begins without viviparous capacity and then acquires the complete condition while investigators watch. Geographic populations are arranged into a proposed historical sequence by comparative analysis. The evidence is valuable, but the observation and the reconstruction must not be conflated.

***Zootoca vivipara*, Gene Flow, Barriers, and the 2026 Genomic Result**

The common lizard Zootoca vivipara is the most informative and the most frequently overstated case. Oviparous and viviparous lineages can hybridize. Laboratory crosses and an Austrian contact zone have produced hybrids with intermediate reproductive traits, and some hybrid females are at least partly fertile (Arrayago et al., 1996; Lindtke et al., 2010). It is nevertheless false to say that all parity lineages interbreed without constraint. Cornetti and colleagues (2015) found no first generation hybrids, later generation hybrids, or backcrosses in one Alpine contact zone and concluded that interbreeding there was absent or extremely rare. Reduced hybrid fitness and steep contact boundaries show that parity differences can contribute to reproductive isolation.

The 2026 whole genome analysis by Xie and colleagues is now the strongest study in this debate. It analyzed 101 lizards from 61 sites and more than 14.6 million autosomal variants. The authors inferred that viviparity arose once in the species, rejecting the widely cited reversal to egg laying. They also inferred extensive long term gene flow from oviparous into viviparous populations, substantial gene tree discordance, and selection distributed across many genomic regions. Ninety six gene flow barrier regions were identified across 16 autosomes, covering about 1.89 percent of autosomal sequence. The architecture is polygenic, not a literal single switch.

This study corrects both sides. It strengthens the evolutionary account by showing that selection can accumulate many regulatory differences while gene flow continues. It also destroys the careless claim that free interbreeding makes reproductive barriers irrelevant. Yet it does not turn historical reconstruction into direct observation. The origin, direction, and duration are inferred from contemporary genomes. Most importantly, the mechanism is primarily regulatory. The 23 genes that fell in concordant barrier and selection regions contained no coding variants in the analysis, while fixed differences were concentrated in putative regulatory regions. The authors explicitly noted that structural variants, chromosomal effects, gene gain, gene loss, and newly evolved genes remain unresolved. The warranted statement is therefore precise: no core de novo coding innovation has been demonstrated for the key concordant gene set. The unwarranted statement is absolute: the transition contains no newly originated genes of any kind.

Decisive correction: Zootoca does not support a one gene toggle, universal free hybridization, or a demonstrated reversal to egg laying. It supports a polygenic regulatory architecture, variable reproductive isolation, historical gene flow, and one reconstructed origin of viviparity.

The Molecular Evidence

Regulatory Reuse Is the Dominant Demonstrated Pattern

Pregnancy in squamates draws on familiar biological functions. Transcriptomic work in *Chalcides ocellatus* identified changes involving metabolism, cell proliferation, cellular transport, tissue remodeling, vascular development, immune regulation, and nutrient provisioning. Studies of Saiphos and Zootoca likewise emphasize expression differences, endocrine signaling, shell formation, uterine remodeling, angiogenesis, and immune control. These are not irrelevant housekeeping changes. Their coordination is the phenotype. The crucial point is that the measured components belong to standing cellular systems rather than to a newly observed organ building program.

Foster and colleagues strengthened this conclusion in 2022 by comparing uterine expression across eight independently viviparous vertebrates. They found no more overlap in specific genes than expected by chance and no single gene shared across every viviparous lineage in the comparison. Nevertheless, the same core physiological functions appeared repeatedly. Different lineages recruited different genes from lineage constrained genomic toolkits to reach similar functional outcomes. This finding does not disprove evolution, because evolutionary theory includes cooption and redundancy. It does defeat the claim that repeated viviparity is a repeated construction by one universal novel gene program.

Smout and colleagues added another layer in 2026 by tracking uterine expression and alternative splicing across the reproductive cycle of a viviparous lizard. They reported hundreds of expression changes and more than one hundred cases of differential transcript use, most of which were not also differentially expressed. Alternative splicing therefore supplies a distinct regulatory layer. The study title refers to novel genes for pregnancy, but in context novel means newly identified candidate involvement, not genes shown to have originated from noncoding sequence during the transition. This distinction matters because titles and abstracts can be rhetorically mined beyond what the experiments establish.

Polygenic Does Not Mean Unbounded

The design case should not depend on genetic simplicity. Xie and colleagues show that the relevant architecture is genome wide and polygenic. Recknagel and colleagues likewise found that live bearing engages more genes and more complex regulatory networks than egg laying. A complex control architecture is exactly what should be expected when endocrine timing, shell secretion, uterine retention, vascular exchange, immune tolerance, and birth must remain coordinated.

The better design claim is not one switch. It is bounded modularity: many adjustable nodes operate inside a preexisting reproductive network whose components are already functional and mutually integrated.

Evolutionary theory can describe regulatory cooption, selection on standing variation, mutation, and the accumulation of barriers. The issue is explanatory depth. Selection can sort variants only because variants act within a viable architecture. It can explain why longer retention spreads when embryos gain a thermal advantage. It does not, by that fact alone, explain the origin of the endocrine, uterine, vascular, immunological, and developmental systems that make retention selectable. The mechanism measured in the present should not be inflated into a complete origin account.

Climate and Selection

The cold climate hypothesis has strong current support. Zimin and colleagues assembled a global dataset of 9,061 squamate species and found viviparity strongly associated with cold climates. Garcia Costoya and colleagues then built a process based model incorporating behavior, thermal physiology, life history, local climate, and nest conditions. Across 89 lizard populations, the model accurately predicted longer gestation in cold settings, supporting the mechanism by which maternal thermoregulation can improve embryonic conditions relative to a cold nest.

This result should be granted without hesitation. It shows why selection can favor longer retention. It does not show that temperature authored the underlying capacity. Moreover, the historical climatic claim is more delicate than the present association. Recknagel, Kamenos, and Elmer found that a correlation between inferred transition timing and paleoclimate disappeared after controls for lineage diversification and simulated trait evolution. They also showed that transition counts and timing depend heavily on model settings. The present ecological mechanism is strongly supported. Deep historical reconstruction remains conditional.

Model distinction: Cold climate can select among viable reproductive settings. The biblical creation model accepts that process. The point of dispute is whether selection and climate also explain the origin of the integrated system that makes those settings possible.

A Biblical Creation and Design Interpretation

Scripture presents living organisms as created to reproduce according to their kinds. That statement does not require species to be genetically static, ecologically rigid, or incapable of rapid diversification. A serious biblical creation model expects variation, recombination, mutation, selection, migration, developmental plasticity, and population divergence within created lineages. It also expects biological systems to possess enough robustness and flexibility for descendants to occupy changing environments after creation and the Flood. Our model poses that at the start species were created with high levels of created heterozygosity and over time it gets lost. Sometimes mosaics are discovered and they retain more traits that were lost in other species.

Squamate reproduction fits that expectation with striking force. Closely related animals use the same basic amniote tissues to produce eggs, retain embryos, reduce shells, form placental contact, regulate maternal immunity, exchange gases and solutes, and complete birth. Environmental selection alters which configurations spread. Regulatory variants alter timing and dosage. Alternative splicing expands functional output. Hybridization can exchange much of the genome even while selected regions resist gene flow. The system is flexible, but its flexibility is not shapeless. It remains squamate reproduction throughout. The term created kind should not be assigned automatically to a modern family, genus, or species. Scripture does not equate the kind with any one Linnaean rank, and exact boundaries must be investigated through ancestry, reproductive continuity, morphology, development, and genetics. The argument does not need an unsupported rule tied to a modern

taxonomic rank. It needs only the narrower and defensible observation that the changes under review remain inside homologous squamate reproductive architecture and do not demonstrate the origin of a new body plan or organ class.

Doyle proposed that reproductively bimodal lizards may preserve a broader ancestral capacity from which later populations specialized. The direct demonstration of both parity outcomes in one Saiphos pregnancy, reported eight years later, gave that proposal unexpected empirical support. The Zootoca genome result adds necessary discipline. The capacity is not controlled by one simple toggle, and some genomic regions resist gene flow. Designed adaptability is therefore best conceived as distributed and modular, not mechanically simple. A sophisticated design model grows stronger when it absorbs hard data instead of leaning on slogans.

Competing Explanations Tested Against the Evidence

Empirical pattern	Evolutionary interpretation	Biblical creation interpretation	Critical assessment
Many inferred origins across squamates	Repeated selection produced viviparity in separate lineages	Lineages repeatedly expressed an adaptable reproductive capacity	Compatible with both. The count is reconstructed and does not by itself identify the source of the capacity
Regulatory and expression change dominates measured mechanisms	Coooption and selection altered established networks	Designed networks were reconfigured within bounded architecture	Both can describe the mechanism. Design directly predicts functional reuse, while evolution must explain the prior availability of the integrated toolkit
Different genes converge on the same uterine functions	Redundancy permits multiple genetic routes	A modular toolkit permits multiple routes to stable functions	Shared compatibility. The result rejects one universal pathway and strengthens the case for modularity
One Saiphos pregnancy produced eggs and a live neonate	Facultative expression illuminates a transitional mechanism	One animal retained both outcomes within one reproductive system	Direct evidence of retained dual capacity. It does not determine historical direction, but it is a successful design model anticipation
Zootoca has historical gene flow plus genomic barriers	Selection built a polygenic innovation despite gene flow	Selection differentiated settings while much of the lineage remained connected	Strong evidence for selection and divergence, but not a witnessed origin event. It refutes claims of universal free interbreeding
Complex skink placenta	Integrated placental phenotypes evolved through coordinated modification	Homologous membranes and existing networks were elaborated by designed capacity	The strongest evolutionary objection. Existing tissues and networks are demonstrated, but the origin of their coordinated capacity remains the central explanatory question
No longitudinal observation of a complete origin	Historical science legitimately reconstructs unobserved events	Present change does not establish an unbounded origin process	Absence of direct observation does not falsify evolution, but it decisively falsifies the claim that macroevolution was simply watched

The Strongest Objections

Modern evolutionary theory explicitly invokes co-option, regulatory evolution and network modification when needing to answer hard or unresolvable questions. But giving an answer without evidence is not confirming anything, it's a scientific opinion. The experiments are clear and show reuse and reconfiguration. When this is presented as direct observation of the creative origin of complex machinery, the conclusion exceeds the result. The opposition may possess a vocabulary for reuse, but naming reuse is not the same as explaining the origin of the reusable system.

The 2026 Study Shows Gradual Accumulation

Xie and colleagues inferred that many regulatory variants accumulated over considerable time. But gradual does not mean directly observed, and accumulation does not mean construction from nothing. The selected regions act on pregnancy, parturition, nutrient homeostasis, immune function, and vascular remodeling within an already viable reproductive system. The study traces genomic differentiation associated with parity. It does not experimentally derive the integrated system from an oviparous baseline lacking the necessary functions.

Reproductive Isolation Can Develop

Correct. One Zootoca contact zone shows extremely rare or absent interbreeding, and hybrid fitness can be reduced. The design model does not and has no reason to deny reproductive isolation within a created lineage. Population separation, chromosomal differences, selection against hybrids, and genomic barriers can generate species boundaries. Speciation in this sense is diversification. It does not demonstrate transformation beyond the reproductive and developmental architecture of the lineage. The accurate argument is bounded divergence, not universal interbreeding.

Historical Inference Is Still Science

Historical reconstruction can be rigorous, quantitatively tested, and strongly corroborated. The mistake is marketing inference as direct observation and then treating the rhetorical substitution as evidence. A reconstruction should be judged by its assumptions, alternatives, sensitivity, and independent predictions. The 2026 Zootoca result is a reconstruction and does not convert it into a witnessed origin event.

Reversibility Favors Evolution

Reversals between egg laying and live bearing remain disputed across squamates. Blackburn showed that the classical claim of irreversibility deserves reconsideration, but reconstructing reversals is difficult because shell glands, eggshell traits, and phylogenetic placement must all be evaluated. The common lizard can no longer be used confidently as the flagship reversal. Xie and colleagues inferred one origin of viviparity and rejected the proposed return to oviparity. Reversibility should therefore be treated as an open comparative question, not ignored based on conjecture.

A Testable Design Research Program

A creation and design interpretation is bold in its predictive power and whose accuracy over the decades makes our model superior. The following predictions distinguish bounded, preconfigured adaptability from an unrestricted origin narrative and direct future work.

Core functions required for squamate viviparity should map predominantly to homologous amniote tissues and conserved cellular systems rather than to an indispensable organ class with no functional precursors.

Regulatory architecture, including timing, dosage, tissue specificity, chromatin control, and alternative splicing, should explain a major share of parity differences, while different lineages recruit different genes toward the same constrained functions.

Experimental manipulation of established endocrine and uterine control nodes should shift component traits such as retention, shell deposition, tissue remodeling, and parturition without requiring the origin of new coding genes during the experiment.

Residual facultative capacity and mixed phenotypes should be concentrated near bimodal lineages where both reproductive outcomes remain developmentally accessible.

Genomic divergence may be distributed and polygenic, but selected regions should remain functionally integrated with established reproductive pathways rather than reveal an unconnected sequence of viable, system building intermediates.

Conclusion

Lizards are not being watched while macroevolution constructs live birth. Researchers are observing extant reproductive diversity, measuring physiological and genetic differences, crossing lineages, and reconstructing history from present data. Those achievements are substantial. They do not justify the stronger slogan.

The empirical picture is now clearer than ever. Saiphos demonstrates that one reproductive system can produce both laid eggs and a live neonate within one pregnancy. Lerista shows geographic variation in retention, shell condition, and parity. Zootoca shows one inferred origin of viviparity, long term gene flow, real genomic barriers, variable reproductive isolation, and a polygenic regulatory architecture. Comparative transcriptomics shows that different lineages recruit different genes toward the same core uterine functions. Ecological work strongly supports cold climate selection for longer retention. Complex placentation confirms that the phenotype is coordinated and biologically impressive.

None of these findings requires denial or retreat. They expose the weakness of the popular evolutionary presentation. What has been directly demonstrated is selection and regulation acting within an already functional amniote reproductive architecture. What has not been directly demonstrated is the origin of that architecture through an unguided process. The biblical creation model expects organisms to reproduce according to created lineages while possessing the robust capacity to diversify, adapt, and survive environmental change. Squamate viviparity displays exactly that combination: striking flexibility within a coherent and bounded reproductive system.

The claim of observed macroevolution therefore fails on its own wording. Present mechanisms have been measured. Historical scenarios have been reconstructed. A new organ class has not been seen arising. Selection may explain which viable configuration spreads, but it cannot be credited with inventing the integrated architecture merely because it sorts variants inside that architecture. The evidence is best read as designed adaptability expressed through regulation, selection, and functional reuse, not as an irrefutable demonstration of evolutionary creation.

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