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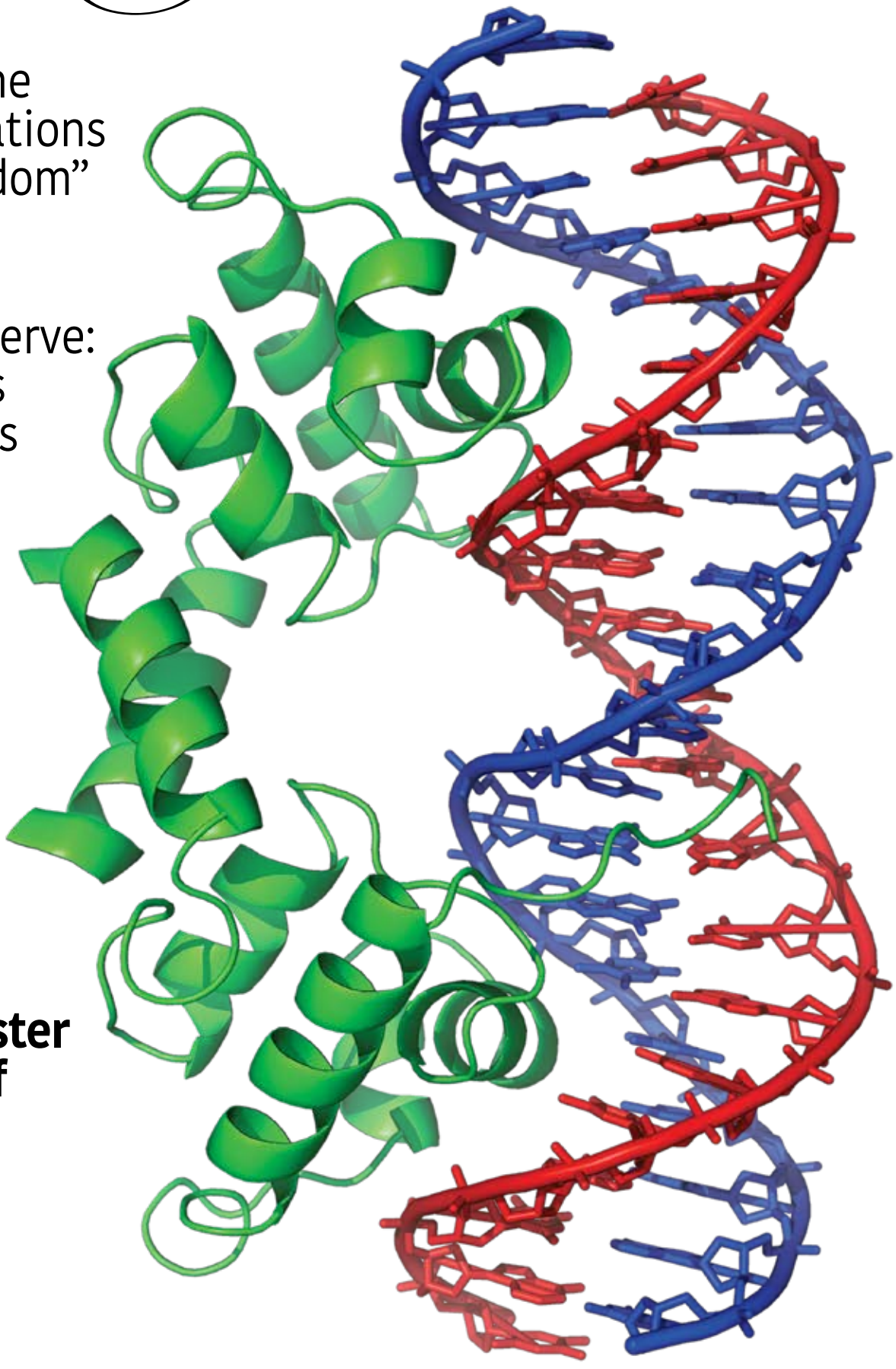

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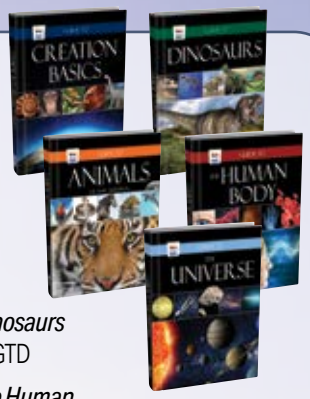

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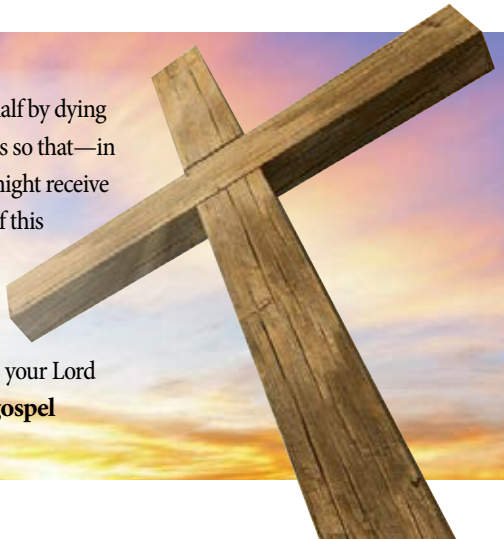
You are deeply loved by God! This certain truth is expressed in a Scripture that sums up the gospel of Jesus Christ: "For God so loved the world that He gave His only begotten Son, that whoever believes in Him should not perish but have everlasting life" (John 3:16). We all need Jesus as our Savior because we are all sinners and can't by our own efforts fulfill the requirements of God's justice. But Jesus Christ, our Creator, could satisfy the Father's holiness, so He suffered the punishment for sin on our behalf by dying on the cross. Jesus was made to be sin for us so that—in the most remarkable exchange ever—we might receive the righteousness of God. We can be sure of this because Jesus rose again from the dead. What a gift of love! You can have the promise of everlasting life when you turn from your sin and believe in Jesus Christ as your Lord and Savior. To learn more, visit **ICR.org/gospel**



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DESIGNER
Dennis Davidson

[Jesus Christ] is the image of the invisible God, the firstborn over all creation. For by Him all things were created that are in heaven and that are on earth, visible and invisible, whether thrones or dominions or principalities or powers. All things were created through Him and for Him. And He is before all things, and in Him all things consist. And He is the head of the body, the church, who is the beginning, the firstborn from the dead, that in all things He may have the preeminence. For it pleased the Father that in Him all the fullness should dwell, and by Him to reconcile all things to Himself, by Him, whether things on earth or things in heaven, having made peace through the blood of His cross.
(Colossians 1:15–20)

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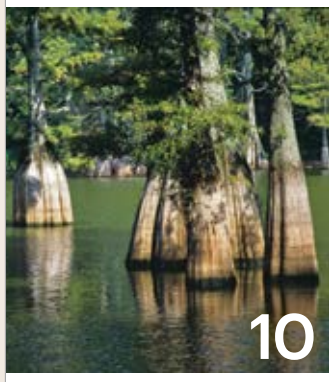
All Scripture quotations are from the New King James Version unless otherwise indicated.



Front cover: Lambda repressor. The lambda repressor transcription factor (green) binds as a dimer to major groove of DNA target (red and blue) and disables initiation of transcription. From PDB: 1LMB.
Image credit: Zephyris at English Wikipedia, CC BY-SA 3.0

Dethroning the Dogma "Mutations Occur at Random"

RANDY J. GULIUZZA, P.E., M.D.

Honesty is good for the soul…especially when the evidence against you is piling up. Some evolutionary biologists held an astoundingly candid conference in Lisbon, Portugal, called On the Nature of Variation: Random, Biased and Directional. The conference's aim was to provide a context for "critically evaluating the rationale behind" evolutionary assumptions about "variation randomness in the light of new developments." On center stage for reevaluation was "the underlying assumption supporting adaptationism…that variation is somehow random, namely, that it is neither biased nor directional." It's hard to imagine evolutionists seriously asking the questions "Why was variation characterised as random in the first place?" and "How useful is the doctrine of variational randomness? And how should it be characterised?"[1]

Skeptical questions abound. Two recent papers are titled "What prevents mainstream evolutionists teaching the whole truth about how genomes evolve?"[2] and "Who ever thought genetic mutations were random?"[3] Likely, most scientists embracing Darwinism would be surprised to know that hundreds of research papers published since the 1970s identify *non*random "adaptive" or controlled genetic modifications that produce purposeful outcomes. I've had discussions with evolutionary biologists who'd never heard of controlled genetic modifications and were disinclined to believe me.

That's because longstanding evolutionary theory "is based on the tenet that new phenotypes arise through a process relying on the raw material supplied by accidental, numerous, successive, and slight genetic changes."[4] But did a reliable base of scientific evidence *ever* justify the assertion that most adaptive traits could be attributed to random genetic errors, i.e., "mutations" as commonly understood?

The backstory helps us find the answer. We need to see how nearly everyone is taught to parrot the mantra "mutations occur at random." This basic creed strongly influences an evolutionist's thinking—even when staring at contrary evidence. A powerful mental conditioning of successive generations of biologists has virtually ensured that when a genetic change associated with an adaptive trait is observed, it will instinctively be interpreted as an accidentally broken genetic mutation.

Most people absorb this barrage of biased interpretations and also begin intoning "mutations occur at random." I know that I did. But like everyone else, I was wrong all along. The thought of purposefully directed genetic change wasn't even in my mind. I didn't understand *why* the concept of purposeless genetic accidents is so vital to Darwinism that it has existed akin to an inviolable doctrine for decades.

Carpathian lynx

article highlights

- Directed genetic change seems to be the norm—creatures internally direct their own genetic adaptation.
- New discoveries appear to show DNA changes are purposeful and rapid, which are Scripture-affirming findings and point to design.
- Each year, honest conventional scientists chip away at evolution's facade and expose a wondrous creation only a Creator could design. And His name is Jesus.

Questioning Randomness Brings Professional Risks

The evolutionary biologists organizing the Lisbon conference are fully familiar with the mantra "mutations occur at random." No biology student escapes indoctrination. They've heard the sacred confession "mutations occur at random" endlessly repeated in chant-like fashion at conferences and in literature. From their conference description,[1] which is well worth the time to read, they knew that presenting evidence for nonrandom genetic change is one thing, but questioning the belief that mutations occur at random could place

them out on a limb as Darwinian heretics.

For instance, here's how orthodox Darwinists are expected to behave. Bacteriologists conducting research on bacteria uncovered that at least some "mutations" were not random. Their conclusive findings were summed up in an article titled "Predictable evolution trumps randomness of mutations."[5] Yet, even as the writer presented contradictory evidence, he still respectfully genuflected to the random mutation creed, saying,

> Although mutations, the driver of evolution, occur at random, a study of the bacterium *Escherichia coli* reveals that nature often finds the same solution to the same problem again and again…. The DNA showed that in some cases identical mutations appeared independently in all three test tubes.[5]

As a bonus, this Darwinist's scientific explanation for the *cause* of nonrandom genetic changes was to personify nature as a mystical agent that somehow "finds" identical solutions to biological problems.

That's why it was shocking, yet refreshingly honest, when the Lisbon conference organizers asked why variation was characterized as random in the first place. But that reveals a remarkable lack of insight that's widespread in contemporary evolutionary biology regarding why evolutionary theory has been fashioned the way it is today.

Likewise, creationists and Intelligent Design (ID) advocates in general don't understand *how* evolutionary theory advances an anti-designer worldview. But we should know why. One of the best ways to identify the specific tenets of evolutionary theory we should target for demolition is to observe what elements knowledgeable evolutionists safeguard at all costs.

The noted evolutionary theorist Stephen J. Gould often castigated colleagues for publishing proposals that recklessly strayed from core Darwinian tenets. He recoiled at flippant suggestions to fundamentally change the theory by associates who "never understood the full logic and implications of this issue" as they proceeded "without grasping the theoretical problems entailed by such excursions" or alternatively failed to grasp a core tenet "which should be emblazoned into the consciousness of all evolutionary biologists."[6] Gould understood how pioneering Darwinists had meticulously crafted essential parts of evolutionary theory so that it could explain the undeniable design of organisms without resorting to God.

Undirected Variation Is Fundamental to Evolutionary Theory

If creatures were static and could not adapt to changing conditions, then a theory of evolution could never get going. But creatures can change. Thus, it is the explanation of adaptation that is steering the direction of the creation-evolution debate. *How* adaptation happens, it seems, is a question of vital importance.

Here's a hypothetical mechanism: most biological adaptation happens when highly regulated innate systems direct modifications of genes and traits toward purposeful outcomes. This hypothesis has long been intolerable to most biologists, not because it's scientifically untenable, but because it's repugnant to Darwinian philosophy. Why? A hypothesis like this could be associated with words like foresight, purposeful, regulated, directed, or targeted. These words characterize the outcome of engineered systems designed by a rational engineer. Ordinary people might intuitively begin to think the forbidden thought that God engineered creatures to be adaptable.

The anti-theistic power of Darwinism lies in one thing only—its anti-engineering assumptions. Darwin's key followers developed a model of adaptation that assumes genetic changes are random, accidental, broken, trial-and-error, noncontrolled, and purposeless. That's why most evolutionary biologists believe that genetic changes are essentially random errors and mistakes, i.e., mutations.[7]

How are random mutations and anti-theistic thinking linked? If a relentless avalanche of scientific literature can persuade people that organisms really did come about via a chaotic, purposeless process, then this fact would negate God directly creating them, and Darwinism would seem to make more causal sense. Thus, the core of anti-theistic doctrine is spread via a longstanding, non-negotiable tenet of Darwinism: genetic change in adaptation is *un*directed toward any *purposeful* outcome.

Gould gives the history behind the anti-design concepts built into Darwinian theory. He summarizes three criteria for genetic variability:

> Variation, in short, must be copious, small in extent, and undirected. A full taxonomy of non-Darwinian evolutionary theories may be elaborated by their denial of one or more of these central assumptions.[8]

He clarifies the meaning of directed variation as "adaptive pressures [that] automatically trigger heritable variation in favored directions." Gould adds that wholly unbiased variation is *fundamental* to evolutionary theory. "In a sense, *the specter* of directed variability threatens Darwinism" in the most serious way. Why? Because automatic responses sound like the outcomes of elements corresponding to human-engineered systems. Thus, "Darwin clearly understood the threat of directed variability to his cardinal postulate of creativity for natural selection."[8]

The Lisbon conference organizers underscored the lethality of directed genetic change to the anti-design purpose of evolutionary theory, saying,

> Futuyma (2005, p. 179) makes the same point by invoking *the spectre* of Lamarckism: "The argument that adaptively directed mutation does not occur is one of the fundamental tenets of modern evolutionary theory. If it did occur, it would introduce a Lamarckian element [nonrandom, useful changes to traits in response to changing conditions] into evolution, for organisms would then acquire adaptive hereditary characteristics in response to their environment."[9]

After presenting evidence for nonrandom genetic change, they added that Futuyma only makes "reference to **theoretical reasons** for dismissing the possibility that mechanisms of directional mutagenesis might exist."[10]

It's remarkable that well-informed Darwinists like Gould and Futuyma see nonrandom, directed genetic change as a nightmare (i.e., "a specter") to evolutionary theory. Perhaps creationists and ID advocates should be investing focused effort to make the nightmare come true.


Eurasian eagle owl

Abundant Evidence of Nonrandom Genetic Change

Likely no one disputes that copying errors and truly random mutations happen. But there's always been an absence of direct evidence that *all* mutations, especially genetic changes associated with suitable adaptations to environmental challenges, are fully random. By the 1980s, contrary findings made one researcher ask, "The great primary problem is evidently set by the mutations. Are they random or nonrandom?"[11]

Today, James Shapiro, another evolutionist, assembles evidence for nonrandom "natural genetic engineering" in *Evolution: A View from the 21st Century.* A reviewer notes that Shapiro "rejects this [random mutation] view by taking into account an extraordinary amount of molecular evidence (the book's impressive bibliography refers to over 1,100 research articles)."[12]

There's a growing body of evidence that many mutations are not random in their formation.[13] In fact, many genetic changes seem to be specially programmed as targeted responses to specific external conditions. When cells detect different environmental conditions, innate mechanisms that are currently not well understood can change their chromosome state and alter the patterns of chemical tags on DNA.[14] Adaptive responses in bacteria can result from the same independently occurring genetic change in different populations.[15] Short segments of DNA can be inverted to generate new patterns in human chromosomes.[16]

Work on yeast exposed to toxins found that they seemed to be directing greater genetic variation to the exact location to produce protective traits and provide "cells with a remarkable and unexpected ability to alter their own genome in response to the environment."[17] Intracellular enzymes may control the location of genetic changes on chromosomes in humans.[18] Recent research on genetic changes in the plant *Arabidopsis thaliana* "found a lower mutation frequency inside gene bodies and certain essential genes, shattering the long-standing idea that mutations are entirely random across the genome."[19]

This is just a foretaste. Two researchers summarize what they and others have found:

> But this view [random mutation] is being revised by discoveries of molecular mechanisms….These mechanisms reveal a picture of highly regulated mutagenesis, up-regulated temporally by stress responses and activated when cells/organisms are maladapted to their environments—when stressed—potentially accelerating adaptation. Mutation is also nonrandom in genomic space, with multiple simultaneous mutations falling in local clusters, which may allow concerted evolution….Assumptions about the constant, gradual, clock-like, and environmentally blind nature of mutation are ready for retirement.[20]

Taking Aim at the Dogma "Mutations Occur at Random"

Fortunately, we're at a unique time in biological research where a flood of discoveries identifies many apparently nonrandom ways that DNA is changed. This also makes theological sense. The belief in a chaotic mechanism for adaptation is inconsistent with all the other incredibly complex and purposeful biological systems the Lord Jesus created. In this and future *Acts & Facts* issues, the ICR science staff will be honoring the Lord Jesus by highlighting nonrandom mechanisms for adaptation.


Cuttlefish

References

1. On the Nature of Variation: Random, Biased and Directional, a CFCUL/BIODECON International Conference held October 3-4, 2017, at the University of Lisbon.
2. Shapiro, J. and D. Noble. 2021. What prevents mainstream evolutionists teaching the whole truth about how genomes evolve? *Progress in Biophysics and Molecular Biology.* 165: 140-152.
3. Veitia, R. A. 2022. Who ever thought genetic mutations were random? *Trends in Plant Science.* 27 (8): 733-735.
4. Vecchi, D. 2013. The Trouble with Natural Genetic Engineering: James A. Shapiro: *Evolution: A View from the 21st Century*. *Biological Theory.* 7 (1): 80-88.
5. Laursen, L. Predictable evolution trumps randomness of mutations. *Nature*. Posted on nature.com February 19, 2013.
6. Gould, S. J. 2002. *The Structure of Evolutionary Theory*. Cambridge, MA: Belknap Press of Harvard University Press, 544-545 and 251.
7. The word mutation technically means any change to a genetic sequence resulting from any cause. Thus, a purposefully directed genetic change would still be called a mutation. The overwhelming usage of the word mutation in technical literature refers to a genetic change interpreted to be a purposeless error or broken gene. Since a definitive test to show that a genetic change is either a mistake or purposeful doesn't exist, ICR researchers prefer not to mislead readers and instead use the non-stigmatizing term "genetic change" instead of "mutation," unless the genetic change is unambiguously linked to debility or disease.
8. Gould, *Structure of Evolutionary Theory*, 145. Emphasis added.
9. On the Nature of Variation: Random, Biased and Directional. Emphasis added. Quotation drawn from Futuyma, D. J. 2005. *Evolution*. Sunderland, MA: Sinauer Associates.
10. Ibid, emphasis in original.
11. Brundin, L. Z. 1986. Evolution by Orderly Stepwise Subordination and Largely Nonrandom Mutations. *Systematic Biology.* 35 (4): 602-607.
12. Vecchi, The Trouble with Natural Genetic Engineering.
13. Hogeweg, P. 2015. Non-Random Random Mutations: A Signature of Evolution of Evolution (EVOEVO). *Proceedings of the European Conference on Artificial Life 2015,* 1.
14. Zhu, J. et al. 2013. Genome-wide Chromatin State Transitions Associated with Developmental and Environmental Cues. *Cell.* 152 (3): 642-654.
15. Herron, M. D. and M. Doebeli. 2013. Parallel Evolutionary Dynamics of Adaptive Diversification in *Escherichia coli*. *PLoS Biology.* 11 (2): e1001490.
16. Löytynoja, A. and N. Goldman. 2017. Short template switch events explain mutation clusters in the human genome. *Genome Research.* 27 (6): 1039-1049.
17. Hull, R. M. et al. 2017. Environmental change drives accelerated adaptation through stimulated copy number variation. *PLoS Biology*. 15 (6): e2001333.
18. Pinto, Y. et al. 2016. Clustered Mutations in Hominid Genome Evolution are Consistent with APOBEC$_3$G Enzymatic Activity. *Genome Research.* 26 (5): 579-587.
19. Veitia, Who ever thought genetic mutations were random?
20. Fitzgerald, D. M. and S. M. Rosenberg. 2019. What is mutation? A chapter in the series: How microbes "jeopardize" the modern synthesis. *PLoS Genetics.* 15 (4): e1007995.

Dr. Guliuzza is President of the Institute for Creation Research. He earned his Doctor of Medicine from the University of Minnesota, his Master of Public Health from Harvard University, and served in the U.S. Air Force as 28th Bomb Wing Flight Surgeon and Chief of Aerospace Medicine. Dr. Guliuzza is also a registered Professional Engineer and holds a B.A. in theology from Moody Bible Institute.

CHARLES C. (CHAS) MORSE, D.MIN.

Sharing the Message of Christ Our Creator

The Institute for Creation Research's founder, the late Dr. Henry M. Morris, emphasized that "we must try not only to win individual scientists and educators to Christ, but also to win *science* itself, and *education* itself, to Christ."[1] We continue to build on the solid foundation laid down by those who came before us. I'd like to share with you some of ICR's current initiatives.

Credit Jesus Christ as Creator. ICR's mission is to consistently exalt the Lord Jesus in everything we do. Our message through events, articles, books, and presentations highlights the workmanship of Christ, especially as expressed in living creatures. We at ICR are privileged to showcase the use of science to rightfully credit Christ as our Creator and Savior, demonstrating why Jesus is worthy to be the center of our deepest love, affection, and devotion.

Forge close relationships with pastors, congregations, and schools. We're here to help lead, feed, and equip believers by providing scientific responses to attacks on the authority and historicity of God's Word. Our pioneering research targets areas that affirm the Bible's historical narrative, principally the accounts of recent creation and the global Flood. We provide answers to the challenges believers face in a world opposed to God's truth.

Defend the biblical creation gospel message. Few people realize how closely the gospel is tied to the Bible's doctrine of creation. For one thing, a correct understanding of creation leads people to see that Jesus is Creator as well as Lord and Savior. Second, people may not realize how belief in evolution undermines the clarity and authority of Scripture. My father, Charles P. Morse, was evolutionary in his ideology until, through the ministry of ICR and Dr. Henry Morris, he was presented with the stark reality of Jesus Christ as Creator of the universe.

Produce quality resources for both evangelism and discipleship. Our articles, books, and videos are designed to further relay ICR's message to people of all ages and stages. One example of the quality resources ICR produces is our new children's book *God Created Birds*. It offers a bird's-eye view of these animals' fascinating features and delightful details that point to the expert handiwork of our Creator and Savior, the Lord Jesus Christ.

UPCOMING MEET AND GREET EVENTS

Free event • registration required • limited seating

- **July 31**—ICR Discovery Center in Dallas, TX
- **August 13-14**—Grace Bible Church in Tempe, AZ
- **October 2**—ICR Discovery Center in Dallas, TX

For more information, email **ICRmeetandgreet@icr.org**

We want to send a heartfelt thank you to all of you who are faithful in prayer and giving as ICR's co-laborers. Because of His goodness and mercy evidenced in your support for ICR, we can meet the future's uncertainties with confidence and hope. Your partnership means the world to us.

If you'd like to donate to the John D. Morris Memorial Fund for Geological Research, visit **ICR.org/donate** and select the memorial fund in the "Use this gift" field. This fund will support ICR's geological research and the sharing of its results.

Reference

1. Morris, H. M. 1994. Beginning at Genesis. *Acts & Facts*. 23 (2).

Dr. Morse is Director of Donor Relations at the Institute for Creation Research and earned his D.Min. from The Master's Seminary.

JULY 1

Dallas, TX
ICR Discovery Center
Independence Day Celebration
ICRDiscoveryCenter.org/Special-Events or 800.743.6374

JULY 15 and AUGUST 19

Dallas, TX
ICR Discovery Center
Day 4 Astronomy Meeting
Free event, no registration needed
info@day4.org or 903.692.1111

JULY 15

Dayton, OH
Centerville Community Church
Science and the Bible Conference
(R. Guliuzza, T. Clarey)
ArkFoundation@arky.org or 937.256.2759

JULY 16-19

Cedarville, OH
Cedarville University
9th International Conference on Creationism
(R. Guliuzza, T. Clarey, J. Tomkins, B. Thomas, J. Hebert)
Register at InternationalConferenceOnCreationism.com

JULY 16-29

Lookout Mountain, GA
Covenant College
Summit Ministries Student Conference
(B. Thomas)
Register at Summit.org/programs/student-conferences/georgia or 719.685.9103

JULY 29

McKinney, TX
Redemption Point Alliance Church
Unmistakable Conference
(T. Clarey, B. Thomas)
Register at ICR.org/McKinneyTX or 214.615.8306

AUGUST 8-13

Grand Canyon, AZ
Landmark Events Grand Canyon Raft Adventure
(T. Clarey)
ICR.org/raftGC or 214.615.8325

AUGUST 12-13

Senoia, GA
Legacy Christian Church
Creation Weekend
(F. Sherwin)
ICR.org/SenoiaGA or 214.615.8325

AUGUST 24-26

Bend, OR
Calvary Chapel Bend
The Berean Call Conference
(R. Guliuzza featured speaker)
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TheBereanCall.org/conference

SAVE THE DATE

SEPTEMBER 2

Dallas, TX
ICR Discovery Center
Labor Day Celebration
ICRDiscoveryCenter.org/Special-Events or 800.743.6374

SEPTEMBER 9

Sioux Center, IA
Sioux Center United Reformed Church
Conference on Biblical Creation
(F. Sherwin)
ReformationGospelMinistries.org or 712.441.5793

SEPTEMBER 17

Cordova, TN
First Assembly Memphis
Creation Sunday
(F. Sherwin)
ICR.org/MemphisTN or 214.615.8325

SEPTEMBER 29–OCTOBER 1

Upland, CA
Foothills Bible Church
Creation Weekend
(T. Clarey)
ICR.org/UplandCA or 214.615.8325

OCTOBER 12-14

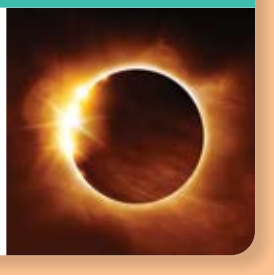
Phoenix, AZ
ICR Creation Mega Conference
(R. Guliuzza, T. Clarey, B. Thomas, F. Sherwin)
ICR.org/Phoenix2023 or 214.615.8306

OCTOBER 15-19

Parks Across America Tour: Grand Canyon
(T. Clarey, B. Thomas, F. Sherwin)
ICR.org/GrandCanyon2023 or 214.615.8306

APRIL 2024 *(Specific dates announced soon!)*

Dallas, TX
ICR Discovery Center
Great American Solar Eclipse 2024
Featuring Apollo 16 astronaut Gen. Charlie Duke and NASA astronaut Col. Jeff Williams
ICR.org/Eclipse2024 or 214.615.8325



ICR DISCOVERY CENTER

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Please check **ICR.org/events** for the most up-to-date event information. If you have questions about a specific event, please send an email to **events@icr.org** or call **800.337.0375** and press 6.

Day 4 Astronomy Meeting at the ICR Discovery Center in Dallas, Texas

Drs. Jake Hebert, Randy Guliuzza, and Tim Clarey (L-R) answer questions during the Uncovering the Truth About Creation Conference at Dale Evangelical Free Church in Harris, Minnesota, in May.

ICR Video Producer Clint Loveness films Drs. Clarey and Hebert on the chilly shore of Lake Superior.

BIG THICKET NATIONAL PRESERVE

PITCHER PLANTS AND BUSY BEES

BRIAN THOMAS, PH.D.

In the early 1800s, pioneers of Southeast Texas initially avoided Big Thicket. Its more than three million acres embraced dense forests, swamps, and few people. Subsistence farmers soon penetrated the thicket in search of solitude. They traded with Coushatta and Alabama Native Americans who had hunted bear and deer there for over a century. Those who kept cattle contended with Karankawas and Comanches. Outlaws and Civil War draft dodgers hid from authorities within its vast foliated lowlands.

Tar and oil oozed to the surface in some spots. The early 20th-century oil boom brought overnight prosperity to those who har-

A Texaco station in Galveston, Texas, in the 1910s

Image credit: Public domain

article highlights

- Big Thicket originally covered over three million acres. Today's park is only about 100,000 acres, but it still offers a glimpse into its remarkable environment.
- The pitcher plant found there is an example of specified design. No evolutionary process could've produced its insect-enticing, drugging, and digesting capabilities.
- Instead of eating a bee, the otherwise carnivorous pitcher plant is engineered to lead it through a determined path that's ideal for pollination.
- These Scripture-affirming designs require the foresight and ingenious engineering of our Creator.

Iconic bald cypress trees in Big Thicket National Preserve in Southeast Texas
Image credit: USDA photo by Larry Rana, CC BY 2.0

vested the crude. Texaco, Inc. was born in Big Thicket. Entrepreneurs depleted those deposits, but the people who had pursued oil or timber thinned out the Big Thicket.

By 1974, after long negotiations between government, landowners, and businesses, Big Thicket National Preserve was established. Today, it includes a patchwork of almost 100,000 acres.[1] A hike through its biodiverse pine forests evokes appreciation for the providence of God, who lets us enjoy these fruits of pioneer and preservationist labors. One creation wonder found here is the pale pitcher plant (*Sarracenia alata*).

The author accesses one of the many trails into Big Thicket.
Image credit: Brian Thomas

A pale pitcher plant attracts a wasp at Big Thicket
Image credit: NPS Photo / Scott Sharaga

Pitcher plants in a Big Thicket bog
Image credit: NPS Photo / Chuck Hunt

A Day in the Life of a Pitcher Plant

Pitcher plants grow from swamp-submerged roots every spring. Small leaves appear first, then flowers. Pitcher-shaped leaves grow after the flowers fade. Each pitcher looks like a vase made out of one leaf with a hood (operculum) like a tiny tarp draped over the opening. These pitchers use a suite of features to catch creepers like insects or slugs. The plant absorbs nutrients such as nitrogen from its captives. This comes in handy in areas where sandy soils have few nutrients.

Three facets of each pitcher point to divine design. First, the specificity of its shapes declares design. Each pitcher's hood exposes enough of the pitcher's mouth to receive rainwater. This mixes with trapped insects and plant-produced enzymes to make a nutritious soup. The hood's underside and the pitcher's lip manufacture nectar laced with a narcotic.[2] When insects from the wet forest floor partake of the nectar, the drug makes them sluggish. Fine inward- and downward-pointing hairs positioned on the hood's underside and on the pitcher's lip nudge prey toward the plant's tube. Once inside, a waxy inner lining proves too smooth for even insect feet to cling to. The pitcher itself is too narrow for a takeoff, preventing flying insects from escaping.

A second facet comes from coordinated features, which always arise from engineering. The insect drug alone, which would require lab experiments to replicate, offers enough evidence to convince us it was created. But someone integrated the plant's chemistry set with fine-tuned shapes, textures, and colors that together confirm creation.

And there's more. The plant places its laced nectar with enticing scents and sights at the top of the pitcher to attract lunch. It also secretes enzymes into the bottom of the pitcher, where it can digest that lunch. Shapes and textures combine with biochemistry and colors to coordinate a complete package.

Pitcher plants absorb the internal contents of their trapped arthropods and leave the exoskeletons behind.
Image credit: NPS Photo

Hard to "Bee"lieve

Only after its flowers fade do pitcher plants grow pitchers. Unlike the pitchers' drugging nectar, these plants' harmless flower nectar attracts and feeds honeybees. This way, their pitchers do not trap the honeybees they need to transfer pollen to the flowers of other plants. This process, called outcrossing, maintains hybrid vigor and thus the plants' long-term genetic health. Without it, the flower would self-pollinate, which would result in inbreeding depression.

How does it ensure this outcrossing? It uses an elaborate setup. The arrangement of its flower's parts anticipates honeybee bodies and behaviors. The flower's petal and sepal arrangement permits bees only one entrance. On its way in, pollen from another flower brushes off the bee and onto the perfectly positioned part of the pistil

Flower petals of the pale pitcher plant provide one-way exit flaps for pollinating honeybees.
Image credit: NPS Photo / Scott Sharaga

that receives pollen, the stigma.

One flower petal hangs from the stalk like an upside-down umbrella. It gives the bee a platform from which to collect pollen placed just overhead. Then, in an expert arrangement, the honeybee cannot exit via the same path it entered. If it did, then it would pollinate the same flower. This presents no problem for our great Creator, the Lord Jesus. He designed *Sarracenia* flower petals as one-way-exit flap doors. He thought ahead when He put all this together. Thus, purposeful or goal-oriented construction is our third creation facet. It requires intelligence to anticipate needs.

Beware Nature-First Words

People often refer to pitcher plant design features with phrases like "highly evolved" or "highly modified." Hogwash. Where can we see evidence that any natural process either could or did craft coordinated specifications for targeted purposes like nutrient capture or outcross pollination? Surely the plant itself has no knowledge of its need to preserve genetic fidelity. Someone outside the plant thought of that.

Romans 1:25 warns about those who would use nature-first phrases to deny the agency and preeminence of their Creator. They have "exchanged the truth of God for the lie, and worshiped and served the creature rather than the Creator, who is blessed forever. Amen." Shame on anyone for crediting (worshiping) nature and time as though they were capable of the kind of craftsmanship that only our Creator could accomplish.

By including a Creator in our thinking, we obtain a real Engineer who ordered up the suite of specifications that demonstrate His handiwork in pitcher plants. Instead of "highly modified" (from what, nobody knows), we can say "highly specified." We can then rightly praise the Lord Jesus, "through whom also He made the worlds" (Hebrews 1:2)—including the specific shapes, coordinated components, and purposeful parts in His pitcher plants.

References

1. Callicott, J. B. et al. 2006. Biocomplexity in the Big Thicket. *Ethics, Place and Environment*. 9 (1): 21-45.
2. Perhaps only some of the eight to 10 *Sarracenia* species produce the drug. Patel, N. R. and R. Krishnamurthy. 2014. Carnivory in pitcher plants: An enigmatic meat-eating plant. *Research and Reviews in Biosciences*. 8 (3): 94-106.

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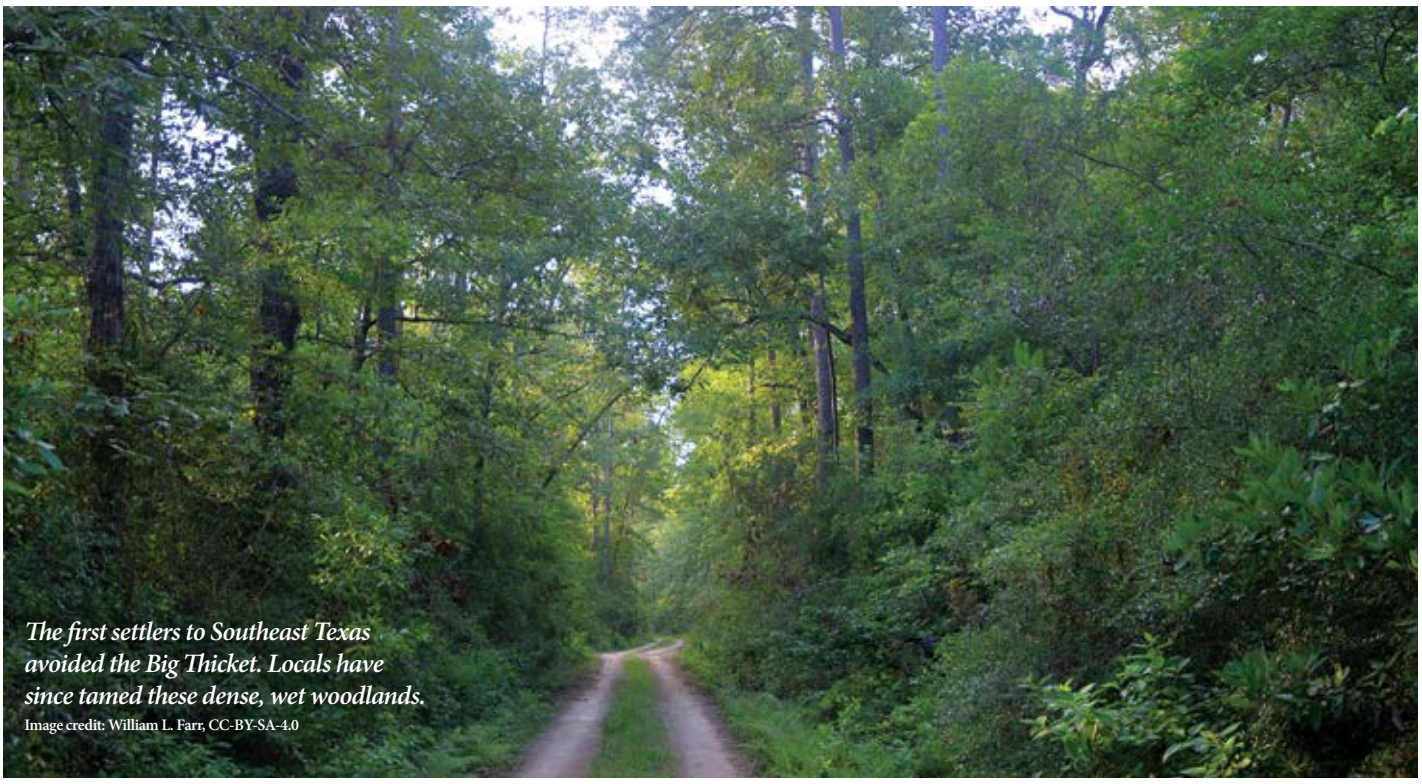
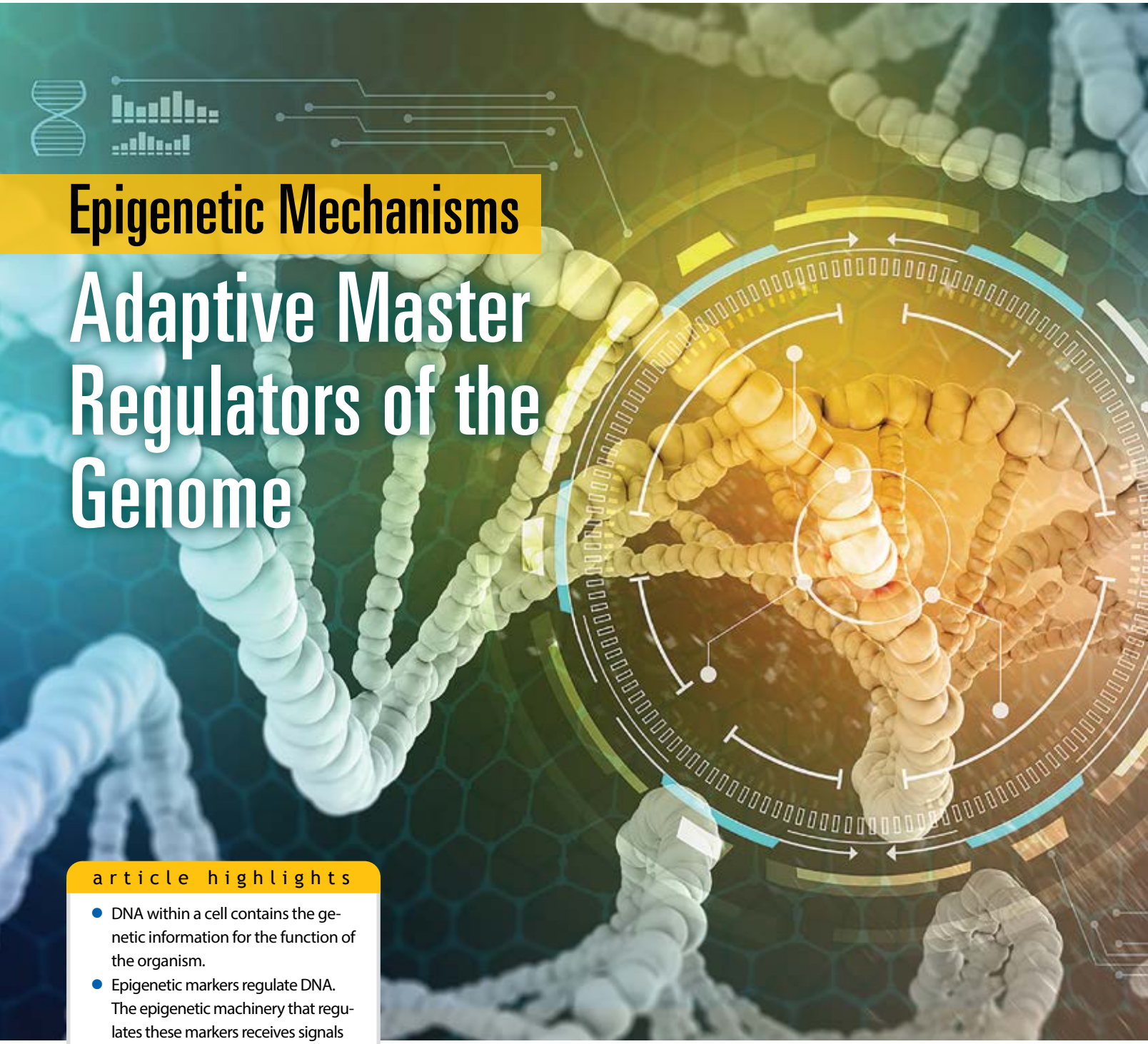


The first settlers to Southeast Texas avoided the Big Thicket. Locals have since tamed these dense, wet woodlands.
Image credit: William L. Farr, CC-BY-SA-4.0

JEFFREY P. TOMKINS, PH.D.



Epigenetic Mechanisms

Adaptive Master Regulators of the Genome

article highlights

- DNA within a cell contains the genetic information for the function of the organism.
- Epigenetic markers regulate DNA. The epigenetic machinery that regulates these markers receives signals from the creature's body as it constantly monitors its environment.
- Precise epigenetic signal responses demonstrate that creaturely adaptations aren't random but are clearly designed systems.
- Creatures possess innate abilities to adaptively respond. These dynamic genetic responses shout design, and design points to a Designer.

The field of epigenetics is one of the most exciting and rapidly expanding scientific research areas in the study of the genome and how it responds adaptively in organisms. The term epigenetics is derived from genetics plus the Greek prefix *epi*, which means "on top of" or "in addition to." In other words, it's an additional type of genomic language that overlays the DNA code that controls how genes are switched on or off. It even determines the three-dimensional structure of the chromosomes in the cell's nucleus.

Epigenetic changes in the genome are modulated dynamically according to sensory input that the body detects from its physical surroundings, signaling molecules it receives from other creatures

(e.g., gut microbes), diet, and even stress. In fact, many epigenetic changes can be heritable and affect traits passed along to children and grandchildren. In many animals and plants, these heritable changes also prime the offspring to be specifically adapted to some aspect of the environment—giving them a preconditioned jumpstart on life.

Two different systems can epigenetically modify an organism's chromosomes. The first and most easily studied system is known as cytosine methylation, which is the addition of chemical methyl groups to the actual DNA base molecules or nucleotide letters. The second system is the modification of proteins called histones that integrate with the DNA and allow it to be packaged and spatially structured in different ways. Both of these types of epigenetic modification determine the accessibility of DNA to protein regulators called transcription factors that bind to regulatory sites in the DNA and control gene activity. This article will discuss each of these modification systems and then show how our current knowledge of epigenetics is connected to creaturely adaptation.

Cytosine Methylation

The DNA code comprises the ordered sequence of the nucleotide letters A (adenine), C (cytosine), T (tyrosine), and G (guanine).[1,2] Epigenetic modification of the actual DNA molecule occurs specifically on the cytosines by the addition of small epigenetic tags called methyl groups—hence the term cytosine methylation. This type of modification is especially pronounced in regions of the genome that have not only a high C content but Gs as well, since Cs pair with Gs in the double-stranded DNA molecule. The presence of these methyl tags in the DNA molecule plays a major role in the way that genes are expressed, i.e., turned off and on.

The DNA sequence of an organism is generally the same across the creature's body in the various different tissues. However, the methylation status or profile across the genome will vary dynamically depending on what kind of tissue the cell is located in, such as heart, lung, bone, or brain tissue. In fact, the methylation states can even vary across cells within the same tissue, since many organs are composed of different types of cells. In humans, greater than 4% of the cytosines in the three-billion-base genome are methylated. In the regions where there are dense amounts of cytosines, greater than 80% are methylated.[2]

In general, when the control regions of genes known as promoters are heavily methylated, the gene is turned down like an adjustable light switch being dimmed. In addition, many other switches called enhancer elements that are around the genome outside of genes can also become methylated, which regulates the level of gene activity as well. But not only are these regulatory switches regulated by DNA methylation, but the main body of genes following the promoter are also subject to different levels of methylation, which has an effect on the activity of that particular gene. The more methylated the DNA is at the start of a gene region, the less active the gene generally is.

The methylation state of DNA across the genome is highly controlled, altered, and maintained by specialized machinery called readers, writers, and erasers.[2] The readers monitor the epigenetic state of DNA methylation across the genome. The writers attach methyl groups to Cs dynamically according to the needs of the cell and the tissue in which it is located. The erasers remove the methyl groups across the genome also according to the cell's demands. The end result is that these actions change and regulate gene expression.

The addition of methyl tags in the writing process is done by enzymes called DNA methyltransferases.[2] In humans and other mammals, scientists have discovered at least three different methyltransferases that function as writers. The erasing function of methyl tags is done by enzymes called demethylases, which remove methylcytosines and replace them with regular cytosines using specialized enzymatic machinery. The exact cellular machinery of specified demethylation remains much less understood than that of methylation. In addition, demethylation can also occur when the DNA is replicated during the process of cell division (mitosis), a process known as passive demethylation.

While the DNA code is very similar

in all cells throughout the human body, the epigenetic code and its patterns vary depending on cell and tissue type. The specific genome-wide epigenetic profile in a particular cell type as it relates to these cytosine tags is called the methylome. In its relation to human health and disease, much research has attempted to find aberrant methylome profiles in certain cell types relating to things like cancer, diabetes, and heart disease. Furthermore, methylome profiles are radically different between various types of organisms. For example, DNA methylation in insects is mostly within gene bodies (coding region of the gene), whereas in plants and mammals it's mostly within a class of DNA called transposable elements.[3]

Histone Modifications

Nearly every cell in the human body has the same genetic code contained within approximately two linear meters of DNA. This huge amount of DNA in the nucleus of a cell presents a considerable organizational and functional engineering challenge. The DNA must be packaged within a microscopically small space while also being dynamically accessible to a host of specialized genetic machinery in a spatially and temporally coordinated manner.

The divinely engineered solution is achieved by the DNA molecules being spooled around a specialized structure containing two pairs of four different proteins called histones.[4] These proteins are designated H2A, H2B, H3, and H4, and form a spool-shaped structure that allows for 147 bases of DNA to be wrapped around it to form a bead called a nucleosome (Figure 1). In between each nucleosome is a small stretch of DNA called linker DNA that's about 10 to 80 nucleotides long, depending on the organism. This whole packaging layout is often referred to as the beads-on-a-string model.

The DNA and histones that together form the basic structure of chromosomes is collectively called chromatin. This chromatinized DNA can also be progressively folded into more compact and condensed chromosomal structures. In general, the more folded and packaged DNA is along a chromosome, the less gene activity there is in that particular region. The more decondensed and even depleted of nucleosomes the DNA is, the more genetically active it is. In fact, DNA templated processes such as transcription (making an RNA copy), recombination (DNA region exchange and shuffling during meiosis), DNA replication, or DNA repair rely on unpackaged "open" chromatin.[4]

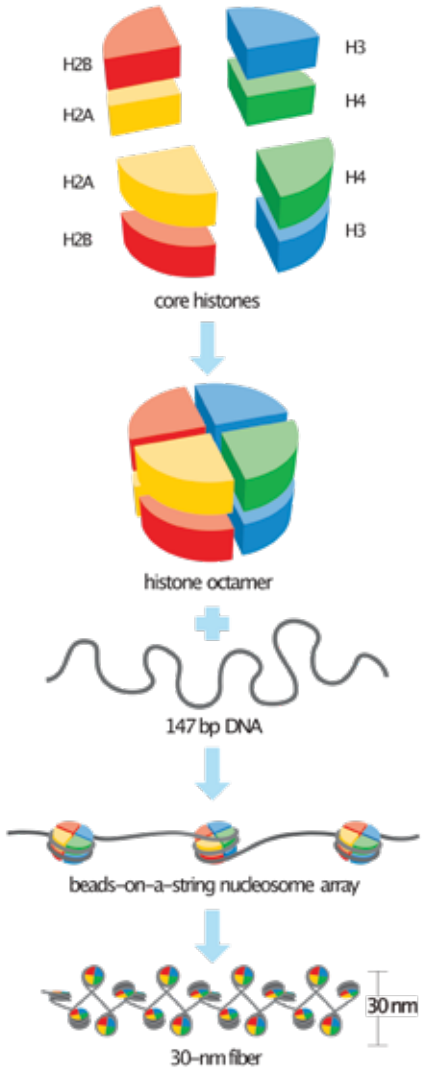


Figure 1. *Basic chromatin structure showing the packaging of DNA around histones to form nucleosomes (beads on a string)*

Image credit: David O Morgan

Histones have the ability to be modified in highly specific ways, which is another important feature of nucleosomes in the accessibility of DNA to various chromatin processes such as gene activity. Each histone protein has a tail that sticks out that can be modified with specialized tags.[4] These histone tail modifications cause the DNA to become more or less accessible to the machinery involved in gene expression.

These protein modifications are called post-translational because they occur after the histone proteins are made. The modifications include methylation, acetylation, phosphorylation, sumoylation, and ubiquitylation. Because these different tags can be added in different ways to eight of the different histone proteins in the nucleosome, a language of over 100 different histone character states can be achieved, leading to a very complex system of chromatin regulation. In addition, the combination of histone modifications also interacts with the system of cytosine methylation in the DNA discussed above, thus controlling the activity and access of the DNA methylases.

Current research in chromatin structure points toward a continuously and dynamically changing genomic architectural landscape. In other words, chromatin is continuously morphing and interconverting between various states of accessibility and three-dimensional structure. Thus, chromatin and its nucleosomes represent much more than a merely static and inert packaging structure. In fact, the genome as a whole is a dynamic scaffold that's capable of responding to specific cues that regulate the accessibility of DNA to various systems and components of the cellular machinery in the nucleus.

Epigenetics in Adaptation

One of the main ways epigenetics facilitates adaptation is by providing altered and heritable gene expression that increases the adaptability of a creature's offspring to novel environments or conditions.[5] In other words, different heritable adaptive traits can be produced from the same genetic background depending on prior events that lead to heritable epigenetic modifications.

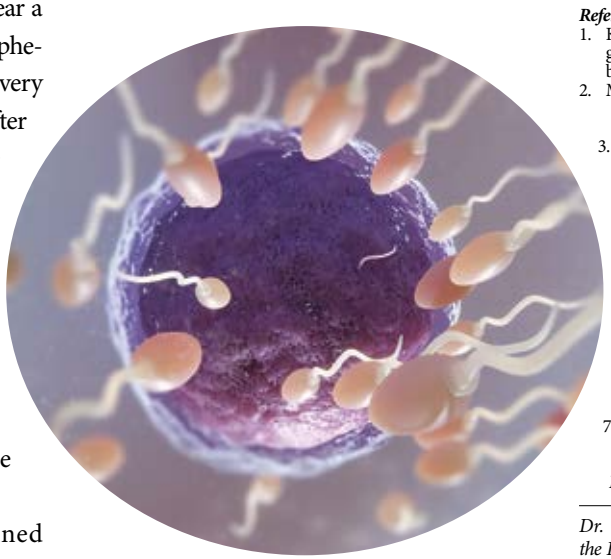
Epigenetic inheritance is especially important for plants because they can't get up and move around to find a more favorable environment. In this respect, one of the first studies highlighting heritable epigenetic adaptation was in the small weedy plant *Arabidopsis* (thale cress). The study was so novel and anti-Darwinian that the paper was titled "Evolution heresy? Epigenetics underlies heritable plant traits."[6]

In this study, researchers tested 80 different *Arabidopsis* strains that were nearly genetically identical except for some that lacked a gene controlling proper DNA methylation patterns. Thus, the test focused on a large population of genetically similar plants that had both normal and aberrant levels of methylation in their genomes. The researchers tested the plants over several generations for flowering time and root growth. The goal of the study was to determine if variability in these traits was passed along from generation to generation by genetic or epigenetic differences. They found that the DNA sequence in the regions of the *Arabidopsis* genome that control both flowering time and root length was identical for all 80 plants and did not contribute the observed variability. What they discovered was that the inherited variability for these important traits was associated with cytosine methylation changes.

In another experiment with animals, researchers conditioned male mice to fear a cherry blossom-like scent called acetophenone by giving them electric shocks every time it was pumped into their cages.[7] After 10 days of this treatment, whenever the cherry blossom scent was in the air, even without an electric shock the mice went into panic mode, expecting to get electrocuted. The researchers also found that these mice developed more smell receptors specifically associated with the scent, which allowed them to detect the acetophenone chemical at lower concentrations.

When the researchers examined the sperm of the males that were shock-conditioned, they found that the odorant receptor gene responsible for acetophenone detection was cytosine-methylated differently compared to the same gene in control mice. In fact, the gene had much less methylation, indicating that it was upregulated to create more odorant receptors. The researchers then inseminated females with the traumatized mice's sperm. The baby mice, who had never interreacted with their fathers, had more acetophenone odorant receptors and also became agitated when acetophenone filled the air. Amazingly, this same trait was epigenetically passed on for several generations.

While these two examples in plants and mice documented adaptive epigenetic inheritance related to cytosine methylation, adaptive histone modifications are also being reported in several different types of creatures. In both fission and budding yeast, up to 20 generations can heritably maintain a variety of specifically induced histone modifications that were regulated by environmental conditions in the yeast's culture medium.[5] In the fruit fly (*Drosophila*), histone modifications were found to be modified related to temperature changes or starvation.[5] And in the small roundworm (*Caenorhabditis elegans*), histone-related gene expression patterns were found to be generationally passed on in response to both heat stress and exposure to bacterial pathogens.[5]



Sperm and egg cell during fertilization

Conclusion

Discoveries in epigenetics present a variety of substantial problems for evolution's failed mutation-selection paradigm. If random genetic alterations of the DNA sequence are not connected with adaptative traits, then nature as a mythical selective agent has nothing to work with.

In fact, the reality of the scientific evidence is that creatures contain innate systems of epigenetic modification as an engineered adaptive response. First, the methylation of DNA and histone modifications are not random features in the genome. These purposeful chemical tags are placed at specific chromatin addresses all over the genome in response to various environmental cues.

Second, complex cellular machinery and surveillance systems must interpret the huge diversity of epigenetic tags not only according to the creature's environment but also based on the type of cell and tissue in which the chromatin is located. Third, for the complete epigenetic system to be passed along during cell growth and to the next generation, there exists yet another separate and necessary system that copies the chromatin profile when the cells are replicated or sperm and egg are produced for reproduction.

The evolutionary story of random mutations and natural selection can't account for DNA's exquisitely engineered systems. Only our Creator Jesus Christ can.

References

1. Kumar, S., V. Chinnusamy, and T. Mohapatra. 2018. Epigenetics of modified DNA bases: 5-methylcytosine and beyond. *Frontiers in Genetics.* 9: 640.
2. Mattei, A. L., N. Bailly, and A. Meissner. 2022. DNA methylation: A historical perspective. *Trends in Genetics.* 38 (7): 676-707.
3. Ashe, A., V. Colot, and B. P. Oldroyd. 2021. How does epigenetics influence the course of evolution? *Philosophical Transactions of the Royal Society B: Biological Sciences.* 376 (1826): 20200111.
4. Millán-Zambrano, G. et al. 2022. Histone post-translational modifications—cause and consequence of genome function. *Nature Reviews Genetics.* 23: 563-580.
5. Stajic, D. and L. E. T. Jansen. 2021. Empirical evidence for epigenetic inheritance driving evolutionary adaptation. *Philosophical Transactions of the Royal Society B: Biological Sciences.* 376 (1826): 20200121.
6. Pennisi, E. 2013. Evolution heresy? Epigenetics underlies heritable plant traits. *Science.* 341 (6150): 1055.
7. Dias, B. G. and K. J. Ressler. 2014. Parental olfactory experience influences behavior and neural structure in subsequent generations. *Nature Neuroscience.* 17: 89-96.

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"The works of the Lord are great, studied by all who have pleasure in them."

Psalm 111:2

*Agreeable tiger moth (*Spilosoma congrua*), ventral view of the head*

Image credit: Micrograph captured and edited by Michael J. Boyle, Ph.D.,The William B. Dean, MD Imaging Center of the Institute for Creation Research

STAFF WRITER

THE MYTH OF TREE THINKING

The instructions to build, maintain, and reproduce every kind of animal on Earth were placed within these organisms when the Lord Jesus created them. The totality of those instructions are called a genome, and they were once thought to be encoded exclusively within deoxyribonucleic acid (DNA) and ribonucleic acid (RNA) molecules.[1] However, researchers are uncovering a far more elaborate set of molecular codes that regulate form and function within each division of life (microbes, protists, fungi, plants, animals) and ultimately determine their stunning biodiversity—both past and present.

As the pace of technology increases, the known number and types of encoded instructions also increase. Compared to what we understood just over 20 years ago when the DNA of the human genome was sequenced, we currently find ourselves in awe of an impressive range of coded instructions that manage many interconnected systems in every organism. This inventory includes epigenetic codes; histone codes; genetic codes; alternative genetic codes; regulatory, enhancer, and promotor codes; and both noncoding DNA and RNA molecules with important roles in almost every cell type.[1,2]

Additionally, where evolutionary biologists once predicted that approximately 2 to 3% of our genome provided functional instructions, it's now estimated that more than 80% of the human genome participates in at least one biochemical function.[1,2]

The Current Evolutionary Explanation

According to evolutionary models for the origin and diversification of life on this planet, every molecular code within organisms is *believed* to have evolved from atoms (e.g., carbon, nitrogen, oxygen) over deep time in a process that began sometime between 4.5 to 3.9 billion years ago.[3,4]

Furthermore, evolutionary views suggest that every cell type, tissue, organ, and organ system produced from these complex codes came about through numerous trial-and-error changes to DNA and RNA. These changes are commonly characterized as mutations that are assumed to be errors and mistakes that occur during copying and decoding of molecular codes.

More complicated mutations are assumed to occur when individual letters of DNA code (nucleotides) or large stretches of DNA sequence (genes) are lost or gained during reproduction. In the most extensive changes, vast sections of chromosomes or

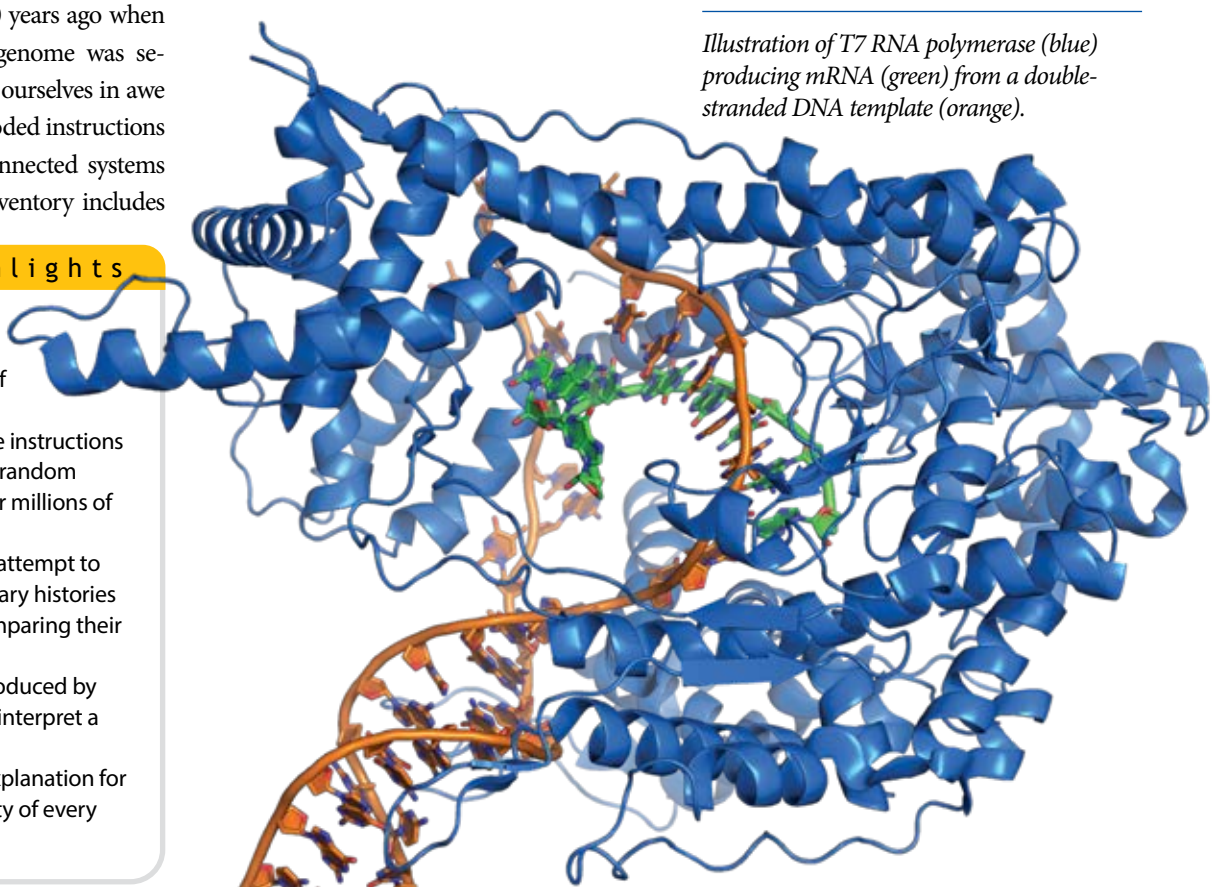


Illustration of T7 RNA polymerase (blue) producing mRNA (green) from a double-stranded DNA template (orange).

article highlights

- Each creature kind has a unique genome containing a variety of encoded instructions.
- Evolutionists claim the instructions for life have arisen by random natural processes over millions of years of Earth history.
- Phylogenetic studies attempt to reconstruct evolutionary histories of all creatures by comparing their genomic instructions.
- Tree-like diagrams produced by phylogenetic studies interpret a false history of life.
- Creation is the true explanation for the origin and diversity of every organism on Earth.

entire genomes are thought to be rearranged or even duplicated, producing multiple copies of genes and/or chromosomes.

Evolutionists envision that the plants and animals that tolerate these changes are somehow *selected* by nature to survive. And given enough time, their body plans and behaviors become significantly altered from the presumed body plans and behaviors of their ancestors. This mutation-selection process is called Darwinian evolution because it describes the primary mechanism of Darwin's original theory of evolution and all subsequent revisions. Evolutionary biologists remain convinced that Darwinian evolution is the most informative explanation for the diversity of all extinct and extant life, while they search deeper and deeper into the past for the origin of life itself.

Improbable Origins of Life

Ever since Charles Darwin and Alfred Russel Wallace independently "conceived the same very ingenious theory to account for the appearance and perpetuation of varieties and of specific forms on our planet,"[5] there have been repeated efforts to explain the primitive origins of life. This area of investigation is recognized today as origins of life research (OoL). In simple terms, OoL proposes to demonstrate the production of living matter from nonliving matter.[6]

There are tremendous barriers to the success of such a production. Researchers would need to (1) synthesize and purify all chemical precursors of the four information-rich macromolecules that are essential for life on Earth: nucleotides, amino acids, lipids, and carbohydrates; (2) generate polymers of each macromolecule that are spatially oriented, self-organizing, replicable, and functional; (3) fabricate a self-dividing cell with a phospholipid bilayer that's interlaced with structural, enzymatic, catalytic, and communicative proteins; (4) establish precise electrostatic properties permitting flow of molecular and chemical information within that cell and between the internal and external cellular environments;[6] and the most fundamental barrier of all—(5) produce the information underlying the codes of all living systems that "has never been observed to arise from purely physical or chemical processes."[7]

These barriers are only a short list of the fundamental challenges that must be overcome to produce eukaryotic cells, which are the basic functional units of life in fungi, plants, animals, and humans. To date, OoL investigators have never produced de novo (anew) any of the essential macromolecule polymers, any structural or heritable components of a functional cell, or any genetic codes required to specify, maintain, and replicate life.[6] Never!

Tree Thinking

Unwavering belief in the natural origin and diversification of life from nonliving matter remains a prominent paradigm worldwide. If only there were an assailable scientific cornerstone upon which the entire evolutionary stronghold teeters.

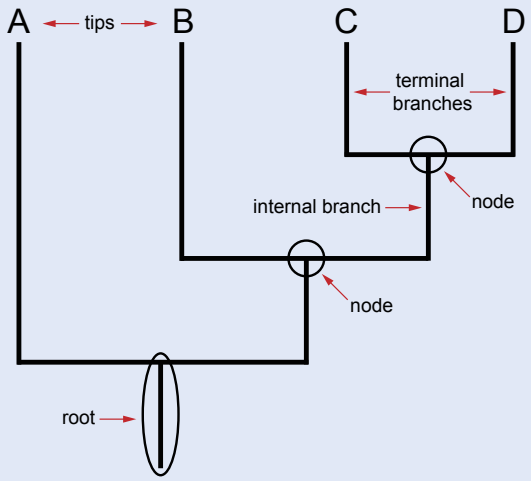
Well, there is. Interpretations of the origin and diversification of life are dependent upon a singular concept—*tree thinking*. Specifically, tree thinking refers to the use of phylogenetic (*phyl-o*, tribe + *-geny*, production) tree diagrams to graphically "visualize evolution as descent from common ancestors."[8] Different branches within such trees are hypothesized to represent distinct lineages of organisms.

The trees are constructed with computer programs. These programs compare statistical similarities and differences among a highly selective set of protein-coding (amino acids) and noncoding sequences from the genomes of organisms living on Earth today. In the grand scheme, the broadest hypotheses are aimed at resolving deep histories leading to major groups of animals and plants. Or, as Charles Darwin once imagined, "each great kingdom of nature."[9]

Following the "Molecular Phylogeny of the Animal Kingdom"[10]—inferred from a single RNA molecule (18S rRNA)—collaborations have steadily increased the amount of sequence data and diversity of taxa under investigation. Across animals, we now have several published studies on the animal tree of life.[11-13] Within animals, there is an arthropod tree,[14] molluscan tree,[15] annelid tree,[16] and mammalian tree,[17] with more trees on the way. In almost every case, the primary goal is to reconstruct evolutionary histories of animal form and function from deep time to the present. And time is the key element. As we are told, "the tree is a historical chronicle: the nodes and branches represent ancestral populations that lived at some particular time in the past" (Figure 1).[8]

So, what do these trees actually show? Of the objects that evolutionary biologists include within a phylogenetic tree, each analysis is limited to showing which objects are more or less similar to each other. However,

Figure 1



Standard phylogenetic tree diagram. A) ctenophores, B) sponges, C) cnidarians, D) all other animals. Ancestral lineages begin at the root where time enters the tree; lineages split at a node and diversify; internal branches connect splitting events at nodes; terminal branches represent current evolution; tips may represent major divisions of life, organisms, species, or genes.

a major flaw in support of tree thinking is the assumption that similarity relationships represent historical relationships. Without the key element of time, tree thinking could not demonstrate ancestor-descendent relationships. As stated above, the grand scheme of tree thinking attempts to explain the origin and diversification of life from prebiotic chemistry to the entirety of Earth's biodiversity across history.

Let's consider an example under intense debate. There are four distinct groups of animals that are thought to comprise the *earliest branches* in the tree of living animals.[12,18] These groups include sponges (Porifera), flat animals (Placozoa), sea anemones and jelly fish (Cnidaria), and comb jellies (Ctenophora). In recent years, phylogenetic reconstructions have promoted two very different arrangements for the position of comb jellies: (1) sponges are the most genetically distant sister group to all other animals,[12] with comb jellies and cnidarians sharing a common ancestor; or (2) comb jellies are the most genetically distant sister group to all other animals and thus the "most basal" lineage.[12,19] Most recently, chromosome-scale comparisons suggest that ctenophores share genetics with non-animal species and likely diverged first among animals.[20]

The comb jellies have distinct nerve and muscle cells; sponges do not have these cells. One of two competing interpretations suggests that nerve, muscle, and other complex cell types would have been present in the last common ancestor (LCA) of animals prior to the evolutionary split between comb jellies and sponges. Therefore, sponges have lost these cell types and the genetic architecture that codes for them.

The alternative interpretation is that nervous and other "innovative" cellular systems would have evolved at least twice—once in comb jellies and then in the ancestor of all other animals.[19] In other words, genes, cells, tissues, and organ systems may be lost or gained to satisfy the most favorable phylogenetic interpretation.

Such interpretations derive from a comparative alignment of thousands of gene-specific amino acids, chromosome content variation, and a presumed tree-like radiation of most major animal lineages over the past 540 million years.[18] This is classic tree thinking: the visualization of evolution as a continuously modifiable tree, which unfortunately today is considered "an essential element of biological literacy."[8]

One Tree of Life

From the example above, it's easy to imagine how molecular phylogenetics has become popular. And as technology advances, tree thinking will continue to grow as a principle application of evolutionary biology.

But is there any truth to it? Are we to believe that the complex molecular instructions of biological life (e.g., epigenetic, genetic, regulatory, noncoding) have been undergoing rearrangement, loss, gain, duplication, doubling, corruption, or other mutational alterations? Should we accept that an unguided, random, error-prone mechanism Darwin called natural selection has been constructing the wondrous diversity of microbes, protists, fungi, plants, and animals? Let's also remember that the origins of prebiotic chemistry (nucleotides, amino acids, lipids, carbohydrates) and their respective products (DNA/RNA, proteins, phospholipids, sugars) are under the same challenges as the most basic unit of all life—the cell.

Collectively, mankind can scarcely begin to describe the molecular, biochemical, and cellular engineering required to construct one microscopic single-cell organism, let alone a human body, which is comprised of 20 to 40 trillion cells. Undaunted by these facts, evolutionary biologists attempt to reconstruct divergent biological histories that can only show that birds are more similar to birds than they are to bees. They carefully survey the nodes and branches of computer-generated tree-like diagrams and fill in the events that supposedly led from one common ancestor to all descendants that swim, crawl, fly, and walk across the earth today. Regardless, while they insist on gaining insights from these *other* trees of life, the scientific cornerstone of tree thinking has begun to crumble under the weight of their bold assumptions.

Why does any of this matter? Because there is only one true Cornerstone who created and sustains all life, including the Tree of Life that mankind has been prevented to take from and eat until Christ returns and we join Him in the new Jerusalem (Genesis 3:22; Revelation 22:14).

As the instructions for life continue to surpass the totality of human understanding, we must also continue to recognize our true origin from a common Architect—the Lord Jesus Christ!

References

1. Mattick, J. and P. Amaral. 2023. *RNA, the Epicenter of Genetic Information: A New Understanding of Molecular Biology*. Boca Raton, FL: CRC Press, Taylor & Francis Group.
2. The ENCODE Project Consortium. 2012. An integrated encyclopedia of DNA elements in the human genome. *Nature.* 489: 57.
3. Makarov, M. et al. 2023. Early selection of the amino acid alphabet was adaptively shaped by biophysical constraints of foldability. *Journal of the American Chemical Society.* 145 (9): 5320-5329.
4. Higgs, P. G. and N. Lehman. 2015. The RNA World: Molecular cooperation at the origins of life. *Nature Reviews Genetics.* 16: 7-17.
5. Darwin, C. and A. Wallace. 1858. On the tendency of species to form varieties; and on the perpetuation of varieties and species by natural means of selection. *Zoological Journal of the Linnean Society.* 3 (9): 45-62. Published online July 27, 2011.
6. Tour, J. 2019. Time out. *Inference: International Review of Science*, 4.
7. Gitt, W. W., R. W. Compton, and J. A. Fernandez. 2011. *Without Excuse*. Powder Springs, GA: Creation Book Publishers.
8. Baum, D. A. and S. D. Smith. 2012. *Tree Thinking: An Introduction to Phylogenetic Biology*. Greenwood Village, CO: Roberts and Company Publishers.
9. Darwin, C. 1903. Letter to T. H. Huxley, September 26, 1857. *More Letters of Charles Darwin*. London: John Murray.
10. Field, K. G. et al. 1988. Molecular Phylogeny of the Animal Kingdom. *Science.* 239 (4841): 748-753.
11. Philippe, H., N. Lartillot, and H. Brinkmann. 2005. Multigene Analyses of Bilaterian Animals Corroborate the Monophyly of Ecdysozoa, Lophotrochozoa, and Protostomia. *Molecular Biology and Evolution.* 22 (5): 1246-1253.
12. Hejnol, A. et al. 2009. Assessing the root of bilaterian animals with scalable phylogenomic methods. *Proceedings of the Royal Society B: Biological Sciences.* 276 (1677): 4261-4270.
13. Philippe, H. et al. 2009. Phylogenomics Revives Traditional Views on Deep Animal Relationships. *Current Biology.* 19: 706-712.
14. Meusemann, K. et al. 2010. A Phylogenomic Approach to Resolve the Arthropod Tree of Life. *Molecular Biology and Evolution.* 27 (11): 2451-2464.
15. Kocot, K. M. et al. 2011. Phylogenomics reveals deep molluscan relationships. *Nature.* 477: 452-456.
16. Weigert, A. et al. 2014. Illuminating the Base of the Annelid Tree Using Transcriptomics. *Molecular Biology and Evolution.* 31 (6): 1391-1401.
17. Foley, N. M. et al. 2023. A genomic timescale for placental mammal evolution. *Science.* 380 (6643): eabl8189.
18. Dunn, C. W. et al. 2014. Animal Phylogeny and Its Evolutionary Implications. *Annual Review of Ecology, Evolution, and Systematics.* 45: 371-395.
19. Moroz, L. L. et al. 2014. The ctenophore genome and the evolutionary origins of neural systems. *Nature.* 510: 109-114.
20. Schultz, D. T. et al. Ancient gene linkages support ctenophores as sister to other animals. *Nature*, published online before print May 17, 2023.

ICR Discovery Center 5-Star Yelp Review

My family enjoyed this beautiful center. It's very organized, clean, family-friendly, and there's a lot to see and do. We booked one of the planetarium shows, which was really enjoyable…. This is a Christian-based science center, so they provide another perspective to history, sciences, and discovery…always good to have an open mind! The walk-through area was really fun; there are interactive displays, come-to-life portraits of inventors and discoverers debating their findings, and there's a to-scale [room] that shows what the inside of Noah's Ark could have been like. Makes for a fun family outing!

— J. H.

I got my latest edition of *Acts & Facts* May/June 2023 magazine. I turned to the article about Jupiter's young moons. When I saw the picture, the first thing I thought of is how different they are in glory. It reminds me of 1 Corinthians 15:40-41: "There are also celestial bodies and terrestrial bodies; but the glory of the celestial is one, and the glory of the terrestrial is another. There is one glory of the sun, another glory of the moon, and another glory of the stars; for one star differs from another star in glory." I am amazed how they all are so different.

— R. M.

I served on the ICR board in the 1980s during Dr. John's [Morris] tenure as president. Years before that, I remember him telling us about his first trip to Ararat [while] sitting on the floor of our living room. He and his father made a powerful impression on us and our children, and I credit their strong faith as adults to the grounding they had in the most important truth in this world—"In the beginning God created the heavens and the earth." May God comfort his family and continue to bless ICR for generations to come.

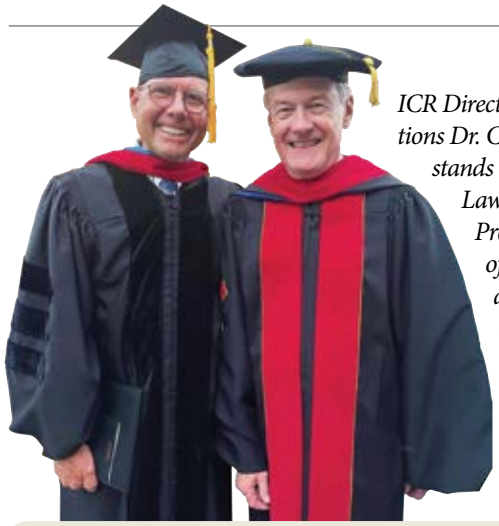
— B. P. A.

Editor's note: Thank you for sharing your memory of Dr. John. ICR is honoring his life and legacy through a new memorial fund. Please see page 7 for more details.

Dear ICR, The money I've enclosed is all that I have. I would donate more, but I'm only eleven years old. It's awesome to hear about your blind cavefish research. May the Lord bless you.

— J. D.

Editor's note: Thank you so much for supporting ICR. We're glad you're learning more about God's glorious creation through our work. God bless you as well.



ICR Director of Donor Relations Dr. Chas Morse (left) stands with Dr. Steven J. Lawson, Professor of Preaching and Dean of D.Min. Studies at The Master's Seminary. Chas received his Doctor of Ministry degree from the seminary on May 7, 2023.

Have a comment?
Email Editor@ICR.org or write to
Editor, P. O. Box 59029, Dallas, TX 75229.
Unfortunately, ICR is unable to respond to all correspondence or accept unsolicited manuscripts, books, email attachments, or other materials.

Written by Michael Stamp. Illustrated by Lori Fausak.

Creation Kids

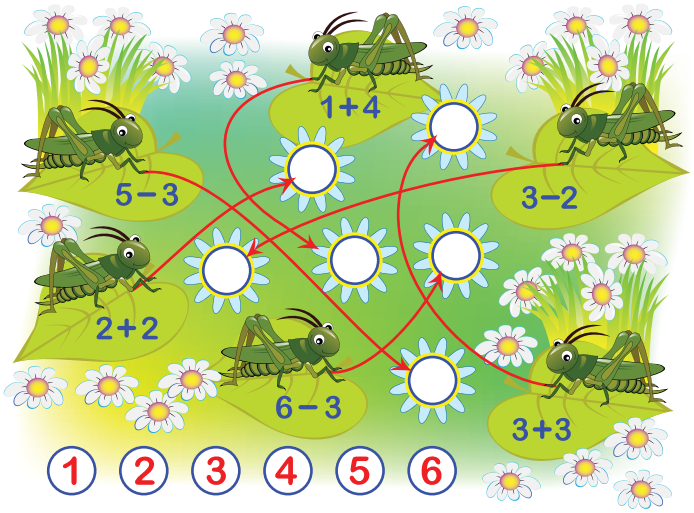
Sounds of Summer

ICR INSTITUTE FOR CREATION RESEARCH

Step into your backyard on an early summer morning and you might hear an orchestra of creatures. Chirp, croak, tweet, buzz! And when the sun sets, another group of creatures tunes up. Did you also know...

- ✔ Male cicadas are the loudest daytime insect singers. They use special abdominal organs called tymbals to make their noisy buzzing sound.
- ✔ During the day, the common true katydid's leaf-green color keeps it camouflaged. But at night, it sings "ch-ch-ch" from the treetops.
- ✔ Crickets and katydids rub a "scraper" on their hind leg against a "file" on the base of their forewing. It's like playing a violin!
- ✔ Each frog species has its own unique croak to attract a mate or warn other frogs to get out of its territory.

Help the crickets solve these problems.



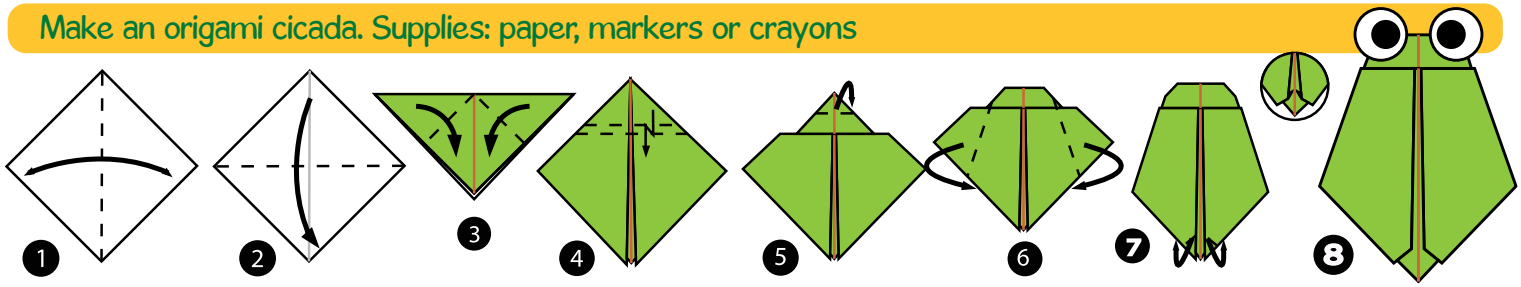
Can you name these summer songsters?

1. _____

2. _____ 3. _____

4. _____ 5. _____

Make an origami cicada. Supplies: paper, markers or crayons



DESIGNED BY SUSAN WINDSOR

Answers: 1. gray treefrog, 2. mourning dove, 3. cricket, 4. cicada, 5. barred owl

NEW!

God Created BIRDS

"In the beginning God created..." (Genesis 1:1)

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BGCB

In *God Created Birds*, explore the funky feathers, wacky wings, and brilliant beaks of these colorful creatures. What's the world's fastest bird? Can ravens do gymnastics? And are bluebirds actually...blue? Discover a bird's-eye view of these animals' fascinating features that point to the expert handiwork of our Creator and Savior, the Lord Jesus Christ.

God Created MONKEYS

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What makes a monkey, well....a monkey? In *God Created Monkeys*, you'll find answers to your questions, colorful pictures, crazy hairstyles, cool fossil facts, and more! Best of all, you'll discover that our world's amazing monkeys point to the incredible power and creativity of our Creator and Savior, the Lord Jesus Christ.

God Created T. REX

God created *Tyrannosaurus rex* with the rest of the land animals on Day 6 of the creation week. This famous theropod dinosaur stomped on Earth just thousands of years ago. What did *T. rex* eat? Did it somehow turn into a bird? In *God Created T. rex*, you'll find answers, fascinating dino facts, and stories of fossil discoveries!

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