



Southwest Florida Archaeological Society (SWFAS)

OUR 46th YEAR

September 2026 Newsletter

<https://swflarchaeology.org/>

PRESIDENT'S CORNER By *John F. Furey M.A., RPA*, jffurey@charter.net



The National Park Service has announced that improvements to the seawall protecting the Castillo de San Marcos National Monument in Saint Augustine will begin this fall. Rising sea levels and storm surges necessitate this construction and it is expected to be completed by January 2028.

Below I have included a new article on DNA titled *We May Have Been Wrong About The Origin of Life All Along*, and while it may seem a bit technical, I urge you to read it. It discusses the origin of the genetic codes, DNA and RNA and posits that their origins may go back four billion years. Every protein in every organism that has ever lived on earth is built from the same set of 20 amino acids. This article

challenges the timeline of which came first and which came last and suggests that the current entire foundation on which scientists built the genetic code is, in part, flawed.

RECENT RESEARCH

ASKING TREE RINGS TO SOLVE A ROMAN CONSPIRACY

In 367 A.D. Roman Britain collapsed into chaos from the “Barbarian Conspiracy” when the Picts from the west and the Saxons from the south rebelled, attacked, and defeated the Roman garrisons across Britain.

Archaeologists and historians know what happened but did not know why. Ulf Buntgen from Cambridge University decided to look at tree rings from living and dead trees to find answers. It turns out that there were three years of severe droughts that preceded the Barbarian Conspiracy and it is believed that harvest failures and food shortages created instability and were factors in the attacks on the Roman garrisons that led to Rome’s withdrawal from Britain. Source: *Nautilus* at <https://nautil.us/asking%20trees-to-solve-a-roman-conspiracy-1207113>

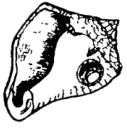
WOODEN SPEARS IN A GERMAN COAL MINE WERE 200,000 YEARS-OLD

A set of wooden spears, one spruce and one of pine, were unearthed in a German coal mine. Originally thought to be attributed to *Homo heidelbergensis* at 300,000 years-old, but recent dating to 200,000 years-old changes them to Neanderthals. The spears appear to be well made and well balanced. Source: *Archaeology News* at <https://archaeologymag.com/2025/05/wooden-spears-in-germany-made-by-neanderthals/>

THE ATLATL IN THE AMERICAS: AN INDEPENDENT INVENTION?

A recent publication in the *Proceedings of the National Academy of Sciences* where anthropologists applied statistical models to radiocarbon-dated Stone Age atlatl's associated with the Clovis Culture found that they fell between 9,300-6,100 years old. If the Clovis Culture died out about 12,000 years ago then these tools belonged to hunters that lived after Clovis and hypothesized that the atlatl would have been independently invented in the New World. It was not designed to hunt big game but would have been used on smaller and faster game and used much smaller stone points than the Clovis points. They also hypothesized that the use of the atlatl would have allowed women with less upper body strength to hunt. Source: *Archaeology News* at <https://archaeologymag.com/2026/07/atlatls-appeared-in-north-america-after-the-clovis-culture/>

SWFAS DUES REMINDER 2026



SWFAS dues for 2026 are due. Thanks to everyone that has already renewed their 2026 tax deductible membership. Your support of archaeology, history, preservation, and education in Southwest Florida is critical. Our sole source of revenue is your dues and gifts as we strive to offer educational programming in the area of archaeology and history free to all members of the public.

SWFAS is a 501(c)(3) registered non-profit organization. If you have not done so, we have two ways, you can renew online with a credit card at <https://swflarchaeology.org>. On the Home page, go to “ Select Member Level” and then “ Add to Cart.” Or send a check to: Charlie Strader, SWFAS Treasurer, 27655 Kent Road, Bonita Springs, FL 34135. If you have question re membership status, you may call/text Charlie at 239-992-6133.

SWFAS PRESENTATION SCHEDULE 2026

Note that all SWFAS presentations are free to the public

JUNE – OCTOBER – NO LECTURES, NEWSLETTERS DISTRIBUTED EACH MONTH

NOVEMBER 18, 2026, 7:00 PM, BONITA SPRINGS FIRE STATION 24

(enter building in front by the flag poles. Parking is in front.)

Lecturer: Steve Koski

Presentation: Submerged Indigenous Archaeological Sites on Florida’s West Coast:

Sea Level Rise, Incidental Discoveries, Predictive Modeling, and Preservation Methodologies

Join SWFAS board members and our speaker for dinner before the program!

DECEMBER 5 OR 12, 2026 Field Trip: TBA

ARTICLES - *PREVIEW*

WE MAY HAVE BEEN WRONG ABOUT THE ORIGIN OF LIFE ALL ALONG

Something written in every biology textbook of the past 70 years may need a rewrite. It was not that science was careless but that the tools available at the time created a blind spot so fundamental that it quietly shaped a generation of assumptions about how life arose on this planet. It reaches back in time four billion years to the very first coded instructions that life used to build itself. And, it turns out that those instructions may be older and stranger than anyone expected. See below.

THE BLACK SEMINOLE INDIAN SCOUTS AND FOUR MEDAL OF HONOR RECIPIENTS

We read about escaped black slaves being integrated into the Seminole Tribe in Florida but many of these “Black Seminoles” were relocated to the Western Indian Territories along with other tribes and Florida Seminoles. Few know about the heroic exploits of these Black Seminoles as US Army scouts in the western Indian wars, and that four of these scouts were recipients of the US Medal of Honor for their service and gallantry. With the end of the Plains War, many of these former scouts enlisted with the Buffalo Soldiers. See below.

DNA STUDY FILLS GAPS IN INDIGENOUS AMERICAN ANCESTRY

A new study by Elena Gusareva et al. in the journal *Science* traces the genetic background of the early settlers into South America and their splitting into four distinct groups: Amazonian, Andean, Chaco American, and Patagonian groups. The Amazon rain forest and the Andes Mountain range contributed to the isolation and genetic mutation differences despite their similar Eastern Asian roots. See below.

ARTICLES

WE MAY HAVE BEEN WRONG ABOUT THE ORIGIN OF LIFE ALL ALONG, SCIENTISTS SAY

By Julie Hambelton

From MSN at <https://www.msn.com/en-us/news/technology/we-may-have-been-wrong-about-the-origin-of-life-all-along-scientists-say/ar-AA24lFEz>



Something written in every biology textbook of the past 70 years may need a rewrite. Not because the science was careless, or the scientists were wrong to try – but because the tools available at the time created a blind spot so fundamental that it quietly shaped a generation of assumptions about how life first arose on this planet. The implications are not minor. They reach back four billion years, to the very first coded instructions life ever used to build itself. And, it turns out, those instructions may be older and stranger than anyone expected.

The question at the heart of this is deceptively simple: in what order did the alphabet of life assemble itself? Every protein in every organism that has ever lived on Earth is built from the same set of 20 amino acids (the molecular building blocks that proteins are made of). Scientists have long believed they understood, broadly, which of those amino acids came first and which came last. New research published in late 2024 has challenged that timeline in ways that matter deeply – both for understanding life on Earth and for knowing where to look for it elsewhere in the cosmos. The study came out of the University of Arizona, and its findings are generating serious attention in origin-of-life research circles. The conclusions are not just a minor recalibration. They suggest that the entire foundation on which scientists built their model of genetic code evolution may rest, at least in part, on a flawed set of assumptions – assumptions that date back to a legendary laboratory experiment conducted in 1952.

The Genetic Code, and Why Its Origins Matter

The genetic code, as senior study author and University of Arizona professor of ecology and evolutionary biology Joanna Masel describes it, is “this amazing thing in which a string of DNA or RNA containing sequences of four nucleotides is translated into protein sequences using 20 different amino acids.” Every protein your body makes – every enzyme, every structural molecule, every antibody – is the product of that code executing its instructions.

The modern genetic code was likely assembled in stages, beginning with “early” amino acids that may have been delivered to Earth by asteroids or formed by simple chemistry, and ending with “late” amino acids requiring biological synthesis. The order in which those amino acids were added was previously inferred from a consensus among some forty different metrics – many of which reflect the abundance of those molecules in the non-living chemistry of ancient Earth.

The last universal common ancestor, known as LUCA, is the hypothesized common ancestral cell population from which all subsequent life – bacteria, archaea, and all complex organisms – ultimately descends. Most studies suggest LUCA existed by around 3.5 billion years ago, and possibly as early as 4.3 billion years ago. A landmark 2024 study in *Nature Ecology and Evolution* led by researchers at the University of Bristol pinpointed LUCA’s existence more precisely, inferring that LUCA lived approximately 4.2 billion years ago and possessed a genome of at least 2.5 megabases encoding roughly 2,600 proteins, comparable in scale to modern prokaryotes, functioning as a complex anaerobic acetogen that was already part of an ecosystem. LUCA did not come from nowhere. The protein-building machinery it relied on had a history, and that history is what the University of Arizona team set out to excavate.

The Flaw at the Foundation

One of the cornerstones of conventional thinking about genetic code evolution rests on the famous Miller-Urey experiment, conducted in 1952 and published in 1953, which attempted to simulate conditions on early Earth.

While valuable in demonstrating that non-living matter could give rise to amino acids through simple chemical reactions, the experiment's implications have been called into question. Crucially, it did not yield any amino acids containing sulfur, despite sulfur being abundant on early Earth. As a result, sulfur-containing amino acids were assumed to have joined the code much later – but that conclusion is hardly surprising, given that sulfur was omitted from the experiment's ingredients in the first place.

The Miller-Urey experiment simulated early Earth's atmosphere and oceans to test whether organic molecules could form abiotically – that is, through chemistry alone, without living organisms. It documented the production of amino acids and other organic molecules, demonstrating that chemical evolution (that is, the formation of complex chemicals from simple ones) is possible. But as Britannica reports, the experiment's gas mixture – methane, ammonia, hydrogen, and water – was a representation of what scientists at the time believed the early atmosphere looked like. Later work revealed that the gases Miller used did not exist in large amounts on early Earth. The current “consensus” order in which amino acids were added to the genetic code is therefore based on potentially biased criteria. More broadly, the abiotic abundance of a molecule in a laboratory flask might not reflect its biotic abundance inside the primitive cells where the genetic code was actually evolving. This distinction turns out to be enormously consequential.

What the University of Arizona Team Did Differently

Sawsan Wehbi, a doctoral student in the Genetics Graduate Interdisciplinary Program at the University of Arizona, found strong evidence that the textbook version of how the universal genetic code evolved needs revision. Wehbi is the first author of a study published in PNAS suggesting the order in which amino acids were recruited is at odds with what is widely considered the “consensus” of genetic code evolution.

The methodological shift that made this possible was a move away from full protein sequences and toward something smaller and more ancient. Unlike previous studies, which used full-length protein sequences, Wehbi and her group focused on protein domains – shorter stretches of amino acids. “If you think about the protein being a car, a domain is like a wheel,” Wehbi explained. “It's a part that can be used in many different cars, and wheels have been around much longer than cars.” This distinction matters enormously. Full proteins are relatively recent evolutionary inventions. The domains within them are far older – some surviving virtually unchanged across billions of years of evolution. By analyzing domains rather than whole proteins, the team could peer further back into the past than previous analyses allowed.

To determine when specific amino acids were likely recruited into the genetic code, the researchers used statistical analysis tools to compare the enrichment of each amino acid in protein sequences dating back to LUCA and even farther back. The team identified more than 400 families of sequences dating back to LUCA. More than 100 of them originated even earlier and had already diversified prior to LUCA.

The Key Findings: A Rewritten Timeline

The study overturned several long-held assumptions about which amino acids are early and which are late. Three findings stand out as particularly significant.

Smaller Is Older – But Not in the Way Previously Thought

The team found that smaller amino acids were added to the code earlier. Metal-binding amino acids, including cysteine and histidine, and sulfur-containing ones, including cysteine and methionine, were added to the genetic code much earlier than previously thought. This is a direct contradiction of what the Miller-Urey-era model predicted. Sulfur-containing amino acids were assumed to be late additions because the Miller-Urey experiment failed to produce them – but as the Arizona team demonstrates, that failure was an artifact of leaving sulfur out of the experiment, not evidence that ancient life lacked sulfur.

Cysteine and methionine are the only sulfur-containing amino acids in the contemporary genetic code, and modern prokaryotes living in hydrogen sulfide-rich environments use them more heavily than species in other

environments. The enrichment of these amino acids in ancient LUCA sequences likely reflects an early life environment that was rich in hydrogen sulfide gas.

Early Life Liked Rings

The pre-LUCA protein sequences turned out to contain more amino acids with aromatic ring structures (ring-shaped molecular structures that confer particular chemical properties) – like tryptophan and tyrosine – despite these amino acids being considered late additions to the current genetic code. “This gives hints about other genetic codes that came before ours, and which have since disappeared in the abyss of geologic time,” said Masel.

This is one of the study’s most striking conclusions. Even more ancient protein sequences – those that had already diversified into multiple distinct copies prior to LUCA – have significantly higher frequencies of aromatic amino acids, including tryptophan, tyrosine, phenylalanine, and histidine. If at least some of these sequences predate the current genetic code, their distinct enrichment patterns provide hints about earlier, alternative genetic codes. Masel summarized the discovery with characteristic directness: “Early life seems to have liked rings.”

The Tryptophan Paradox

Tryptophan holds a unique place in biology. It is the largest of all 20 amino acids. Its side chain is an indole group – an aromatic structure with a binuclear ring – and the biosynthetic pathway to produce it is the most complex and energetically expensive among all amino acids. Tryptophan is widely regarded as the last of the 20 amino acids to have evolved. Its large size and complex chemical structure make its late appearance, in the current model, seem perfectly logical.

Yet the Arizona team found tryptophan showing up prominently in the most ancient protein sequences they analyzed – those predating LUCA itself. Sequences that had already diversified into multiple distinct copies in LUCA would be expected to be enriched in early amino acids and depleted in late ones. Surprisingly, these more ancient sequences showed a different pattern – significantly less depleted for tryptophan and tyrosine, and enriched rather than depleted for phenylalanine. This is compatible with at least some of these sequences predating the current genetic code, and their distinct enrichment patterns provide hints about earlier, alternative genetic codes.

The implication is that tryptophan may not have been a late addition to all genetic codes – only to the particular one that eventually won out and became universal. Before that, older codes that used tryptophan freely may have competed, evolved, and ultimately gone extinct.

A Code That Replaced Other Codes

This brings the research to its most conceptually striking claim: the genetic code every living thing uses today is not the original. The genetic code we use today likely came after other codes that have since disappeared. The researchers argue that the current understanding of how the genetic code evolved needs to be revised.

The modern genetic code was likely assembled in stages, hypothesized to begin with early amino acids possibly delivered by extraterrestrial sources and ending with late amino acids requiring biological synthesis. But the pre-LUCA sequences suggest there was an intermediate chapter in this story – older codes, now extinct, that used a different amino acid vocabulary. Some of these earlier codes may have preferentially used aromatic amino acids, including tryptophan, which the modern code later relegated to “late addition” status because they were costly and complex to synthesize.

Science Daily’s reporting on the Bristol LUCA study provides useful context here: LUCA represents the root of the tree of life before it splits into bacteria, archaea, and eukarya. Modern life evolved from LUCA from various different sources, including the same amino acids used to build proteins in all cellular organisms, the shared energy currency ATP, and the cellular machinery like the ribosome associated with translating genetic

information into proteins. If the Arizona team is right, LUCA itself inherited some of its molecular toolkit from predecessor organisms that ran on a different code entirely.

What This Means for Astrobiology – and the Search for Life

The implications extend beyond Earth. Co-author Dante Lauro, Regents Professor of Planetary Science and Cosmochemistry at the University of Arizona's Lunar and Planetary Laboratory, points out that early life's sulfur-rich nature offers insights for astrobiology, particularly in understanding the potential habitability and biosignatures of extraterrestrial environments. Lauro noted that "on worlds like Mars, Enceladus, and Europa, where sulfur compounds are prevalent, this could inform our search for life by highlighting analogous biogeochemical cycles or microbial metabolisms."

The mention of Enceladus – Saturn's icy moon – is particularly relevant. NASA's Jet Propulsion Laboratory reported that data from the Cassini spacecraft revealed organic compounds freshly ejected from Enceladus' subsurface ocean. Together with confirmed aromatic, nitrogen- and oxygen-bearing compounds, these compounds can form the building blocks to support chemical reactions and processes that could have led to more complex organic chemistry – the kind of interest to astrobiology. The high pH of Enceladus' ocean is interpreted as a consequence of serpentinization of chondritic rock, leading to the generation of hydrogen gas – a geochemical source of energy that could support both abiotic and biological synthesis of organic molecules such as those detected in Enceladus's plumes.

Research published in *Astrobiology* has taken this further. The active plume at Enceladus' south pole makes indirect sampling of its global ocean possible. The partially resolved chemistry of the plume points to conditions seemingly compatible with life, and hydrothermal activity is estimated to be sufficient to sustain both abiotic and biotic amino acid synthesis.

If ancient genetic codes on Earth could use aromatic amino acids like tryptophan – and if those compounds can form abiotically at the water-rock interface of a moon like Enceladus – then the Arizona team's findings have quietly widened the window of where in the solar system chemistry might shade into biology.

What This Means for You

The University of Arizona research, published in *PNAS* in December 2024, does not overturn everything known about the origin of life. What it does is reveal a significant methodological flaw in a framework that has guided origin-of-life science for decades – and replaces it with direct evolutionary evidence drawn from the most ancient protein structures on Earth.

The core lessons are worth sitting with. What happens in a laboratory flask does not necessarily mirror what happened inside the first cells. The Miller-Urey experiment's failure to produce sulfur-containing amino acids reflected the design of the experiment, not the chemistry of early life. Sulfur-rich amino acids appear to have been central to the earliest genetic code, not peripheral to it.

Beyond that, the genetic code we all share today was not the first genetic code. It competed with, and eventually replaced, older codes that ran on a different amino acid vocabulary – one that may have favored aromatic molecules like tryptophan far earlier than the current model allows. That history is still readable in the deepest, most conserved protein domains in every living organism on Earth today. The instructions life wrote four billion years ago did not disappear. They just got buried under layers of time – and researchers are only now learning how to read them again.

For those who follow science closely, the practical takeaway is this: the origin-of-life field is not settled, and that is a good thing. The sulfur chemistry and aromatic compounds found at hydrothermal vents – whether on Earth's ocean floor or under the ice of Enceladus – deserve more attention than they have historically received. The universe did not necessarily follow the same recipe our textbooks described. That, in itself, changes where scientists will look next, and what they will be hoping to find.

BLACK SEMINOLE INDIAN SCOUTS

From The National Park Service at <https://www.nps.gov/articles/000/black-seminole-indian-scouts.htm>



A group of Black Seminole Indian Scouts from Mexico helped the Buffalo Soldiers during the Plains Wars to track other American Indian groups. These men used their knowledge of the land to effectively do their job. Four of them were awarded the Medal of Honor. Who were the Black Seminole Indian Scouts and how did they come to be an integral part of the Buffalo Soldiers on the frontier?

The Black Seminole Indians followed a circuitous and difficult path from the swamps of Florida to the borderlands of Texas and Mexico. In the Antebellum South, enslaved

people in Georgia and South Carolina self-emancipated south into Spanish-held Florida. The Spanish would not send the now-freed Blacks back to enslavement in the colonies. The freedmen and women would make their way into the hinterland of Florida and encounter the Seminole people, who welcomed them. The newly freed men and women assimilated into Seminole life. The historical record shows that the Black Seminoles lived in their own towns and fought alongside Seminoles as equals in battle. The Black Seminoles adopted some of the Seminole ways and occasionally intermarried.

During Indian Removal before the Civil War many Seminole people, including the Black Seminoles, were moved West to Indian Territory, modern-day Oklahoma. The Black Seminoles endured the similar hardships of starvation and disenfranchisement as other native peoples during that time. Upon arrival in Indian Territory, they remained vulnerable to kidnapping and re-enslavement.

In 1850, this threat became too much for the Black Seminole Indians. A group led by John Horse and Coacoochee, known as Wild Cat, left Indian Territory and traveled to Mexico, where they could live without fear of re-enslavement. The Mexican government received them warmly and welcomed their help in fighting against Apache and Comanche raiding parties that crossed into Mexico. They also helped fend off bandits and slave raiders attempting to annex parts of Mexico to create a pro-slavery state.

After 20 years in Mexico, the Black Seminoles were interested in returning to the United States. They hoped to reclaim their land rights set out in original treaties at the time of Indian Removal. Major Zenas R. Bliss of the Twenty-fifth Infantry encouraged the Black Seminoles to emigrate back to the United States and offered them positions as scouts. On July 4, 1870, the first group of Black Seminoles arrived at Fort Duncan, Texas, to offer their scouting services. Six weeks later, in August, the U.S. Army created the Seminole Negro Indian Scouts.

The first group consisted of John Kibbetts and 10 other men and their families. Kibbetts, their leader, was appointed sergeant. All 11 men signed up for a six-month enlistment. Many of the white officers at Fort Duncan thought they were hiring scouts that looked like the Seminole people in Oklahoma. They were surprised to see that these scouts were Black. The scouts quickly adapted to their new environment. Major Bliss said they were “excellent hunters, and trailers, and brave scouts...splendid fighters.” Bliss and other officers were more than happy to give the scouts and their families a place to live in exchange for their skills on the frontier.

Throughout the 1870s, more Black Seminoles emigrated back to the United States from Mexico. Most of them settled at Fort Duncan and later Fort Clark in Texas. The ranks of the Seminole Negro Indian Scouts also increased at this time. The scouts numbered no more than 50 enlisted men at any one time.

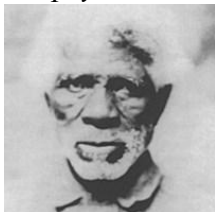
From 1873 until 1881, Lieutenant John Lapham Bullis led the scouts. They engaged in 26 campaigns and were often heavily outnumbered, but the scouts never lost a man killed or wounded in action. Four of the Black Seminoles received the Medal of Honor for their actions: Private Adam Paine, Private Pompey Factor,

Trumpeter Isaac Payne, and Sergeant John Ward. All four are buried in the Seminole Negro Indian Scout Cemetery west of Fort Clark, Texas.

As the Plains Wars ended, the U.S. Army no longer needed the Seminole Negro Indian Scouts. Many of them enlisted in the segregated Buffalo Soldier regiments. In 1914, the U.S. Army officially disbanded the Seminole Negro Indian Scouts. The Black Seminoles were displaced from Fort Clark and moved to nearby Brackettville, Texas. Some of the Black Seminole scouts' descendants remain in Brackettville, keeping their unique culture and heritage alive for future generations.

Black Seminole Indian Scouts Medal of Honor Recipients

Pompey Factor



Pompey Factor was born in 1849 in Arkansas. He was a Black Seminole Indian Scout for 10 years, from 1870 to 1880. He helped the Buffalo Soldiers track various groups throughout the Southwest. He received the Medal of Honor for his actions on April 25, 1875.

Isaac Payne



Isaac Payne was a Black Seminole born in Musquiz, Mexico in 1854. He enlisted as a trumpeter in the Seminole Indian Scouts in October of 1871. He was awarded the Medal of Honor for his actions on April 25, 1875. He died on January 12, 1904 and is buried in the Seminole Indian Scout Cemetery in Brackettville, Texas.

John Ward



John Ward was a Black Seminole Indian born in 1847 in Arkansas. He served for 25 years in the Black Seminole Indian Scouts working along the Buffalo Soldiers on the Texas frontier. He was awarded the Medal of Honor for his actions of April 25, 1875. He died in 1911 and was buried at the Seminole Indian Scout Cemetery in Brackettville, Texas.

Adam Paine



Adam Paine was born in Florida in 1843. He personally experienced Indian Removal in the 1840s. Paine and other Black Seminoles relocated to Mexico in the 1850s. He later joined the Black Seminole Indian Scouts in 1873. He was awarded the Medal of Honor for his actions on September 26, 1874. He died on January 1, 1877.

DNA STUDY 'FILLS GAPS' IN INDIGENOUS AMERICANS' ANCESTRY

By Fred Schwaller

May 17, 2025

From DW at <https://www.dw.com/en/dna-study-fills-gaps-in-indigenous-americans-ancestry/a-72558361>



The first people to inhabit the Americas migrated from modern-day Russia about 20,000 to 30,000 years ago, a new study has found. Published on May 15 in the journal *Science*, the study suggests that the languages and traditions of Indigenous groups living in the Americas today can be traced back to these early settlers. Traces of their cultures exist in the genes of modern Indigenous groups. The study also found that the early settlers split into groups that became isolated in different environmental settings. The findings provide a new genetic and cultural understanding of present-day South American communities, said the researchers. "[It fills] key gaps in our understanding of how the diverse populations of present-day South America

came to be," said Elena Gusareva, the study's lead author, who is based at Nanyang Technological University in Singapore.

Gusareva said the participants in the study had been "deeply motivated" to uncover their people's history, showing the importance of ancestral knowledge for people's identities. The researcher cited an "urgent case" involving the Kawesqar people of Patagonia, whose population and 6,000-year-old cultural heritage is in danger of disappearing. "This genetic record is one of the last chances to preserve their legacy."

Eurasian roots of Indigenous Americans

Gusareva and other researchers sequenced the genomes of 1,537 individuals from 139 ethnic groups in northern Eurasia and the Americas. They compared the millions of tiny variations in the genes of modern-day Indigenous people to ancient DNA from the first peoples to arrive in the Americas, creating a genomic dataset from people previously underrepresented in ancestral science. Tracing how these genetic codes changed in people from different geographical regions and various Indigenous groups allowed them to study patterns of population history, migration and adaptation over thousands of years. "Our genetic analysis of Indigenous groups is crucial because their genomes carry unique insights into the earliest human history in the region," said Gusareva's colleague, Hie Lim Kim, a geneticist at Nanyang Technological University.

Their analysis appears to corroborate existing archaeological evidence, showing the first peoples in the Americas diverged from North Eurasians between 19,300 and 26,800 years ago. The dates are "consistent with a large body of archaeological evidence," said Francisco Javier Aceituno, an archaeologist at the University of Antioquia, Colombia, who was not involved in the new study.

By comparing genetic datasets, the researchers said they had been able to find the closest living relatives of Indigenous North Americans are west Beringian groups, such as the Inuit, Koryaks and Luoravetlans. Beringia was an ice bridge between modern-day Russia and North America during the last ice age. Foundation of South America's Indigenous groups. Gusareva and Kim's study found that after the early settlers had arrived in South America and then split into four distinct groups — Amazonian, Andean, Chaco Amerindian and Patagonian — they each became isolated in different environments.

Aceituno told DW these groups of hunter-gatherers probably divided "to occupy new territories, generate new family groups and avoid isolation." Gusareva believes the new genetic data shows natural barriers, such as the Amazon rainforest and the Andes mountain range, led to the isolation of these Indigenous groups. "This made their genetic makeup more uniform, similar to what is seen in island populations," Gusareva said.

Ancient gene mutations affect modern South Americans' health

The study also found Indigenous groups have distinct genetic traits, which may have evolved through their adapting to extreme environments and long-term isolation from other groups. For instance, a group of Andean highlanders carries a gene mutation that helps them adapt to low levels of oxygen. Mutations in the gene EPAS1 stimulate new blood vessel formation and produce more red blood cells. EPAS1 mutations have also been found in people from Tibet. "As people adapted to diverse and often extreme environments — like high altitudes or cold climates — their genomes evolved accordingly," said Kim.

Previous studies have found genetic variations among Brazil's Indigenous groups may cause them to respond differently to medication for blood clots or high cholesterol. Kim said the new research had revealed more than 70 gene variations that could increase [people's] vulnerability to emerging infectious diseases. "Many of these populations are already small. It's critical to provide tailored health care and disease prevention efforts to support their well-being," said Kim.

SWFAS OFFICERS AND BOARD OF DIRECTORS FOR 2026

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Find us on Facebook at Southwest Florida Archaeological Society!

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SWFAS AND FAS MEMBERSHIP APPLICATIONS

We encourage those interested in Florida archaeology to become members of The Florida Anthropological Society (FAS) and The Southwest Florida Archaeological Society (SWFAS). Annual dues are due in January and membership applications to both organizations are attached. Membership in the FAS provides you with four annual volumes of *The Florida Anthropologist* and occasional newsletters on anthropological events in Florida in addition to the annual statewide meeting. More information on FAS can be found online at: www.fasweb.org. Membership in SWFAS offers you a local series of talks on archaeological and anthropological subjects that you can attend. The SWFAS monthly newsletter keeps you up to date on local events as well as other important archaeological topics. We urge you to support both with your membership. The SWFAS Lecture Series is open to all members of the public at no charge.



JOIN US!

The Southwest Florida Archaeological Society

<http://swflarchaeology.org/>

The Southwest Florida Archaeological Society (SWFAS) was founded in 1980 as a not-for profit corporation to provide a meeting place for people interested in the area's past.

Our goals are to:

- Learn more of the area's history
- Create a place for sharing of this information
- Advocate for preservation of cultural resources

Its members include professional and amateur archaeologists and interested members of the general public. Members come from all walks of life and age groups. They share a lively curiosity, a respect for the people who preceded them here, and a feeling of responsibility for the conservation of the places and objects they left behind.

The Society holds monthly meetings between October and April, attracting speakers who are in the forefront of archaeological and historical research. Occasionally members join in trips to historical and archaeological sites.

A monthly newsletter, Facebook page, and website keep members abreast of our events and happenings.

The organization is a chapter of the Florida Anthropological Society, a statewide organization that publishes quarterly newsletters and a journal, *The Florida Anthropologist*, and holds an annual conference.

I want to help The Southwest Florida Archaeology Society preserve and interpret Florida's heritage!

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Donation to Support SWFAS Speakers and Programs _____

Skills, training, interests: _____

I hereby agree to abide by the rules and bylaws of the Southwest Archaeological Society. I further release from any and all liability due to accident and injury to myself, dependents and any property owners cooperating with the society.

Signature: _____ Date _____

Please make your check out to SWFAS and mail to:

Charlie Strader
SWFAS Treasurer
27655 Kent Road
Bonita Springs, FL 34135

REV. 12052017

FAS Membership Categories

Membership in the Society is open to all interested individuals who are willing to abide by the Florida Anthropological Society Statement of Ethical Responsibilities, which can be found on our website fasweb.org. *Membership is for one year.* SELECT LEVEL BELOW.

☐ Student*	\$20	☐ Institutional	\$50
☐ Regular	\$40	☐ Sustaining	\$100
☐ Family	\$45		

*Student membership is open to graduate, undergraduate and high school students. A photocopy of your student ID must accompany payment. **Add \$25 for foreign addresses.

Member Name: _____

Email: _____

Address: _____

City: _____ State: _____ ZIP: _____

Phone: _____ FAS Chapter: _____

Please choose how you wish to receive the quarterly journal, *The Florida Anthropologist*.

☐ Digital Only (via a password protected web link) Note: Student members only receive digital access.

☐ Both Digital and Printed

This is a Gift Membership from: _____

In addition to this Membership, I also wish to make a donation to:

\$ _____ Dot Moore/FAS Student Grant Fund \$ _____ Florida Archaeology Month Account

\$ _____ Florida Anthropologist Monograph Fund \$ _____ Florida Anthropologist Endowment Fund

Total Enclosed: \$ _____

☐ I agree to abide by the Code of Ethics of the Florida Anthropological Society.

Signature

Date

Send Membership Form and Dues Payment to:

Florida Anthropological Society, P O Box 1561 Boynton Beach, FL 33425

You can join online or pay Membership dues renewals via PayPal on our website fasweb.org.

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