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## **Radiation discovered to be a major overlooked source of natural gas generation in shales**

*A large fraction of shale gas – over 25% has been produced by radioactive decomposition of organic matter*

By [Tim Wogan](#)

A substantial fraction of shale gas – potentially more than 25% in some regions – has been produced by radioactive decomposition of organic matter, a mechanism that had been dismissed as unimportant, researchers claim. They believe the discovery could prove crucial for monitoring emissions near fracking sites to ensure that the potent greenhouse gas methane is not inadvertently released into the atmosphere.

The mixture of methane and smaller quantities of ethane, propane and butane that makes up ‘natural gas’ has traditionally been extracted from oil wells. However, as these run out and prices rise, new technologies have been developed to extract gas from other sources. The most controversial is hydraulic fracturing, or fracking. This involves horizontal drilling deep into shale rocks before injecting pressurised water to crack open the shales and release hydrocarbons. Among many environmental objections is the potential for methane to leak from buried sediments into the atmosphere, and the petroleum industry is therefore required to monitor ‘fugitive emissions’.

One complication is that surface methane emissions can occur without fracking, as microbes can produce methane from carbon dioxide or acetic acid. Like all living organisms, microbes preferentially take up carbon-12 over other, heavier isotopes of carbon, so the methane they subsequently emit is isotopically light. Three processes are known to produce subterranean natural gas: microbial, thermal decomposition of organic matter under pressure and inorganic reactions between rocks. The latter two cause less

isotopic fractionation, so the isotopic composition of methane emissions from soils is used to infer their origins.

In the new work, however, researchers in France, Switzerland and Canada found that many deep shales from around the world, which are rich in radioactive elements such as thorium and especially uranium, also emitted isotopically light natural gas. The researchers turned to previous laboratory reports that irradiation of organic matter could produce gaseous hydrocarbons and, based on those reports, they calculated that such hydrocarbons would be isotopically light. ‘The difference is that, basically, microbes produce only methane, whereas radiolytic gases have a lot of ethane, propane and heavier,’ says [Maria Naumenko-Dèzes](#) of the French Geological Survey in Orléans, France.

This makes monitoring both the chemical and the isotopic composition of any gaseous hydrocarbons emitted near a fracking site crucial to ensure that leaks are not occurring, explains [Wolfram Kloppmann](#) of the University of Bern in Switzerland. ‘If you take into account that you can get this pseudo-microbial signature, but it can still be the reservoir gas you’re exploiting, then you have to think again about your monitoring strategy and the conclusions you can get from this monitoring,’ he says.

Geochemist [John Eiler](#) of Caltech in the US says the paper ‘focuses a spotlight on a side issue that has been percolating for a couple of years’. ‘This paper tries to integrate some prior experiments showing that radiolysis can be an energy source that leads to the creation of natural gas components and connect those to geochemical data,’ he says. ‘It does so in a way that is in some ways plausible and in other ways not fully developed. There’s no “A-ha!” moment... If I were a lawyer for the defence, so to speak, I could find ways to explain all the data in some more conventional way ... but it makes you want to go and do more.’ Future work, he says, should focus on finding and testing detailed mechanisms for

how the gases supposedly form.

### References

M Naumenko-Dèzes et al, *Proc. Natl. Acad. Sci. USA*, 2022, **119**, e2114720119 (DOI: [10.1073/pnas.2114720119](https://doi.org/10.1073/pnas.2114720119))

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## World's first computer, the Antikythera Mechanism, 'started up' in 178 B.C., scientists claim

*Not everyone agrees with the conclusion.*

By [Owen Jarus](#)

The mysterious Antikythera mechanism, thought by some to be the world's first computer, was first "started up" on Dec. 22, 178 B.C., archaeologists have now found.



*This 1970s reconstruction of the Antikythera Mechanism was designed by Derek de Solla Price and constructed by R. Deroski. (Image credit: Have Camera Will Travel | Europe / Alamy)*

Discovered by sponge divers in a Roman-era shipwreck near the Greek island of Antikythera in 1901, the elaborate ancient computer, which looks like a shoebox-size contraption with gears and dials that have numerous tiny inscriptions written on them, could predict eclipses and determine when various athletic games took place, among other functions.

Over the years, researchers have painstakingly pieced together the many fragments of the [Antikythera mechanism](#) to figure out how it was created and how it would have been used 2,000 or so years ago. There are many questions plaguing the device: Who made it? Where did they live? Why create it and what start date did it have? Now, a team of scientists has determined that "turn on" date, detailing their findings online March 28 on the preprint database [arXiv](#), an online journal where research can be uploaded before peer review.

However, scientists not affiliated with the study cast doubt on this claim, telling Live Science that the start date was probably in 204 B.C.

### Finding a start date

In their new paper, the researchers specify a number of reasons why they think Dec. 22, 178 B.C. was the mechanism's start date, which is the earliest date on which all calculations made on the mechanism are based. It's sort of like the temperature absolute zero on the kelvin scale.

For one, there was a [solar eclipse](#) on that day, one that lasted over 12 minutes. Secondly, the following day, Dec. 23, was the [winter solstice](#), an important day among many ancient peoples. They also note that the Isia festival — celebrating the Egyptian goddess Isis — was celebrated in both Egypt and Greece at this time. Additionally, the phases of the moon started Dec. 22 of that year, the team wrote in their paper.

This combination of events created a "very rare coincidence" that would make for a memorable starting day, the researchers wrote. The starting date "should be very characteristic, important and easily detected," Aristeidis Voulgaris, the lead author of the paper and team leader of the Functional Reconstruction of Antikythera Mechanism-The FRAME Project, told Live Science in an email.

It's possible that whoever made the Antikythera Mechanism — another unresolved question, with some experts suggesting Archimedes was the engineer who crafted the marvel — witnessed this day and remembered the cosmic events, but there is no way to be certain. "Usually, in order to perform time calculations, it is more common to select a date from the recent past rather than one in the future," the researchers wrote.

This initiation date matters because it is the date in which all calculations using the mechanism would be based on. "In order to

use a measuring instrument, a reference point is needed, before the measuring procedure," the researchers wrote in the paper. Like a calendar which needs a fixed date — such as A.D. 1 — whoever used the mechanism would need a starting date on which to base all calculations.

The date is one of the mysteries regarding the mechanical marvel that remains to be solved. Previous research has succeeded in deciphering many of the inscriptions and understanding what many of the gears and dials were used for. In 2021, a team of scholars [announced](#) the creation of a computer model of the mechanism that they believe is accurate.

### Scholars react

Live Science reached out to several scholars not affiliated with the research to get their thoughts on the team's findings. Many were not able to respond at press time, but those who did were skeptical.

"It's not a paper that would withstand competent peer-review," Alexander Jones, a professor of the History of the Exact Sciences in Antiquity at New York University's Institute for the Study of the Ancient World, said in an email. "There are a lot of problems with it, ranging from major issues to minor ones that nevertheless are symptomatic of lack of good grounding in the broad context of ancient astronomy and science," Jones said.

For instance, Jones pointed out that this start date would put

Kraneios, a season inscribed on the Antikythera mechanism that is associated with wine, in the month of February, which is "not a particularly good month for ripe grapes," Jones said.



[This image shows a reconstruction of the Antikythera mechanism.](#) (Image credit: Aristeidis Voulgaris)

Two papers [published](#) in 2014 showed that the starting date was in 204 B.C., Jones added. Those two papers showed "that the eclipse prediction sequence had been computed for a unique 223-lunar-month interval beginning in 204 B.C.," Jones said. This was timed to start on May 12 204 B.C. and start and end with a lunar eclipse.

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### Scientists Have New Theory on Origin of State

*Researchers propose that hierarchy arose as a result of the shift to dependence on appropriable cereal grains*

The conventional theory about the origin of the state is that the adoption of farming increased land productivity, which led to the production of food surplus; this surplus was a prerequisite for the emergence of tax-levying elites and, eventually, states. Hebrew University of Jerusalem's Professor Joram Mayshar and colleagues challenge this theory and propose that hierarchy arose as a result of the shift to dependence on appropriable cereal grains.

"A theory linking land productivity and surplus to the emergence of hierarchy has developed over a few centuries and became conventional in thousands of books and articles," Professor Mayshar said. "We show, both theoretically and empirically, that this theory is flawed."

Underpinning the study, Professor Mayshar, Professor Omer Moav from the University of Warwick and Reichman University, and Professor Luigi Pascali from the Universitat Pompeu Fabra and the Barcelona School of Economics developed and examined a large number of data sets including:

- (i) *the level of hierarchical complexity in society;*
- (ii) *the geographic distribution of wild relatives of domesticated plants;*
- (iii) *and land suitability for various crops to explore why in some regions, despite thousands of years of successful farming, well-functioning states did not emerge, while states that could tax and*

***provide protection to lives and property emerged elsewhere.***

“Using these novel data, we were able to show that complex hierarchies, like complex chiefdoms and states, arose in areas in which cereal crops, which are easy to tax and to expropriate, were de-facto the only available crops,” Professor Pascali said.

“Paradoxically, the most productive lands, those in which not only cereals but also roots and tubers were available and productive, did not experience the same political developments.”

The researchers also employed the natural experiment of the Columbian Exchange, the interchange of crops between the New World and the Old World in the 15th century CE which radically changed land productivity and the productivity advantage of cereals over roots and tubers in most countries in the world.

“Constructing these new data sets, investigating case studies, and developing the theory and empirical strategy took us nearly a decade of hard work,” Professor Pascali said.

“Following the transition from foraging to farming, hierarchical societies and, eventually, tax-levying states have emerged,” Professor Moav said. “These states played a crucial role in economic development by providing protection, law and order, which eventually enabled industrialization and the unprecedented welfare enjoyed today in many countries.”

“The conventional theory is that this disparity is due to differences in land productivity. The conventional argument is that food surplus must be produced before a state can tax farmers’ crops, and therefore that high land productivity plays the key role.”

“We challenge the conventional productivity theory, contending that it was not an increase in food production that led to complex hierarchies and states, but rather the transition to reliance on appropriable cereal grains that facilitate taxation by the emerging elite,” Professor Mayshar said.

“When it became possible to appropriate crops, a taxing elite

emerged, and this led to the state.” “Only where the climate and geography favored cereals, was hierarchy likely to develop.”

“Our data shows that the greater the productivity advantage of cereals over tubers, the greater the likelihood of hierarchy emerging.” “Suitability of highly productive roots and tubers is in fact a curse of plenty, which prevented the emergence of states and impeded economic development.” The team’s [paper](#) was published in the *Journal of Political Economy*.

Joram Mayshar et al. 2022. *The Origin of the State: Land Productivity or Appropriability?* *Journal of Political Economy* 130 (4); doi: 10.1086/718372

<https://go.nature.com/3Odvuju>

## **Record-breaking simulation hints at how climate shaped human migration**

***Model suggests that a shift in weather patterns in southern Africa might have contributed to the rise of Homo sapiens.***

[Freda Kreier](#)

A colossal simulation of the past two million years of Earth’s climate provides evidence that temperature and other planetary conditions influenced early human migration — and possibly contributed to the emergence of the modern-day human species around 300,000 years ago.



***The early human species Homo heidelbergensis (skull shown) might have been able to spread across Earth because wetter, more migration-friendly weather conditions arose, according to a climate model. Credit: Javier Trueba/MSF/Science Photo Library***

The finding is one of many to come out of the largest model so far to investigate how changes in Earth’s movement have influenced climate and human evolution, published in *Nature*<sup>1</sup> today. “This is another brick in the wall to support the role of climate in shaping human ancestry,” says Peter de Menocal, director of the Woods

Hole Oceanographic Institution in Falmouth, Massachusetts.

The idea that climate might have a significant role in human evolution has been around since at least the 1920s<sup>2</sup>, when scientists started debating whether drier conditions had led early human ancestors to begin walking on two feet, to adapt to life on the savannah. But so far, researchers have struggled to provide strong evidence that climate played a part in shaping humanity.

### **Orbital influence**

In the latest study, Axel Timmermann, a climate physicist at Pusan National University in South Korea, and his colleagues ran a climate model on a supercomputer for six months to reconstruct how temperature and rainfall might have shaped what resources were available to humans over the past few million years. Specifically, the researchers examined how long-term fluctuations in climate brought about by Earth's astronomical movement might have created the conditions to spur human evolution.

The push and pull of other planets alters Earth's climate by changing both the planet's tilt, and the shape of its orbit. Over 41,000-year cycles, Earth's tilt oscillates, affecting the intensity of seasons and changing how much rain falls over the tropics. And over 100,000-year cycles, Earth goes from having a more circular orbit — which brings more sunlight and longer summers — to having a more elliptical orbit, which reduces sunlight and can lead to periods of glacial formation.

Timmermann and his colleagues used a simulation that incorporated these astronomical changes, and then combined their results with thousands of fossils and other archaeological evidence to work out where and when six species of humans — including the early *Homo erectus* and the modern *Homo sapiens* — could have lived.

### **Movements and mixing**

The study pumped out a dizzying amount of data, and Timmermann

says that several interesting patterns emerged. For instance, the researchers' analysis showed that an early human species, *Homo heidelbergensis*, started expanding its habitat around 700,000 years ago. Some scientists have thought that this species might have given rise to a slew of others across the globe, including Neanderthals (*Homo neanderthalensis*) in Eurasia and *H. sapiens* somewhere in Africa.

The model suggests that the distribution of *H. heidelbergensis* across the globe was possible because a more elliptical orbit created wetter climate conditions that allowed the species to migrate more widely. The simulation also showed that the most habitable regions, in terms of climate, shifted over time, and the fossil record tracked along with them.

“The global collection of skulls and tools is not randomly distributed in time,” Timmermann says. “It follows a pattern” that overlaps with climate change driven by Earth's movement. “This is amazing to me — here is a pattern that nobody so far was able to see.”

One part of this pattern might provide fresh insight into where and how our own species emerged. Some genetic studies of modern-day hunter-gather groups in sub-Saharan Africa — who tend to be genetically isolated — suggest that *H. sapiens* is the outcome of a single evolutionary event in southern Africa. But other studies point to a more complex story, in which humanity began as a hotchpotch of many different groups of ancient Africans that, together, evolved into modern-day humans.

Timmermann and his colleagues say that their climate reconstruction favours the single-evolutionary-path hypothesis. The model suggests that our species evolved when *H. heidelbergensis* in southern Africa started losing liveable habitat during an unusually warm period. This population could have evolved into *H. sapiens* by adapting to the hotter, drier conditions.

But this finding is unlikely to end debate. “To make the case that a particular climate event led to a speciation event is really hard”, in part because of gaps in the fossil and genetic record, says Tyler Faith, a palaeobiologist at the University of Utah in Salt Lake City.

The same goes for many of the other patterns reported in the paper. “The people who’ve spent a career studying this will either be in violent agreement or disagreement with the propositions here,” de Menocal says. The model, however, is a “phenomenal accomplishment in and of itself” and “gives you a template to ask these questions”.

Most researchers that spoke to *Nature* say that more evidence will be needed to prove that astronomical cycles influenced the trajectory of human ancestry. “If solving the mystery of climate change and human evolution could be dealt with in one paper, it would have been done 40 years ago,” Faith says.

Which is why Timmermann and his colleagues are planning to run even larger models, including ones that integrate genetic data.

doi: <https://doi.org/10.1038/d41586-022-01050-1>

#### References

1 Timmermann, A. et al. *Nature* <https://doi.org/10.1038/s41586-022-04600-9> (2022).

[Article Google Scholar](#)

2 Dart, R. A. *Nature* **115**, 195–199 (1925). [Article Google Scholar](#)

[Download references](#)

<https://bit.ly/3L2bChv>

## Life With Longer Genetic Codes Seems Possible — but Less Likely

*Life could use a more expansive genetic code in theory, but new work shows that improving on three-letter codons would be a challenge.*

As wildly diverse as life on Earth is — whether it’s a jaguar hunting down a deer in the Amazon, an orchid vine spiraling around a tree in Congo, primitive cells growing in boiling hot springs in Canada, or a stockbroker sipping coffee on Wall Street

— at the genetic level, it all plays by the same rules. Four chemical letters, or nucleotide bases, spell out 64 three-letter “words” called codons, each of which stands for one of 20 amino acids. When amino acids are strung together in keeping with these encoded instructions, they form the proteins characteristic of each species. With only a few obscure exceptions, all genomes encode information identically.

Yet, in a new study published [last month in eLife](#), a group of researchers at the Massachusetts Institute of Technology and Yale University showed that it’s possible to tweak one of these time-honored rules and create a more expansive, entirely new genetic code built around longer codon words. In principle, their discovery points to one of several ways of expanding the genetic code into a more versatile system that synthetic biologists could use to create cells with novel biochemistries that make proteins found nowhere in nature. But the work also showed that an extended genetic code is hampered by its own complexity, becoming less efficient and even surprisingly less capable in some ways — limitations that hint at why life may not have favored longer codons in the first place.

It’s uncertain what these findings mean for how life elsewhere in the universe could be encoded, but it does imply that our own genetic code evolved to be neither too complicated nor too restrictive, but just right — and then ruled life for billions of years thereafter as what Francis Crick called a “frozen accident.” Nature opted for this Goldilocks code, the authors say, because it was simple and sufficient for its purposes, not because other codes were unachievable.

For example, with four-letter (quadruplet) codons, there are 256 unique possibilities, not just 64, which might seem advantageous for life because it would open opportunities to encode vastly more than 20 amino acids and an astronomically more diverse array of proteins. [Previous synthetic biology studies](#), and even some of

those rare exceptions in nature, showed that it's sometimes possible to augment the genetic code with a few quadruplet codons, but until now, no one has ever tackled creating an entirely quadruplet genetic system to see how it compares with the normal triplet-codon one.

"This was a study that asked that question quite genuinely," said Erika Alden DeBenedictis, the lead author of the new paper, who was a doctoral student at MIT during the project and is currently a postdoc at the University of Washington.

### Expanding on Nature

To test a quadruplet-codon genetic code, DeBenedictis and her colleagues had to modify some of life's most fundamental biochemistry. When a cell makes proteins, snippets of its genetic information first get transcribed into molecules of messenger RNA (mRNA). The organelles called ribosomes then read the codons in these mRNAs and match them up with the complementary "anti-codons" in transfer RNA (tRNA) molecules, each of which carries a uniquely specified amino acid in its tail. The ribosomes link the amino acids into a growing chain that eventually folds into a functional protein. Once their job is complete and the protein is translated, the mRNAs get degraded for recycling and the spent tRNAs get reloaded with amino acids by synthetase enzymes.

The researchers tweaked the tRNAs in *Escherichia coli* bacteria to have quadruplet anti-codons. After subjecting the genes of the *E. coli* to various mutations, they tested whether the cells could successfully translate a quadruplet code, and if such a translation would cause toxic effects or fitness defects. They found that all of the modified tRNAs could bind to quadruplet codons, which showed that "there's nothing biophysically wrong with doing translation with this larger codon size," DeBenedictis said.

But they also found that the synthetases only recognized nine out of 20 of the quadruplet anticodons, so they couldn't recharge the rest with new amino acids. Having nine amino acids that can be

translated with a quadruplet codon to some degree is "both a lot and a little," DeBenedictis said. "It's a lot of amino acids for something that nature doesn't ever need to work." But it's a little because the inability to translate 11 essential amino acids strictly limits the chemical vocabulary that life has to play with.

Moreover, many of the quadruplet code translations were highly inefficient, and some were even detrimental to the cell's growth. Without a major fitness advantage, it's very unlikely nature would have selected a more complex code, especially once it had settled on a working code, DeBenedictis said. The authors concluded that the reason why nature didn't select for a quadruplet code wasn't because it was unachievable, but rather because the triplet code was simple and sufficient. After all, even if life needed to expand its repertoire of 20 amino acids, there's still lots of room within the existing 64 codons to do so.

Triplet codons work well on Earth, but it's not clear if that would be true elsewhere — life in the cosmos might differ significantly in its chemistry or in its coding. The genetic code is "presumably derivative and subservient to the biochemistry of peptides" that are required for life to work, said [Drew Endy](#), an associate professor of bioengineering at Stanford University and president of the BioBricks Foundation, who was not involved in the study. In environments more complex than Earth, life might need to be encoded by quadruplet codons, but in much simpler settings, life might get by with mere doublet codons — that is, of course, if it uses codons at all.

### The Entrenched Competition

No matter how life is encoded on our planet or on others, the real impact of the paper is that now we know it's "totally possible to make a quad-code organism," and the findings suggest it will be straightforward, Endy said. With one study, they're almost halfway to getting it to work, he added, which is "an infinitely amazing

accomplishment.”

Not everyone agrees that creating a full quad-coded life form will be simple. “I don’t think anything they show suggests that it’s going to be easy — but they do show it’s not impossible and that’s interesting,” said [Floyd Romesberg](#), a synthetic biologist who co-founded the biotech company Synthorx. Getting something that works poorly to work better is a “very, very different game” than trying to do the impossible.

How much effort it will take to make a true quadruplet code work well is an open question, DeBenedictis said. She thinks you would also likely need to reengineer much of the translation machinery to work well with a larger code. She and her team are hoping to bring their work to the next level by adding an extra “tail” to the engineered tRNAs so that they will interact with a set of ribosomes designed to work with them alone. That might improve the efficiency of translation by reducing competition with any triplet-coding aspects of the system.

Overcoming the competition from the triplet code will always be a major challenge, she added, because it already works so well.

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### **Hubble Confirms Largest Comet Nucleus Ever Seen – A Staggering 500 Trillion Tons Headed This Way 4-Billion-Year-Old Relic From The Early Solar System Is Headed This Way**

Denizens of deep space, comets are among the oldest objects in the solar system. These icy “Lego blocks” are leftover from the early days of planet construction. They were unceremoniously tossed out of the solar system in a gravitational pinball game among the massive outer planets. The kicked-out comets took up residence in the Oort Cloud, a vast reservoir of far-flung comets encircling the solar system out to many billions of miles into deep space.

A typical comet’s spectacular multimillion-mile-long tail, which

makes it look like a skyrocket, belies the fact that the source at the heart of the fireworks is a solid nucleus of ice mixed with dust — a dirty snowball. Most comet nuclei measure a few miles across and so would fit inside a small town, but Hubble astronomers have uncovered a whopper. Comet C/2014 UN271 (Bernardinelli-Bernstein) could be as big as 85 miles across, over twice the width of the state of Rhode Island.

Comet C/2014 UN271 was discovered by astronomers Pedro Bernardinelli and Gary Bernstein in archival images from the Dark Energy Survey at the Cerro Tololo Inter-American Observatory in Chile. It was first serendipitously observed in 2010. Hubble observations in 2022 were needed to discriminate the solid nucleus from the huge dusty shell enveloping it, with help from radio observations. The comet is now less than 2 billion miles from the Sun, and in a few million years will loop back to its nesting ground in the Oort Cloud.

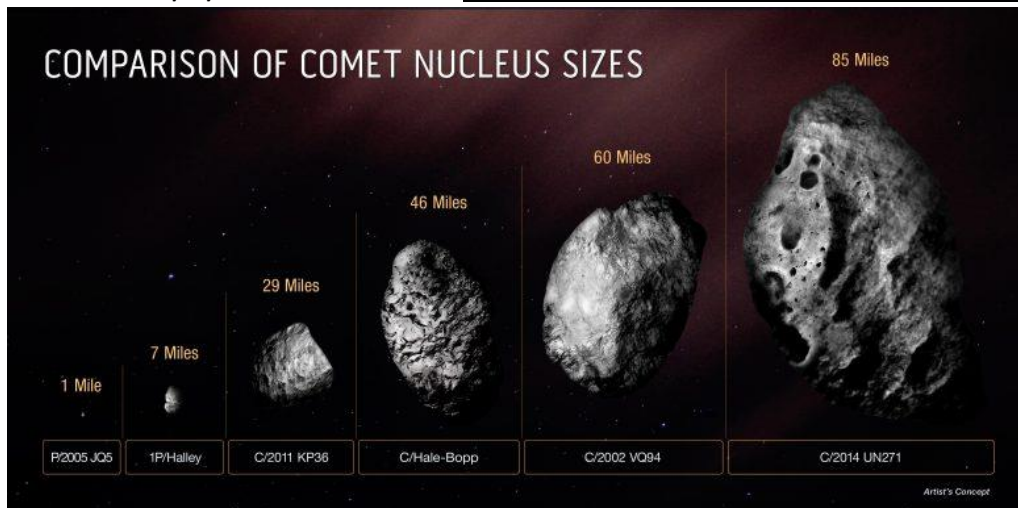
### **Hubble Confirms Largest Comet Nucleus Ever Seen**

NASA’s Hubble Space Telescope has determined the size of the largest icy comet nucleus ever seen by astronomers. The estimated diameter is approximately 80 miles across, making it larger than the state of Rhode Island. The nucleus is about 50 times larger than found at the heart of most known comets. Its mass is estimated to be a staggering 500 trillion tons, a hundred thousand times greater than the mass of a typical comet found much closer to the Sun.

The behemoth comet, C/2014 UN271 (Bernardinelli-Bernstein) is barreling this way at 22,000 miles per hour from the edge of the solar system. But not to worry. It will never get closer than 1 billion miles away from the Sun, which is slightly farther than the distance of the planet Saturn. And that won’t be until the year 2031.

The previous record holder is comet C/2002 VQ94, with a nucleus estimated to be 60 miles across. It was discovered in 2002 by the Lincoln Near-Earth Asteroid Research (LINEAR) project.





*This diagram compares the size of the icy, solid nucleus of comet C/2014 UN271 (Bernardinelli-Bernstein) to several other comets. The majority of comet nuclei observed are smaller than Halley's comet. They are typically a mile across or less. Comet C/2014 UN271 is currently the record-holder for big comets. And, it may be just the tip of the iceberg. There could be many more monsters out there for astronomers to identify as sky surveys improve in sensitivity. Though astronomers know this comet must be big to be detected so far out to a distance of over 2 billion miles from Earth, only the Hubble Space Telescope has the sharpness and sensitivity to make a definitive estimate of nucleus size. Credit: Illustration: NASA, ESA, Zena Levy (STScI)*

“This comet is literally the tip of the iceberg for many thousands of comets that are too faint to see in the more distant parts of the solar system,” said David Jewitt, a professor of planetary science and astronomy at the University of California, Los Angeles (UCLA), and co-author of the new study in *The Astrophysical Journal Letters*. “We’ve always suspected this comet had to be big because it is so bright at such a large distance. Now we confirm it is.”

Comet C/2014 UN271 was discovered by astronomers Pedro Bernardinelli and Gary Bernstein in archival images from the Dark Energy Survey at the Cerro Tololo Inter-American Observatory in

Chile. It was first serendipitously observed in November 2010, when it was a whopping 3 billion miles from the Sun, which is nearly the average distance to Neptune. Since then, it has been intensively studied by ground- and space-based telescopes.

“This is an amazing object, given how active it is when it’s still so far from the Sun,” said the paper’s lead author Man-To Hui of the Macau University of Science and Technology, Taipa, Macau. “We guessed the comet might be pretty big, but we needed the best data to confirm this.” So, his team used Hubble to take five photos of the comet on January 8, 2022.

The challenge in measuring this comet was how to discriminate the solid nucleus from the huge dusty coma enveloping it. The comet is currently too far away for its nucleus to be visually resolved by Hubble. Instead, the Hubble data show a bright spike of light at the nucleus’ location. Hui and his team next made a computer model of the surrounding coma and adjusted it to fit the Hubble images. Then, the glow of the coma was subtracted to leave behind the starlike nucleus.

Hui and his team compared the brightness of the nucleus to earlier radio observations from the Atacama Large Millimeter/submillimeter Array (ALMA) in Chile. This combined data constrains the diameter and the reflectivity of the nucleus. The new Hubble measurements are close to the earlier size estimates from ALMA, but convincingly suggest a darker nucleus surface than previously thought. “It’s big and it’s blacker than coal,” said Jewitt.

The comet has been falling toward the Sun for well over 1 million years. It is coming from the hypothesized nesting ground of trillions of comets, called the Oort Cloud. The diffuse cloud is thought to have an inner edge at 2,000 to 5,000 times the distance between the Sun and the Earth. Its outer edge might extend at least a quarter of the way out to the distance of the nearest stars to our Sun, the Alpha

Centauri system.

The Oort Cloud's comets didn't actually form so far from the Sun; instead, they were tossed out of the solar system billions of years ago by a gravitational "pinball game" among the massive outer planets, when the orbits of Jupiter and Saturn were still evolving. The far-flung comets only travel back toward the Sun and planets if their distant orbits are disturbed by the gravitational tug of a passing star — like shaking apples out of a tree.

Comet Bernardinelli-Bernstein follows a 3-million-year-long elliptical orbit, taking it as far from the Sun as roughly half a light-year. The comet is now less than 2 billion miles from the Sun, falling nearly perpendicular to the plane of our solar system. At that distance temperatures are only about minus 348 degrees Fahrenheit. Yet that's warm enough for carbon monoxide to sublime off the surface to produce the dusty coma.

Comet Bernardinelli-Bernstein provides an invaluable clue to the size distribution of comets in the Oort Cloud and hence its total mass. Estimates for the Oort Cloud's mass vary widely, reaching as high as 20 times Earth's mass.

First hypothesized in 1950 by Dutch astronomer Jan Oort, the Oort Cloud still remains a theory because the innumerable comets that make it up are too faint and distant to be directly observed. Ironically, this means the solar system's largest structure is all but invisible. It's estimated that NASA's pair of Voyager spacecraft won't reach the inner realm of the Oort Cloud for another 300 years and could take as long as 30,000 years to pass through it.

Circumstantial evidence come from infalling comets that can be traced back to this nesting ground. They approach the Sun from all different directions meaning the cloud must be spherical in shape. These comets are deep-freeze samples of the composition of the early solar system, preserved for billions of years. The reality of the Oort Cloud is bolstered by theoretical modeling of the formation

and evolution of the solar system. The more observational evidence that can be gathered through deep sky surveys coupled with multiwavelength observations, the better astronomers will understand the Oort Cloud's role in the solar system's evolution.

*Reference: "Hubble Space Telescope Detection of the Nucleus of Comet C/2014 UN<sub>271</sub> (Bernardinelli-Bernstein)" by Man-To Hui, David Jewitt, Liang-Liang Yu and Max J. Mutchler, 12 April 2022, The Astrophysical Journal Letters.*

[DOI: 10.3847/2041-8213/ac626a](https://doi.org/10.3847/2041-8213/ac626a)

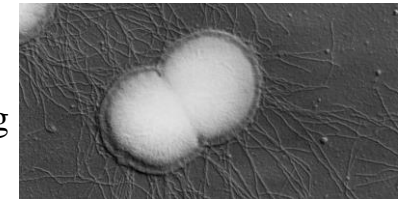
<https://bit.ly/3KQ7PU2>

## As gonorrhea becomes untreatable, a repurposed vaccine may prevent it

*The effectiveness is modest but could still prevent a large number of infections.*

[Beth Mole](#)

An existing vaccine that prevents meningococcal disease may also be up to 40 percent effective at preventing gonorrhea infections, which are becoming increasingly resistant to antibiotics, with some strains [completely incurable](#).



[Enlarge](#) / *A scanning electron micrograph of Neisseria gonorrhoeae.* [NIH](#)

This discovery is according to a series of studies and commentaries published Tuesday in The Lancet Infectious Diseases.

Though the estimated effectiveness is modest, shots of the vaccine—4CMenB aka Bexsero—could still prevent many infections, researchers reported. The vaccine could prevent more than 100,000 gonorrhea infections over 10 years in the UK, saving an estimated \$10.4 million. In the meantime, the vaccine's effectiveness could provide significant clues for vaccine developers to make a more effective gonorrhea-specific shot.

The need for such a vaccine is clear. Not only is gonorrhea quickly becoming more drug-resistant, but it is also on the rise in the US and other countries. The World Health Organization estimates there

were [more than 82 million gonorrhea cases worldwide in 2020](#). The US Centers for Disease Control and Prevention estimates there were nearly [680,000 cases in the US in 2020](#), up 10 percent from 2019 and up 45 percent from 2016.

In a press conference Tuesday, Jonathan Mermin, director of the CDC's National Center for HIV, Viral Hepatitis, STD, and TB Prevention, highlighted the optimism around using 4CMenB to prevent gonorrhea. "There's more research going into that," Mermin noted, "but it does show at least some hope that in the future we could be developing effective and safe vaccines against gonorrhea, which would help us more successfully reverse some of the trends that we've been seeing over the past 10 years."

The effectiveness of a meningococcal vaccine against gonorrhea stems from the fact that the two diseases are caused by related bacteria—*Neisseria meningitidis* and *Neisseria gonorrhoeae*, respectively. Previous research has suggested that the vaccine could provide cross-reactive immune responses, given that the [two microbes share significant amounts of their genetic code](#) and key proteins targeted by the vaccines.

### **Multipurpose vaccine**

In the series of studies published Tuesday, two were case-controlled observational studies looking at the real-world effectiveness of 4CMenB against gonorrhea infections in specific populations in the US and Australia.

In [the US-based study](#), led by the CDC's Winston Abara, researchers used health records of gonorrhea cases in people ages 16 to 23 in New York City and Philadelphia from 2016 to 2018. The cases were matched to others in the same age group who had chlamydia—the control group.

The researchers had records of nearly 168,000 infections (approximately 18,000 gonorrhea infections, 125,000 chlamydia infections, and 25,000 co-infections) among almost 110,000 teens

and young adults. Of those, nearly 7,700 were vaccinated with at least one dose—about 4,000 had one dose, and 3,600 had two doses. The researchers estimated that having two doses provided 40 percent protection against gonorrhea, and one dose was 26 percent effective.

In [the second study](#), Australian researchers tapped into data on more than 53,000 teens and young adults who received one dose and 46,000 who received two doses in South Australia as part of a statewide program. Looking at the vaccination status of gonorrhea cases and using chlamydia cases as controls, the researchers estimated that the 4CMenB vaccine was 33 percent effective at preventing gonorrhea.

The studies have several limitations. For instance, the researchers cannot determine how long such protection may last against gonorrhea after vaccination. The studies looked at specific populations, so the estimates may not be generalizable. Still, any modest benefits could significantly impact disease spread, especially in high-risk groups, such as young adults and men who have sex with men (MSM).

In [a third study](#) released Tuesday, researchers in the UK modeled the cost-effectiveness of using the meningococcal vaccine 4CMenB to prevent gonorrhea infections. They estimated that vaccinating at-risk MSM could prevent 110,000 cases in the UK over the next 10 years, saving \$10.4 million in testing and treatment costs. And those estimates are conservative. The researchers assumed that one dose of the vaccine does not provide any protection. The study also didn't account for extra costs that may be associated with drug-resistant gonorrhea infections.

"With a gonorrhea-specific vaccine likely to take years to develop, a key question for policymakers is whether the meningitis vaccine 4CMenB should be used against gonorrhea infection," lead author of the modeling study, Peter White, of Imperial College London,

said in a statement. "Our analysis suggests that giving the vaccine to those at the greatest risk of infection is the most cost-effective way to avert large numbers of cases."

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## DNA Mutation Research Reveals Why Most Smokers Never Get Lung Cancer

*Some smokers may have robust mechanisms that shield them from lung cancer by limiting mutations*

Cigarette smoking is overwhelmingly the main cause of lung cancer, yet only a minority of smokers develop the disease. A study led by scientists at Albert Einstein College of Medicine and published online on April 11, 2022, in *Nature Genetics* suggests that some smokers may have robust mechanisms that protect them from lung cancer by limiting mutations. The findings could help identify those smokers who face an increased risk for the disease and therefore warrant especially close monitoring.

"This may prove to be an important step toward the prevention and early detection of lung cancer risk and away from the current herculean efforts needed to battle late-stage disease, where the majority of health expenditures and misery occur," said Simon Spivack, M.D., M.P.H., a co-senior author of the study, professor of medicine, of epidemiology & population health, and of genetics at Einstein, and a pulmonologist at Montefiore Health System.

### Overcoming Obstacles to Study Cell Mutations

It's long been assumed that smoking leads to lung cancer by triggering DNA mutations in normal lung cells. "But that could never be proven until our study, since there was no way to accurately quantify mutations in normal cells," said Jan Vijg, Ph.D., a study co-senior author and professor and chair of genetics, professor of ophthalmology and visual sciences, and the Lola and Saul Kramer Chair in Molecular Genetics at Einstein (also at the Center for Single-Cell Omics, Jiaotong University School of

Medicine in Shanghai, China). Dr. Vijg overcame that obstacle a few years ago by developing an improved method for sequencing the entire genomes of individual cells.

Single-cell whole-genome sequencing methods can introduce sequencing errors that are hard to distinguish from true mutations—a serious flaw when analyzing cells containing rare and random mutations. Dr. Vijg solved this problem by developing a new sequencing technique called single-cell multiple displacement amplification (SCMDA). As [reported](#) in *Nature Methods* in 2017, this method accounts for and reduces sequencing errors.

The Einstein researchers used SCMDA to compare the mutational landscape of normal lung epithelial cells (i.e., cells lining the lung) from two types of people: 14 never-smokers, ages 11 to 86; and 19 smokers, ages 44 to 81, who had smoked a maximum of 116 pack years. (One pack year of smoking equals 1 pack of cigarettes smoked per day for one year.) The cells were collected from patients who were undergoing bronchoscopy for diagnostic tests unrelated to cancer. "These lung cells survive for years, even decades, and thus can accumulate mutations with both age and smoking," said Dr. Spivack. "Of all the lung's cell types, these are among the most likely to become cancerous."

### Mutations Caused by Smoking

The researchers found that mutations (single-nucleotide variants and small insertions and deletions) accumulated in the lung cells of non-smokers as they age—and that significantly more mutations were found in the lung cells of the smokers. "This experimentally confirms that smoking increases lung cancer risk by increasing the frequency of mutations, as previously hypothesized," said Dr. Spivack. "This is likely one reason why so few non-smokers get lung cancer, while 10% to 20% of lifelong smokers do."

Another finding from the study: The number of cell mutations detected in lung cells increased in a straight line with the number of

pack years of smoking—and, presumably, the risk for lung cancer increased as well. But interestingly, the rise in cell mutations halted after 23 pack years of exposure.

“The heaviest smokers did not have the highest mutation burden,” said Dr. Spivack. “Our data suggest that these individuals may have survived for so long in spite of their heavy smoking because they managed to suppress further mutation accumulation. This leveling off of mutations could stem from these people having very proficient systems for repairing DNA damage or detoxifying cigarette smoke.”

The finding has led to a new research direction. “We now wish to develop new assays that can measure someone’s capacity for DNA repair or detoxification, which could offer a new way to assess one’s risk for lung cancer,” said Dr. Vijg.

*Reference: “Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking” by Zhenqiu Huang, Shixiang Sun, Moonsook Lee, Alexander Y. Maslov, Miao Shi, Spencer Waldman, Ava Marsh, Taha Siddiqui, Xiao Dong, Yakov Peter, Ali Sadoughi, Chirag Shah, Kenny Ye, Simon D. Spivack and Jan Vijg, 11 April 2022, Nature Genetics. DOI: 10.1038/s41588-022-01035-w*

*The study is titled, “Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking.” Additional Einstein authors include: Zhenqiu Huang, Ph.D., Shixiang Sun, Ph.D., Moonsook Lee, M.S., Yakov Peter, Ph.D., Ali Sadoughi, M.D., Chirag Shah, M.D., and Kenny Ye, Ph.D., Miao Shi, Ph.D., Spencer Waldman, B.S., Ava Marsh, B.A., Taha Siddiqui, M.B.B.S., Alexander Y. Maslov, M.D., Ph.D. (also at Voronezh State University of Engineering Technology, Voronezh, Russia), and Xiao Dong, Ph.D. (also at University of Minnesota, Minneapolis MN).*

*This study was supported by grants from the National Institutes of Health (U01 ES029519-01, U01HL145560, AG017242, and AG056278).*

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## **A New Therapy Attacking a Common Virus Shows Huge Promise For Multiple Sclerosis**

*Treatment designed to attack EBV hiding in our bodies could ease decline caused by multiple sclerosis, and may reverse some symptoms.*

[Mike Mcrae](#)

A treatment designed to attack a common [virus](#) that hides in our bodies could ease the decline caused by multiple sclerosis (MS), according to new trial results. Excitingly, it may even reverse some of the symptoms.

A phase 1 clinical trial by the California-based immunotherapy company Atara Biotherapeutics confirms latent Epstein-Barr (EBV) infections are viable targets for treating MS in at least some patients, reinforcing a curious link between the virus and a deadly illness that [affects millions around the world](#).

Out of the trial's 24 volunteers, 20 showed signs of either improvement or at least a halt in their health's steady decline. Importantly, there were no signs of serious side effects.

Promising as these results might seem, the study hasn't yet been peer reviewed. What's more, the path from small [clinical trials](#) to approved medicine is a rocky one.

Years of research based on larger, ever more diverse groups of volunteers are needed to reveal hidden risks or demonstrate the worth of the treatment.

But there's good reason to think targeting the dormant virus could be key to putting the brakes on a particular aspect of MS – progressive decay of myelin, the 'insulation' protecting nerve cells.

Around 95 percent of people catch EBV at some point in their lives; the virus, also known as human herpesvirus 4, causes the illness known as mono, or glandular fever.

[Symptoms are rarely severe](#), but the virus sticks around in the body, ready for potential future reactivation. [The consequences](#) of its reappearance range from benign to deadly, although most people don't notice if EBV pipes up again.

However, research has now uncovered suspected [links between EBV](#) and various autoimmune diseases, cancers, and [chronic fatigue syndrome/myalgic encephalomyelitis](#) (CFS/ME).

As far back as the [early 1980s](#) medical researchers were noticing

that an inordinate number of blood samples from people with MS had elevated levels of Epstein-Barr virus [antibodies](#).

How the two might be related [is an ongoing question](#), though a [recent longitudinal study](#) published by researchers at Harvard found that an EBV infection "greatly increased the risk of subsequent multiple sclerosis".

Another [recent study](#) by Stanford University researchers showed nearly a quarter of MS patients have antibodies that bind to both an EBV protein called EBNA1 and a protein produced by our own nervous system called glial cell adhesion molecule, or GlialCAM.

"Part of the EBV protein mimics your own host protein – in this case, GlialCAM, found in the insulating sheath on nerves," [says](#) Stanford immunologist William Robinson.

"This means that when the immune system attacks EBV to clear the virus, it also ends up targeting GlialCAM in the myelin."

That loss of myelin could be what's primarily responsible for the diverse symptoms of multiple sclerosis. These range from difficulty walking to cognitive dysfunction, numbness and tingling, and in some cases, pain, problems with vision, and even clinical [depression](#).

Why EBV tricks the immune systems of some people and not others isn't known, though [genetics might play](#) some kind of predisposing role, possibly making it harder for their own white blood cells to respond to recurring EBV infections.

If the constant presence of the virus triggers some people's immune systems to attack their own myelin, helping them clear the infection could help treat MS symptoms as a result. This [idea was first tested](#) just under a decade ago, through the transfer of EBV-targeting immune cells into a single 42-year-old patient.

Encouraged by the experiment's results, researchers in Australia ran a slightly larger study on 10 patients [back in 2018](#), taking the patients' own T cells and training them to hunt down virus-laden

cells.

With seven of the 10 showing signs of improvement, an even larger, more rigorous clinical trial was called for to really put the concept to the test.

Instead of using the patients' own cells, this latest trial by Atara Biotherapeutics relied on specially-selected donor white blood cells, hoping it might provide a more rapid, 'off-the-shelf' delivery system. Called ATA188, they hope the therapy may not only give MS patients a chance to stay on top of EBV infection and thus improve their symptoms, but the 'donor model' would be easily scaled up to reach a greater number and higher diversity of patients.

The team's findings were [presented](#) at an investor meeting recently and a conference late last year. They claimed that of the 18 patients who agreed to participate in a more extensive data-collection period, nine reported a sustained improvement in their disability over a year or more.

There were also no reports of adverse immune responses, further demonstrating a strong need to continue research. Most exciting of all, the study also evaluated the regrowth of myelin.

Keeping in mind the small sample size and moderate improvements, the fact there are hints of re-myelination around some nerves provides solid ground for hope, since this is not something typically seen in MS patients.

"When a patient reaches a certain level of advanced disability, it is rare for them to naturally revert, and any improvement that is sustained would not be expected from the natural history of the disease," [says](#) University of Ottawa neurologist Mark Freedman.

With nearly 1 million people living with MS in the US alone, an illness that not only compromises quality of life but can shorten lifespans by years, a treatment that puts on the brakes can't come soon enough.

<https://bit.ly/36j87UF>

## Earth's oldest living landscape spotted in South African rock cores

*Campaign probes for earliest signs of oxygen-producing life*

By [Paul Voosen](#)

Beneath the [Barberton Makhonjwa Mountains](#), home to South Africa's original gold rush, lies something more scientifically valuable than any precious metal: Earth's first land ecosystem, trapped in a 3.2-billion-year-old rock formation called the Moodies Group. In roadcuts and mineshafts, scientists had already glimpsed fossilized remnants of the slimy microbial mats thought to have covered the ancient rivers, beaches, and estuaries. Now, they are drilling into the terrain for the first time, retrieving fresh samples of what may have been Earth's first microbial producers of oxygen.

"It's really lucky there are places as old as this," says Tanja Bosak, a geobiologist at the Massachusetts Institute of Technology who is unaffiliated with the project. Although older signs of life have been found in South Africa and Australia—and potentially Greenland—in what were once ocean deposits, no other spots record primordial life on land so convincingly, she says. "This covers a not-well-understood time in Earth's history."

When the Moodies Group formed, Earth would have been nearly unrecognizable. Its atmosphere, rich in methane and carbon dioxide but nearly devoid of oxygen, kept the planet warm while the Sun was young and faint. Land was scarce because plate tectonics, the process that assembles continents, was just getting going. Here and there, however, volcanic archipelagos like the Moodies Group pierced the waters. Beaches ringing the volcanoes would have been ideal spaces for life to evolve and spread, says Christoph Heubeck, a sedimentary geologist at the Friedrich Schiller University of Jena. He leads the \$2 million [Barberton Archaean Surface Environments](#) (BASE) project, which plans to complete drilling its eighth and

final core next month.

The cores the team has already extracted, from deposits 200 meters below the surface, are rich in fossilized slimes. "We've drilled through hundreds of meters of them," Heubeck says. Their nature, however, is a mystery.

Other ancient microbial fossils in the Moodies Group, found in what were marine and subsurface deposits, probably fed on sulfates or used a primitive form of photosynthesis to feed on iron. But those metabolic pathways would not have worked well in the Sun-soaked shallow waters in which the slimes lived. Heubeck [believes these microbes](#) were early ancestors of cyanobacteria, which some 800 million years later flooded the atmosphere with oxygen in what's called the Great Oxidation Event. "The production of oxygen appears to be a process invented early in Earth's history," he says.

It's a controversial claim. If oxygen-producing photosynthesis had evolved so early, some researchers argue, the Great Oxidation Event would have promptly followed. But evidence for early "oxygen oases" [has grown](#). Geochemists have found mineral deposits from well before the Great Oxidation Event that needed oxygen to form. And genetic analysis of cyanobacteria suggests they evolved, on land, [around the same time as the Moodies Group](#), says Patricia Sanchez-Baracaldo, a paleobiologist at the University of Bristol who is unaffiliated with BASE. "The genomic record is independent and consistent with the idea that those were early ancestors of cyanobacteria."

Heubeck and colleagues hope the fresh, unaltered microbial mats in the cores will yield decisive evidence: geochemical traces of oxygen production that have been missing in previous, exposed samples. That hunt will begin in earnest later this year, when the team begins to pore over half of the cores at a "sampling party" in Germany; the other half will remain in South Africa as an archive.

The cores could contain other scientific treasures. In 2010, Emmanuelle Javaux, an astrobiologist at the University of Liège, [reported finding walled spherical microbial fossils](#) up to 300 micrometers in diameter, hundreds of times the size of a typical bacterium, in mudstones extracted from a gold mine in the Moodies Group. Some thought the jumbo microbes were the world's oldest eukaryotes—organisms with complex cells like our own—by 1 billion years, but confirmation proved elusive. Javaux hopes the BASE cores will capture the same fossils in better condition. “Now we just have to find them,” she says.

The BASE cores could also hold clues to the climate of that ancient landscape. One core contains what appears to be lithified layers of soil, which could capture indicators of the atmosphere's composition. Offshore shales may record how the islands' volcanic basalt eroded. Whether it broke off in chunks, as happens in today's Arctic, or was ground down into bits as in tropical climates could hint at the ancient temperatures. Other samples capture an interwoven pattern of sand and mud layers, assembled by the ancient tides. The Moon was much closer to Earth at the time, and the tidal record could pin down its distance.

The cores should also contain a record of lightning strikes, which create strong magnetic fields that can be imprinted on rocks. Lightning might have supplied a key nutrient to the ancient ecosystem by splitting apart the tough molecular bonds of atmospheric nitrogen, enabling the atoms to form the compounds that life depends on. Because the microbes that break down nitrogen today were scarce or even nonexistent, the strike rate alone would reveal how much of this important nutrient was being added to the surface. “This nitrogen flux is potentially a major component of the biosphere at the time,” says Roger Fu, a planetary scientist at Harvard University.

In many ways, the Moodies Group cores are preparing geologists

for the work to come when rock samples are returned from another 3-billion-year-old terrain—on the surface of Mars. Later this month, NASA's Perseverance rover [will reach a fossilized river delta](#) and begin to drill cores. If, as hoped, future Mars missions return those cores to Earth, the lab techniques used on the BASE cores will come in handy, Bosak says. “Looking at these well-preserved sediments on Earth will tell us what the ideal case will be from Mars.”

<https://bit.ly/3Ehyoiy>

## **Complex Life May Have Started on Earth Much Earlier Than We Thought**

*Findings would push the date for the first signs of life on Earth back by at least 300 million years*

**Conor Feehly**

All life on Earth likely emerged from one spark in Earth's early history. Some time later, it diversified, branching off into lineages that helped it survive. Exactly when these moments occurred has been a point of contention in the scientific community, but new [research](#) suggests both steps may have taken place earlier than we previously thought.

The [study](#), led by University College London researchers builds on evidence of diverse microbial life inside a fist-sized piece of rock from Quebec in Canada, dated to around 3.75 billion to 4.28 billion years.

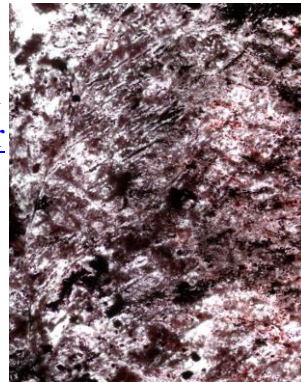
[In 2017](#), the researchers who discovered it speculated that structures in the rock – tiny filaments, knobs, and tubes – had been left by ancient bacteria. But not everyone was convinced that these structures – which would push the date for the first signs of life on Earth back by at least 300 million years – were biological in origin. However, after further extensive analysis of the rock, the team discovered an even larger and more complex structure than those which were previously identified. Within the rock was a stem-like



structure with parallel branches on one side that are nearly a centimeter long, as well as hundreds of distorted spheres, or ellipsoids, alongside the tubes and filaments.

"This means life could have begun as little as 300 million years after Earth formed. In geological terms, this is quick – about one spin of the Sun around the galaxy," [says lead author of the study](#), geochemist Dominic Papineau from UCL.

The key question for Papineau and his colleagues was whether it was possible for these structures to have formed through chemical reactions not related to living things.



*The filaments seen here are the stem-like structures indicating oldest known fossils. (D. Papineau)*

According to the paper, some of the smaller structures could have conceivably been the product of abiotic reactions, however, the newly identified 'tree-like' stem is most likely biological in origin, as no structure like it, created through chemical reactions alone, has been found before.

In addition to the structures, researchers identified mineralized chemicals in the rock that could have been byproducts of different types of metabolic processes.

The chemicals are consistent with energy-extraction processes in the bacteria that would have involved iron and sulfur; depending on the interpretation of chemical signatures, there could even be hints of a version of photosynthesis. This finding points to the possibility that the early Earth – only 300 million years after its formation – was inhabited by an array of microbial life.

The rock was analyzed through a combination of optical observations through Raman microscopes (which use light scattering to determine chemical structures), and digitally recreating

sections of the rock with a supercomputer that processed thousands of images from two high-resolution imaging techniques.

The piece of rock in question was collected by Papineau in 2008 from Quebec's Nuvvuagittuq Supracrustal Belt (NSB), which was once a part of the seafloor. The NSB contains some of the oldest sedimentary rocks known on Earth. The fossil-laden rock was also analyzed for levels of rare Earth elements, with researchers finding it did indeed have the same levels as other ancient rock specimens, confirming it was as old as the surrounding volcanic rocks.



*Bright red iron and silica-rich rock which contains tubular and filamentous microfossils. (D. Papineau)*

Prior to this discovery, the earliest fossil evidence of life [was found in Western Australia](#), which dates back 3.46 billion years. However, [similar contention](#) exists around whether these fossils were biological in origin.

Perhaps the most exciting implications from this discovery are what it means for the potential distribution of life in the Universe. If life was able to develop and evolve in the harsh conditions of the very early Earth, then it may be more common throughout the cosmos than we think.

"This discovery implies that only a few hundred million years are needed for life to evolve to an organized level on a primordial habitable planet," [state the authors of the paper](#).

"We therefore conclude that such microbial ecosystems could exist on other planetary surfaces where liquid water interacted with volcanic rocks, and that these oldest microfossils and dubiofossils reported here from the NSB suggest that extraterrestrial life may be more widespread than previously thought."

The study was published in the journal [Science Advances](#).

<https://bit.ly/3M9Lbqe>

## Ancient Peruvian was buried with tools for cranial surgery

*He was also buried with the partial skulls of two former patients.*

[Kiona N. Smith](#)

Archaeologists recently unearthed an unusual tomb in a temple complex at the Huaca Las Ventanas archaeological site near Lambaeque, in northern Peru. The site belonged to the Sican culture, one of the several complex societies that flourished prior to the rise of the Inca Empire (around 1400 CE) in northern Peru.

The tomb reveals that the Sican—like several other Indigenous cultures spanning the length of Peru and about 4,000 years of history—practiced a type of cranial surgery called trepanation.



Sican National Museum

### The surgeon's tomb

Trepanation is the delicate art of cutting or drilling a hole in a person's skull. It sounds brutal, but it can help relieve pressure on the brain from inflammation or bleeding, such as might occur after a head injury. Modern surgeons sometimes use a similar procedure, called a craniotomy, to relieve pressure from bleeding under the membrane that surrounds the brain.

Of course, modern craniotomies are guided by CT scans and MRIs. Ancient surgeons just had to go by sight and feel, which makes their success rates pretty remarkable. Archaeologists in Peru have found the remains of about 800 trepanation patients from the last 4,000 years, and the majority of them show signs of bone healing around the edges of the hole—which means they survived serious head trauma *and* cranial surgery to treat it.

Assuming that the tools belonged to the tomb's occupant, it tells us that the Sican surgeon buried at Huaca Las Ventanas wasn't a butcher; he was, as Sican National Museum director Carlos Elera put it in a press statement, "a specialist in cranial trepanations, and his surgical instruments were oriented to everything that was human skull surgery."

A whole suite of surgical tools wrapped in a bundle was lying alongside the long-dead surgeon; archaeologists found dozens of wooden-handled bronze awls, needles, and knives in various sizes. Most of the knives were single-edged blades, but one was clearly special. The semicircular blade, called a tumi, was a staple of both surgery and ritual sacrifice for the Sican, their predecessors the Moche, and later the Inca. Ritual tumis were large and elaborate, but ancient surgeons used a smaller, more utilitarian version for trepanation.

"We are comparing the instruments of a modern surgeon with these objects, to see what similarities they have," said Elera. One difference is obvious: The bronze in most of the tools contains a fairly large amount of arsenic, which would probably raise some eyebrows in a modern surgical suite.



*The surgeon's toolkit included at least 50 knives, along with needles and awls in various sizes.* Sican National Museum

On the other hand, the Sican surgeon would probably have recognized the tools used by his colleagues several hundred years earlier and several hundred miles to the south, in the Paracas culture of what's now southern Peru. Archaeologists have found very similar surgical tools—awls, knives, needles, and tumis—at Paracas sites. But while the Sican surgeon used bronze tools, Paracas surgeons favored razor-sharp obsidian blades. They share that

preference with some modern surgeons, who use obsidian scalpels for their sharpness and precision.

Two examples of the surgeon's work also joined him in his grave; archaeologists found two frontal bones (the bone that makes up the forehead). One belonged to an adult, one belonged to a child, and neither originally belonged to the surgeon (his was still attached to the rest of his skull). Both had been carefully cut using a classic trepanation technique.

### **Impressive survival rates**

Elera and his colleagues dated the surgeon's tomb at Huaca Las Ventanas to sometime between 950 and 1000 CE—about 400 years before the rise of the Inca Empire. By the time the Sican surgeon first picked up a bronze tumi, surgeons from cultures all over what's now Peru had already been performing trepanations for about 3,000 years. The oldest evidence of trepanation in Peru dates to around the same time ancient Greek physicians were first writing down guidelines for the procedure.

And, based on the archaeological record, they actually saved lives. Archaeologists in Peru have found the remains of at least 800 people, dating from 4,000 years ago up until the cusp of Spanish colonization, with neatly drilled or cut holes in their skulls. In [a 2018 study](#), University of Miami School of Medicine professor David Kushner, along with a team of archaeologists, examined those skulls for evidence of surgical survival rates. They found that Inca cranial surgeons kept their patients alive about twice as often as American Civil War surgeons, who also practiced trepanation 800 years later.

From 1000 CE to about 1400 CE (which mostly includes the Sican surgeon's lifetime), between 75 and 83 percent of cranial surgery patients lived long enough for the bone to start remodeling itself around the opening. Some surgeons were clearly better than others; Kushner and his colleagues found survival rates as high as 91

percent at some sites. Surgeons during the US Civil War, on the other hand, managed only a 44 to 54 percent survival rate.

The difference, Kushner and his colleagues speculated, was hygiene. Civil War hospitals, especially in the field, were notoriously dirty. Surgeons didn't sterilize their tools or even wash their hands. Infection probably killed more soldiers on both sides than bullets alone could have done. Most of the ancient Peruvian surgeons probably weren't working under battlefield conditions.

"We do not know how the ancient Peruvians prevented infection, but it seems they did a good job of it," said Kushner back in 2018. "Neither do we know what they used as anesthesia, but since there were so many [surgeries], they must have used something. There are no written records, so we just don't know."

The recently unearthed surgeon's tomb at Huaca Las Ventanas may shed some light on that. His kit included a piece of bark, which Elera and his colleagues speculate may have been medicinal. Some types of willow bark, for instance, have traditionally been used as painkillers and anti-inflammatories (that's where the compound in aspirin comes from).

### **The good doctor**

Although cranial surgery was a refined practice in Peru 1,000 years ago, ancient surgeons faced a bit of a learning curve. In Kushner and his colleagues' 2018 study, people who had trepanations between 400 and 200 BCE had about even odds of surviving. But over time, Peru's ancient surgeons clearly improved their knowledge of anatomy and surgical techniques.

The trick, according to Kushner, was to make smaller holes, avoid piercing the dura (the membrane that surrounds the brain), and avoid areas that are likely to bleed heavily.

And by 950-1000 CE, when the Sican surgeon at Huaca Las Ventanas practiced his trade, the profession was highly skilled and—based on the riches with which the surgeon was buried—well

respected. His grave goods included not just surgical tools but a golden mask with feathers around the eyes, a large bronze breastplate, and a set of gilded copper bowls.

<https://bit.ly/38X4FA1>

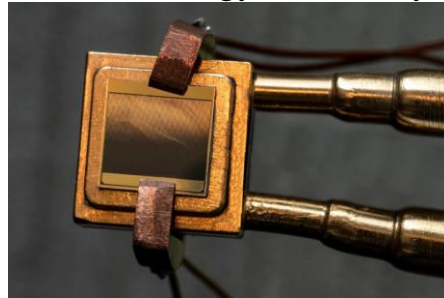
## **New Heat Engine With No Moving Parts Could Fully Decarbonize the Power Grid**

### ***A New Heat Engine With No Moving Parts Is As Efficient as a Steam Turbine***

*The design could someday enable a fully decarbonized power grid, researchers say.*

**By Jennifer Chu, Massachusetts Institute of Technology**

Engineers at MIT and the National Renewable Energy Laboratory (NREL) have designed a heat engine with no moving parts. Their new demonstrations show that it converts heat to electricity with over 40 percent efficiency — a performance better than that of traditional steam turbines.



*A thermophotovoltaic (TPV) cell (size 1 cm x 1 cm) mounted on a heat sink designed to measure the TPV cell efficiency. To measure the efficiency, the cell is exposed to an emitter and simultaneous measurements of electric power and heat flow through the device are taken. Credit: Felice Frankel*

The heat engine is a thermophotovoltaic (TPV) cell, similar to a solar panel's photovoltaic cells, that passively captures high-energy photons from a white-hot heat source and converts them into electricity. The team's design can generate electricity from a heat source of between 1,900 to 2,400 degrees Celsius, or up to about 4,300 degrees Fahrenheit.

The researchers plan to incorporate the TPV cell into a grid-scale thermal battery. The system would absorb excess energy from renewable sources such as the sun and store that energy in heavily

insulated banks of hot graphite. When the energy is needed, such as on overcast days, TPV cells would convert the heat into electricity, and dispatch the energy to a power grid.

With the new TPV cell, the team has now successfully demonstrated the main parts of the system in separate, small-scale experiments. They are working to integrate the parts to demonstrate a fully operational system. From there, they hope to scale up the system to replace fossil-fuel-driven power plants and enable a fully decarbonized power grid, supplied entirely by renewable energy.

“Thermophotovoltaic cells were the last key step toward demonstrating that thermal batteries are a viable concept,” says Asegun Henry, the Robert N. Noyce Career Development Professor in MIT's Department of Mechanical Engineering. “This is an absolutely critical step on the path to proliferate renewable energy and get to a fully decarbonized grid.”

Henry and his collaborators have published their results on April 13, 2022, in the journal *Nature*. Co-authors at MIT include Alina LaPotin, Kyle Buznitsky, Colin Kelsall, Andrew Rohskopf, and Evelyn Wang, the Ford Professor of Engineering and head of the Department of Mechanical Engineering, along with Kevin Schulte and collaborators at NREL in Golden, Colorado.

### **Jumping the gap**

More than 90 percent of the world's electricity comes from sources of heat such as coal, natural gas, nuclear energy, and concentrated solar energy. For a century, steam turbines have been the industrial standard for converting such heat sources into electricity.

On average, steam turbines reliably convert about 35 percent of a heat source into electricity, with about 60 percent representing the highest efficiency of any heat engine to date. But the machinery depends on moving parts that are temperature-limited. Heat sources higher than 2,000 degrees Celsius, such as Henry's proposed thermal battery system, would be too hot for turbines.

In recent years, scientists have looked into solid-state alternatives — heat engines with no moving parts, that could potentially work efficiently at higher temperatures.

“One of the advantages of solid-state energy converters are that they can operate at higher temperatures with lower maintenance costs because they have no moving parts,” Henry says. “They just sit there and reliably generate electricity.”

Thermophotovoltaic cells offered one exploratory route toward solid-state heat engines. Much like solar cells, TPV cells could be made from semiconducting materials with a particular bandgap — the gap between a material’s valence band and its conduction band. If a photon with a high enough energy is absorbed by the material, it can kick an electron across the bandgap, where the electron can then conduct, and thereby generate electricity — doing so without moving rotors or blades.

To date, most TPV cells have only reached efficiencies of around 20 percent, with the record at 32 percent, as they have been made of relatively low-bandgap materials that convert lower-temperature, low-energy photons, and therefore convert energy less efficiently.

### **Catching light**

In their new TPV design, Henry and his colleagues looked to capture higher-energy photons from a higher-temperature heat source, thereby converting energy more efficiently. The team’s new cell does so with higher-bandgap materials and multiple junctions, or material layers, compared with existing TPV designs.

The cell is fabricated from three main regions: a high-bandgap alloy, which sits over a slightly lower-bandgap alloy, underneath which is a mirror-like layer of gold. The first layer captures a heat source’s highest-energy photons and converts them into electricity, while lower-energy photons that pass through the first layer are captured by the second and converted to add to the generated voltage. Any photons that pass through this second layer are then reflected by the

mirror, back to the heat source, rather than being absorbed as wasted heat.

The team tested the cell’s efficiency by placing it over a heat flux sensor — a device that directly measures the heat absorbed from the cell. They exposed the cell to a high-temperature lamp and concentrated the light onto the cell. They then varied the bulb’s intensity, or temperature, and observed how the cell’s power efficiency — the amount of power it produced, compared with the heat it absorbed — changed with temperature. Over a range of 1,900 to 2,400 degrees Celsius, the new TPV cell maintained an efficiency of around 40 percent.

“We can get a high efficiency over a broad range of temperatures relevant for thermal batteries,” Henry says.

The cell in the experiments is about a square centimeter. For a grid-scale thermal battery system, Henry envisions the TPV cells would have to scale up to about 10,000 square feet (about a quarter of a football field), and would operate in climate-controlled warehouses to draw power from huge banks of stored solar energy. He points out that an infrastructure exists for making large-scale photovoltaic cells, which could also be adapted to manufacture TPVs.

*Reference: “Thermophotovoltaic efficiency of 40%” by Alina LaPotin, Kevin L. Schulte, Myles A. Steiner, Kyle Buznitsky, Colin C. Kelsall, Daniel J. Friedman, Eric J. Tervo, Ryan M. France, Michelle R. Young, Andrew Rohskopf, Shomik Verma, Evelyn N. Wang and Asegun Henry, 13 April 2022, Nature. DOI: [10.1038/s41586-022-04473-y](https://doi.org/10.1038/s41586-022-04473-y)*

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<https://bit.ly/3EoL7Qt>

**Cancer Tied to Reduced Risk of Alzheimer’s Disease**  
*Observational evidence for the connection is solidifying, and some clues are emerging about the mechanisms that may explain it.*

**Dan Robitzski**

In recent years, scientists around the world have been probing an unexpected trend: The risk of developing cancer seems to have an

inverse relationship with the risk of developing Alzheimer's disease. Research published earlier this year in [Brain](#), in which researchers autopsied study subjects to verify whether they had in fact died with Alzheimer's disease, further solidifies the hypothesis, experts tell *The Scientist*.

Thanks to those data, which showed participants with cancer had fewer hallmarks of Alzheimer's disease in their brains as well as a reduced likelihood of neurodegenerative symptoms during their lifetimes, lead study author Erin Abner, a University of Kentucky epidemiologist and aging researcher and her team were able to offer the clearest picture yet of a molecular mechanism that seems to link the two diseases.

"The connection is becoming more and more apparent," New York University cancer researcher Eva Hernando-Monge, who didn't work on the study, tells *The Scientist*.

#### **A neurological link between cancer and Alzheimer's**

Nearly every prior study exploring the connection between cancer and Alzheimer's in humans did so by analyzing epidemiological evidence. For example, a 2020 meta-analysis and literature review published in [JAMA Network Open](#) combined 22 cohort studies representing more than 9.6 million people to calculate that cancer diagnoses are associated with an 11 percent reduction in Alzheimer's disease occurrence.

The *Brain* study expands on that approach. In it, researchers monitored volunteers through the University of Kentucky's Alzheimer's Disease Research Center, which follows people throughout their lives—often for decades—and allows their symptoms and pathologies to be directly connected to biological data from their autopsies after they die, Abner tells *The Scientist*.

The researchers used data including clinical diagnoses and scores on the Mini-Mental State Exam, a popular tool used to diagnose dementia and track its progression. Those data were compared to

cohort members' records from the University of Kentucky's cancer registry, which is legally required to include every cancer diagnosis and treatment in the state. Participants were included in the analysis regardless of the stage or treatment status of their cancer, though the researchers repeated the analysis among just those who were cancer-free at baseline.

As cohort members passed away, the team autopsied their brains to look for biomarkers associated with Alzheimer's disease, including structures such as [neurofibrillary tangles](#) and neuritic plaques. They also noted when someone carried the [APOE ε4 allele](#), a known genetic risk factor for the neurodegenerative condition. This allowed for a more accurate diagnosis than studies without access to autopsies or with less access to the patients. In order to avoid confounding factors, the team only included data from subjects who didn't show signs of dementia at their baseline examination, explaining in their paper that such a diagnosis might prompt behavioral changes that could potentially complicate the analysis. While this reduced the number of participants to 785, far lower than most cohort studies, experts tell *The Scientist* that the multifaceted methodology means that the data were of particularly high quality.

The analysis revealed "less Alzheimer's pathology in the people who had cancer, both amyloid and tau," Abner says. "We also saw evidence [that] another amyloid pathology—cerebral amyloid angiopathy, which is amyloid aggregation in blood vessel walls—was lower. Another contribution of our study is that we found an inverse association with *APOE*, a major genetic driver of Alzheimer's risk, and cancer. Most of the existing studies on cancer and dementia have not been able to use these kinds of data."

Jane Driver, who studies aging and the Alzheimer's-cancer link at the US Department of Veterans Affairs and Harvard Medical School but didn't contribute to the *Brain* paper, says that the new publication fills in a gap "for which there isn't a lot of evidence,

which is a biological-level correlation between what people's brains look like when they die, a real objective assessment of Alzheimer's-type pathology, and a good definition of cancer from a cancer registry."

Biologist Ovais Shafi from Sindh Medical College in Pakistan, who also was not involved in the research, similarly tells *The Scientist* over email that the study's design and methodology "make the findings of the study more impactful and clear" than those of previous purely epidemiological papers on the link.

Experts say that diagnosing Alzheimer's disease—by examining autopsied brains for specific Alzheimer's biomarkers—is crucial for cutting noise from the data and painting a clear picture of the relationship between cancer and Alzheimer's.

That's because there are many kinds of dementia that can be caused by myriad factors such as strokes, Driver says, and it's impossible to diagnose a dementia patient with perfect accuracy until after they've died and their brain can be autopsied. Without the ability to confirm an Alzheimer's diagnosis, data from people with other forms of dementia can muddle the results: as Driver explains, the inverse correlation with cancer diagnosis only seems to exist for Alzheimer's disease, not with dementia in general.

#### **Possible mechanisms for a cancer-Alzheimer's risk connection**

Compared to the evidence that a correlation exists, scientists' understanding of the mechanisms driving the link between Alzheimer's and cancer is far less robust. However, there have been some attempts to explain the link at the molecular scale.

For example, Shafi scoured existing literature to write a 2016 review in *BMC Neurology* that suggested each disease downregulates processes in the brain that would support the other condition. Processes related to cell growth and survival, as well as the production of specific molecules including the antistress response protein [vimentin](#) and the enzyme [carbonic anhydrase](#), are

all upregulated in cancer, he finds. Alzheimer's occurs when these processes and proteins are downregulated.

Another review, published in *Molecular Psychiatry* in 2021, identifies the proteins p53 and PIN1 as implicated in both cancer and Alzheimer's. PIN1 overexpression is [associated with myriad cancers](#), but its absence [is linked to](#) the formation of the Alzheimer's biomarkers tracked in the *Brain* study. Meanwhile, p53 has a well-established [anticancer role](#), but can also [contribute to neurodegenerative disease](#).

While the *Brain* paper primarily focused on the onset of Alzheimer's disease among cancer patients and not vice versa, the evidence in these reviews suggests that the correlation may be bidirectional and dictated at least in part by the genetic drivers of those various processes.

#### **Picture imperfect**

Still, questions remain about exactly how the diseases are connected. For example, Shafi says it's imperative that future research "seeks out which factors greatly contribute to [Alzheimer's] or are causative directly or indirectly," establishing a clearer link than the correlation identified by existing studies.

In addition to experimental studies, improving our understanding of the link will require access to even better and broader human data.

One challenge is that the volunteers in the *Brain* study were overwhelmingly white and highly-educated—with an average of 15 years of schooling—making them poorly representative of the broader population and potentially skewing the study results, explains University of Michigan School of Public Health social epidemiologist Lindsay Kobayashi, a coauthor of the *JAMA Network Open* meta-analysis.

"An important thing to remember about research studies that use autopsy data is that they have used data from people who have died, and these people might have different neuropathology than those

who live for a long time,” Kobayashi adds. Among the participants whose data were included in the final study, the average age of death was just under 84 years old, plus or minus about nine years—a number unaffected by cancer diagnosis.

It’s also possible that people who survive cancer and stave off Alzheimer’s happen to be healthier than the general population for some unknown reason, Driver speculates, which is to say that further studies will need to investigate and attempt to rule out other possible explanations for the phenomenon.

The burning, unanswered question is what this means for people living with dementia, cancer, or both. As far as immediate clinical applications go, the *Brain* paper offers little to go on. However, continuing to explore the link between cancer and Alzheimer’s could one day reveal new ways to treat or prevent both, experts tell *The Scientist*.

“This understanding may ultimately lead to a revolution in the development of new therapies that will be focusing on new targets in terms of molecular mechanisms and cellular pathways based on the inverse relationship between Alzheimer’s disease and Cancer,” Shafi writes.

Driver adds that there may be a biological profile of people who are more likely to develop Alzheimer’s and less likely to develop cancer—or vice versa. If scientists “can understand what’s driving those differences” and “discover what is it [that] the body’s doing to protect itself from cancer and increase the risk of Alzheimer’s,” Driver says, then there may be “something we could modulate there to come up with a new treatment.”

### **The melanoma exception**

The *Brain* study identified a general trend but didn’t correlate the risk of Alzheimer’s disease with any individual type of cancer.

“Cancers are all quite different,” US Department of Veteran Affairs researcher Jane Driver tells *The Scientist*, with pathology that is

“very different from cancer to cancer.”

Standing out from other cancers is melanoma, which has a more complicated relationship with Alzheimer’s—as well as Parkinson’s—than cancer as a whole does, New York University cancer researcher Eva Hernando-Monge tells *The Scientist*. Based on her work on the mechanistic connections between neurodegenerative disease pathology and melanoma metastasis, she asserts that the inverse correlation between Alzheimer’s disease and cancer risk doesn’t hold true when looking specifically at melanoma. She adds that there’s a strong positive correlation between melanoma and another neurodegenerative condition, Parkinson’s disease—a trend that’s [been supported](#) by [multiple studies](#).

Hernando-Monge, along with colleagues primarily from New York University, published a paper this month in [Cancer Discovery](#) in which a proteomic analysis of melanoma cells from human patients revealed that the cancer, which has one of the highest rates of brain metastasis among malignancies, can adapt to better survive the brain environment. The study, which also involved injecting human melanoma cells into mice, found that metastasizing melanoma tumors secrete amyloid beta, the peptide that builds up in the brains of people with Alzheimer’s, indicating that there’s a plausible positive connection between that cancer type and Alzheimer’s instead of the inverse relationship turned up by the *Brain* paper.

Those secretions, she explains, inhibit the immune system’s ability to fight melanoma cells by neutralizing astrocytes in the area. That, in turn, prevents astrocytes from summoning microglia that would target and consume the tumors—telling the astrocytes that “nothing is going on, stay there, don’t call the microglia, everything is alright,” Hernando-Monge says. That, ultimately, may prevent the brain from staving off not only melanoma but neurological conditions as well.



<https://bit.ly/3jKfB63>

## Zoo anteater exposed people to rabies in first-of-its-kind case

*The unusual case marks the first time that rabies has been reported in this species of anteater.*

By [Rachael Rettner](#)

An anteater infected with rabies at a Tennessee zoo potentially exposed more than a dozen people to the deadly virus, according to a new report.



(Image credit: Mikael Drackner/Getty Images)

The unusual case marks the first time that rabies has been reported in this species, a type of anteater from South America known as the southern tamandua or lesser anteater (*Tamandua tetradactyla*), according to the report, published Thursday (April 14) in [Morbidity and Mortality Weekly Report](#), a journal from the Centers for Disease Control and Prevention (CDC).

What's more, the anteater in question had recently been transferred from a zoo in Virginia and was infected with a variant of rabies not typically seen in Tennessee, meaning the animal likely caught the virus before its transfer, the report said. This case highlights the potential for "rabies translocation" from one geographic area to another through the movement of captive animals, the authors said.

The case began in early May 2021, when the anteater was transferred from the Virginia zoo to a zoo in Washington County, Tennessee, where it was housed with one other anteater. In late June 2021, the transferred anteater started showing signs of illness, including lethargy, loss of appetite and diarrhea, the report said. At first, veterinarians presumed the anteater had a bacterial infection and prescribed antibiotics.

When the animal's symptoms continued to get worse, veterinarians

at a nearby college examined the animal. But at first, staff at the college did not consider rabies as a possible diagnosis because the animal wasn't known to have any bites (which can spread rabies) and rabies had never been reported in this type of anteater (tamanduas) before.

Interestingly, tamanduas have a very low body temperature of 91 degrees Fahrenheit (33 degrees Celsius) — one of the lowest body temperatures of any active land mammal, according to the [San Diego Zoo Wildlife Alliance](#) — and such a low body temperature was thought to reduce the risk of infection with rabies, the authors said.

Ultimately, the anteater got so sick that it was euthanized on July 6, 2021, the report said. Veterinarians performed a necropsy to try to understand why the animal died, and samples of the anteater's [brain](#) tissue tested preliminary positive for rabies on Aug. 16, 2021. Additional testing was performed by the CDC, and the agency confirmed the diagnosis of rabies on Aug. 21, 2021.

Because anteaters don't have teeth, there was no risk of the animal biting people and giving them rabies. But some people may have been exposed to the animal's saliva or brain tissue (during the necropsy), which could have spread the virus, the report said. After an assessment of people who came into contact with the anteater, officials recommended that 13 of these people receive rabies postexposure prophylaxis, which consists of multiple shots of the rabies vaccine. All 13 people agreed to receive the treatment.

As of April 1, 2022, no additional cases of rabies related to this case — in either humans or animals — were identified in Tennessee or Virginia, the report said.

Further analysis revealed that the anteater was infected with a variant of the rabies virus seen in raccoons in the eastern United States, including those in Virginia, but not previously seen in Tennessee. This suggests that the anteater acquired its infection at

the Virginia zoo, the researchers said. The Virginia zoo was notified about concerns of rabid raccoons on their property, and the zoo confirmed that native wildlife (including raccoons) had been seen inside the zoo's fencing perimeter, the report said.

"Captive mammals maintained in exhibits or zoological parks typically are not completely excluded from rabies host species and can become infected," the authors wrote. They noted that "all employees who work with animals in areas where rabies is endemic should receive preexposure rabies vaccination."

In the current case, three of the 13 people who were exposed to the anteater hadn't received rabies vaccination before, and they needed a dose of rabies antibodies as part of their treatment in addition to the rabies vaccine shots.

"This case also highlights the importance of continued public health efforts to expand awareness and education about rabies prevention and control," the authors said.

<https://bit.ly/3vjHIOW>

## **Mysterious hepatitis outbreak sickens young children in Europe as CDC probes cases in Alabama**

*Researchers suspect an adenovirus may be involved, but are still searching for the cause of illness*

By [Meredith Wadman](#)

La Paz University Hospital in Madrid admitted a 22-month-old with acute hepatitis, *El País* newspaper reported this week. The child is one of dozens of European and U.S. children with serious hepatitis of unknown cause.

Puzzled scientists are searching for the cause of a strange and alarming outbreak of severe hepatitis in young children, with 74 cases documented in the United Kingdom and three in Spain. Clinicians in Denmark and the Netherlands are also reporting similar cases. And in the United States, the Centers for Disease Control and Prevention (CDC) said late yesterday it is investigating

nine cases in Alabama.

Viruses can cause hepatitis, an inflammation of the liver, but otherwise-healthy children rarely become seriously ill. As of 12 April, none of the U.K. or Spanish children have died, but some are very sick: All have been admitted to hospitals and seven required liver transplants, [six of them in the United Kingdom](#), according to a World Health Organization (WHO) statement issued today. Two of the nine affected children in Alabama have required liver transplants, the state's Department of Public Health [announced](#) this afternoon.

The leading theory is that an adenovirus, a family of viruses that more typically cause colds, is the culprit—up to half of the sickened children in the United Kingdom tested positive for such a virus, as did all the children in Alabama. But so far, the evidence is too thin to resolve the mystery, researchers and physicians say.

"This is a severe phenomenon," says Deirdre Kelly, a pediatric hepatologist at Birmingham Children's Hospital in England. "These [were] perfectly healthy children ... up to a week ago." Not all the news is bad, however. "Most of [the children] recover on their own," Kelly notes.

"This should be taken seriously," WHO's Regional Office for Europe said in an emailed statement. "The increase is unexpected and the usual causes have been excluded."

Scottish investigators first identified the outbreak on 31 March, when they alerted Public Health Scotland to a cluster of 3- to-5-year-olds admitted to the Royal Hospital for Children in Glasgow in the first 3 weeks of March. Each was diagnosed with severe hepatitis of unknown cause. Typically, Scotland sees fewer than four such cases annually, the investigators wrote in a [paper published yesterday](#). But there have been 13 cases in Scottish children as of 12 April, all but one in March and April.

Kelly, who works at one of England's three centers for pediatric

liver disease and transplantation, says that since the start of this year, her unit has seen 40 cases of childhood hepatitis of uncertain cause. Over the same January to April period in 2018, her unit saw only seven such children.

Most of the U.K. children are 2 to 5 years old, according to [a statement](#) issued on 8 April by the UK Health Security Agency. The European Centre for Disease Prevention and Control [issued a public alert](#) on 12 April about the U.K. outbreak, noting that vomiting and jaundice—yellowing of the skin and the whites of the eyes—are common symptoms.

Early hypotheses about what might be making the children sick included a toxic exposure from food, drinks, or toys, but suspicion now centers on a virus. None of the U.K. or Spanish kids had the hepatitis A, B, C, or E viruses, typical infectious causes of the disease. But a handful of children tested positive for SARS-CoV-2 infection shortly before or upon hospital admission; none had received a COVID-19 vaccine. In addition, as many as half had adenovirus, a common virus passed by respiratory droplets and from touching infected people or virus on surfaces. It can cause vomiting, diarrhea, conjunctivitis, and cold symptoms but rarely causes hepatitis.

“The leading hypotheses center around adenovirus—either a new variant with a distinct clinical syndrome or a routinely circulating variant that is more severely impacting younger children who are immunologically naïve,” the Scottish investigators wrote.

Isolation of the youngest children during the pandemic lockdown may have left them immunologically vulnerable because they haven’t been exposed to the multiplicity of viruses, including adenoviruses, that typically attend toddlerhood. “We are seeing a surge in typical childhood viral infections as children come out of lockdown, [as well as] a surge in adenovirus infections”—but can’t be sure that one is causing the other, says Will Irving, a clinical

virologist at the University of Nottingham.

Researchers continue to study other possibilities. For example, the immunological effects of a prior episode of COVID-19 might have left children more vulnerable to infection or the illness could be a long-term complication of COVID-19 itself. An unidentified toxin has also not been ruled out.

All the cases might not have a single cause, cautions Jim McMenamin, an epidemiologist who heads the infection service of Public Health Scotland. “It’s awfully important that we ensure we are looking for everything, that we are not confining ourselves to saying this is simply one viral cause.”

In the United States, CDC is helping the Alabama Department of Public Health investigate nine cases of hepatitis in children ranging in age from 1 to 6 years old and who also tested positive for adenovirus. The cases have occurred since October 2021, Kristen Nordlund, a CDC spokesperson, said in the statement emailed to *ScienceInsider* last night.

“CDC is working with state health departments to see if there are additional U.S. cases, and what may be causing these cases,” she wrote. “Adenovirus may be the cause for these, but investigators are still learning more—including ruling out the more common causes of hepatitis.”

Wes Stubblefield, a medical officer with the Alabama Department of Public Health, said in an interview today that the most recent case in Alabama occurred in February, and that five of the nine children tested positive for adenovirus-41, a strain that commonly causes gastroenteritis.

Meanwhile, in Spain, the government of the Madrid region announced on 13 April that three regions—Madrid, Aragón, and Castilla-La Mancha—had each reported a case of severe hepatitis of unknown origin in young children. One child has received a liver transplant.

Physicians at major pediatric liver centers in the Netherlands and Denmark told *ScienceInsider* yesterday they are seeing similar trends. “There are children that are very sick and have been referred for transplantation, says Ruben de Kleine, a pediatric liver transplant surgeon at University Medical Center Groningen. “We have assessed a similar number of kids for transplantation within the first 4 months of 2022 [to what we] normally do in a whole year.”

At Copenhagen University Hospital, too, “we have more cases with [acute liver failure] than we normally have,” says pediatric hepatologist Marianne Hørby Jørgensen. No children there have needed transplants.

Hørby Jørgensen and de Kleine both stress that parents should not panic. To date, clinicians have identified small numbers of cases in their countries where, combined, more than 230,000 infants are born each year.

*Update, 15 April, 3:00 p.m.: This story has been updated to include more details about the Alabama cases.*

<https://wb.md/3JNGBft>

## Case Study: Lead Poisoning From Ayurvedic Medicine

*Drug users are not the only ones who need to watch out for lead — believers in certain traditional remedies do too*

Thomas Kron, MD

### Core Messages

Lead is used as a diluting agent for illegal drugs such as heroin and [marijuana](#). However, drug users are not the only ones who need to watch out for the toxic heavy metal — believers in certain traditional remedies do as well.

The case history of a young man, as related by Victor Suárez, MD, and his colleagues from the University Hospital of Cologne, Germany, which was [published](#) in the *German Medical Weekly*, illustrates this point.

### Presentation and History

The 24-year-old man came to the emergency department because of crampy lower abdominal pain and poor performance status, according to the authors.

Investigations that were conducted during a previous inpatient hospital stay had not yielded any indicative findings. The patient had no preexisting conditions other than previous cocaine and [cannabis abuse](#). When asked, the patient reported that he had received an Indian (Ayurvedic) remedy from a friend. He had been taking two capsules of it each day for about a month.

### Findings

- *Patient in reduced general condition but with normal nutritional status*

- *Normal vital signs*
- *Diffuse abdominal pressure pain*
- *Pale gray skin color and slight gingival gums on the edges*
- *No evidence of a focal neurologic deficit*
- *Elevated liver enzyme and [lipase](#) levels*
- *Normocytic, normochromic [anemia](#)*
- *No vitamin B12, [folic acid](#), or iron l deficiency*
- *Normal kidney function*
- *Elevated ferritin level (671 µg/L)*
- *Abdominal ultrasonography and CT without additional findings*

- *Testing for heavy metals: significantly elevated blood levels of lead (70 µg/dL; normal value, <5 µg/dL)*

- *Elevated urine levels of δ-aminolevulinic acid (42 mg/L; normal value, <4.5 mg/L)*

- *Peripheral blood smear: basophilic spotting of erythrocytes*

- *Lead also detected in the hair (12.1 µg/g)*

According to the authors, the analysis of the capsules taken by the patient revealed that there was 34 mg of lead per two capsules. This

corresponds to about 136 times the permissible dose.

### Therapy and Course

The patient received chelation therapy (250 mg of dimercaptopropane sulfonate [DMPS] intravenously every 4 hours). The dose was gradually reduced, and the patient was switched to oral administration after 4 days (DMPS 100 mg 3x daily p.o.). The patient's blood level of lead dropped from 70 µg/dL initially to 57 µg/dL after 5 days on this therapy, according to the authors. The symptoms regressed, and the patient was discharged in good general condition.

During a follow-up examination after 3.5 months, the patient was symptom free and in very good general condition. The blood level of lead was 30 µg/dL. The hemoglobin level and levels of liver enzymes and lipase were normal.

### Discussion and Recommendations

Suárez and his colleagues report that lead exposure in the population has steadily declined since the 1980s, owing to the ban on lead-based paint and the switch to unleaded gasoline. What is less well known is that drugs and traditional natural remedies that are contaminated with lead can also cause [lead poisoning](#). Around 20% of Ayurvedic remedies contained at least one heavy metal at a potentially toxic dose. Of these medicines, lead was the heavy metal most often detected.

Symptoms of lead poisoning are nonspecific. Initially, patients often have abdominal discomfort ("lead colic"), and there are often changes in the blood count.

A thorough study of the patient's history with regard to occupation, living situation, hobbies, medications — including alternative medicine and drug use — is a key part of the diagnostic process. A suspicion of lead poisoning warrants determining the blood lead level and  $\delta$ -aminolevulinic acid in the urine.

<https://bit.ly/3uRuMRk>

## Green eggs and scam: Cuckoo finch's long con may be up

*For two million years African cuckoo finches have been tricking other birds into raising their young by mimicking the colour of their eggs, but new research suggests the tables may be turning in this evolutionary scam.*

by Pierre Celerier and Daniel Lawler

The cute yellow appearance of the [cuckoo](#) finch belies its nefarious nature: it smuggles its forged eggs into foreign nests, where unwitting foster parents treat them like their very own.

The cuckoo finch eggs then hatch a little earlier than the others in the nest, allowing them to grow quicker and beg more loudly for food than the host chicks—which starve to death as their confused parents prioritise the imposter.

Aiming to save their young from this grisly fate, [birds](#) like the African tawny-flanked prinia, a common victim of the ruse, have evolved ever more colourful and elaborate patterns for their eggs to avoid falling for counterfeits. But the wily cuckoo finch has responded in kind, evolving the ability to copy a variety of egg colours and signatures of several different bird species.

Way back in 1933, British geneticist Reginald Punnett hypothesised that cuckoo finches inherited this remarkable talent of mimicry from their mothers.

His theory has been proved for the first time by a study published in the *PNAS* science journal this week, which confirmed that the skill is inherited via the W chromosome which only [female birds](#) have—similar to how only human males have the Y chromosome.



*The far larger cuckoo finch hatchling, centre, demands all the food in the nest, leaving the hosts chicks to starve to death.*

However the study said that "in this particular arms race, played out in grasslands of central Africa, [natural selection](#) has shaped a genetic architecture that appears to be a double-edged sword."

Studying the DNA samples of 196 cuckoo finches from 141 nests of four grass-warbler species in Zambia, the researchers found that the long-term dupes have evolved new ways to sniff out the cuckoo finch's deceptions.

### **The uncrackable green egg**

Claire Spottiswoode, an evolutionary biologist of the University of Cambridge and University of Cape Town who led the research, gave the example of the olive-green egg, laid by the tawny-flanked prinia.

A single female cuckoo finch cannot produce an infinite variety of differently coloured eggs, she said. It can only mimic the egg of the bird that raised it—the cuckoo finch is "imprinted" with how to target its future victims from the shells of its foster siblings.

This means that different cuckoo finches can lay blue or white eggs, while others can produce them in red and white—but because the skill is inherited via the female chromosome, they can never combine those pigments to make that olive green.

"Maternal inheritance is the reason why they're unable to mimic that particular deep olive green colour," Spottiswoode told AFP.

That puts the cuckoo [finch](#) at a evolutionary disadvantage—their rivals the prinias can inherit the genetic talents of both parents to make increasingly complicated [eggs](#).



*The tawny-flanked prinia has evolved more elaborate eggs to filter out fakes, including a green colour that cuckoo finches cannot mimic.*

"We may see the emergence of unforgeable egg signatures which

could force cuckoo finches to switch to other naive host species," Spottiswoode said.

Even now cuckoo finches "make a lot of mistakes" she said, and once prinias spot a forgery they spear the egg and throw it out of the nest. But if an egg avoids detection long enough to hatch, the parents lose all ability to detect the much larger fraud in their nest.

"It's really remarkable how you have this beautiful adaptation at the egg stage, then at the chick stage the hosts seem to be completely stupid and raise a chick that looks completely unlike their own," Spottiswoode said.

*More information: Genetic architecture facilitates then constrains adaptation in a host-parasite coevolutionary arms race, Proceedings of the National Academy of Sciences (2022). DOI: [10.1073/pnas.2121752119](https://doi.org/10.1073/pnas.2121752119)*