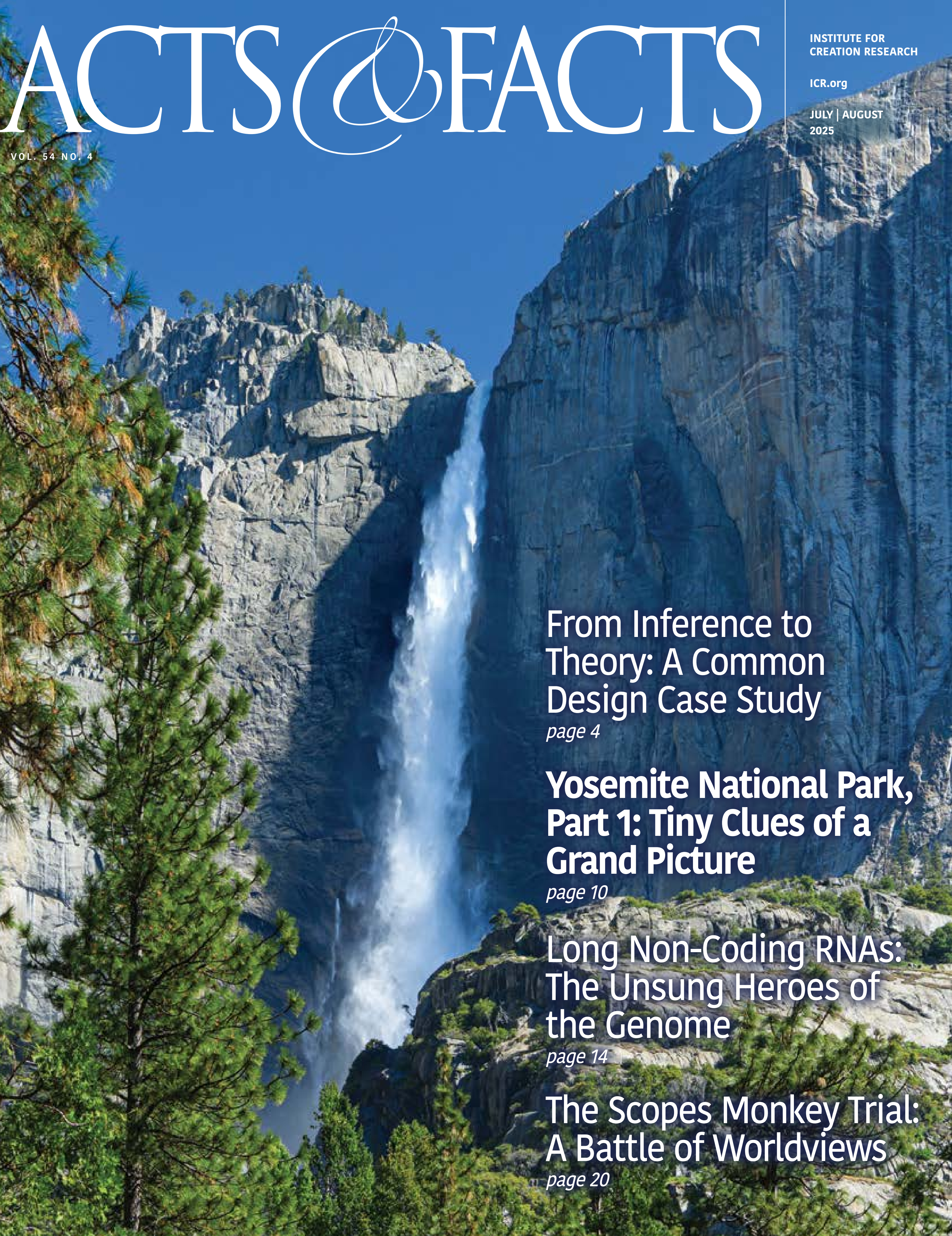

ACTS & FACTS

INSTITUTE FOR
CREATION RESEARCH

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JULY | AUGUST
2025

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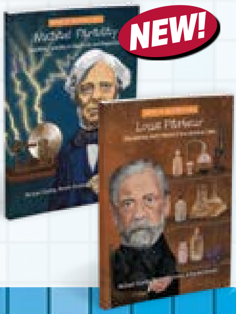

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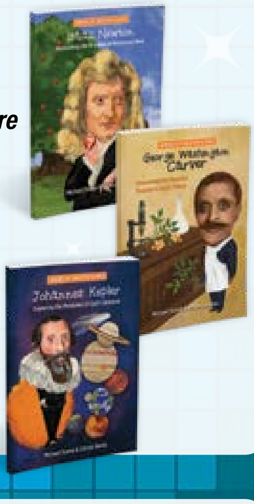

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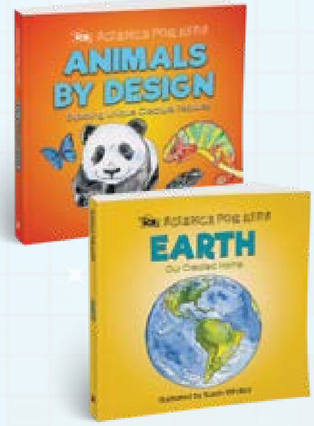

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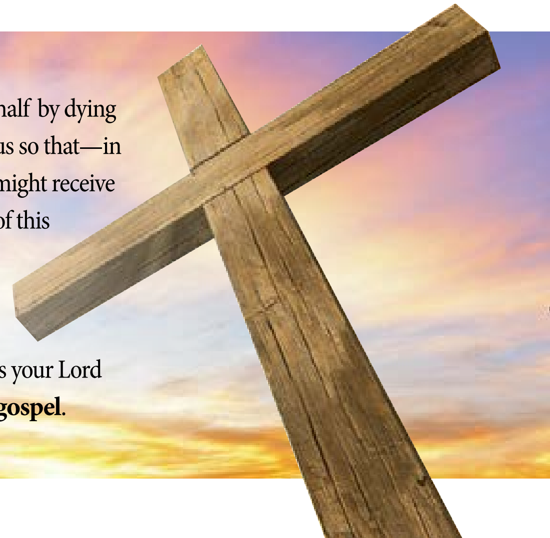

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DESIGNER
Dennis Davidson

[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)

ISSN (print): 1094-8562
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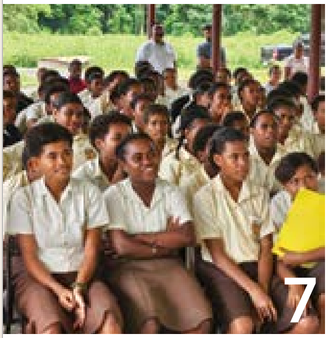
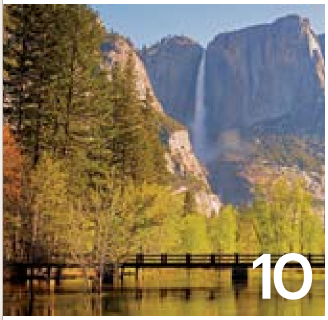
All Scripture quotations are from the New King James Version unless otherwise indicated.

Front cover: Yosemite Falls, Yosemite National Park
Image credit: iStock | GomezDavid





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From Inference to Theory
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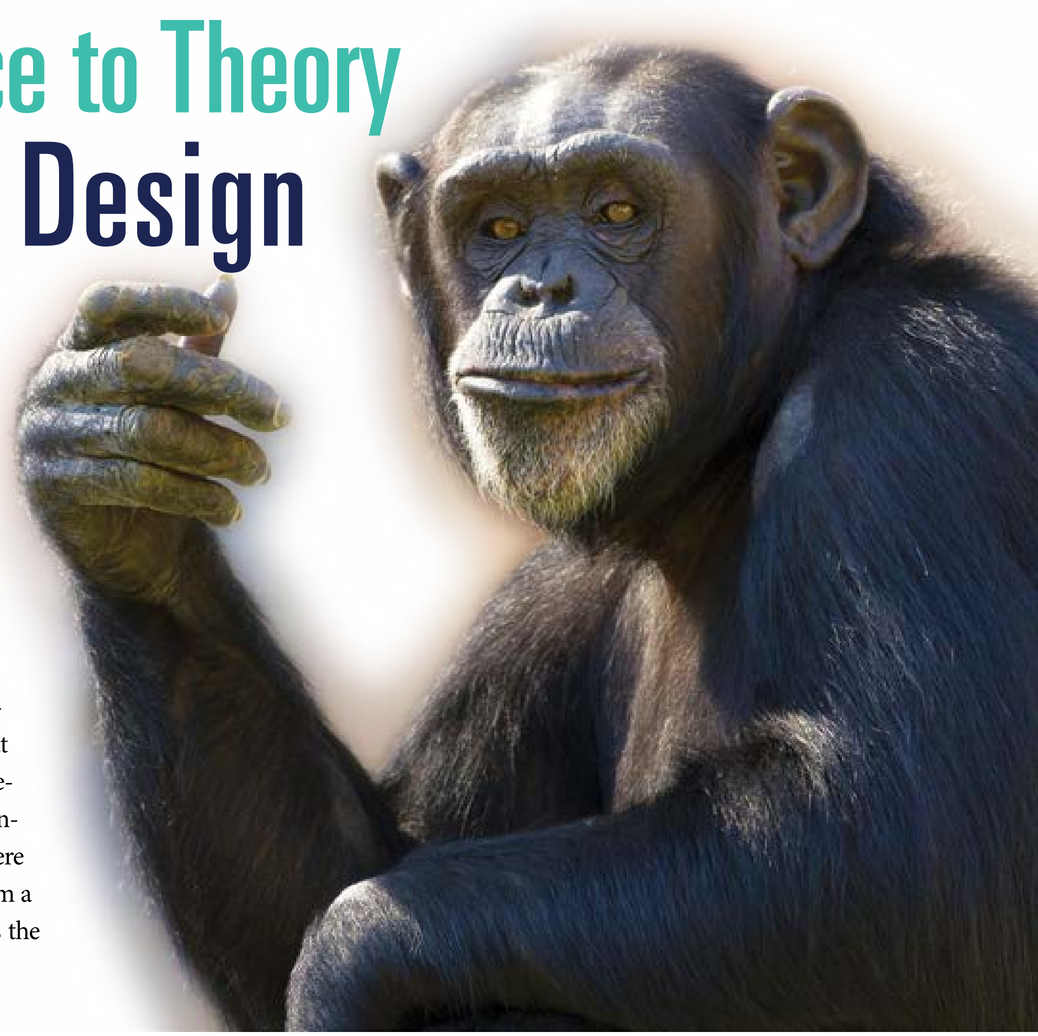


RANDY J. GULIUZZA, P.E., M.D.

Without a doubt, humans, chimpanzees, and other organisms share similar features. An early explanation was that these features reflect similar designs because they serve similar purposes. Then evolutionary theory hypothesized that similar features were explained by (and are evidence for) descent from a common ancestor. Which explanation matches the evidence?

Case Study: Common Design vs. Common Ancestry

The history of the debate between whether common design or common ancestry better explains biological similarity is a fascinating case study. It starts at a time before researchers could identify the order of DNA's building blocks and deals with what each side expected to find when technology became more advanced—either that the building blocks would be similar (common design) or dissimilar (common ancestor).

This is a head-to-head match between the design-based intuitions of creationists and the predictions of the foremost evolutionary theorist, Ernst Mayr. This case study tests the quality of each theory by evaluating the accuracy of its predictions and also shows the value of having an accurate theory so that researchers can think correctly and be on the right track from the outset.

We'll trace the development of thought by some creationists and intelligent design (ID) advocates from early design-based intuitions to a *historical* science. This enabled inferences based on design detection and finally led to the bona fide, hypothesis-based theory of biological design (TOBD). ICR is developing the TOBD into a fully *operational* theory that helps craft detailed research questions and enables specific predictions.[1] Finally, we'll see how evolutionary predictions made to explain similar features proved instead to be major blunders.

Design-Based Predictions: Common Central Design—Unique Details

As early as 1802, William Paley, a pioneer of design-based explanations, compared living things to human-engineered machines. He postulated that the origins of similar features in diverse creatures could be explained by how man-made machines are copied and uniquely modified for similar—but not identical—uses. He wrote,

> Whenever we find a general plan pursued, yet with such variations in it as are, in each case, required by the particular exigency for the subject…we possess, in such a plan and such adaptation…the strongest evidence for intelligence and design….Arkwright's mill was invented for spinning cotton. We see…such modification of the original principle, such variety of the same plan…to observe it in different applications [for spinning wool, flax, and hemp]….Very much of this reasoning is applicable to what has been called comparative anatomy. In their general economy, in the outlines of the plan, in the construction as well as offices of their principal parts…[2]

Paley held that similar comparative anatomy was due to similar functions by design. It wasn't until the mid-twentieth century that links between anatomy and genetic information were better understood. So the different explanations for similarity naturally extended past anatomy to genetics.

In 1975, Dr. Henry Morris claimed there would be common underlying design patterns to explain similar structures. He wrote,

> The creative process would have designed similar structures for similar functions and different structures for different functions….In the creation model, the same similarities are predicted on the basis of a common purposive designer.[3]

The "creative [or engineering design] process" referenced includes a minimum of (1) recognizing the purpose of a design, (2) identifying its constraints, and (3) producing the needed underlying information (specifications, spatial layout and orientation, schedule, etc.) for construction.

This set the stage decades in advance for techniques that could conduct detailed genetic analysis and allow for a rare head-to-head test of ID and evolutionary expectations. While the differing traits of various organisms let them occupy diverse environmental niches, advocates for design-based explanations still expect that similar features fulfilling similar purposes are based on similar information. Extreme multistep, specified regulation over thousands of details produces organisms that are unique but still have similar overall plans.

Evolutionary Predictions: Not Similar Information but Convergent Evolution

All prominent evolutionists reject the common design predictions, but their rationales differ. Darwin's was theological, doubting "that it has pleased the Creator to construct all the animals and plants in each great class on a uniform plan."[4] He derided any hypothesis that claimed similar anatomy and information reflect common design as "not a scientific explanation."[4]

Ernst Mayr, Harvard's leading evolutionary theorist, predicted in 1963 that looking for similar DNA between very diverse organisms would be pointless. He explained differences in creatures' traits by random genetic changes over millions of years that obliterated genetic similarities.

> Much that has been learned about gene physiology makes it evident that the search for homologous genes [similar codes due to common ancestry] is quite futile except in very close relatives. If there is only one efficient solution for a certain functional demand, very different gene complexes will come up with the same solution, no matter how different the pathway by which it is achieved. The saying "Many roads lead to Rome" is as true in evolution as in daily affairs.[5]

Since common ancestry does not explain similarities in organisms whose ancestors "diverged" eons ago, new evolutionary explanations have emerged. Now "convergent evolution" is frequently invoked, as denoted in Mayr's "Many roads lead to Rome" pronouncement.

For example, what explains similar parts found in diverse creatures' eyes? Evolutionists claim similar environments "pressured" the creatures to independently converge upon comparable complex features at least 40 times, and probably as many as 65.[6] This evolutionary naturalistic explanation counterintuitively posits that millions of years of genetic tinkering propels organisms to *diverge* into increasingly different classes while simultaneously cobbling their traits to *converge* upon "the same solution" to problems.[5]

Creationists remain skeptical that highly complex structures independently evolve over and over again. They also characterize the evolutionist's imagined convergent evolution as a mystical rescuing device to explain biological observations that are contrary to the belief in universal common ancestry.[7]

Evolutionary Predictions Were Spectacularly Wrong

A landmark discovery between 1978 and 1984 identified a *common* genetic basis prescribing how similar structures can be built across diverse organisms.[8] One example is *Hox* genes, whose regulatory and developmental functions are responsible for core basic design patterns in developing embryos.

This astounding find was so *opposite* evolutionists' notions that it clearly constituted a spectacular evolutionary blunder. Evolutionary biologist Sean Carroll described the implications of the discovery.

> When the sequence of these homeoboxes were examined in detail, the similarities among species were astounding. Over the 60 amino acids of the homeodomain, some mice and frog proteins were identical to the fly sequences at up to 59 out of 60 positions. Such sequence similarity was just stunning. The evolutionary lines that led to flies and mice diverged more than 500 million

> years ago….No biologist had even the foggiest notion that such similarities could exist between genes of such different animals. The *Hox* genes were so important that their sequences had been preserved throughout this enormous span of animal evolution.[9]

He continued,

> The discovery that the same sets of genes control the formation and pattern of body regions and body parts with similar functions (but very different designs) in insects, vertebrates, and other animals has forced a complete rethinking of animal history, the origins of structures, and the nature of diversity. Comparative and evolutionary biologists had long assumed that different groups of animals, separated by vast amounts of evolutionary time, were constructed and had evolved by entirely different means.[10]

Yet evolutionists still won't consider that these genes may have a common designer. Rather than concede their predictions were greatly mistaken, they're just "stunned" at the appearance of this supposedly new, unexpected evidence for evolution. The only evidence that *Hox* genes *can* be "preserved throughout this enormous span of animal evolution" is the belief that life evolved from a common ancestor.[9]

And what about all of those "sure" claims of convergence? They get promptly but quietly scrapped. *Voilà*, *Hox* genes instantly turn into preserved ancient DNA, which is now used—with equivalent certainty—as evidence of common ancestry.

Creationist Expectations of Common Design and Information Confirmed

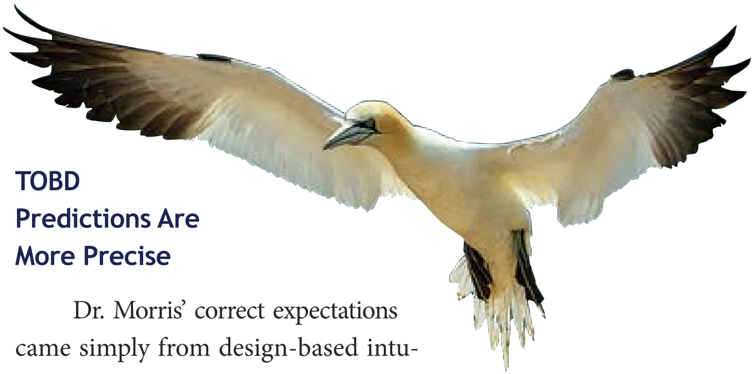
It is now factually confirmed that similar genetic regulatory information is *common* to many classes of organisms and aids in achieving similar *functional anatomy*—many with remarkably similar *designs*. Sean Carroll again relates the confounding weight of this finding.

> It was inescapable. Clusters of *Hox* genes shaped the development of animals as different as flies and mice, and now we know that includes just about every animal in the kingdom, including humans and elephants. Not even the most ardent advocate of fruit fly research predicted the universal distribution and importance of *Hox* genes. The implications were stunning. Disparate animals were built using not just the same kinds of tools, but indeed, the very same genes![11]

What about the teaching that 40 independent evolutionary events developed eyes? That proved to be *another* incredible evolutionary blunder and validation of creationists' design-based expectations. As Carroll candidly continues,

> Natural selection has not forged many eyes completely from scratch; there is a common genetic ingredient to making each eye type, as well as to the many types of appendages, hearts, etc.[12]

Hox genes appear to be the "smoking gun" of common design that creationists expected for decades. Eyes as sensors are the common design, and *Hox* genes are the common information across diverse groups of organisms. In other areas of research, this fact would be ascribed to common engineering instructions.



TOBD Predictions Are More Precise

Dr. Morris' correct expectations came simply from design-based intuitions. ICR's theory of biological design is even more useful. It assumes that basic research of biological functions is within the domain of engineering practice and that these functions will be accurately characterized by engineering principles.

A TOBD extends Paley's 1802 principle that corresponding similar features between different creatures is due to similar function to predict that we will find corresponding elements between *human-engineered* and biological systems performing similar functions. Thus, analyzing human engineering practices can inform biological predictions.

Scientific predictions will be more precise, and likely more accurate, if science adopts the *operational* theory of biological design that hypothesizes that the best explanation for why creatures appear so highly engineered is that they are engineered. And the glory will belong to the Master Designer, our Creator Jesus Christ.

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This article is adapted from Guliuzza, R. J. 2015. Major Evolutionary Blunders: Evolutionary Predictions Fail the Reality Test. *Acts & Facts*. 44 (9): 17–19.

Dr. Guliuzza is the 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 received an honorary doctor of divinity from Southern California Seminary. He 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.

Creation Mission in Fiji

BRIAN THOMAS, PH.D.

In 2024 my wife, Michele, and I went to Fiji for a fantastic creation mission.[1] We had the opportunity to go again this year, and what a joy it was to partner with such great workers and supporters.[2] We all shared one goal for the week: present evidence for creation, our Creator, and our Savior. Like last year, we had toasty, tropical, fast-paced, power-packed visits to Fijian high schools. Here's a snapshot of what we did and what to pray for.

Our desire is to reach every high school in Fiji with the gospel. Teams visited about 40 high schools near the capital, Suva, last year. This time we traveled to the north side of the main island, Viti Levu. Most folks there are Indian or Indo-Fijian and follow Hinduism.

During our week, two teams each traveled to two schools per day for five days. At every school, our organizer would find the principal and a large place for students to assemble. Perhaps half the schools had a covered space.

Each team brought a projector, screen, laptop, speaker, microphone, and hands-on demonstrations. The speakers traded sections, so this year I gave evidence for Noah's Flood and warned students to prepare for the next worldwide judgment.[3] Just when I sounded the most boring, my wife ran through the crowd in a sweltering *T. rex* suit. My co-teacher, Chris Lowes,[4] shared the way to salvation: repent of one's sins and trust in Jesus. At the end of our presentation, we handed each student a copy of *Explore the World* by Bruce Malone and Julie Vonn Vett.[5,6] Its full-color pages illustrate Christ as Creator and Savior.

Why would someone ride for hours on gravel roads in a hot cargo van? Why survive on granola bars or visit places with no bathrooms or clean water? These are paltry prices to pay to reach these students. Each precious face beckons us toward the heart of our Lord Jesus, who said, "Let the little children come to Me, and do not forbid them; for of such is the kingdom of heaven" (Matthew 19:14).

Some plow the rough ground of human hearts. Others sow gospel seeds, like we did in Fiji. And then God sends people to water those seeds, like team leader Fred Brashear and Sister Lagi.[7,8] Please pray with us for a harvest of Fijian souls "that both he who sows and he who reaps may rejoice together" (John 4:36).

Fijian high school students enjoy our team's hour-long assembly where they hear that their Creator wants to be their Savior

Image credit: Tracy Lowes

Michele discusses pages from Explore the World *with boys at an orphanage*

Image credit: Brian Thomas

Michele waits for her cue to accost the crowd as part of our team's school presentation

Image credit: Tracy Lowes

Dr. Brian Thomas with students who attended the assembly

Image credit: Tracy Lowes

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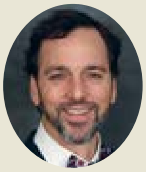
2. We thank the Institute for Creation Research, friends, and family for their support and the Creation Science Association of Fiji for this missions opportunity.
3. Tomkins, J. P. Coming Judgment. *Days of Praise*, July 12, 2022.
4. Chris and Tracy Lowes represent Search for the Truth Ministries.
5. *Explore the World* is available at SearchForTheTruth.net/product/explore-the-world.
6. Bruce and Robin Malone run Search for the Truth Ministries, which supplies the content for these student assemblies in Fiji and other countries.
7. Fred Brashear is an American missionary to Fiji. He runs Character Under Construction, a follow-up discipleship program for students.
8. Sister Lagi helps organize the mission trips and faithfully prays for her country.



Dr. Thomas is a research associate at the Institute for Creation Research and earned his Ph.D. in paleobiochemistry from the University of Liverpool.

JULY 11–12

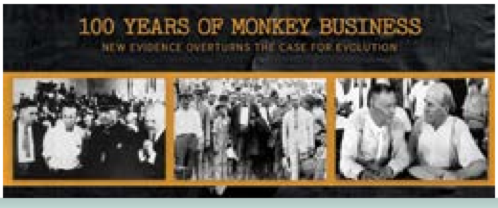
Scotts, MI
Country Christian Evangelical Free Church
Creation Weekend Seminar
(T. Clarey)
ICR.org/ScottsMI or 214.615.8325

AUGUST 3

Weatherford, TX
Parker Bible Church
(F. Sherwin)
ICR.org/WeatherfordTX or 214.615.8325

AUGUST 6–10

Chattanooga, TN
100 Years of Monkey Business Conference
(R. Guliuzza, T. Clarey, B. Thomas, D. Napier, E. Steele)
Featured speakers: Michael Farris of Patrick Henry College and Josh Timonen, former atheist and Richard Dawkins' "right-hand man."
Field trips to geological and historical sites with ICR scientists!
Family fun night! Conference sessions for children and youth!
Registration required
ICR.org/ChattanoogaTN or 214.615.8306



AUGUST 13–16

Glendive, MT
Glendive Dinosaur and Fossil Museum
ICR Dinosaur Dig Experience
(T. Clarey)
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ICR.org/DinoDig or 214.615.8306

AUGUST 29–31

Reno, NV
Granite Hills Baptist Church
(R. Guliuzza)
Registration required
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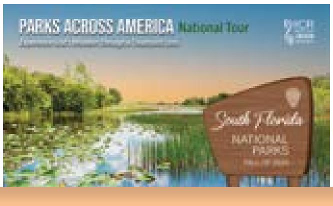
SAVE THE DATE

SEPTEMBER 18–21

Lafayette, LA
First Baptist Church
Foundations of Creation Conference
(R. Guliuzza, T. Clarey, B. Thomas, F. Sherwin, J. Hebert, D. Napier, E. Steele)
Youth conference with Matt Miles of Creation Truth Foundation and children's sessions with ICR's Kids on Mission Director Miss Emmy Steele!
Registration required
ICR.org/LafayetteLA or 214.615.8333

OCTOBER 1–6

Homestead, Florida
Parks Across America Tour:
South Florida Parks
Registration required
ICR.org/Parks-Across-America-Tour or 214.615.8325



OCTOBER 17–18

Beaverton, OR
Southwest Bible Church
Portland Area Creation Conference
(R. Guliuzza, T. Clarey, B. Thomas, J. Hebert, D. Napier, E. Steele)
Featured speakers: NASA astronaut Colonel Jeff Williams, Bill Hoesch of the Mount St. Helens Creation Center, and Judy Salisbury of Logos Presentations.
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OCTOBER 24–25

Edmonton, Alberta, Canada
Creation Weekend Conference
Sponsored by Creation Science Association of Alberta
(B. Thomas)
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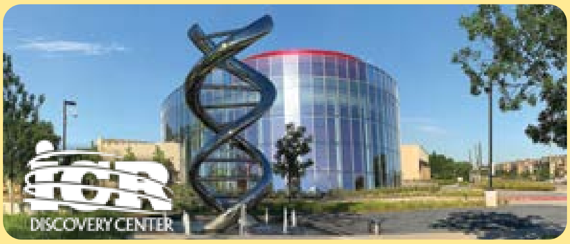

JULY 4

Independence Day

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SEPTEMBER 1

Labor Day Celebration

Enjoy educational presentations, food trucks, a petting zoo, fun activities, and discounted tickets!

SEPTEMBER 18

North Texas Giving Dollar Day at the Discovery Center

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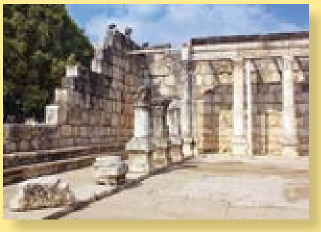
OCTOBER 11

Dallas, TX
ICR Discovery Center
Estate Planning Workshop
ICRgiving.org or 214.615.8353

NOVEMBER 8

Biblical Archaeology Conference: Evidence for the Bible



Join us for an insightful conference featuring scholars Dr. Titus Kennedy, Dr. Randall Price, and Dr. Jim Johnson presenting archaeological discoveries and research highlighting the compelling evidence for the Bible. Tickets available at our website.

SERIOUS SCIENCE TALKS

Last Saturday of select months

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DAY4 ASTRONOMY MEETING

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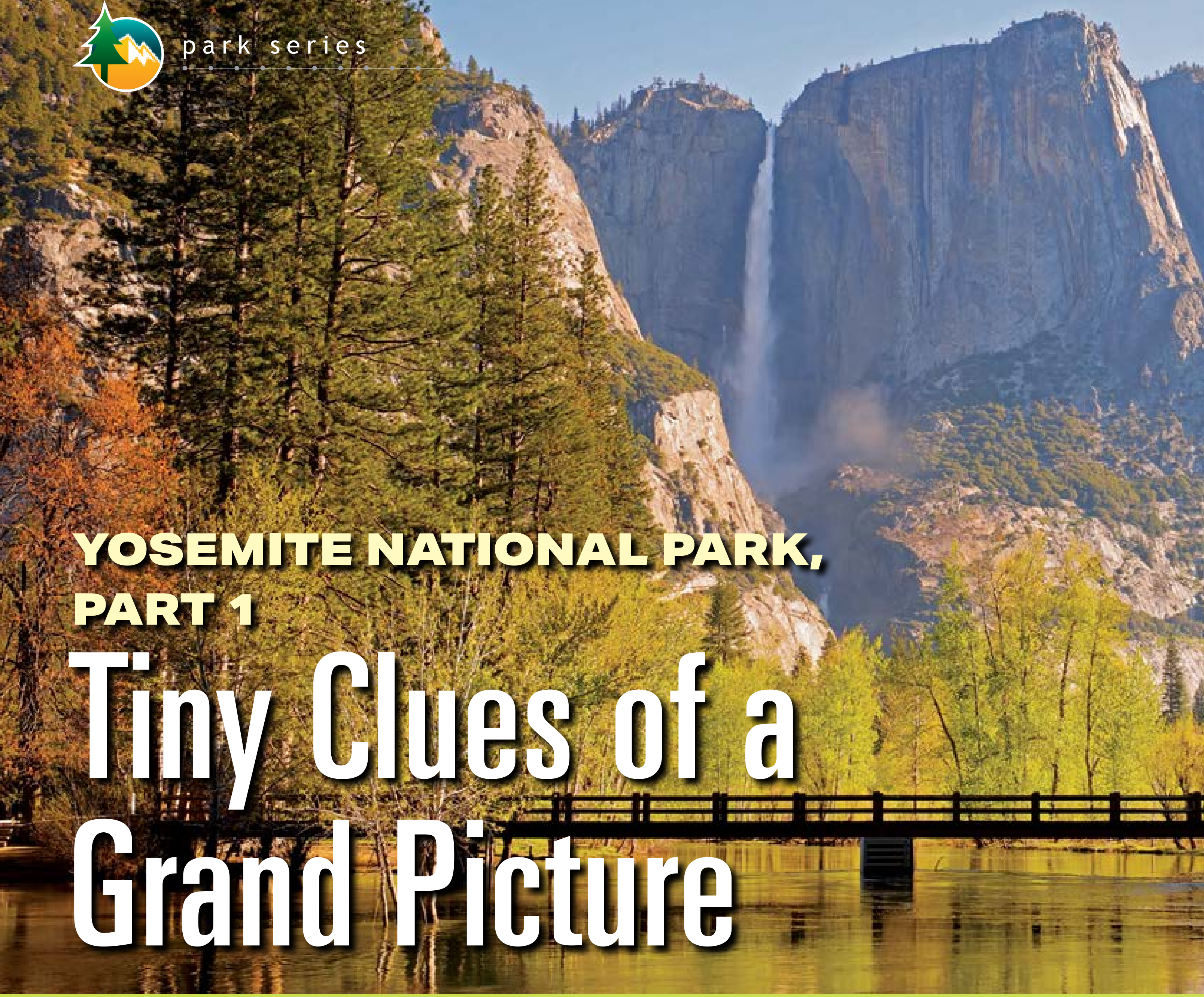
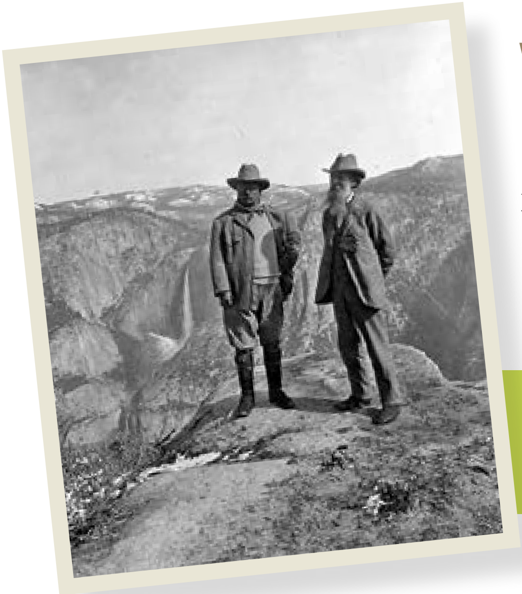


YOSEMITE NATIONAL PARK, PART 1

Tiny Clues of a Grand Picture

BRIAN THOMAS, Ph.D.



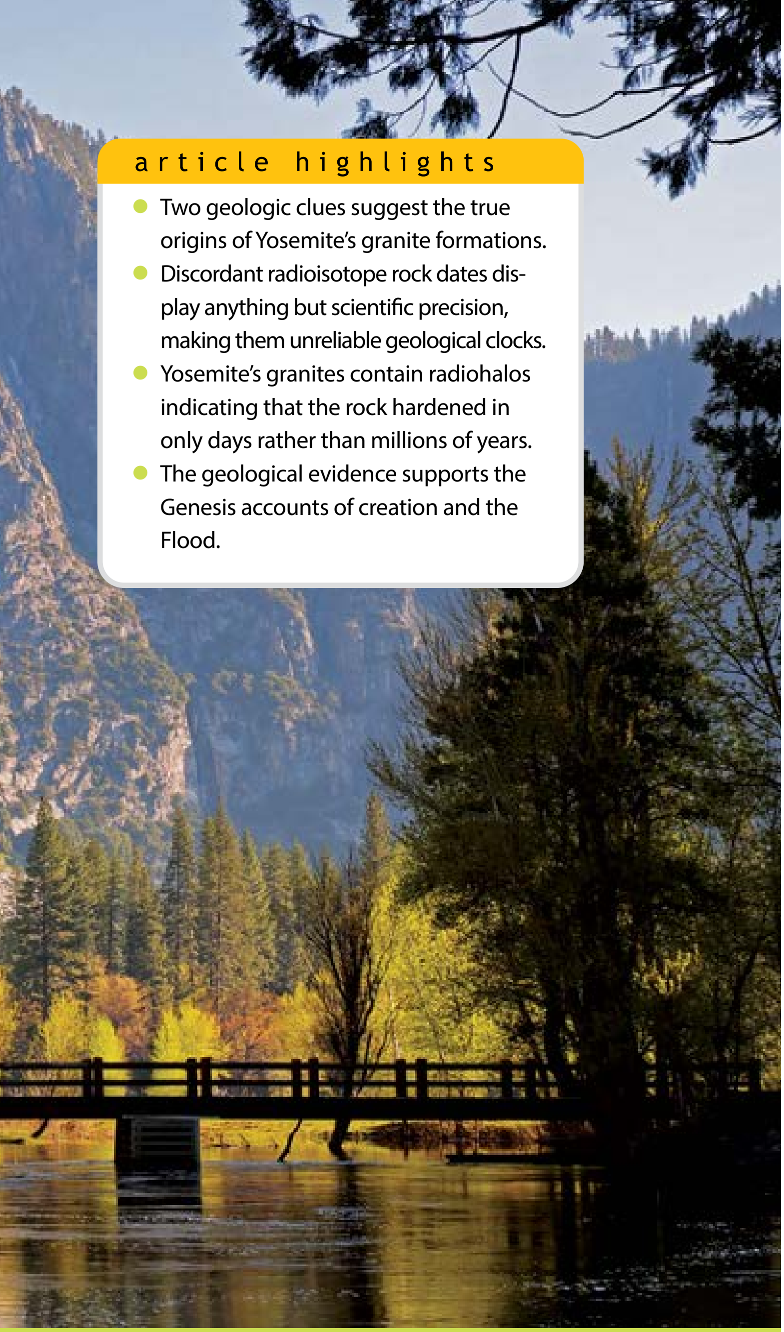
President Theodore Roosevelt (left) with John Muir at the top of Glacier Point in Yosemite in 1903

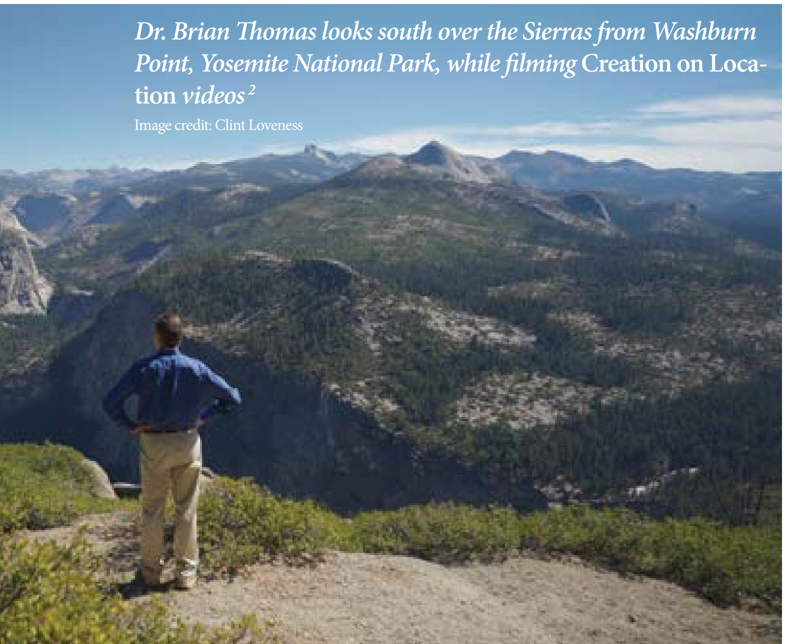
Image credit: National Park Service

Yosemite National Park in California is a sure source of stunning scenery. It's no wonder that American naturalist John Muir persuaded President Theodore Roosevelt to preserve Yosemite Valley.[1] But how and when did this park's dramatic peaks rise? Two clues in particular should clarify the origins of Yosemite's mountain granites.

article highlights

- Two geologic clues suggest the true origins of Yosemite's granite formations.
- Discordant radioisotope rock dates display anything but scientific precision, making them unreliable geological clocks.
- Yosemite's granites contain radiohalos indicating that the rock hardened in only days rather than millions of years.
- The geological evidence supports the Genesis accounts of creation and the Flood.





Dr. Brian Thomas looks south over the Sierras from Washburn Point, Yosemite National Park, while filming Creation on Location *videos*[2]

Image credit: Clint Loveness

A Mental Setting

Before investigating this, one must first consider one's beliefs—e.g., whether Noah's Flood actually covered the earth—because they inevitably affect a person's decision tree.[3] Creation scientists treat the Bible's report of Noah's Flood as true, not just the account recorded in Genesis but also those by David (Psalm 29), Peter (2 Peter 3:5–6), and even Jesus (Matthew 24:37–38). Those who welcome this perspective recognize the geological effects of world-destroying water.

For example, geology shows that North America's western edge suffered great stresses. Sediments were deposited, subducted, faulted, stretched, and compressed. Volcanoes spewed vast volumes of ash through great gashes in Earth's crust into continent-covering water.[4] One of the last western-edge geologic episodes occurred when molten material rose through Earth's crust and quickly cooled. It was later uplifted and exposed by erosion, forming the Sierra Nevada mountain range in which the now-scenic Yosemite Valley rests.

The vast sedimentary layers and deformed rocks that flank the Sierras, plus countless deeply buried fossils, already point to past geologic processes that exceedingly surpassed today's energy levels. In addition to water, the Flood involved tectonic, magmatic, and volcanic aspects, like those involved in the formation of the Sierras, that rearranged Earth's entire surface in mere months.[5] In contrast, conventional scientists reject the Flood outright—often without testing it against the rock and fossil evidence.

One similarity between Flood and anti-Flood models is the relative timing of geologic events. Both models agree that waterborne sediments blanketed the region first, after which the Sierras formed, which was then followed by an ice age. However, anti-Flood models reject evidence of youth, like that discussed below. But why? Those committed to evolution need to give natural processes enough time to evolve all plants and animals from a one-cell ancestor. So if these rocks show evidence of recent formation, which they do, then out goes evolution, forcing the Bible and its holy God into consideration.[7]

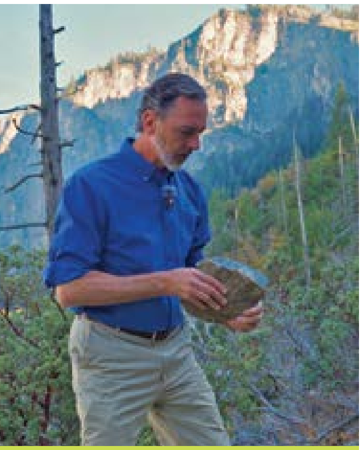
Tan region shows how far sediments were spread—much of it offshore—as "the waters receded continually from the earth" in the final months of the Flood (Genesis 8:3)

Image credit: Screenshot from the ICR documentary *Carved in Stone*[6]

Inconsistent Dating

Our first origins-orienting clue comes from inconsistent radioisotope results. Conventional scientists performed radioisotope dating on Yosemite granites. One such method (uranium-lead) gave ages that ranged from 80 to 120 supposed million years.[8]

But are isotope-based ages like these reliable? Well, the dating methods do require workers to make unprovable assumptions.[9] Plus, they have failed to accurately test rocks of known historic ages.[10] And different techniques often give different ages for the same rock.[11]

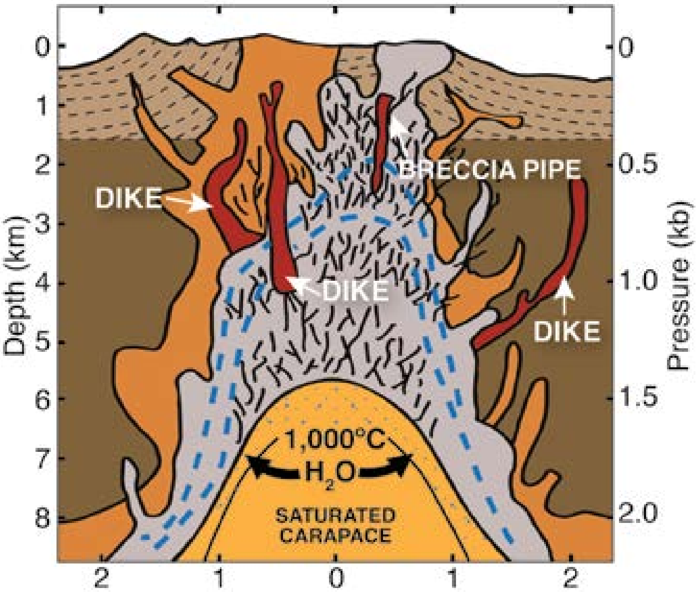


Dr. Brian Thomas inspects a piece of granite at Yosemite

Image credit: Clint Loveness

The Sierras are no exception. One conventional geologist wrote about Sierra samples that "some potassium-argon hornblende [another mineral in granite] ages are inexplicably older than uranium-lead ages for the same rocks."[8] These inconsistencies suggest that isotope systems make poor clocks. The next example makes them seem even more meaningless.

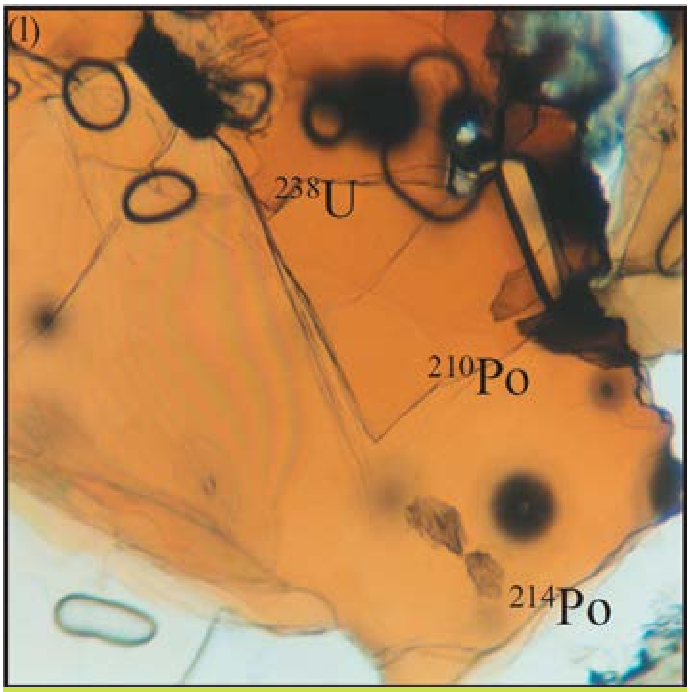
Granites have chemical signatures—like fingerprints. Granites that are quite similar from peak to peak came from the same magma source. Radioisotope ages for similarly sourced Yosemite granites called plutons suggest that it took 10 million years for them to form. However, in the researchers' own words, "Simple thermal considerations preclude the possibility that a magma chamber the size of the Half Dome pluton could have existed as a liquid at shallow crustal depths for that long."[12] That magma would have cooled long before even one million years, let alone 10. One solution to this inconsistency is to replace isotope ages with more reliable sources.



Schematic cross-section of a small granitic intrusion in its last stages of cooling. Orange indicates volcanic rock, gray shows granite, brown is sedimentary rock, and chaotic black lines display fractures in the rock above the cooling water-saturated granite magma. Granite intruded into volcanic rocks that had just formed, with both from the same magma supply.

Put a Ring on It

Microscopes reveal radiohalos in biotite from granites worldwide. Radiohalos look like dark, concentric rings. They form when a radioactive center emits energy and particles. Too much heat erases them, so they form when the granites are about 150°C.[13] Each radioisotope leaves behind a characteristic ring pattern. The ICR Radioisotopes and the Age of the Earth (RATE) project sampled many granites for radiohalo analyses, including samples from six Yosemite locations.[14]



In granite, polonium radiohalos were frozen in time before they could decay in days or even minutes

Image credit: ICR RATE project[14]

The RATE scientists often found polonium (Po) near uranium (U). U turns into Po as it decays to lead. Biotite mineral forms into sheets as magma cools and releases water. Therefore, the team reasoned that hot water carried Po between the crystal's sheets away from its parent U. So what? Well, Po doesn't last long. If these granites took more than 10 days to cool, then they would not have captured polonium radiohalos.[13] If we go by what Po radiohalos say, then these granites formed not over millions of years but in mere days.[15]

Black minerals contain polonium radiohalos that point to fast formation of Yosemite granite

Image credit: Brian Thomas

Isotope	Half-life
^{218}Po	3.1 minutes
^{214}Po	164 microseconds
^{210}Po	138 days

The half-life of three polonium isotopes

Conclusion

The two clues covered in this article have narrowed down the options for how quickly Yosemite's granite mountains formed. First, radioisotope ages are too inconsistent in several ways to trust. Second, the existence of polonium radiohalos implies that granites cooled in days after all.

What does all this mean? When correctly interpreted, the geological evidence supports the Bible's timeline of a recent creation and Flood. Since God got His history right, then we have more reason to trust His every word.

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3. By "decision tree" I mean everything pertaining to decision-making, including which research questions to ask, which models to employ, which results to emphasize, and what conclusions to draw.
4. All that volcanism left behind the Independence dike swarm that extends for hundreds of miles across California's southeastern deserts.
5. Psalm 29 appears to give illustrations of global events from the Flood year, including leveled forests (v. 5), extensive volcanism (v. 7), and violent earthquakes (v. 8), with floodwater first and last. See Dr. Henry M. Morris' notes on this in *The Defender's Study Bible* free online at ICR.org/bible/psalm/29/.
6. The DVD set *Carved in Stone: A Creationist Road Trip Across America* is available for purchase as a digital download. Visit ICR.org/store, enter code 1886 in the search bar, and click the download link at the bottom of the DVD description.
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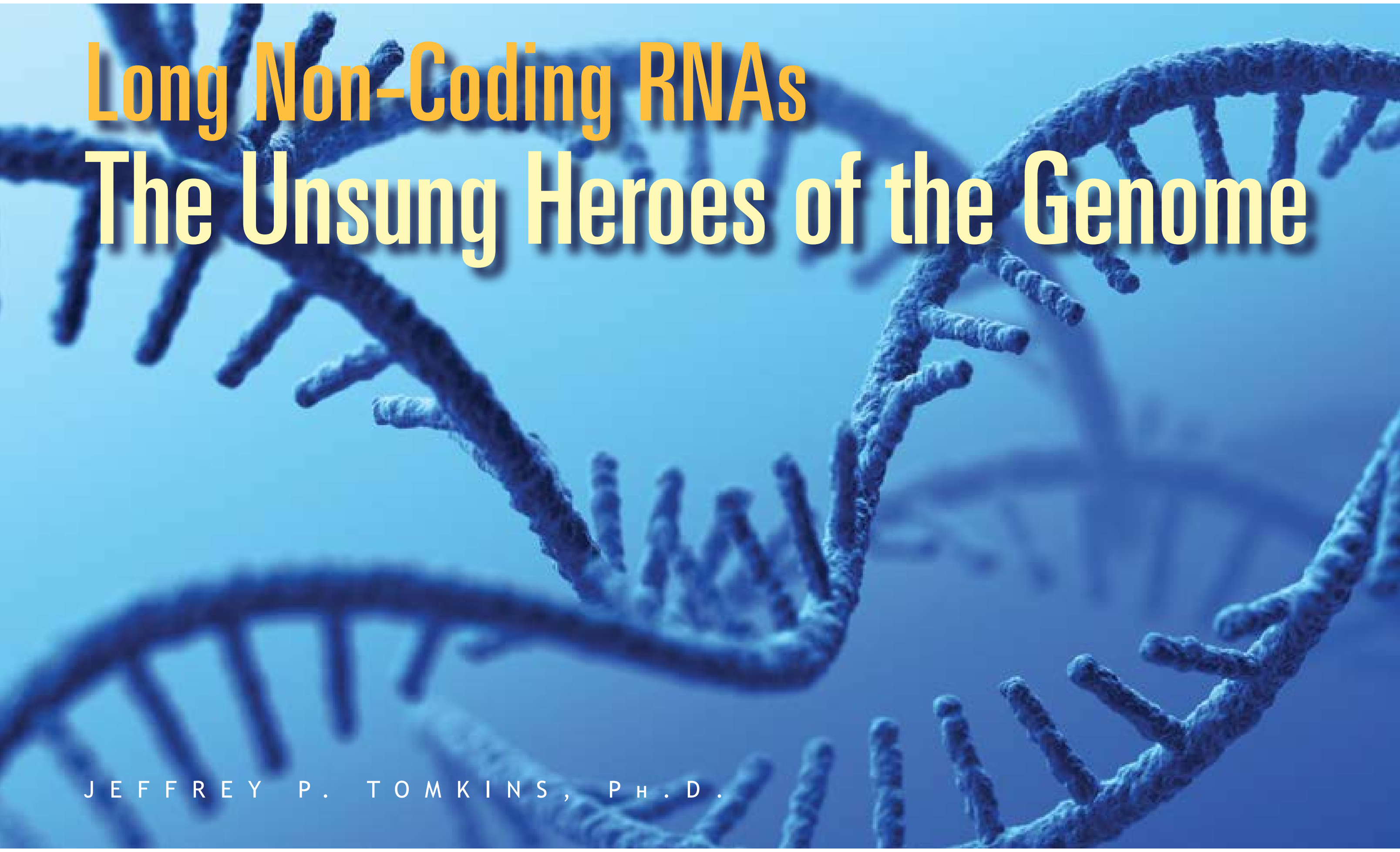
15. Another implication of Po radiohalos is that millions of years' worth of U-decay at today's slow rates must have occurred in mere minutes to generate enough Po to make radiohalos. See reference 12 for details.

Dr. Thomas is a research scientist at the Institute for Creation Research and earned his Ph.D. in paleobiochemistry from the University of Liverpool.

Half Dome, seen in center, showed isotope ages that conflicted with cooling rates

Long Non-Coding RNAs
The Unsung Heroes of the Genome



JEFFREY P. TOMKINS, Ph.D.

article highlights

- Top scientists have called the genome an "RNA machine" since nearly the entire genome is transcribed into a diversity of RNAs.
- Evolutionists used to consider long non-coding RNAs (lncRNAs) largely nonfunctional because they don't code for proteins, but research has shown that lncRNAs play many crucial functional and structural roles in cells.
- Studies of fruit flies, butterflies, and plants show that lncRNAs are invaluable for a wide variety of processes, including those pertaining to adaptation.
- Biomedical researchers, who are far less hamstrung by evolutionary theories because of their focus on curing disease, have linked lncRNAs to many aspects of human health.
- Each year more of the incredible complexity of the genome is unveiled, and with it the glory of our Creator Jesus Christ.

Evolutionary theory holds that all living things came about through random, natural processes. So conventional scientists believe the genome has developed through these means, and large sections of it have therefore been assumed to be nonfunctional. These alleged nonfunctional regions supposedly are a source of new gene evolution. But these evolutionary presuppositions of nonfunctionality are being challenged by an unexpected group—members of the biomedical genomics community.

These scientists, healthcare providers, industry professionals, and others are dedicated to studying the role of all parts of the genome in health and disease. Their practical focus on developing and improving diagnoses and treatments means they are freer to follow evidence where it leads. And that evidence doesn't lead to evolution.

Background

The genome is the complete set of chromosomes in a cell. It's like a computer hard drive that encodes critical information for growth, development, physiology, and adaptation. Protein-coding genes are DNA segments that carry instructions for making proteins. These segments are copied (transcribed) into RNA in a temporary fashion, just like copies of software programs are put into short-term memory on a computer.[1] These temporary RNA instructions are then used as templates to make proteins.

As genome research technologies became more advanced and comprehensive, scientists realized that protein-coding genes are only a small portion of the genome transcribed into RNA. In fact, researchers discovered that nearly the entire genome is transcribed. This is

called pervasive transcription.[2,3] The initial and ongoing discovery of pervasive transcription has led some scientists to call the genome an "RNA machine."[3]

One significantly large component of this transcriptional landscape is produced from long non-coding RNAs (lncRNA). This diverse class of genes doesn't code for proteins but instead produces a variety of structural or functional RNAs typically longer than 200 bases. These lncRNA genes outnumber protein-coding genes by at least three to one and perform a wide variety of critical activities in the cell.[4,5]

Because evolutionists didn't understand lncRNA gene function in the early days of the human genome project, they originally and prematurely labeled these regions "junk DNA." A wide variety of these genes have since been investigated and found to have important functions,[6–11] although it has been difficult to assign specific functions to many of the human lncRNAs.[12] As far as gene structure goes, lncRNAs have essentially the same exon-intron system that protein-coding genes have along with the same regulatory regions such as promoters and enhancers (Figure 1).[13]

On a historical note, the first nearly complete draft of the human genome was published about 20 years ago. The assessment of its information content attributed only a small percentage of the genome to protein-coding sequences (exons as represented in mRNAs), ribosomal RNAs (rRNAs), transfer RNAs (tRNAs), and introns from protein-coding genes.[14,8]

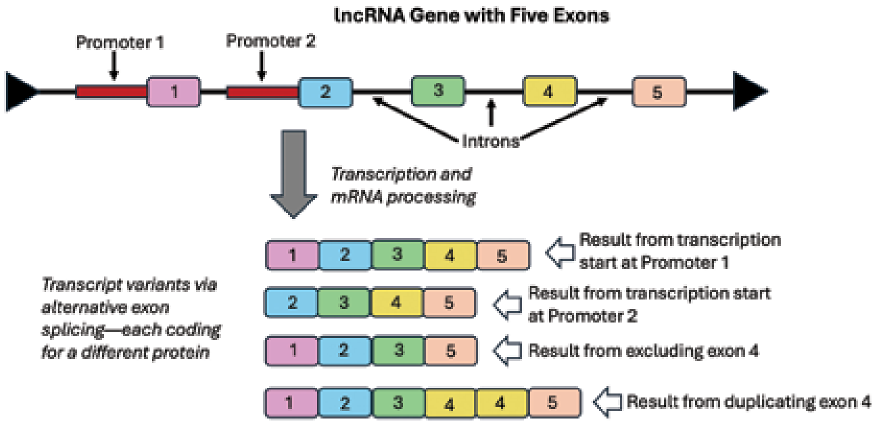


Figure 1. *Diagram illustrating alternative splicing of an lncRNA gene*

As of 2023, the known landscape of the human genome had not changed much concerning these features, which make up about 25% of the genome. The overall information content, however, has been radically altered by the addition of numerous lncRNAs, which constitute about 75% of the genome (Figure 2).[8] Numerically speaking, there are about 20,000 protein-coding genes and over 100,000 lncRNA genes in the human genome.[6]

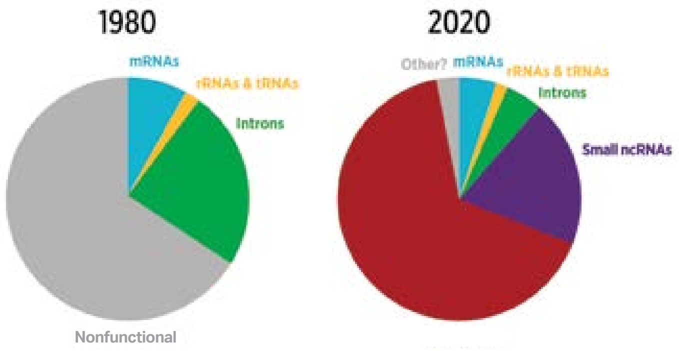


Figure 2. *A comparison of the known genomic landscape between 1980 and 2020. Image adapted from figure 1 in reference 8.*

Role and Function of lncRNAs

The cell's nucleus contains a greater proportion of lncRNAs than protein-coding mRNAs. The lncRNAs' roles there are both functional and structural. Functionally, they are important for regulating gene transcription, stabilizing chromosomes, assisting in epigenetic modifications of both the DNA and histones, binding to certain proteins and acting as nuclear address delivery guides, and helping modify the three-dimensional structure of the genome. In fact, one interesting study showed that all the chromosomes of the human genome are literally painted with a specific class of repeat-rich lncRNAs. When these lncRNAs are eliminated with an enzyme called RNAse, the chromosomes literally collapse.[15]

Many studies show that lncRNAs participate in virtually all levels of chromosome organization and in defining cell type and structure, and they widely regulate gene expression. These functional roles are formed through RNA-RNA, RNA-DNA, and RNA-protein interactions. Regarding RNA-RNA interactions, lncRNAs form complex networks with both microRNAs[16] and messenger RNAs in the nucleus and cytoplasm.[17,18] In the nucleus these three-way interaction networks regulate gene expression, and in the cytoplasm they regulate protein production (translation). One particularly interesting class of regulatory lncRNAs are those produced from the opposite DNA strand of a gene.[19] Called antisense RNAs, they're key to regulating the splicing of a newly copied RNA from a gene.

In the cell's cytoplasm, lncRNA interactions are involved in protein production and the subsequent transport and localization of that protein to a specific location in the cell. While RNA editing primarily takes place in the nucleus of a cell via the aid of lncRNAs,[20] it can also take place within cytoplasm organelles like the mitochondria and chloroplasts (photosynthetic sites in plants).

Many lncRNAs are also involved in the regulation of cell differentiation and development in animals and plants. In mice, we now know that five different lncRNAs are involved in maintaining the proper amount of developmental and growth-related proteins in a process called dosage compensation.[9] Several other lncRNAs have been shown to regulate mouse brain development, and others control limb development (one lncRNA), organism viability (seven lncRNAs), the immune system (six lncRNAs), fertility (one lncRNA), and overall chromosome stability (one lncRNA).

Besides growth and development, lncRNAs also play a wide range of roles in mammals' physiological processes.[9] Some of these processes are involved in DNA damage control and repair, antibody diversity in immune cells, secretion by immune cells of specialized disease-fighting substances (cytokines), inflammation and neuropathic pain, cholesterol biosynthesis and homeostasis, growth hormone and prolactin production, glucose metabolism, cellular signal transduction and transport pathways, and brain cell synapse function. Research also shows lncRNAs are important for the structure and function of the cell membrane.[9]

Brown mouse

Adaptation and lncRNAs

Fruit Flies

Cold tolerance is an important adaptive trait that allows creatures to inhabit a wide array of latitudes on a continent. The fruit fly (*Drosophila melanogaster*) is one of the most studied creatures in researching genetic mechanisms of adaptation. In a 2008 study, researchers captured hundreds of fruit flies on the east coast of Australia from 41 different locations along a latitudinal cline from 15° to 43°.[21] The gene associated with heat tolerance that they targeted for analysis was *hsr-omega*, which encodes a large lncRNA. In fact, the gene itself encodes two different lncRNAs: *omega-c* operates in the cell cytoplasm, and *omega-n* stays in the nucleus.

Additionally, the gene encodes a long series of tandem repeats where the repeated unit is 280 nucleotides long. The *omega-n* variant in the nucleus is the long version of the gene that includes the repeats. The *omega-c* variant is much shorter and excludes the long section of repeats. It only comprises the front section of the gene minus a small section.

*Fruit flies (*Drosophila melanogaster*)*

As location shifts from north to south, the transcription of the *hsr-omega* gene as a whole decreases in response to latitude. The amount of repeats in the *omega-n* variant decreases in response to cold, and the quantity of the *omega-n* RNAs decreases. Finally, during fly recovery from cold exposure, there is a large increase of the *omega-c* variant in the cytoplasm.

Butterflies and Moths

Variations in the wing pigmentation of butterflies and moths (lepidopteran insects) are striking examples of adaptation. They allow the insect to hide itself from predators by blending into its environment or even mimicking another creature's appearance. In lepidopterans, there is a chromosomal region called the cortex locus, a complex segment containing multiple genes and regulatory elements that work together to control wing patterns.[22] While the specific number of genes within the cortex locus varies depending on the kind of lepidopteran, the region is vital for understanding the genetic basis of wing pattern diversity in these insects.

A recent study revealed the pivotal role of an lncRNA gene transcribed from the cortex locus.[22] Named *ivory*, the gene modulates and controls color patterning in butterflies and kicks in gear during pupal development in the cocoon, which is the metamorphosis stage of the lepidopteran. The gene is turned on after about 20% of pupal development and persists until about 60 hours after pupal formation stops.

Hawk moth

Overall, the data show that the *ivory* lncRNA gene functions as a master switch for color pattern specification, making it invaluable for adaptive diversification of wing patterns in butterflies and moths.

Plants

Since plants are sessile organisms and can't move around, they need a robust molecular genetic toolkit to adapt to a wide variety of environmental challenges. lncRNA genes and their RNA products play an important role in this.[23] And because plants are more easily studied than animals due to fewer regulations and less required maintenance, lncRNA research in various grasses, herbaceous plants, vines, shrubs, and trees has exploded in the past 10 years.

These lncRNAs in plants are encoded in genes outside protein-coding genes, in the introns of protein-coding genes, on the opposite strand of protein-coding genes (producing antisense transcripts), and are even produced from the promoters of protein-coding genes. Their functions range from regulating gene transcription to regulating protein production, regulating epigenetic modifications, and modifying the genome's 3-D structure.

The major environmental cues they respond to are cold, heat, salt stress, light, and water availability. They also help regulate plant growth and development by coordinating changes in plant hormones in response to all sorts of environmental stimuli. Nearly every aspect of plant adaptation and physiology involves the precise coordinated action of lncRNAs.


Grass

Conclusion

In the evolutionary paradigm, the incredible complexity of the genome is believed to have somehow evolved by random processes. Much of it is therefore thought to be useless evolutionary junk. The leading proponents of evolution are steeped in this type of speculation, called theoretical evolution, and have tried to downplay recent discoveries of pervasive function across the genome, which is largely based on lncRNAs.

However, the biomedical genomics community is pragmatically focused on diagnosing and curing disease. As a result, biomedical researchers are not as limited by false evolutionary presuppositions and have associated lncRNAs with many different aspects of human health. Thanks to these efforts and the work of plant and animal researchers in adaptive systems, the incredible functionality of the entire genome and all of its seemingly infinite complex workings are glorifying the omnipotent Creator, the Lord Jesus Christ who made it all.


Biomedical researcher

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TIM CLAREY, PH.D.

Megasequences Down Under Support Progressive Global Flood

article highlights

- ICR's Column Project recently completed analysis for Australasia—its sixth continent!
- Northern Australia has vast oil and natural gas reserves found in Precambrian sedimentary rocks—some of the oldest sedimentary rock layers—that are difficult for evolutionists to explain.
- We now have evidence from six continents that the Genesis Flood was global and progressive. Every continent contains similar deposition patterns from the same time and in the same order.

The Institute for Creation Research's Column Project team recently completed analysis of the Australasian continent, which encompasses Australia, New Guinea, and New Zealand. The study compiled 486 stratigraphic columns from oil wells, cores, seismic profiles, and outcrop data. We correlated six megasequences across Australasia and mapped their extent and thicknesses.[1] We also tracked a seventh pre-Sauk Megasequence, conventionally known as the Upper Precambrian or Proterozoic. The data show Australasia contributes its own unique evidence for the historicity of the progressive global Flood.

Australasia's Rich Pre-Sauk

A graph of the sediment volume preserved for each megasequence shows a chapter-by-chapter progression of the Flood similar to the other five continents (North and South America, Africa, Asia, and Europe) with one exception: Australasia has more pre-Sauk sediment than most (Figure 1).[2] And in Australia's McArthur Basin, some of these Precambrian rocks are producing oil and gas. Detailed chemical analysis indicates these oils are from buried marine plankton.[3]

These discoveries, and similarly productive pre-Sauk sediments in Russia, China, and Oman, are difficult for evolutionists to explain because tremendous volumes of organic material must have been quickly buried to provide these oil and gas resources. But the Flood's rapid and catastrophic nature means it could have encapsulated ample organic material, even in its earliest days or weeks, explaining this basin's oil and gas potential. More research on these resources and sediments is needed.

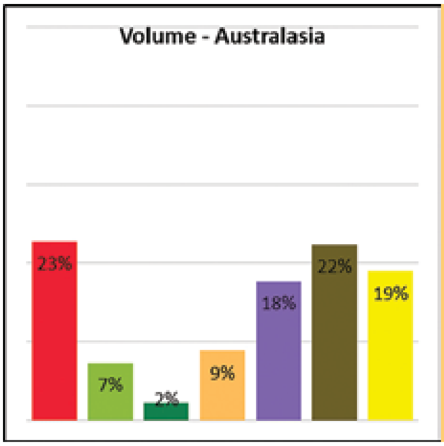


Figure 1. Graph of the sediment volume percentage by megasequence for Australasia. Pre-Sauk is red, Zuni is brown, and Tejas is yellow.
Image credit: Davis J. Werner

Australasia's Progressive Flood

The earliest generally accepted Flood sediments begin with Cambrian System rocks, corresponding to the Sauk Megasequence. Hereafter, the volumetric pattern across Australasia exhibits the same pattern as the rest of the world. Figure 1 shows minimal sediments deposited in the first three megasequences and progressively more in the Absaroka until peaking in the Zuni.

The latter three megasequences also increased dramatically in surface coverage. The Zuni has the most sedimentary volume (after the pre-Sauk) and the second most surface coverage, corresponding to the Flood's peak.[2] The final megasequence (Tejas) has the most widespread surface coverage, suggesting it formed during the Flood's receding phase.[2]

Six Continents of Data

The Australasia rock data show the same pattern of a progressive global Flood recognized in our earlier studies.[2] Figure 2 shows total sediment volumes from all six continents according to megasequence. Even the high percentage of pre-Sauk in Australasia is tempered in the global snapshot. The Zuni still contains the most volume globally, and the Tejas is a close second.

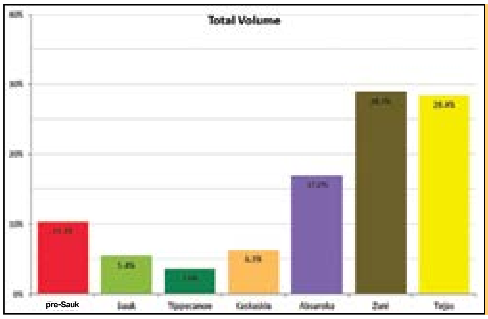
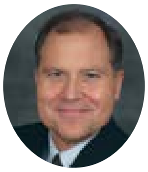


***Figure 2.** Graph of the sediment volume percentage by megasequence. The values represent the totals for all six continents.*
Image credit: Davis J. Werner

With Australasia's data, we have even stronger evidence that the Flood was historical and global. Every continent shows similar deposition patterns from the same time and in the same order. What else could explain these findings?[4]

References

1. A megasequence is a thick, definable package of sedimentary rock bounded top and bottom by extensive erosional surfaces. Each megasequence represents a major sea level rise and fall across the continents.
2. Clarey, T. L. and D. J. Werner. 2023. A Progressive Global Flood Model Confirmed by Rock Data Across Five Continents. *Proceedings of the International Conference on Creationism*. 9: article 23, 412–445.
3. Jarrett, A. J. M. et al. 2022. Petroleum Supersystems in the Greater McArthur Basin, Northern Territory, Australia: Prospectivity of the World's Oldest Stacked Systems with Emphasis on the McArthur Supersystem. *The APPEA Journal*. 62 (1): 245–262.
4. Genesis 7 and 8 provide answers to these rock data and explain why there was a progressive global Flood.



Dr. Clarey is the director of research at the Institute for Creation Research and earned his Ph.D. in geology from Western Michigan University.

JAMES GADBERRY

ENTERING BY THE DOOR

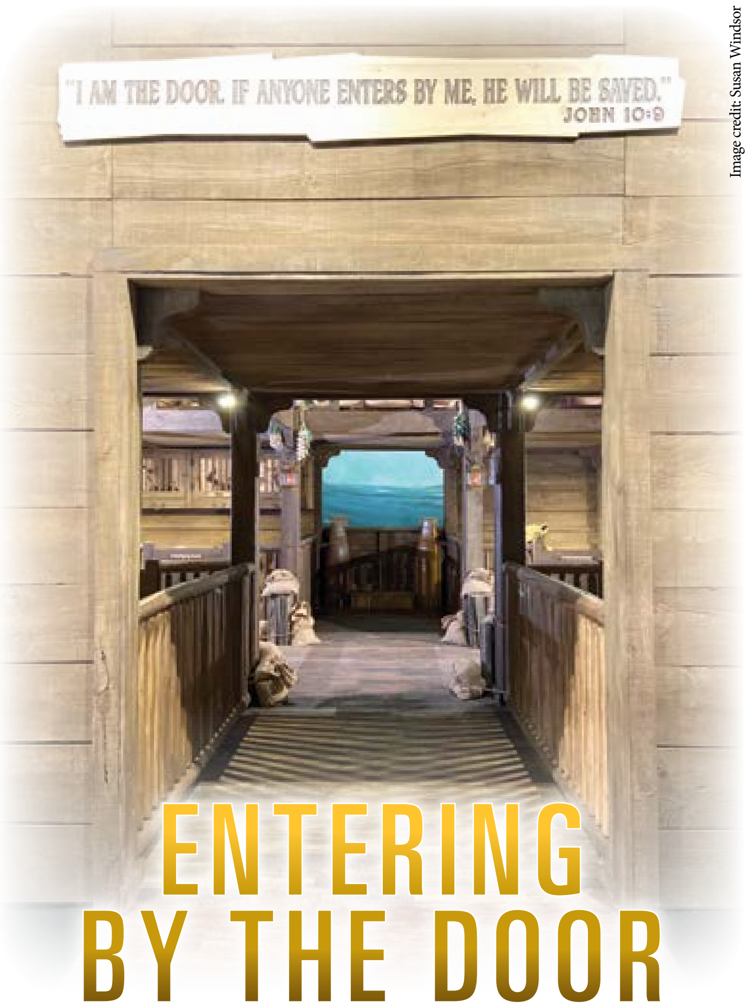


Image credit: Susan Windsor

Recently, I hosted a visiting pastor from a large church at ICR's Discovery Center. As I guided him through our Dallas museum, one conversation affirmed how important ICR's mission is—not only to proclaim the scientific evidence that aligns with Scripture but to educate, equip, and encourage church leaders in their calling.

We stopped at one of my favorite exhibits: Noah's Ark. The entrance is framed by a sign that says, "I am the door. If anyone enters by Me, he will be saved" (John 10:9). It's a powerful reminder of the salvation Noah and his family experienced through the Ark and parallels the eternal salvation offered through our Lord and Savior, Jesus Christ.

Jesus Himself draws this connection in Matthew 24:37: "But as the days of Noah were, so also will the coming of the Son of Man be." And Peter echoes the historicity of the Genesis narrative as he recounts "when once the Divine longsuffering waited in the days of Noah, while the ark was being prepared, in which a few, that is, eight souls, were saved through water" (1 Peter 3:20). Truly, the global Flood was a real, catastrophic event with deep theological and spiritual significance.

Standing before the Ark entrance, I could see in the pastor's eyes that he was impacted by this truth. As we continued the tour, however, he presented a question that stopped me in my tracks. With genuine curiosity and excitement, the pastor asked, "Does ICR teach about the other civilizations of humanity that survived the Flood as well?"

My knees almost buckled, not because I was shaken in my belief, but because this evidenced how even faithful church leaders can be misled by unbiblical narratives. I gently and confidently replied, "The Bible tells us that none but Noah and his family survived this event. We at ICR believe that the Bible is true and accurate."

By the end of his visit, this pastor was not only encouraged but energized. He began making plans to return with his church's leadership team, eager to share about ICR's faith-affirming scientific research.

The need to exhort pastors in biblical accuracy is more urgent than ever. In a world filled with compromise and confusion, church leaders must be rooted in the authority of God's Word from the very first verse. It's our joy and responsibility to come alongside these shepherds and provide resources to help them stand firm and boldly lead others.

The enemy has long deceived God's children by sowing doubt and distorting Scripture. But thanks to your faithful support, ICR has the scientific muscle, intellectual prowess, and research capabilities to combat these threats. We remain unwavering in our mission to defend the truth of God's Word, proclaim the gospel of Jesus Christ, and provide biblically sound scientific education to leaders and laypeople alike. As ICR hires a critically needed Ph.D. biologist to augment our pioneering efforts, please consider increased prayers and generosity to help us cover this new expense.

To our friends of the ministry: thank you. Your prayers, gifts, and uplifting words are a vital part of ICR's mission. Every life touched, every leader equipped, every church encouraged—it's thanks to you, standing with us. Together, we're pointing the world to the glorious Door of salvation, our Lord Jesus Christ.

Mr. Gadberry is the director of development and donor relations at the Institute for Creation Research.

The Scopes Monkey Trial

A Battle of Worldviews

MIKE MUELLER, M.S.

Rhea County Courthouse in Dayton, Tennessee, and its statue of William Jennings Bryan

Image credit: M. Mueller

Defense Attorney Clarence Darrow (right) cross-examining Prosecuting Attorney William Jennings Bryan (left) outside the courthouse

Image credit: Smithsonian Institution Archives, public domain

The Scopes Monkey Trial, an event that's often called the trial of the century, was truly a battle—not physical like the American Revolution but spiritual. Its outcome cast doubt on the authority of God's Word, implying that either Scripture is true or science is. This has impacted views on faith and science for the past 100 years.

Why does this matter? It is by God's Word, Genesis to Revelation, that we can know God's plan for our salvation. If any part isn't completely true, why would we trust the rest of it? Let's take a look at the 1925 trial to see what it actually proved.

The Trial

In March 1925 the Tennessee state legislature passed the anti-evolution law HB 185, called the Butler Act after legislator John Washington Butler. He'd heard about a young woman who came home from college believing the evolutionary theory and had therefore rejected her religious heritage. Butler introduced the bill in hopes of limiting the dangerous teaching of evolution.[1]

Residents of Dayton, Tennessee, decided to test the new law in court. High school teacher John T. Scopes agreed to be charged with illegally teaching evolution. Two national icons faced off in the subsequent trial—William Jennings Bryan for the prosecution and Clarence Darrow for the defense. They and their teams went at it for eight days in the Dayton courthouse.

The trial reached a tipping point when Darrow called Bryan to the stand. He poked holes in Bryan's arguments by exposing his lack of scientific knowledge and inconsistencies in his position. Scopes was ultimately found guilty and fined, but that courtroom exchange presented the Christian creation position as unscientific and the Bible as nonfactual.

Eventually the Butler Act was overturned. Today's public schools generally provide only one-sided evolutionary teaching. Just as Christians feared in 1925, the idea that science has disproven the Bible has prompted many young people to question or leave their faith.

The Scientific Case for...Evolution or Scripture?

In the 1925 trial, Clarence Darrow and his team of attorneys used testimonies from so-called experts to demonstrate that evolution was true science. The supposed experts presented some of the following topics as proof. Many are still used, but the scientific evidence actually supports creation, not evolution. Consider the claims and our brief responses.

Defense Attorney Clarence Darrow (left) and Prosecutor William Jennings Bryan (right)

Image credit: Rhea County Historical Society, used by permission

Claim: Evolution from simple cells to complex life, bacteria to man, is a fact.

Response: The trial experts admitted they didn't know where the first cell came from and weren't clear on the process or method evolution uses.

Biological science has advanced considerably since then, and it overwhelmingly disproves evolutionary ideas about how

High school teacher John Scopes appearing in court
Image credit: Rhea County Historical Society, used by permission

life operates. In fact, ICR President Dr. Randy Guliuzza recently introduced a new theory proposing that God equipped each life form with the ability to adapt to environmental changes using its own innate systems.[2] Modern science supports the Bible like never before.

Claim: Ape-to-human evolution is demonstrated by fossils.
Response: The so-called missing links between ape and man are still missing. No discoveries show that humans descended from primates, and the fossil specimens presented in the trial and since have turned out to be fully human, fully ape or animal, a mixture of human and animal, or fraudulent.[3]

Claim: The geological record proves evolution because simple life forms are buried in the deepest geological layers.
Response: The fossil record documents the ecological zones that were progressively flooded and buried in the global Flood of Genesis. This interpretation is supported by ICR geologist Dr. Tim Clarey's research using core drilling samples from all over the world.[4]

The Flood also explains the Cambrian Explosion, the fossil creatures whose living counterparts show no signs of evolution, and the original tissue found in fossils that suggests recent burial.[5] The Bible best explains the geological observations.

Claim: The earth is millions of years old, allowing for evolution to have occurred.
Response: Many dating methods used to assign millions-of-years ages to rock specimens are based on unprovable assumptions and/or produce inconsistent results.[6] Most evidence clearly supports a young earth and coincides with the biblical timeframe of around 6,000 years.

Claim: The tailbone, appendix, wisdom teeth, and other organs are vestigial features.
Response: Parts of organisms once thought to be useless evolutionary leftovers are today known to have important functions.[7] They were designed according to God's plan.

Claim: Genetic similarity and breeding results support evolution.
Response: Human and ape DNA are now known to be 84% similar, not 98% as initially claimed.[8] And variation between plant and animal species can be managed by controlled genetic breeding. This is not evidence of gradual change driven by random mutations over millions of years.

Claim: Embryonic development and comparative embryology between animals prove that living organisms came from a common ancestor because their developing embryos echo evolutionary stages.
Response: This idea was popularized in 1866 by Ernst Haeckel. He was later reprimanded for using fraudulent drawings. Unfortunately, students are still told that developing babies go through evolutionary history with gill slits, a tail, and yolk sacs, even though this is false.[9]

Conclusion

Sadly, William Jennings Bryan died just five days after the trial's conclusion. But his last speech, published after his death, demonstrates the convictions he communicated at the trial remained strong.

> Christians know that "the fear of the Lord is the beginning of wisdom" now just as it has been in the past, and they therefore oppose the teaching of guesses that encourage godlessness among the students....Evolution is not truth; it is merely an hypothesis—it is millions of guesses strung together. It had not been proved in the days of Darwin....It had not been proved in the days of Huxley, and it has not been proved up to today.[10]

Indeed, it still has not been proven. If Bryan had had modern scientific evidence and knowledge to take on Darrow's questioning, the Scopes trial outcome might have been very different. However, the great battlefield's results continue to spread misinformation, imaginary histories, and ungrounded speculations as evidence of evolution, even though biological science points to phenomenal complexity and design by the all-wise, all-powerful Creator, Jesus Christ.

Christians have science on their side affirming the truth of God's Word. The evidence shows us we can be confident that the Word of God is completely true and lasting, and we can believe its message of life and hope through Jesus our Redeemer.

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Mr. Mueller is the vice president of the Institute for Biblical Authority and earned his B.S. and M.S. in biology education and natural resource/wildlife management from Pittsburg State University.

letters to the editor

I'm 78 years old…**I went through the first 10 videos on the Creation Connection yesterday, and they are absolutely mind-blowingly wonderful.** You guys are really…informative and funny. God bless you…you guys are so gifted and talented. You guys made my day!

— F. W.

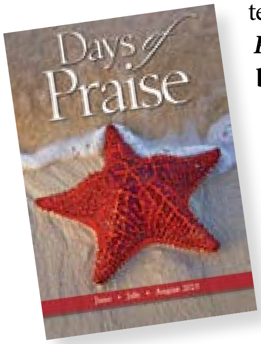
Creation Connection is my love language!!!

— R2B

Editor's note: Watch *Creation Connection* and other ICR videos at **YouTube.com/@ICRscience**.

You have NO idea how valuable *Days of Praise* is to me. Every day's devotional message is so rich in biblical insights. Like full-meated sermons in every one. God has used it so many times to reach and teach my soul.…**In my opinion, *Days of Praise* is the very best daily devotional book anywhere.**

— J. B.



For years [my husband] followed ICR.… Soon after his homegoing I cancelled *Days of Praise* as he was the one who faithfully meditated on it. But you kept sending it, and how grateful I am that you have! When I began feasting on every day's selection I've grown and grown.

— J. F.

★★★★★ I have been getting ICR [*Acts & Facts*] magazines for many years and have also purchased several of their publications or creation-related materials. I have also been to several of their live presentations.…**They have been a favorite ministry of mine for a long time, and I continue to refer people to them.** God bless ICR.

— B. L.

I went here a few years back. **[The ICR Discovery Center is] one of the best museums in DFW, if not the best!** Really liked the section with the scientists. I hope to go again.

— L. P.

Perfect venue for Christian homeschool groups or a family outing or for the deep thinking individual who is open to being presented evidence of the accuracy of the Bible in a fun way.…It's full of animatronic animals, high-tech exhibits, and full of thought-provoking evidence from around the world that gives a powerful argument for the Bible.

— J. C.

Editor's note: Plan your visit to the ICR Discovery Center at **ICRDiscoveryCenter.org**.

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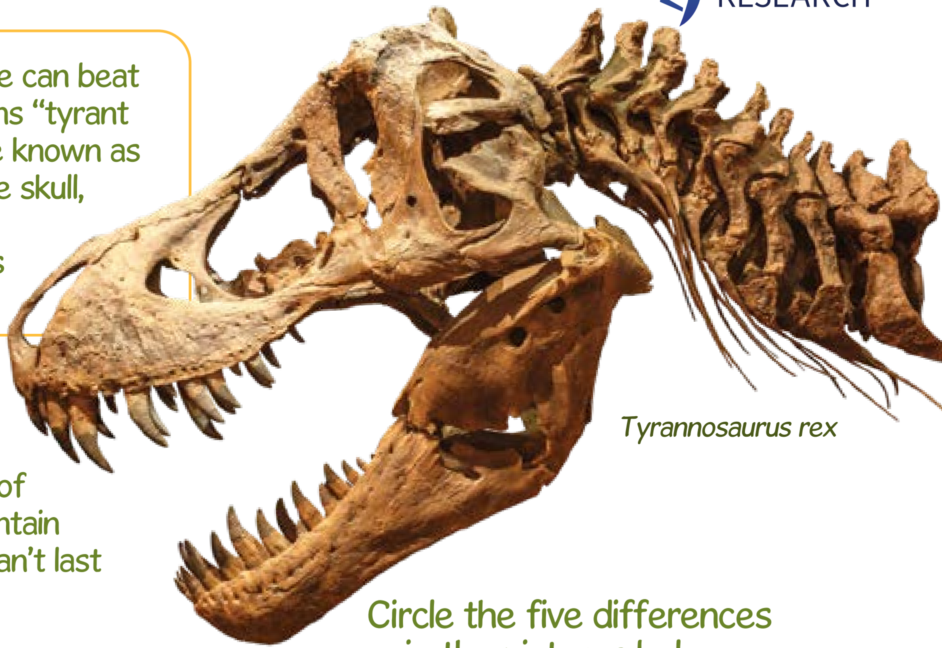
Unfortunately, ICR is unable to respond to all correspondence or accept unsolicited manuscripts, books, email attachments, or other materials.

Watch for *Project Artifact: The Spear* at ICR.org/store

Written by Michael Stamp, illustrated by Lori Fausak

T. rex

When it comes to famous dinosaurs, no one can beat *Tyrannosaurus rex*! With a name that means "tyrant lizard king," *T. rex* was a two-legged reptile known as a theropod. It had razor-sharp teeth, a huge skull, and a really long tail. The largest one found weighed over nine tons—that's as heavy as a school bus! Did you also know...

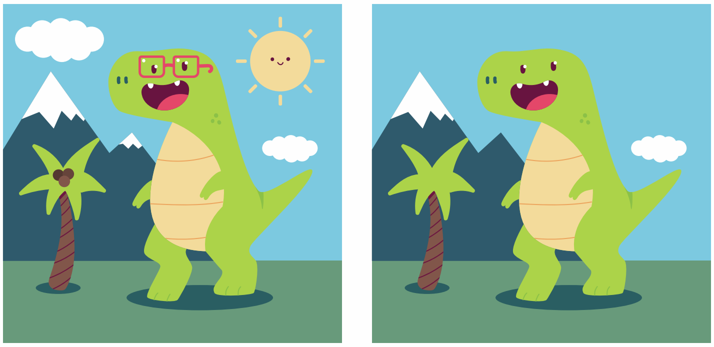

Tyrannosaurus rex

- ✔ The Lord Jesus made *T. rex* on Day 6 of the creation week.
- ✔ Some people think *T. rex* lived millions of years ago. But many of their fossils contain soft tissues, like blood vessels, which can't last that long.
- ✔ Buried *T. rex* fossils were formed during the recent global Flood. Read Genesis 7 to learn more.

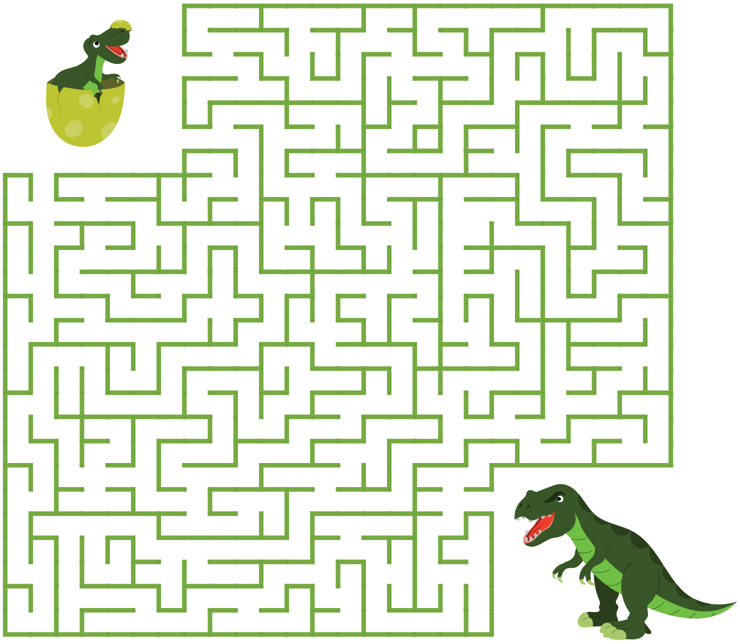
Find the hidden objects in the picture below.

BY MICHAEL STAMP AND SUSAN WINDSOR

Circle the five differences in the pictures below.



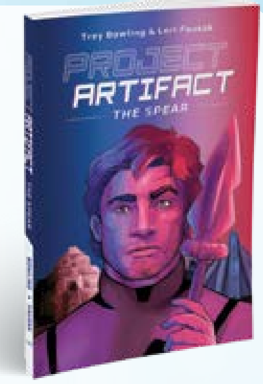
Help the *T. rex* find its baby.



COMING SOON!

Project Artifact: The Spear

Written by Trey Bowling
Illustrated by Lori Fausak



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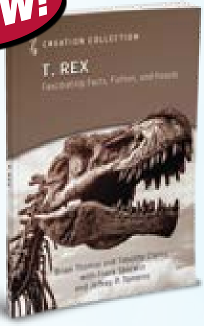

Conventional scientists argue that dinosaurs like *T. rex* evolved and then died out millions of years ago. However, the scientific evidence not only highlights this remarkable reptile's unique design but also points to a global watery catastrophe that buried it and countless other creatures just thousands of years ago.

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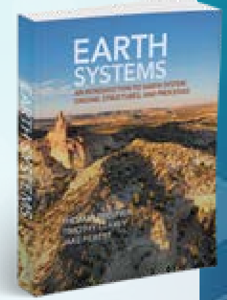

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