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Giant tsunami from dino-killing asteroid impact revealed in fossilized 'megaripples'

For the first time, scientists have discovered fossilized megaripples from this tsunami

By Akila Raghavan

When a giant space rock struck the waters near Mexico's Yucatán Peninsula 66 million years ago, it sent up a blanket of dust that blotted out the Sun for years, sending temperatures plummeting and killing off the dinosaurs. The impact also generated a tsunami in the Gulf of Mexico that some modelers believe sent an initial tidal wave up to 1500 meters (or nearly 1 mile) high crashing into North America, one that was followed by smaller pulses. Now, for the first time, scientists have discovered fossilized megaripples from this tsunami buried in sediments in what is now central Louisiana.

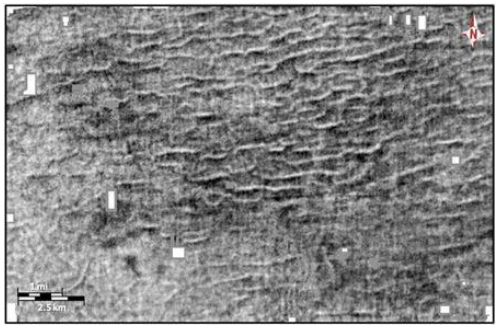
"It's great to actually have evidence of something that has been theorized for a really long time," says Sean Gulick, a geophysicist at the University of Texas, Austin. Gulick was not involved in the work, but he co-led a campaign in 2016 to drill down to the remains of the impact crater, called Chicxulub.

To look for ancient buried structures, researchers rely on seismic imaging techniques to "see" underground. They set off explosives or use industrial hammers to send seismic waves into the earth, and listen for reflections from the layers of sediment and rock below. Companies use the technique to search for oil and gas, and they have mountains of data—especially in areas such as the Gulf of Mexico.

More than 10 years ago, Gary Kinsland, a geophysicist at the University of Louisiana, Lafayette, obtained seismic imaging data for central Louisiana from Devon Energy. At the time of the dino-killing impact, sea levels were higher, and Kinsland thought information from this region would hold clues to what happened in the shallow seas off the coastline.

When Kinsland and his colleagues analyzed a layer about 1500 meters underground—one associated with the time of the impact—they saw fossilized ripples. These "megaripples" were spaced up to 1 kilometer apart and were an average of 16 meters tall, they reported in an *Earth & Planetary Science Letters* study posted online on 2 July.

Kinsland believes the ripples are the imprint of the tsunami waves as they approached the shore in waters about 60 meters deep, disturbing the seafloor sediments. (Tidal waves gain their massive height only when they reach the ramp of the coastline.)



Seismic images of underground layers in Louisiana revealed megaripples associated with a tsunami. **Kaare Egedahl**

Kinsland says the orientation of the ripples was also consistent with the impact. When he drew a line perpendicular to their crests, he says, it went right to Chicxulub. He adds that the location was perfect for preserving the ripples, which would have eventually been buried in sediment. "The water was so deep that once the tsunami had quit, regular storm waves couldn't disturb what was down there."

The discovery is the latest in a flurry of research about the Chicxulub impact, which was first hypothesized in the 1980s. Cores from the 2016 drilling expedition helped explain how the impact crater was formed and charted the disappearance and recovery of Earth's life. In 2019, researchers reported the discovery of a fossil site in North Dakota, 3000 kilometers north of Chicxulub, that they say records the hours after the impact and includes debris swept inland from the tsunami.

"We have small pieces of the puzzle that keep getting added in," says Alfio Alessandro Chiarenza, a paleontologist at the University of Vigo who was not involved with the new study. "Now this research is another one, giving more evidence of a cataclysmic tsunami that probably inundated [everything] for thousands of miles."

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Covid vaccine: Thailand decides to mix jabs as cases spike

Thailand has changed its vaccine policy to mix China's Sinovac with the AstraZeneca vaccine in a bid to boost protection.

The decision comes after hundreds of medical workers caught Covid despite being fully vaccinated with Sinovac. Instead of two Sinovac shots, people will now receive the AstraZeneca vaccine after their first Sinovac shot. Health workers already fully vaccinated with Sinovac will also receive a third booster from a different vaccine.

This can be either the AstraZeneca vaccine, or an mRNA vaccine like Pfizer/BioNTech. This third dose will be given three to four weeks after their second Sinovac jab, said the country's National Infectious Disease Committee on Monday. AstraZeneca is currently the only other vaccine available in the country, with Pfizer/BioNTech shots donated by the US set to arrive soon.

Thailand first received Sinovac vaccines from China and began giving shots to its health workers in February.

On Sunday, the health ministry said out of more than 677,000 medical staff who were fully vaccinated with Sinovac, 618 were infected between April and July. One nurse has died and one medical staff is still in critical condition.

According to a study published in the New England Journal of Medicine showing results from Chile, Sinovac has an efficacy rate of 65.9% against Covid-19, is 87.5% effective at preventing hospitalisation and 86.3% effective at preventing death.

Thailand is currently in the midst of a spike of new infections, reporting a record high of 9,418 on Sunday. The death toll for the previous day stood at 91, also a record number. Concerns over the efficacy of the Chinese vaccine amid rising cases have sharply driven demand for other shots offered by some private clinics.

Last week, one clinic selling the US Moderna vaccine on an online shopping platform saw its offer sold out within minutes. The Phyathai Hospital offered 1,800 vaccination slots for a single Moderna shot at 1,650 Thai baht ($50, £36) via Shopee.

Overall, Thailand has seen more than 345,000 confirmed cases of Covid-19 and nearly 2,800 deaths since the beginning of the pandemic in 2020, according to figures collated by Johns Hopkins University from around the world. There are concerns that the spike in cases in many South East Asian countries is due to the spread of the more infectious Delta variant, first discovered in India.

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A 'wobble' in the moon's orbit could result in record flooding in the 2030s, new study finds

The entire US coastline is in for a one-two punch from the lunar cycle and climate change.

By Brandon Specktor - Senior Writer

Climate change has already increased the frequency and severity of hurricanes and other extreme weather events around the world. — But there's a smaller, less splashy threat on the horizon that could wreak havoc on America's coasts.

High-tide floods, also called "nuisance floods," occur in coastal areas when tides reach about 2 feet (0.6 meters) above the daily average high tide and begin to flood onto streets or seep through storm drains. True to their nickname, these floods are more of a nuisance than an outright calamity, inundating streets and homes, forcing businesses to close and causing cesspools to overflow —

but the longer they last, the more damage they can do.

The U.S. experienced more than 600 of these floods in 2019, according to the National Oceanic and Atmospheric Administration (NOAA). But now, a new study led by NASA warns that nuisance floods will become a much more frequent occurrence in the U.S. as soon as the 2030s, with a majority of the U.S. coastline expected to see three to four times as many high-tide flood days each year for at least a decade.

The study, published June 21 in the journal Nature Climate Change, warns that these extra flood days won't be spread out evenly over the year, but are likely to cluster together over the span of just a few months; coastal areas that now face just two or three floods a month may soon face a dozen or more.

These prolonged coastal flood seasons will cause major disruptions to lives and livelihoods if communities don't start planning for them now, the researchers cautioned.

"It's the accumulated effect over time that will have an impact," lead study author Phil Thompson, an assistant professor at the University of Hawaii, said in a statement. "If it floods 10 or 15 times a month, a business can't keep operating with its parking lot under water. People lose their jobs because they can't get to work. Seeping cesspools become a public health issue."

Several factors drive this predicted increase in flood days.

For one, there's sea level rise. As global warming heats up the atmosphere, glacial ice is melting at a record pace, dumping enormous amounts of meltwater into the ocean. As a result, global average sea levels have risen about 8 to 9 inches (21 to 24 centimeters) since 1880, with about a third of that occurring in just the last 25 years, according to NOAA. By the year 2100, sea levels could rise anywhere from 12 inches (0.3 m) to 8.2 feet (2.5 m) above where they were in 2000, depending on how well humans restrict greenhouse gas emissions in the coming decades.

While rising sea levels alone will increase the frequency of high-tide floods, they will have a little help from the cosmos — specifically, the moon.

The moon influences the tides, but the power of the moon's pull isn't equal from year to year; the moon actually has a "wobble" in its orbit, slightly altering its position relative to Earth on a rhythmic 18.6-year cycle. For half of the cycle, the moon suppresses tides on Earth, resulting in lower high tides and higher low tides. For the other half of the cycle, tides are amplified, with higher high tides and lower low tides, according to NASA.

We are currently in the tide-amplifying part of the cycle; the next tide-amplifying cycle begins in the mid-2030s; — and, by then, global sea levels will have risen enough to make those higher-than-normal high tides particularly troublesome, the researchers found.

Through the combined effect of sea-level rise and the lunar cycle, high-tide flooding will increase rapidly across the entire U.S. coast, the team wrote. In a little more than a decade, high-tide flooding will transition "from a regional issue to a national issue with a majority of U.S. coastlines being affected," the authors wrote. Other elements of the climate cycle, like El Niño events, will cause these flood days to cluster in certain parts of the year, resulting in entire months of unrelenting coastal flooding.

Scary as this pattern sounds, it is also important to understand for planning purposes, the authors wrote. "Understanding that all your events are clustered in a particular month, or you might have more severe flooding in the second half of a year than the first — that's useful information," study co-author Ben Hamlington of NASA's Jet Propulsion Laboratory said in the statement.

Extreme weather events may get all the national media attention as they batter America's coasts, but high-tide flooding will soon be impossible to ignore. Best to start planning for it now, before it's too late, the authors concluded.

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That Scandalous Phosphine on Venus Really Could Come From Volcanoes, Says New Study

Phosphine gas detected in the atmosphere of Venus could have a volcanic origin after all, new research has found.

Michelle Starr

An analysis of potential volcanic activity on the mysterious planet has found that, contrary to findings uploaded to preprint server arXiv last year, there may indeed be sufficient geothermal venting to produce the detected abundances of the gas.

The detection of phosphine on Venus, announced in September of 2020, had scientists around the world shaken.

The gas can be found here on Earth in very limited contexts, one of which is anaerobic, or low oxygen, ecosystems. It's found in swamps and sludges, where anaerobic microbes thrive; it's found in intestines and intestinal gas. Somehow, anaerobic microorganisms produce phosphine - and the clouds of Venus are anaerobic.

As we reported at the time, however, a biological origin was far from the only possible explanation. One phosphine-producing process here on Earth is volcanic activity. And while the team ruled this out, finding that volcanic activity on Venus is insufficient and citing a 2015 study on the matter, more recent research indicated Venus may be more volcanically active than previously thought.

Now scientists from Cornell University have made a careful study of the available information, and concluded that volcanic activity, particularly explosive volcanic activity, could have produced the observed abundance of phosphine.

"The phosphine is not telling us about the biology of Venus," said astronomer Jonathan Lunine of Cornell University. "It's telling us about the geology. Science is pointing to a planet that has active explosive volcanism today or in the very recent past."

The path of the phosphine detection has not been smooth. Initially, the abundance, made using two separate instruments at two different times (the James Clerk Maxwell Telescope in 2017 and the Atacama Large Millimeter/submillimeter Array in 2019) was determined to be about 20 parts per billion.

Then, it turned out there had been an error processing the data from ALMA; the reprocessed data yielded a lower abundance, a global average of 1 to 4 parts per billion, with localized peaks of 5 to 10 parts per billion.

Lunine and his colleague, geologist Ngoc Truong of Cornell University, have reviewed Venus data suggesting active volcanism - if not current, then recent. They used published laboratory data on the production of phosphine gas to determine if a form of phosphorus called phosphide vented from deep under the Venusian mantle could be converted into phosphine.

Here on Earth, phosphorus found in impurities in iron can be converted efficiently to phosphine gas via reactions with hydrochloric acid, and magma rich in phosphide can be found deep in the mantle.

The researchers assumed a Venus mantle oxidation state similar to Earth's - not unreasonable, given that the two planets are so similar in mass and composition, if not habitability. And they found that, if vented by way of explosive volcanism, phosphide in Venusian magma can be converted into phosphine via reactions with the sulfuric acid in Venus' atmosphere.

Surface features on Venus are suggestive of recent volcanism; sulfur dioxide, a gas that can be volcanogenic, has been detected in the Venusian atmosphere. Using these and other studies, the researchers found there can indeed be sufficient volcanic activity on Venus to produce the observed abundances of phosphine.

Of course, the phosphine detection itself is still the subject of a lot of debate and is yet to be confirmed by another instrument (you can read more about that here). The new study doesn't address that, but

simply lays out the case for another means by which the phosphine could have come to be there.

"Given the ongoing debate about the robustness of the phosphine detection itself, our results only suggest a roadmap to assessing the level of Venusian volcanic activity today," the researchers wrote in their paper.

"Should the phosphine be there, it might point to Venus experiencing a modestly elevated epoch of active plume volcanism with magma originating deep in the mantle. That, in turn, would strengthen the case for additional missions to understand the geologic state and history of the planet closest to us in space and bulk physical properties." The research has been published in *PNAS*.

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Maybe not so fast with the phage therapy?

Even though viruses attack harmful bacteria, the immune system attacks viruses.

Diana Gitig

Every living thing on the planet plays host to viruses, and bacteria are no exception. Bacteriophages—or just "phages" to those in the know—are the viruses that attack bacteria. And we are in dire need of things that attack bacteria, since many pathogenic bacterial species have developed resistance to the antibiotics we've thrown at them for decades.

Phage therapy is attractive not only because antibiotic use yields antibiotic resistance but also because the treatment can be targeted specifically to the bacteria causing an infection. Most antibiotics in use are rather broad-spectrum, so they obliterate many of the bacteria they encounter, including the ones that are happily residing in our guts, minding their own business and not causing anyone any problems. Phages can be more precise.

But is phage therapy effective? A new study suggests it may end up being undercut by our own immune systems, which treat the therapies like a hostile invader.

Case studies

One promising case study that makes phage therapy look promising is provided by a 15-year-old girl with cystic fibrosis. He had a nasty bacterial infection, which was successfully treated with a cocktail of three different phages. But he was on immunosuppressants because he had just had a lung transplant. Phage therapy in immunocompetent people has not yet been as thoroughly examined, so we don't really know how our immune system would deal with it.

The researchers who treated the boy learned of an 81-year-old man with lung disease who was infected with a closely related strain of bacteria. He had been treated with different antibiotic regimens for five years to no avail. The researchers took bacteria he coughed up and exposed it to the same three phages they had successfully used to treat the other patient, and they found that the phages killed most, but not all, of the bacteria. The bacteria the phages didn't kill evolved some resistance to the phages, but none of the bacteria that survived were resistant to all three phages.

The researchers put the man on a six-month regimen of IV phage therapy but did not discontinue his antibiotics. There were no serious side effects. After the first month, things looked great; the amount of bacteria in his sputum dropped tenfold. But then they rebounded with a vengeance. At the end of the six months, his bacterial load was even higher than when he began. Phage therapy was discontinued.

Neutralized

Phage resistance did not account for this bacterial explosion; neutralizing antibodies against the phage did. Before the treatment, the patient had no such antibodies. But within a month of treatments starting, he developed antibodies of all subtypes against all three phages. The phages do not share many features, so there was not just one antibody cross-reacting with all of them—different

antibodies were independently generated against each of them.

This does not mean that phage therapy is too good to be true; it just still may be in the "better in theory than in practice" stage of clinical development. We'll need more than a couple of individual patients to understand the scope of the challenge.

Now that we know antibodies can interfere with phages, perhaps administering them serially might be better than giving them all together. Or maybe different phages will ultimately be used for immunosuppressed and immunocompetent people. Like antibiotics, phages are not a miracle cure. They have therapeutic utility, but it is not limitless.

Nature Medicine, 2021. DOI: 10.1038/s41591-021-01403-9. (About DOIs).

https://bit.ly/3esyich

Scientists Discover The First Known Algae Species With Three Distinct Sexes

Algae could actually help us to understand how different sex systems - like male and female - evolved

Jacinta Bowler

Although we might think of ourselves as far removed from blobby green algae, we're not really that different.

An algae explosion a few hundred million years ago is thought to have been what allowed all human and animal life to evolve, and all told there's only about one and a half billion years between us in terms of evolution.

Plus, according to a Japanese team of researchers, algae could actually help us to understand how different sex systems - like male and female - evolved in the first place.

Researchers from the University of Tokyo and a number of other Japanese universities have discovered that a type of green algae called *Pleodorina starrii* has three distinct sexes – 'male', 'female', and a third sex that the team have called 'bisexual'. This is the first time any species of algae has been discovered with three sexes.

"It seems very uncommon to find a species with three sexes, but in natural conditions, I think it may not be so rare," said one of the researchers, University of Tokyo biologist Hisayoshi Nozaki.

Algae isn't a very specific scientific classification. It's an informal term for a huge collection of different eukaryotic creatures that use photosynthesis to get energy. They're not plants, as they lack many plant features; they're not bacteria (despite cyanobacteria sometimes being called blue-green algae); and they're not fungi.

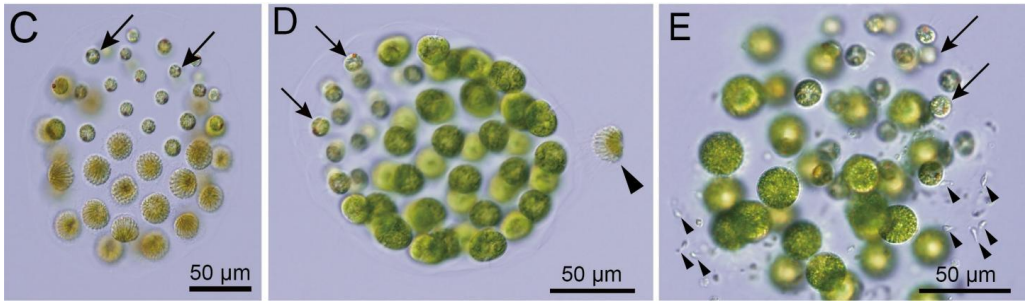
Everything from many-celled giant kelp species, all the way down to cute single-celled dinoflagellates can be classed as algae.

Because algae are such a big, diverse group, there's lots of variation in the way that they get it on, but generally algae are able to reproduce asexually (by cloning themselves) or sexually (with a partner), depending on the life cycle stage they're in. This can be either haploid (with a single set of chromosomes), or diploid (with two sets). There's also hermaphroditic algae that can change depending on the gene expression of the organism. Having three sexes, including hermaphrodites, is called 'trioecy'.

But the volvocine green algae *P. starrii* is different from this again. The bisexual form of this haploid algae has both male and female reproductive cells. The team describe it as a "new haploid mating system" completely unique to algae.

P. starrii form either 32 or 64 same-sex celled vegetative colonies and have small mobile (male) and large immobile (female) sex cells similar to humans. The male sex cells are sent out in the world in sperm packets to find a female colony to attach to.

Bisexual *P. starrii* have both, can form either male or female colonies, and therefore can mate with either a male, a female, or another bisexual. The researchers are particularly excited because other closely related algae have different sex systems, meaning the discovery might be able to tell us more about how these sexual changes evolve.



Above: Sexually induced male colony of algae (left). Female colony with male sperm packet (center). Female colony with dissociated male gametes (right). **(Kohei Takahashi)**

"Mixed mating systems such as trioecy may represent intermediate states of evolutionary transitions between dioecious (with male and female) and monoecious (with only hermaphrodites) mating systems in diploid organisms," the team write in their new paper.

"However, haploid mating systems with three sex phenotypes within a single biological species have not been previously reported."

For 30 years, Nozaki had been collecting algae samples from the Sagami River outside of Tokyo. Samples that were taken from lakes along that river in 2007 and 2013 were used by the team for the new finding.

The team separated the algal colonies and induced them to reproduce sexually by depriving them of nutrients, discovering that the bisexual algae had a 'bisexual factor' gene that was separate to previously discovered male and female specific genes.

The bisexual cells had the male gene as well, but can produce either male or female offspring. "Co-existence of three sex phenotypes in a single biological species may not be an unusual phenomenon in wild populations," the researchers conclude.

"The continued field-collection studies may reveal further existence of three sex phenotypes in other volvocine species."

The research has been published in *Evolution*.

https://bit.ly/2UmkqSB

Post-vaccination Infections Come in 2 Different Flavors

Lumping all breakthroughs together, regardless of symptoms, miscasts what our COVID-19 vaccines can do.

By Katherine J. Wu

The first thing to know about the COVID-19 vaccines is that they're doing exactly what they were designed and authorized to do. Since the shots first started their rollout late last year, rates of COVID-19 disease have taken an unprecedented plunge among the immunized. We are, as a nation, awash in a glut of spectacularly effective vaccines that can, across populations, geographies, and even SARS-CoV-2 variants, stamp out the most serious symptoms of disease.

The second thing to know about the COVID-19 vaccines is that they're flame retardants, not impenetrable firewalls, when it comes to the coronavirus. Some vaccinated people are still getting infected, and a small subset of these individuals is still getting sick—and this is completely expected.

We're really, really bad at communicating that second point, which is all about *breakthroughs*, a concept that has, not entirely accurately, become synonymous with vaccine failure. It's a problem that goes far beyond semantics: Bungling the messaging around our shots' astounding success has made it hard to convey the truly minimal risk that the vaccinated face, and the enormous gamble taken by those who eschew the jabs.

The main problem is this. As the CDC defines it, the word *breakthrough* can refer to *any* presumed infection by SARS-CoV-2 (that is, any positive coronavirus test) if it's detected more than two weeks after someone receives the final dose of a COVID-19 vaccine. But infections can come with or without symptoms, making the term imprecise. That means breakthroughs writ large aren't the most relevant metric to use when we're evaluating

vaccines meant primarily to curb symptoms, serious illness, hospitalizations, and death. "Breakthrough *disease* is what the average person needs to be paying attention to," Céline Gounder, an infectious-disease physician at Bellevue Hospital Center in New York, told me. Silent, *asymptomatic* breakthroughs—those that are effectively invisible in the absence of a virus-hunting diagnostic—are simply not in the same league.

To put this in perspective, consider the original criteria laid out by the FDA about this time last year, back when the United States was still solidly in its second infectious surge. An effective inoculation, the agency said, should be able to "prevent disease or decrease its severity in at least 50 percent of people who are vaccinated." It's an easy benchmark to forget. By the close of 2020, two vaccines absolutely obliterated those expectations; two months later, a third followed, and now there's buzz of a fourth.

If disease is our yardstick, then breakthrough COVID-19 cases—a very small subset of all known breakthroughs—might meet our criteria for concern. These are actual illnesses, events where the shots' protection has apparently crumbled; these cases are the same ones that vaccine makers searched so diligently for in clinical trials, to ensure that their products were working. By the same logic, *asymptomatic* coronavirus infections fall outside our shots' protective purview as we defined it so many months ago. And although they're important to track and glean data from, conflating them with the rest, experts told me, risks misrepresenting what our vaccines can do. (The CDC responded to an inquiry about its designation by saying that while a "SARS-CoV-2 infection" indicates any positive tests for the virus and a "COVID case" refers to a person with a positive test who meets other case definitions, "throughout COVID the terms infection and case have often been used interchangeably.")

The term *breakthrough* has long been a staple of the infectious-disease community, where it's used to describe the detection of vaccine-preventable pathogens in immunized individuals. "This is definitely not a new idea," says Kevin Escandón, a physician and infectious-disease researcher at the University of Valle, in Colombia. But as a popular notion, it was always doomed to cause some confusion. *Breakthrough* is still used as an adjective of praise; the pandemic has now warped the word into a foreboding noun that tends to eclipse all clarifying qualifiers. "It's confusing, it's fuzzy, it's already loaded," Alison Buttenheim, who studies human behavior around vaccines at the University of Pennsylvania, told me. And when news appears in a headline or push alert, or on social media, "people pay attention to the word *breakthrough*" and not much else, Ryan McNamara, a virologist at the University of North Carolina at Chapel Hill, told me. That's unfortunate, when the simple addition of *asymptomatic* or *symptomatic* can make all the difference. As they stand, blanket *breakthroughs* sound far scarier than they should.

Joseph Allen, a public-health researcher at Harvard, recently pointed out on Twitter one such ambiguity, in a study documenting a very small number of breakthrough infections at a prison. All were asymptomatic—though you wouldn't know it from the paper's title.

To be clear, breakthroughs of *any* severity are an entirely expected part of the vaccination process. No vaccines are 100 percent effective at preventing infection or disease. But our current crop of COVID-19 shots comes pretty damn close with regards to stymieing symptoms, especially the severe ones that can signal a deadly case. The Moderna and Pfizer shots have consistently demonstrated very high COVID-prevention rates, often in the 90s; Johnson & Johnson's, for the most part, isn't far behind. Symptomatic breakthroughs are the cases that wedge themselves in the gap between *excellent* effectiveness and *perfect* effectiveness; in

other words, we saw them coming.

Even out in the messiness of the real world, symptomatic breakthrough cases are proving themselves quite rare. The overwhelming majority of the COVID-19 cases we're seeing are among the unvaccinated. And when the virus *does* affect the immunized, it seems to accumulate to lower levels, and spread less enthusiastically to new hosts; it's causing, on average, milder and more transient symptoms.

All of this is a reminder of how vaccines work—by ratcheting up our immunity against the version of SARS-CoV-2 that the shots were formulated to mimic. If humans are wood that fuels a flame, and coronaviruses are the sparks that ignite it, vaccines are the fire suppressants that protect best against the worst of the viral burn: severe disease, hospitalization, and death. Stopping milder cases requires more immune investment, and blocking asymptomatic infections—ones that barely singe the bark—is most difficult of all. It's part of why the vaccines' goalposts were at first set so conservatively. "This is not a magic shield that just bounces coronavirus right off you," McNamara told me.

Considering that we first took aim at stopping disease, it's great news that the majority of known breakthroughs have actually been asymptomatic infections, not COVID-19 cases. The proportions of silent breakthroughs reported by various studies and federal agencies are certainly undercounts, because vaccinated people aren't regularly screened for the coronavirus. (On May 1, the CDC controversially switched its reporting strategy to documenting only breakthrough cases involving some form of hospitalization or death, skewing national counts further.) Since the vaccines first deployed, the news has only improved: Researchers didn't bank on it, but in many people, the shots seem to stop the coronavirus from establishing itself *at all*. "The vaccines are better than anything we ever dreamed of," Gounder told me, exceeding our first expectations in more ways than one.

The shots are even holding their own against SARS-CoV-2 variants. A few versions of the virus have picked up mutations that help them dodge certain anti-coronavirus antibodies. But these genetic alterations chip away only incrementally at immune protection, rather than obliterating it. Against Delta, for instance, vaccines like Pfizer's are still curbing severe disease, hospitalization, and death to an extraordinary degree. And while the shot's strength has slightly slackened when it comes to milder illnesses and silent infections, those are simply lower hurdles for a virus to clear. Pfizer's protection is still hitting its mark where it matters the most. (One asterisk on this is long COVID, a condition whose relationship to vaccination is still being actively researched.)

None of this means, of course, that asymptomatic breakthrough infections should be ignored. To fully understand what the virus is doing and where it might be headed, experts need as comprehensive a picture as they can get of whom it's afflicting, and what form those infections take, across the entire spectrum of disease. They also need to know how and when it's most likely to *spread.* Asymptomatic infections are a part of that. Researchers around the world are still diligently sequencing any and all test-positive coronavirus samples they can, regardless of symptoms, in part to check whether any particular variants are disproportionately infiltrating the inoculated. They're also tabulating who's experiencing breakthroughs, and testing whether select populations might benefit from an early vaccine boost.

And when vaccines start to consistently falter against more severe tiers of disease—because of either a new variant, waning immune memory of the virus, or both—the diligent monitoring of breakthroughs will pick it up. Tracking milder breakthroughs is also crucial to figuring out how well the virus can be transmitted from vaccinated people, something that's much more difficult to

determine than whether inoculations merely block disease. From a surveillance standpoint, casting a broad net for breakthroughs—one that accounts for infections of all types—is essential, Buttenheim said. “That’s how you catch everything.”

The question of which breakthroughs matter ultimately depends on another: What’s the goal of vaccination? Gounder thinks that, for now, the focus should stay on using immunizations to control COVID-19, especially while so much of the world remains unvaccinated; understanding whether we’re accomplishing that goal, then, hinges on symptomatic breakthroughs. Eventually, we’ll have the bandwidth to turn our attention to halting transmission and infection more comprehensively. Then, we’ll pull asymptomatic breakthroughs back into the conversation, with more data to guide our next move.

https://go.nature.com/3kr9CVi

This ‘super antibody’ for COVID fights off multiple coronaviruses

An newly identified immune molecule raises hopes for a vaccine against a range of viruses related to SARS-CoV-2.

Diana Kwon

Scientists have uncovered an antibody that can fight off not only a wide range of SARS-CoV-2 variants, but also closely related coronaviruses[1]. The discovery could aid the quest to develop broad-ranging treatments and vaccines.

Tyler Starr, a biochemist at the Fred Hutchinson Cancer Research Center in Seattle, Washington, and his co-authors set out to shed light on a problem facing antibody treatments for COVID-19: some variants of SARS-CoV-2 have acquired mutations that enable the virus to escape the antibodies’ grasp.

The researchers examined 12 antibodies that Vir Biotechnology, a company based in San Francisco, California, that was involved in the study, isolated from people who had been infected with either SARS-CoV-2 or its close relative SARS-CoV. Those antibodies latch on to a fragment of viral protein that binds to receptors on human cells. Many antibody therapies for SARS-CoV-2 infection grab the same protein fragment, called the receptor binding domain.

The researchers compiled a list of thousands of mutations in the binding domains of multiple SARS-CoV-2 variants. They also catalogued mutations in the binding domain on dozens of SARS-CoV-2-like coronaviruses that belong to a group called the sarbecoviruses. Finally, they assessed how all these mutations affect the 12 antibodies’ ability to stick to the binding domain.

One antibody, S2H97, stood out for its capacity to adhere to the binding domains of all the sarbecoviruses that the researchers tested. S2H97, which the authors dub a pan-sarbecovirus antibody, was able to prevent a range of SARS-CoV-2 variants and other sarbecoviruses from spreading among cells growing in the laboratory. It was also powerful enough to protect hamsters against SARS-CoV-2 infection. “That’s the coolest antibody that we described,” Starr says.

A closer examination of S2H97’s molecular structure revealed that it targets a previously unseen and well-hidden region on the binding domain — a section that is revealed only when the domain pops up to bind to a cell’s receptor. Starr notes that molecules targeting this binding-domain region could generate protection against multiple viruses, and might one day be used in pan-sarbecovirus vaccines.

The other 11 antibodies could target a variety of viruses, but the more effectively an antibody blocked the entry of the earliest known SARS-CoV-2 strain into a cell, the smaller the range of viruses it could bind. The team also found that antibodies that could disable a wide variety of viruses targeted sections of the binding domain that tended not to change as the virus evolved.

It’s good news that the team has identified antibodies that can bind to a range of sarbecoviruses, says Arinjay Banerjee, a virologist at

the University of Saskatchewan in Saskatoon, Canada. “The biggest question that remains is, what about viruses that we don’t know exist yet?”

Although scientists can’t test an antibody’s activity against an unknown virus, Banerjee adds, pan-sarbecovirus treatments and vaccines would help to prepare the world to fight the next coronavirus that jumps from wildlife into humans.

doi: https://doi.org/10.1038/d41586-021-01917-9

Updates & Corrections

Correction 15 July 2021*: An earlier version of this article stated incorrectly that all of the antibodies in the research were from people who had recovered from COVID-19.*

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Article Google Scholar Download references

https://bbc.in/3hJzuu3

Benjamin Jesty: The unsung hero of vaccination

More than 250 years before the coronavirus pandemic, another deadly virus - smallpox - was sweeping Europe.

The epidemic led to the development of the first vaccine - a medical milestone credited to Gloucestershire physician Edward Jenner.

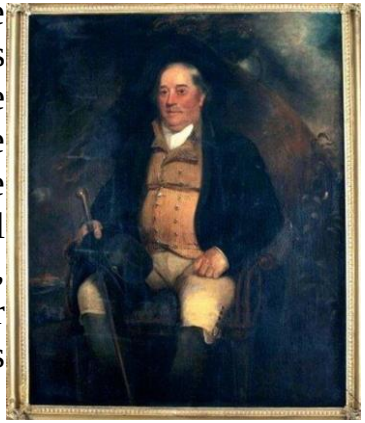
But, while Jenner became rich and famous for his discovery, the technique had been pioneered more than two decades earlier by a Dorset dairy farmer whose social status meant he never received the recognition he deserved.

Fast-forward to 1985 when microbiologist Patrick Pead, on holiday in Dorset, picked up a booklet in a Worth Matravers village shop entitled Benjamin Jesty: The First Vaccinator. "I thought 'that's not right, it was Edward Jenner'," said Mr Pead. "We went to the churchyard and saw his tombstone and that day changed my life."

In the years that followed, Mr Pead turned detective, piecing together the little that was known about Jesty and tracking down new evidence, including the only portrait of the farmer which was believed lost for more than a century but had found its way to the other side of the world.

Jesty's story began in 1774, when the farmer from Yetminster deliberately infected his family with cowpox in a bid to protect them from the deadly smallpox virus. Smallpox was the leading cause of death in the 18th century. Most people became infected during their lifetimes, and about 30% of those infected died.

Jesty had contracted cowpox in his youth and knew that milkmaids seemed, somehow, to be immune from the more virulent human disease. Using pus taken from lesions on a cow's udder, he used a stocking needle to scratch the infected material into the skin of his wife and two sons. But his wife became very ill and, although she eventually recovered, Jesty was vilified. "The last trial for witchcraft had been less than 40 years earlier," said Mr Pead.



Wellcome Library

"Jesty was reviled, people were suspicious.

"In those days, everybody would go to church on Sunday and the human body was sacred but here was a guy taking something from a beast and poking it into a human body."

Jesty's experiment would later be proved successful when attempts to infect his sons indicated they were immune to smallpox.

In 1796, Edward Jenner, who is believed to have heard of Jesty's exploits through his dining club, carried out a similar procedure on an eight-year-old boy but his findings were rejected by the Royal Society.

By 1798 he had conducted experiments on 23 children and, following support from his colleagues and the king, was awarded vast sums by parliament - first £10,000 in 1802, then a further £20,000 in 1807.

But Jesty's contribution did not pass unnoticed, with doctors and clergy calling for him also to be recognised.

In 1805, their lobbying led the Vaccine Pock Institute in London to quiz Jesty about his experiment and he was presented with a scroll and gold lancets.

A prominent artist - Michael William Sharp - was also commissioned to paint his portrait but, despite the gesture, Jenner's well-connected supporters won the day and Jesty looked set to remain a footnote in medical history.

Satirists depicted recipients of the smallpox vaccine growing cow parts **BBC Sport**

Mr Pead's quest to find Jesty's portrait led him to the archives of the Eldridge Pope Brewery in Dorchester - the painting had passed to the Pope family through marriage but had since disappeared.

After making inquiries he was given the telephone number of a Pope family descendant in South Africa.

He said: "I rang them straight away - it was about 10 o'clock at night. They said 'it's hanging here above the fireplace in the family home.'" The owner said he wanted to sell the painting and was keen for it to return to England.

In 2006, the Wellcome Trust in London agreed to acquire the portrait but its journey back to the UK was "a nightmare" according to research development specialist William Schupbach.

"The cost of getting it to the UK was considerable compared with the actual cost of the purchase," he said.

"It was on a farm on a huge estate in the Eastern Cape so we had to identify art handlers who had to drive their lorry hundreds of miles to get to this farm house. "We did not know what condition this painting was in - it had been stored in a barn in Dorset before being taken to South Africa. "And because South Africa is outside the EU there were import regulations."

After a restoration project lasting two years, the painting finally went on public display - first in Dorset Museum in Dorchester, then at the Wellcome Collection galleries.

Since then, interest in Jesty's story has grown, Mr Pead has written books and articles, given hundreds of talks and was awarded a Fellowship of The Historical Association for his research.

He said: "I'm a scientist working in medicine and I know all of the progress is built on the findings of others.

"Vaccination wasn't plucked out of the air by Benjamin Jesty or by Edward Jenner, it was built on out of what went before - that's why Jesty does deserve recognition."

https://wb.md/2UnUVaT

Alcohol Accounts for 4% of Newly Diagnosed Cancers Worldwide

Three quarters of these cancers occur in men

Liam Davenport

Alcohol consumption accounted for 4% of all cancers diagnosed worldwide in 2020, with three quarters of these cancers occurring in men. The most common cancer locations were the esophagus, liver, and breast. The finding comes from an analysis carried out by the International Agency for Research on Cancer. It was published online in *The Lancet Oncology* on July 13.

"We urgently need to raise awareness about the link between alcohol consumption and cancer risk among policymakers and the general public," said lead author Harriet Rumgay, BSc, Cancer Surveillance Branch, the International Agency for Research on Cancer, Lyon, France.

"Public health strategies, such as reduced alcohol availability, labeling alcohol products with a health warning, and marketing bans, could reduce rates of alcohol-driven cancer," she added. She

noted that taxation and pricing policies already in place in Europe could be implemented worldwide.

Commenting on the study, Mark Petticrew, professor of public health evaluation at the London School of Hygiene and Tropical Medicine, London, United Kingdom, agreed that there is a need to raise public awareness about this risk. There is "a lot of misinformation out there, some from the alcohol industry itself.

"The public needs clear, independent information, and this large, robust study makes a significant contribution to clarifying the risks," he added. It "provides further clear evidence that alcohol consumption contributes to a significant burden of cancer, particularly heavy drinking."

Study Details

To estimate the burden of alcohol-attributable cancer, Rumgay and colleagues gathered cancer incidence data from GLOBOCAN 2020 for a range of cancers and for all cancers combined.

Assuming a 10-year latency period between alcohol consumption and cancer diagnosis, they examined per capita alcohol consumption estimates for 2010 from the Global Information System on Alcohol and Health. The estimates were stratified by age and sex.

The results suggested that 741,300 (4.1%) of all incident cancer cases in 2020 were attributable to alcohol consumption, with 568,700 (76.7%) of those cases occurring in men.

The age-standardized incidence rate of alcohol-attributable cancer was 13.4 per 100,000 in men and 3.7 per 100,000 in women.

The most common types of cancer attributable to alcohol consumption were esophageal cancer (189,700 cases; 31.6%), liver cancer (154,700 cases; 17.3%), and breast cancer (98,300 cases; 4.4%).

Heavy drinking (defined as >60 g/d), accounted for 46.7% of the alcool-attributable cancers. Risky drinking (defined as 20–60 g/d), accounted for 29.4%. Moderate drinking (<20 g/d, which is the equivalent of around two daily drinks) contributed 13.9% of cases of alcohol-attributable cancers.

The analysis also found that by region, the largest proportions of cancer cases attributable to drinking were in eastern Asia (5.7%) and in central and eastern Europe (5.6%). The lowest were in western Asia (0.7%) in northern Africa (0.3%).

At the country level, the estimated proportion of cancer cases attributable to alcohol was highest in Mongolia (10%) and lowest in Kuwait (0%).

In China, the estimated proportion of cancer cases linked to alcohol was 6%. In India and France, it was 5%; in Germany, Brazil, and the United Kingdom, 4%; and in the United States, 3%.

Regarding gender differences in cancer rates, the team writes that "increases in alcohol consumption in women have been reported as women have taken on a larger share of paid employment.

"This finding is clearly reflected in countries highly indexed in development, where we saw the highest burden of alcohol-attributable cancers in women and the most similar male-to-female ratios of alcohol-attributable cancer rates.

"In these regions, breast cancer was the main driver of the high alcohol-attributable cancer incidence rates among women," they add.

In an accompanying comment, Amy C. Justice, MD, PhD, from the Department of Medicine and Health Policy and Management, Yale University, West Haven, Connecticut, said that the results are "useful," but she questioned how alcohol consumption was measured.

"Until we address limitations in measurement, we might be underestimating health risks, especially cancer risks, associated with alcohol," she warned.

The use of commercial alcohol sales to estimate consumption has

"major limitations," and the use of self-report is "worse," she said.

"Furthermore, neither commercial sales nor current self-report reflect past alcohol consumption," which has "especially important implications for genetic studies...and for understanding associations between alcohol use and cancers that commonly have extended latency periods. "Surely, we can do a better job," said Justice.

She suggests measuring direct alcohol biomarkers, such as phosphatidylethanol, which is an "abnormal" phospholipid that forms in the presence of ethanol and bonds to red blood cells.

Measuring levels over time, "coupled with a careful history of use," such as one based on a biomarker, could help determine not only current but also past alcohol exposure.

"We do not ask people with diabetes what their glycosylated hemoglobin is, we check it," Justice pointed out. "Then we discuss their risk of adverse health outcomes informed by the test results and their personal risk profile. We should use a similar approach to counseling patients regarding risk from alcohol," she said.

Commenting for the UK Science Media Center, Sadie Boniface, PhD, head of research at the Institute of Alcohol Studies, King's College London, London, United Kingdom, described the new analysis as "comprehensive and well-designed."

She added that the results are "in line with other studies, and scientists already knew that alcohol causes seven types of cancer," including cancer of the breast, esophagus, mouth, and throat.

However, this risk has not been well communicated to the general public, she said. In the United Kingdom, a forthcoming consultation on alcohol labeling represents a "real opportunity" to help consumers to "make fully informed decisions about their drinking."

Beyond labeling, the authors' recommendations on policies to target alcohol pricing, availability, and marketing are needed as "part a comprehensive alcohol strategy in the wake of the pandemic" to address the burden of alcohol, she added.

No funding for the study has been described. Boniface reports working at the Institute of Alcohol Studies, which receives funding from the Alliance House Foundation. No other relevant financial relationships were reported.

Lancet Oncol. Published online July 13, 2021. Full text

https://bit.ly/3kufY6o

Microbial Fossils Found in 3.4-Billion-Year-Old Subseafloor Rock

The material, now part of an African mountain range, bolsters the idea that hydrothermal veins supported early forms of life.

Ruth Williams

Researchers have discovered fossilized cell remnants in rock that roughly 3.4 billion years ago was a hydrothermal vein—a crack in bedrock containing superheated water. The microfossils, described today (July 14) in *Science Advances*, support the theory that such veins were breeding grounds for Earth's earliest lifeforms, as well as the idea that primitive microbes were methane producers.

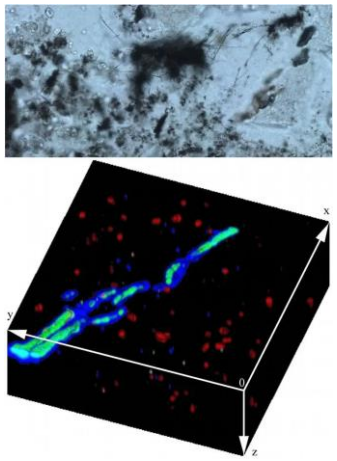
"On the basis of very detailed chemical analyses [the] filamentous . . . structures are interpreted as methane-cycling microbes," Malcolm Walter, an astrobiologist at the Australian Centre for Astrobiology who was not involved in the study, writes in an email to *The Scientist*. "This is a significant addition to the very rare early Archean microfossil record."

Hydrothermal veins in rock contain magma-heated ground water that rises to the surface as hot springs or geysers on land or vents in the seabed, and are believed to be among the first places on Earth that life began. That's because they are enriched with the types of chemical elements thought to "create an environment in which microbes could potentially originate," says Barbara Cavalazzi, a geobiologist and astrobiologist at the University of Bologna. Specifically, she says, they provide the sort of chemical environment suitable for methanogens—microbes that generate methane—which are believed to be among the earliest forms of life. The intervening billions of years since life's infancy mean ancient

hydrothermal veins are long gone, geological processes having crushed them, moved them, filled them with chert—a type of sedimentary rock—or all three. There are few places on Earth where it is possible to find well-preserved, fossil-filled chert, even fewer where the chert represent ancient hydrothermal veins, and fewer still where those veins date back to the Archean Eon, 3–4 billion years ago. One such place is the Barberton Greenstone Belt in the Makhonjwa Mountains of South Africa, where Cavalazzi and her team collected their 3.42-billion-year-old samples.

Other microfossils have been found in similarly aged or even older chert samples, but the appeal of the particular rocks Cavalazzi chose is that they originated from the subseafloor—the rock deep below the seabed. This would mean that the only type of microorganisms that could be present were ones that obtain energy though chemical processes (chemotrophs), such as methanogens. It ruled out the possibility of finding phototrophs, which convert light into energy and which are thought to have evolved more recently, Cavalazzi explains.

Cavalazzi's team sliced the rock into sections 30–50 µm thick for viewing under the microscope. At the interface between the chert (which would once have been aqueous) and the host rock, they found tiny filamentous structures the size and shape of microbes, on average, 42 µm in length and 0.77 µm in diameter. Some were grouped together in formations resembling biofilms—carpets of microbes growing together on a surface.



Top: Optical microscopy image of a rock slice showing filamentous microfossils; Bottom: 3D Confocal Raman image showing carbonaceous matter within microfossil filaments **Cavalazzi; Cavalazzi Et Al., 2021**

The team also used mass spectrometry and a specialized type of imaging called Raman microspectroscopy to examine the chemical composition of the filaments and surrounding chert.

"I'm pretty well convinced," says environmental chemist Eli Moore of Rowan University who was not involved in the research.

"The [fossils'] morphology resembles cellular colonies, and then within the fossils they have high concentrations of carbon, nitrogen, and hydrogen, so it really looks like organic matter . . . most likely representing ancient cells."

The analysis also showed the presence of nickel in the chert, which is "particularly cool," says Moore, because nickel is an important metal cofactor in the biological process of microbial methanogenesis.

"The evidence is definitely strong" that these filaments are indeed fossilized Archean methanogens, and is more definitive than that gleaned from previously discovered microfossils, he says.

Earlier reports of filamentous microfossils had been debated as potential abiogenic biomorphs—that is, organic structures that look like cells but are produced as a result of geochemical, not biological, processes.

"We were able to exclude any possibility that our structures were related to any abiotic process," Cavalazzi says, because they have a different composition from abiogenic biomorphs and formed typically microbial-looking biofilms.

"We can't be completely sure, one hundred percent" that these were once cells, "because we were not there when this stuff was happening," says Cavalazzi. But taking all the data together, she continues, they "strongly support the biological origin of these structures."

https://bit.ly/36Q8NqF

Study shows diet causes 84% drop in troublesome menopausal symptoms--without drugs

Plant-based diet rich in soy reduces moderate-to-severe hot flashes by 84%

Washington--A new study, published by the North American Menopause Society in the journal *Menopause*, found a plant-based diet rich in soy reduces moderate-to-severe hot flashes by 84%, from nearly five per day to fewer than one per day. During the 12-week study, nearly 60% of women became totally free of moderate-to-severe hot flashes. Overall hot flashes (including mild ones) decreased by 79%.

The study, called the WAVS trial--the Women's Study for the Alleviation of Vasomotor Symptoms-shows that diet changes can be much more powerful for treating hot flashes than scientists had thought. Vasomotor symptoms refer to night sweats, hot flashes, and flushes.

The study used no hormone medications or extracts. Instead, the research team tested a combination of a low-fat plant-based diet plus 1/2 cup of ordinary soybeans added to a salad or soup each day. "This is a game changer for women aged 45 and over, most of whom we now know can get prompt relief from the most severe and troubling menopause symptoms without drugs," says lead researcher Neal Barnard, MD, president of the Physicians Committee and adjunct professor at the George Washington University School of Medicine.

As many as 80% of postmenopausal women suffer from hot flashes. Heat wells up from the chest, causing flushing, sweating, and chills. At night, hot flashes interfere with sleep. Estrogen-based medications were once routinely used to treat hot flashes but have been shown to increase the risk of breast cancer and other serious problems. Isoflavone extracts from soybeans work only modestly, leaving women and their doctors with few effective options.

Study Details

Postmenopausal women reporting two or more hot flashes per day were randomly assigned to either an intervention group--consisting of a low-fat, vegan diet, including half a cup of cooked soybeans daily--or to a control group that made no diet changes for 12 weeks. Frequency and severity of hot flashes were recorded using a mobile application, and vasomotor, psychosocial, physical, and sexual symptoms were assessed using the Menopause Specific Quality of Life Questionnaire (MENQOL).

Each participant was given a digital self-calibrating scale to track body weight day by day, a mobile app to track hot flashes in real time, and an Instant Pot to prepare soybeans at home. Each week, the group got together with the research team via Zoom.

"Previous studies have shown that soy could be beneficial, so we decided to put a diet change to the test," says study author Hana Kahleova, MD, PhD, director of clinical research for the Physicians Committee. "We believe that the combination is what is important. By the end of the study, the majority of women on a plant-based diet rich in soy reported that they no longer experienced moderate-to-extreme hot flashes at all and that they experienced significant improvements in their quality of life."

Key Findings

Total hot flashes decreased by 79% and moderate-to-severe hot flashes decreased by 84% in the intervention group. At the study's conclusion, 59% of intervention-group participants reported becoming free of moderate and severe hot flashes. There was no change in this variable in the control group.

In previous randomized trials, soy products have been shown to modestly reduce the frequency of hot flashes. The researchers theorize that the effect may be a result of soy products containing isoflavones, which can be metabolized by gut bacteria into equol--a

nonsteroidal compound that has been shown in some studies to reduce the incidence and severity of hot flashes. Previous studies have also shown that those following vegetarian or vegan diets produce higher levels of equol. The new study showed a more robust response, using the combination of a plant-based diet plus soy.

Many study participants also reported improvements in sexual symptoms, mood, and overall energy.

"This was basically a lifesaver for me," said one study participant. "I've got my quality of life back." Another said, "I am sleeping better, and my hot flashes diminished tremendously." Several participants also noticed significant weight loss and better digestion. "Before you jump to any kind of medication, I would try this route, because it's easy," a study participant said. "Anybody can do it."

The study was based on the new approach to menopausal symptoms described by Dr. Barnard in his book Your Body in Balance. After the book was released in 2020, a reader contacted Dr. Barnard to let him know that his method eliminated her hot flashes within five days. Rather than using isoflavone extracts or soy foods such as soy milk or tofu, she used whole soybeans.

https://bit.ly/3kvWIFQ

Early-Life Penicillin Could Lead to Brain Disorders, New Study Suggests

Antibiotic exposure early in life could alter human brain development in areas responsible for cognitive and emotional functions.

Penicillin in early life changes microbiome and gene expression, which allows cells to respond to its changing environment, in key areas of the developing brain, according to new research.

Penicillin and related medicines (like ampicillin and amoxicillin) are the most widely used antibiotics in children worldwide. In the United States, the average child receives nearly three courses of antibiotics before the age of two. Similar or greater exposure rates occur in many other countries.

"Our previous work has shown that exposing young animals to antibiotics changes their metabolism and immunity," said Professor Martin Blaser, director of the Center for Advanced Biotechnology and Medicine at Rutgers University.

"The third important development in early life involves the brain."

"This study is preliminary but shows a correlation between altering the microbiome and changes in the brain that should be further explored."

In the study, Professor Blaser and his colleagues compared mice that were exposed to low-dose penicillin in utero or immediately after birth to those that were not exposed. They found that mice given penicillin experienced substantial changes in their intestinal microbiota and had altered gene expression in the frontal cortex and amygdala, two key areas in the brain responsible for the development of memory as well as fear and stress responses.

A growing body of evidence links phenomena in the intestinal tract with signaling to the brain, a field of study known as the gut-brain-axis. If this pathway is disturbed, it can lead to permanent altering of the brain's structure and function and possibly lead to neuropsychiatric or neurodegenerative disorders in later childhood or adulthood.

"Early life is a critical period for neurodevelopment," Professor Blaser noted. "In recent decades, there has been a rise in the incidence of childhood neurodevelopmental disorders, including autism spectrum disorder, attention deficit/hyperactivity disorder and learning disabilities."

"Although increased awareness and diagnosis are likely contributing factors, disruptions in cerebral gene expression early in development also could be responsible." "Future studies are needed to determine whether antibiotics directly effect brain development

or if molecules from the microbiome that travel to the brain disturb gene activity and cause cognitive deficits."

The study was published online this week in the journal *iScience*.

Angelina Volkova et al. Effects of early-life penicillin exposure on the gut microbiome and frontal cortex and amygdala gene expression. iScience, published online July 15, 2021; doi: 10.1016/j.isci.2021.102797

https://bit.ly/3wP2NQ7

New Sinai Health research finds common denominator linking all cancers

Scientists divide all cancers into two groups, based on the presence or absence of a protein called the Yes-associated protein

All cancers fall into just two categories, according to new research from scientists at Sinai Health, in findings that could provide a new strategy for treating the most aggressive and untreatable forms of the disease.

In new research out this month in *Cancer Cell*, scientists at the Lunenfeld-Tanenbaum Research Institute (LTRI), part of Sinai Health, divide all cancers into two groups, based on the presence or absence of a protein called the Yes-associated protein, or YAP.

Rod Bremner, senior scientist at the LTRI, said they have determined that all cancers are present with YAP either on or off, and each classification exhibits different drug sensitivities or resistance. YAP plays an important role in the formation of malignant tumours because it is an important regulator and effector of the Hippo signaling pathway.

"Not only is YAP either off or on, but it has opposite pro- or anti-cancer effects in either context," Bremner said. "Thus, YAPon cancers need YAP to grow and survive. In contrast, YAPoff cancers stop growing when we switch on YAP."

Many YAPoff cancers are highly lethal. In their new research, Bremner and fellow researchers from the Roswell Park Comprehensive Cancer Center in Buffalo, NY, show that some cancers like prostate and lung can jump from a YAPon state to a YAPoff state to resist therapeutics.

When cancer cells are grown in a dish in a lab setting, they either float or stick down. The team of researchers found that YAP is the master regulator of a cell's buoyancy, where all the floating cells are YAPoff, and all the sticky cells are YAPon. Changes in adhesive behavior are well known to be associated with drug resistance, so their findings implicates YAP at the hub of this switch, explained Bremner.

Joel Pearson, co-lead author and a post-doctoral fellow in the Bremner Lab at the LTRI, said therapies that tackle these cancers could have a profound effect on patient survival.

"The simple binary rule we uncovered may expose strategies to treat many cancer types that fall into either the YAPoff or YAPon superclasses," Pearson said. "Moreover, since cancers jump states to evade therapy, having ways to treat either the YAPoff and YAPon state could become a general approach to stop this cancer from switching types to resist drug treatments."

The researchers hope by deducing common vulnerabilities of these types of cancer, it may be possible to develop new therapeutic approaches and improve patient outcomes.

The work was funded primarily by the Canadian Institutes of Health Research (CIHR), the Cancer Research Society, and the Krembil Foundation.

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No sign of COVID-19 vaccine in breast milk

Small UCSF study indicates vaccine safety for pregnant and lactating women

Messenger RNA vaccines against COVID-19 were not detected in human milk, according to a small study by UC San Francisco, providing early evidence that the vaccine mRNA is not transferred

to the infant.

The study, which analyzed the breast milk of seven women after they received the mRNA vaccines and found no trace of the vaccine, offers the first direct data of vaccine safety during breastfeeding and could allay concerns among those who have declined vaccination or discontinued breastfeeding due to concern that vaccination might alter human milk. The paper appears in *JAMA Pediatrics*.

Research has demonstrated that vaccines with mRNA inhibit transmission of the virus that causes COVID-19. The study analyzed the Pfizer and Moderna vaccines, both of which contain mRNA.

The World Health Organization recommends that breastfeeding people be vaccinated, and the Academy of Breastfeeding Medicine has said there is little risk of vaccine nanoparticles or mRNA entering breast tissue or being transferred to milk, which theoretically could affect infant immunity.

"The results strengthen current recommendations that the mRNA vaccines are safe in lactation, and that lactating individuals who receive the COVID vaccine should not stop breastfeeding," said corresponding author Stephanie L. Gaw, MD, PhD, assistant professor of Maternal-Fetal Medicine at UCSF.

"We didn't detect the vaccine associated mRNA in any of the milk samples tested," said lead author Yarden Golan, PhD, a postdoctoral fellow at UCSF. "These findings provide an experimental evidence regarding the safety of the use of mRNA-based vaccines during lactation."

The study was conducted from December 2020 to February 2021. The mothers' mean age was 37.8 years and their children ranged in age from one month to three years. Milk samples were collected prior to vaccination and at various times up to 48 hours after vaccination.

Researchers found that none of the samples showed detectable levels of vaccine mRNA in any component of the milk.

The authors noted that the study was limited by the small sample size and said that further clinical data from larger populations were needed to better estimate the effect of the vaccines on lactation outcomes.

Co-authors are Mary Prahl, MD; Arianna Cassidy, MD; Christine Y. Lin, BA; Nadav Ahituv, PhD; and Valerie J. Flaherman, MD, MPH, all of UCSF.

The study was supported by the Marino Family Foundation; the National Institutes of Health (grant numbers K23AI127886 and K08AI141728); the Weizmann Institute of Science-National Postdoctoral Award Program for Advancing Women in Science; the International Society for Research in Human Milk and Lactation Trainee Bridge Fund; and the Human Frontier Science Program. Disclosures can be found in the paper.

https://bit.ly/3zf3YKh

Jumping Spiders Seem to Have a Cognitive Ability Only Previously Found in Vertebrates

Able to distinguish between animate and inanimate objects

Michelle Starr

Tiny little jumping spiders, with their magnificent eyes, seem to be able to do something we'd only ever seen before in vertebrates: distinguishing between animate and inanimate objects.

***Menemerus semilimbatus and its gorgeous peepers*. emanuelkern/iNaturalist, CC BY 4.0**

In a new test, wild jumping spiders (*Menemerus semilimbatus*) behaved differently when presented with simulated objects of both kinds, in ways that indicated an ability to discern between them.

The research doesn't just suggest that this ability can be found more widely in the animal kingdom than we knew, it demonstrates that the team's experimental setup can be used to test other invertebrates in the same way. "These results clearly demonstrate the ability of jumping spiders to discriminate between biological motion cues," the researchers wrote in their paper.

"The presence of a biological motion-based detection system in jumping spiders deepens questions regarding the evolutionary origins of this visual processing strategy and opens the possibility that such mechanisms might be widespread across the animal kingdom."

When you think about it, it makes sense that creatures ought to be able to distinguish between living and nonliving things. It could literally be a matter of life or death - evading predators, or chasing prey. Nevertheless, it was unclear whether or not tiny invertebrate critters rely on the ability to distinguish between motion and non-motion, or animate and inanimate objects.

Jumping spiders seemed to be an excellent candidate for testing, because of their spectacularly good vision. Like all spiders, they have eight eyes; but the eyes of jumping spiders include two large, sparkling pools of limpid black on the fronts of their little faces, which possibly give them tetrachromatic color vision.

A team of researchers led by biologist Massimo De Agrò, formerly of Harvard University, collected 60 specimens of *M. semilimbatus*, common throughout the Northern Hemisphere. These spiders were then subjected to a specially designed point-light test.

Here's how it works. When presented with 11 moving dots corresponding to the positions of the main joints on the human body, human test subjects can recognize the pattern of motion as belonging to a human. Those 11 dots, when still, won't convey the same meaning - they're just 11 dots.

De Agrò and his team designed a similar point-light display based on the joints of a spider. They also designed other point-light displays, including a moving ellipse, and scrambled random motion that didn't resemble the movements of any living creature.

To show the spider the animation, the team held the spider's body fixed in place over a spherical "treadmill" that rolled over a stream of compressed air. The way the spider tried to walk over the treadmill was considered an indicator of its response to the point-light animations. Each of the 60 spiders was then shown the point-light displays, and their reactions carefully recorded.

Interestingly, the jumping spiders swiveled their bodies around to stare with their big eyes at the displays that were less lifelike. The effect was most pronounced with the randomized point-light display, which moved the least like a living organism.

This, the team realized, has to do with how the spiders' eyes work. The secondary eyes on the side of the head may not have the visual acuity of the two large eyes, but they do give the spiders almost 360-degree vision. If the spider spots something with those eyes that it can recognize, but also something that it doesn't recognize, it will prioritize the strange thing, since the recognizable thing will remain in its field of view.

"The secondary eyes are looking at this point-light display of biological motion and it can already understand it, whereas the other random motion is weird and they don't understand what's there," De Agrò explained.

The team hopes that their system could be used to apply their test to other invertebrates, such as insects and snails, in order to try and learn more about how this ability was evolved. All 60 spiders were returned to the wild unharmed… although maybe a little confused.

The research has been published in *PLOS Biology*.

https://bit.ly/3zabjux

The history of animal-based medicine in China

In "Mao's Bestiary," Liz P.Y. Chee explores the contentious use of wild animals in traditional Chinese medicine

By Rachel Love Nuwer

Liz P.Y. Chee vividly remembers the first time she visited a bear farm. It was 2009, and Chee, who was working for a Singapore-based animal welfare group, flew to Laos to tour a Chinese-owned facility. The animals Chee saw "were hardly recognizable as bears,"

she later wrote, "because they had rubbed most of their fur off against the bars of the cages and had grown very long toenails through disuse of their feet."

As at countless other bear farms across China and Southeast Asia, the bears there were being held for their bile. Bear bile — which is either "milked" through a catheter permanently inserted into the animals' gall bladders or extracted by stabbing large needles into the animals' abdomens — is popularly prescribed across the region to treat a host of ailments, including, most recently, Covid-19. It is also marketed as an all-around health tonic. Although there is a growing animal welfare and anti-bear farming movement in China, the industry remains powerful.

Bears stand by a wall at a bear farm of Guizhentang Pharmaceutical Co Ltd on February 24, 2012 in Quanzhou, Fujian Province of China. The Guizhentang Pharmaceutical Co Ltd, which makes medicine using bile extracted from live bears, opened one of its bear farms to the media on Wednesday, to quell growing criticism. **(Photo by Getty Images (Stringer/Getty Images)**

Seeing the suffering bears made Chee wonder about the cultural and historical forces that brought the animals there — a question that propelled her to conduct exhaustive research on animal medicalization in China. In "Mao's Bestiary: Medicinal Animals and Modern China," she details her findings, many of which are distilled from sources never before published in English. Chee, who is now a research fellow and lecturer at the National University of Singapore, also found that, until now, even scholars in China have dedicated scant attention to the history of animal-based medicine, despite the controversy associated with the topic today.

"If Chinese medicine retains an Achilles' heel in the present century, it is the widespread perception that it is contributing to a holocaust among wild creatures," Chee writes, "and in so doing supporting a global criminal enterprise" of animal poaching and trafficking. Moreover, she adds, such medicines are often condemned "as being as ineffective as they are unethical," even by some Chinese physicians. Many of these products are medically useless at best, Chee writes, and in some cases, actually harmful.

Defenders of animal-based Chinese medicine often point to the practice's 2,000-plus year history. In "Mao's Bestiary," however, Chee shows that the roots establishing the use of most animals as ingredients in medicine are not as deeply planted in China's culture as many believe. Instead, the industry as it exists now was purposefully developed, expanded, and promoted over the last century. Today, it is more closely linked to politics and profit than to ancient culture and tradition. This revelation has important implications for both species conservation and for public health, Chee argues, because it leaves room for "possibilities of choice and change."

Chee focuses on the evolution of animal-based medicine throughout the tumultuous period of modern China's formation, from the 1950s through the 1980s. These decades encompassed the early years of the People's Republic of China, Mao's Great Leap Forward and Cultural Revolution and, finally, Deng Xiaoping's reforms.

While animal-derived medicines do have a long history in China, Chee found that their use in the past was nowhere near the "startlingly abundant" level they are at today. Around 400 animals were cited in the 16th century "Compendium of Materia Medica," for example, whereas more than 2,300 are listed today in pharmacopeias.

Many newly medicalized species exist only on distant continents, such as jaguars in South and Central America. Nor is China's use of animals in traditional medicine solely based on Chinese innovation,

Chee found; ideas, approaches, and technologies from the Soviet Union, North Korea, Japan, and the Western world all heavily influenced the industry's development. So while animal-based products may still "hold the aura of tradition," Chee writes, in fact, most are the products of a profit-driven expansion.

Efforts to abolish traditional medicine and replace it with a science-based approach, primarily inspired by Japan, began in the 1920s and continued through the early days of a Communist government that was racing to build an industrialized economy. While researchers acknowledged that some especially efficacious Chinese herbs were worth investigating to find their active ingredients, animal-based remedies were "initially undervalued and underdeveloped" by the new regime as it worked to build up its pharmaceutical sector, Chee writes.

Traditional doctors pushed back on the attempt to phase out their industry, however, and argued that the synergistic effects of the plant, animal, and mineral ingredients of their practice were too complex to be nailed down in a lab. To appease both groups, the state-owned drug-making sector decided that doctors trained in Chinese and Western medicine should learn from each other, "scientizing" Chinese medicine and seeking new innovations from tradition.

"To learn from the Soviet Union" was also a popular phrase in China at this time. Following the example set by the USSR, China was especially interested in creating its own pharmaceuticals from local ingredients to become self-sufficient. Soviet interest in animal-based folk medicine and the USSR's own practice of farming deer for medicinal ingredients soon "provided modern and scientific sanction for the Chinese fascination with faunal drugs," Chee writes.

During the Great Leap Forward's period of rapid industrialization, "animals as well as plants were swept up in this nationwide project," Chee continues. China expanded its export of high-end medicinal products like deer antler, rhino horn, and tiger bone, especially to Chinese expatriates. To meet steep quotas, authorities promoted the creation of "laboratory farms" for scaling up production. Entrepreneurs at these farms were also encouraged to find more uses for existing animal parts, and to engineer additional uses for new parts and species.

"Once a medicinal animal was farmed, there was pressure or incentive to justify the use of all of its parts, regardless of previous traditions that had often been quite selective as to which part should actually be taken as medicine, and for what purpose," Chee writes. Medicine farms popped up for a host of additional species, including geckos, ground beetles, scorpions, snakes, and seahorses.

Wildlife farming also began being presented as something benefiting conservation because it allegedly spared wild animals from being hunted. In fact, it usually had the opposite effect by stimulating the market and relying on hunters to replenish farm stocks, Chee notes. While she does not delve deeply into the impact this has had on animal populations within and outside China, many sources today argue that demand for traditional medicine all but emptied the country's forests of tigers, pangolins, and other highly sought after species.

During the purges and upheavals of the Cultural Revolution, the export of luxury medicines such as rhino horn were scaled up to generate much-needed revenue. Back home, however, a stark lack of medical care and supplies inspired an emphasis on "miracle cures" derived from cheaper, more common animals.

Chicken blood therapy — "the direct injection of chicken blood (from live chickens) into human bodies" — was representative of this time, Chee writes. The doctor who founded the treatment claimed chicken blood therapy could cure more than 100 conditions, and it was heavily promoted throughout the country, becoming

"emblematic of economical grassroots innovations" and "the very expression of 'red medicine,'" Chee writes.

This practice started to be phased out in 1968 when news surfaced of people dying after being injected with chicken blood. But similar remedies soon took its place, including ones that used goose or duck blood, lizard eggs, or toad heads. These new remedies were marketed as magic-like cures for serious and otherwise untreatable conditions, including cancer — "an attribute that has become standard in the marketing of many animal-based drugs today," Chee writes.

After Deng came to power in 1978, wildlife farming and animal-based medicine "became even more popular as part of the official policy to enrich farmers," Chee continues. The government-supported bear bile industry — which was originally inspired by facilities in North Korea and continues to flourish today — was one major result of this period, as was the proliferation of tiger farms.

Policy shifts also had significant ramifications for the regulation of Chinese medicine, and its impact on consumers and the environment. The forestry ministry was "given decision-making power over wild medicinal animals," Chee writes, "and would essentially manage China's forests as extraction sites."

Meanwhile, the health ministry only had full regulatory control of patented drugs, so companies selling animal-based medicines could bypass health or efficacy regulations and make extravagant, unchallenged claims about their products' curative value.

Chinese medicine has become globalized over the last three decades, and animal-based products have "continued to play a central, if increasingly problematic, role," Chee writes. The industry is assailed in the international media for its role in driving species declines, and clashes regularly occur within China between proponents of animal-based medicines and those who value wildlife and conservation.

"Many middle-class Chinese, both on the mainland and in the diaspora, and within Chinese medicine itself, have been on the front lines in the battle to save endangered species from poaching and consumption," Chee points out.

"Mao's Bestiary" went to press in the midst of the Covid-19 pandemic, and Chee writes in the introduction that the likely link between Covid-19's emergence and wild animals fundamentally changes the debate by making wildlife use a global public health issue.

Yet despite the undeniable threats posed by zoonotic diseases, animal-based traditional medicine remains an "immensely profitable, and thus politically influential" force in China, she continues. As evidence, Chinese authorities not only did not ban animal-based medicine during the pandemic, but actually promoted remedies containing bear bile for treating Covid-19.

As for shaping the industry's future to mitigate the dangers for both wildlife and humans, Chee looks not to officials but to Chinese consumers, who can choose to boycott animal-based medicines. There is a large and growing animal welfare movement in China, so this could be more than just a pipe dream.

"Whether they will reinvent the pharmacology of Chinese medicine as a practice less reliant on animals, endangered or otherwise," she concludes, "remains a vital question."

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https://go.nature.com/2UUmvwq

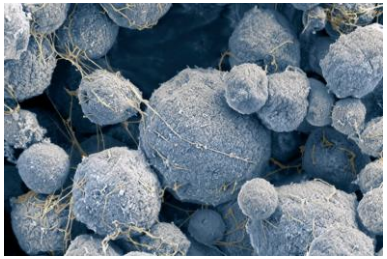
Massive DNA 'Borg' structures perplex scientists

Researchers say they have discovered unique and exciting DNA strands in the mud — others aren't sure of their novelty.

Amber Dance

The Borg have landed — or, at least, researchers have discovered their counterparts here on Earth. Scientists analysing samples from muddy sites in the western United States have found novel DNA

structures that seem to scavenge and 'assimilate' genes from microorganisms in their environment, much like the fictional *Star Trek* 'Borg' aliens who assimilate the knowledge and technology of other species.



Borgs seem to be associated with single-celled microorganisms known as archaea, shown in this scanning-electron microscopy image. **Credit: Eye of Science/SPL**

These extra-long DNA strands, which the scientists named in honour of the aliens, join a diverse collection of genetic structures — circular plasmids, for example — known as extrachromosomal elements (ECEs). Most microbes have one or two chromosomes that encode their primary genetic blueprint.

But they can host, and often share between them, many distinct ECEs. These carry non-essential but useful genes, such as those for antibiotic resistance.

Borgs are a previously unknown, unique and "absolutely fascinating" type of ECE, says Jill Banfield, a geomicrobiologist at the University of California, Berkeley. She and her colleagues describe their discovery of the structures in a preprint posted to the server bioRxiv[1]. The work is yet to be peer-reviewed.

Unlike anything seen before

Borgs are DNA structures "not like any that's been seen before", says Brett Baker, a microbiologist at the University of Texas at Austin. Other scientists agree that the find is exciting, but have questioned whether Borgs really are unique, noting similarities between them and other large ECEs.

In recent years "people have become used to surprises in the field of ECEs", says Huang Li, a microbiologist at the Chinese Academy of Sciences in Beijing. "However, the discovery of Borgs, which undoubtedly enriches the concept of ECEs, has fascinated many in the field."

Their vast size, ranging between more than 600,000 and about 1 million DNA base pairs in length, is one feature that distinguishes Borgs from many other ECEs. In fact, Borgs are so huge that they are up to one-third of the length of the main chromosome in their host microbes, Banfield says.

Banfield studies how microbes influence the carbon cycle — including the production and degradation of methane, a potent greenhouse gas — and, in October 2019, she and her colleagues went hunting for ECEs containing genes involved in the carbon cycle in Californian wetlands. There, they found the first Borgs and later identified 19 different types from this and similar sites in Colorado and California.

Borgs seem to be associated with archaea, which are single-celled microorganisms distinct from bacteria. Specifically, those Banfield and her team have discovered are linked to the *Methanoperedens* variety, which digest and destroy methane. And Borg genes seem to be involved in this process, says Banfield.

Scientists can't yet culture *Methanoperedens* in the laboratory — an ongoing challenge for many microbes — so the team's conclusions that Borgs might be used by the archaea for methane processing are based on sequence data alone.

"They've made an interesting observation," says systems biologist Nitin Baliga, at the Institute for Systems Biology in Seattle, Washington.

But he cautions that when researchers sift through fragments of many genomes and piece them together, as Banfield's team has done, it's possible to make errors. Finding Borgs in cultured *Methanoperedens* will be necessary for the finding to be considered definitive, he adds.

Costs and benefits

Assuming Borgs are real, maintaining such a massive ECE would

be costly for *Methanoperedens*, Banfield and colleagues say, so the DNA structures must provide some benefit. To learn what that might be, the researchers analysed the sequences of hundreds of Borg genes and compared them with known genes.

Borgs seem to house many genes needed for entire metabolic processes, including digesting methane, says Banfield. She describes these collections as "a toolbox" that might super-charge the abilities of *Methanoperedens*.

So what makes a Borg a Borg? In addition to their remarkable size, Borgs share several structural features: they're linear, not circular as many ECEs are; they have mirrored repetitive sequences at each end of the strand; and they have many other repetitive sequences both within and between the presumptive genes.

Individually, these features of Borgs can overlap with those seen in other large ECEs, such as elements in certain salt-loving archaea, so Baliga says the novelty of Borgs is still debatable at this stage. Borgs also resemble giant linear plasmids found in soil-dwelling Actinobacteria, says Julián Rafael Dib, a microbiologist at the Pilot Plant for Microbiological Industrial Processes in Tucumán, Argentina.

Banfield counters that although the individual features of Borgs have been seen before, "the size, combination and metabolic gene load" is what makes them different.

She speculates that they were once entire microbes, and were assimilated by *Methanoperedens* in much the same way that eukaryotic cells gained energy-generating mitochondria by assimilating free-living bacteria.

Now that scientists know what to look for, they might find more Borgs by sifting through old data, says Baker, who used to work in Banfield's lab. He thinks he might already have discovered some candidates in his own genetic database since the preprint was posted.

Resistance is futile

When analysing the Borg genome, Banfield and colleagues also saw features suggesting that Borgs have assimilated genes from diverse sources, including the main *Methanoperedens* chromosome, Banfield says. This potential to 'assimilate' genes led her son to propose the name 'Borg' over Thanksgiving dinner in 2020.

Banfield's team is now investigating the function of Borgs and the role of their DNA repeats. Repeats are important to microbes: differently-structured repeats called CRISPR are snippets of genetic code from viruses that microbes incorporate into their own DNA to 'remember' the pathogens so they can defend against them in the future.

CRISPR and its associated proteins have been a boon for biotechnology because they have been adapted into a powerful gene-editing technique — hinting that Borg genomes might also yield useful tools. "It could be as important and interesting as CRISPR, but I think it's going to be a new thing," says Banfield, who is collaborating on future investigations with her preprint co-author, Jennifer Doudna, a pioneer of CRISPR-based gene editing at the University of California.

One potential application that the researchers see for Borgs could be as an aid in the fight against climate change. Fostering the growth of microbes containing them could, perhaps, cut down the methane emissions generated by soil-dwelling archaea, which add up to about 1 gigatonne globally each year.

It would be risky to do this in natural wetlands, Banfield says, but it might be appropriate at agricultural sites. So, as a first step, her group is now hunting Borgs in Californian rice paddies.

doi: https://doi.org/10.1038/d41586-021-01947-3

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https://go.nature.com/3xJ46Bj

Tied in knots: Zika virus tangles are the most stable RNA known

A dangerous virus uses a ring-shaped structure to make its RNA resistant to attack.

Some viruses tie their RNA into intricate knots to prevent hostile cells from digesting it. Experiments now show that the Zika virus's knotted RNA is the most stable RNA ever observed, paving the way to understanding how the virus eludes cellular defences.

To study the knot's mechanics, Meng Zhao and Michael Woodside at the University of Alberta in Canada used optical tweezers, which rely on a laser beam to hold and move microscopic objects. The authors applied force to both of the RNA strand's free ends, allowing them to repeatedly unfold and refold the knot and observe the steps involved in its formation. This revealed that a ring-shaped structure blocks the cell's enzymes from digesting the RNA and generates the knot's unusual mechanical stability.

By working out the steps required to form the ring, the researchers offer potential targets for future therapeutics to prevent the RNA from knotting. Many members of the flavivirus family — which includes the Zika, West Nile, dengue and yellow fever viruses — contain RNA with knots, and the authors hope their findings will contribute to disarming these viruses. *Nature Chem. Biol.* (2021)

https://bit.ly/3ew6gq6

Greenland scraps all future oil exploration

Greenland dropped all plans for future oil exploration on environmental grounds, saying the price of extraction was "too high."

by Morten Buttler

Oil and natural gas wells require concrete to seal the area between the well casing and the surrounding borehole, but because of the high temperatures and pressures at depth, it has been hard to study how these specialized cements harden. Now, a new method developed at MIT can help to fill in that missing knowledge.

The island's socialist-led government, in office since April, has made climate concerns central to its legislative program. While the decision to scrap planned exploration is a win for environmental groups, it cuts off potential investments that could have aided efforts to gain economic independence from Denmark.

The government "has decided to cease issuing new licenses for oil and gas exploration," it said in a statement. "This step has been taken for the sake of our nature, for the sake of our fisheries, for the sake of our tourism industry, and to focus our business on sustainable potentials."

Ten years ago, Greenland had become a hotspot for drillers as a commodity-price boom attracted not only oil explorers but miners of diamonds, iron, rare earths and other metals. But crude's subsequent crash made extraction uneconomic offshore—where drilling would be hampered by large floating icebergs—and the official ban now puts an end to dreams of energy riches.

Although the Inuit Ataqatigiit ruling party campaigned on seeking greater autonomy from Denmark—which still oversees Greenland's foreign, defense and monetary policies—its program has yet to offer a sustainable alternative to Danish economic support for its 56,000 inhabitants, which amounts to about $600 million a year.

The decision to abandon oil exploration comes amid increasingly alarming signs of global warming for Greenlanders. Average sea levels have risen about 9 inches since 1880, and about a quarter of that increase comes from ice melting in the Greenland and Antarctica ice sheets, along with land-based glaciers elsewhere, according to a study published in Nature in May.

Greenland's west coast alone is estimated to contain about 18 billion barrels of oil, according to a recent study from the Geological Survey of Denmark and Greenland. The U.S.

Geological Survey has previously estimated that there may be double that volume in crude and natural gas in the east.

The island isn't banning all mineral exploration. Earlier this month, Canadian miner AEX Gold Inc.—already the largest exploration license holder on the territory—applied for another permit to explore for copper and gold in the south. But fossil fuels are out.

"The Greenlandic government believes that the price of oil extraction is too high," it said in the statement. "This is based upon economic calculations, but considerations of the impact on climate and the environment also play a central role in the decision."

A number of other European countries have also scrapped plans for oil exploration in recent years, including Denmark itself, France, Spain and Ireland.

https://bit.ly/3z4JIL8

Curiosity rover discovers that evidence of past life on Mars may have been erased

The surprising discovery doesn't make it any less likely that scientists will find life on the Red Planet.

By Ben Turner - Staff Writer

Evidence of ancient life may have been scrubbed from parts of Mars, a new NASA study has found.

The space agency's Curiosity rover made the surprising discovery while investigating clay-rich sedimentary rocks around its landing site in Gale Crater, a former lake that was made when an asteroid struck the Red Planet roughly 3.6 billion years ago.

Clay is a good signpost towards evidence of life because it's usually created when rocky minerals weather away and rot after contact with water — a key ingredient for life. It is also an excellent material for storing microbial fossils.

But when Curiosity took two samples of ancient mudstone, a sedimentary rock containing clay, from patches of the dried-out lake bed, dated to the same time and place (3.5 billion years ago and just 400m apart), researchers found that one patch contained only half the expected amount of clay minerals. Instead, that patch held a greater quantity of iron oxides, the compounds that give Mars its rusty hue. The team believes the culprit behind this geological disappearing act is brine: supersalty water that leaked into the mineral-rich clay layers and destabilized them, flushing them away and wiping patches of both the geological — and possibly even the biological — record clean.

"We used to think that once these layers of clay minerals formed at the bottom of the lake in Gale Crater, they stayed that way, preserving the moment in time they formed for billions of years," study lead author Tom Bristow, a researcher at NASA's Ames Research Center in Mountain View, California, said in a statement. "But later brines broke down these clay minerals in some places — essentially resetting the rock record."

The rover completed its analysis by drilling into the layers of the Martian rock before using its chemistry and mineralogy instrument, known as CheMin, to investigate the samples.

The process of chemical transformation in sediments is called diagenesis, and it could have created new life beneath Mars even as it erased some of the evidence of the old life on its surface, according to the study authors. So even though old records of life may have been erased in the brine patches, the chemical conditions brought about by the influx of salty water may have enabled more life to spring up in its place, the scientists said.

"These are excellent places to look for evidence of ancient life and gauge habitability," study co-author John Grotzinger, a geology professor at the California Institute of Technology, said in the statement. "Even though diagenesis may erase the signs of life in the original lake, it creates the chemical gradients necessary to support subsurface life, so we are really excited to have discovered this."

Curiosity's mission to Mars began nine years ago, but the rover has continued to study the Red Planet well past its initial two-year mission timeline, to establish the historic habitability of Mars for life. It is now working in collaboration with the new Perseverance Mars rover, which landed in February 2021 and has been tasked with collecting rock and soil samples for a possible return to Earth.

The research done by Curiosity has not only revealed how the Martian climate changed but also helped Perseverance determine which soil samples to collect to increase the odds of finding life.

"We've learned something very important: There are some parts of the Martian rock record that aren't so good at preserving evidence of the planet's past and possible life," co-author Ashwin Vasavada, a Curiosity project scientist at NASA's Jet Propulsion Laboratory in California, said in the statement. "The fortunate thing is, we find both close together in Gale Crater and can use mineralogy to tell which is which."

The search for life on Mars has been given fresh animus by a new study that could have triangulated the possible location of the six methane emissions detected by the Curiosity rover during its time in Gale crater, Live Science reported. Since all of the methane in Earth's atmosphere comes from biological sources, scientists are thrilled to find the gas on Mars. The researchers published their findings July 9 in the journal Science.

https://wb.md/3rg5ZTu

The Genius of Recognizing a Familiar Face

For the first time researchers report a new class of cells they say is responsible for flash of familiarity

Leanne Ridgeway

That flash of familiarity we feel when we see someone we know has long fascinated and stumped scientists, who have been unable to pinpoint what is happening in the brain. But for the first time, researchers are now reporting a new class of cells they say is responsible.

The discovery goes against the prevailing understanding in neuroscience that diverse areas of the brain must communicate with each other to process information. Instead, this study shows that one region of the brain appears to be operating for the sole purpose of identifying people we know.

It was thought that a single brain cell — called the grandmother neuron, because of its ability to identify familiar faces, like a person's grandmother's — would be discovered, but that has yet to happen.

The problem is so entrenched in neuroscience that senior author Winrich Freiwald, PhD, professor of neurosciences and behavior at the Rockefeller University in New York City, says that when one scientist wants to ridicule another's argument, they dismiss it as "just another grandmother neuron," or unproven theory.

Now, in an obscure and understudied area of the brain, Freiwald says they have found the closest thing to a grandmother neuron in cells capable of linking face perception to memory.

The Grandmother of Cells

For their study, Freiwald and his colleagues recorded electrical signals from neurons in the brains of two rhesus monkeys as they were shown photos of faces; some of people they knew and some of people they did not.

The team showed that neurons in the lower front of the brain, the temporal pole, play a role in the identification of familiar faces and the ability to tell the difference between known and new faces.

In fact, neuronal responses were three times stronger for faces of people the monkeys were personally familiar with than for faces of those they did not know, even if they had seen those faces multiple times on screens.

This could point to the importance of knowing someone in person, the researchers explain. Given the tendency nowadays to interact

virtually, we must be aware that faces we have seen on a screen might not evoke the same neuronal activity as faces we meet in person.

With this information, scientists can start to investigate how these brain cells encode familiar faces. The researchers say they can now ask how this region is connected to the other parts of the brain and what happens when a new face appears.

https://bit.ly/3eOxf6T

As little as 1.5% of our genome is 'uniquely human'

The rest is shared with ancient human relatives such as Neanderthals.

By Rachael Rettner - Senior Writer

Less than 10% of your genome is unique to modern humans, with the rest being shared with ancient human relatives such as Neanderthals, according to a new study.

The study researchers also found that the portion of DNA that's unique to modern humans is enriched for genes involved with brain development and brain function. This finding suggests that genes for brain development and function are what really set us apart, genetically, from our ancestors.

However, it's unclear what this finding means in terms of the actual biological differences between humans and Neanderthals, said study senior author Richard E. Green, an associate professor of biomolecular engineering at the University of California, Santa Cruz.

"That is a giant question that future work will have to disentangle," Green told Live Science. "At least now we know where to look."

For the new study, published Friday (July 16) in the journal Science Advances, the researchers aimed to tease apart the genes that are unique to modern-day humans as opposed to inherited from ancient ancestors. But this process is tricky because humans have genetic variants that they share with Neanderthals, not only because the two groups interbred, but also because humans and Neanderthals inherited some of the same genetic variants from a common ancestor.

So the researchers developed an algorithm, known as the "speedy ancestral recombination graph estimator," which enabled them to more efficiently tell the difference between parts of the genome modern humans inherited due to interbreeding with Neanderthals and parts that humans shared with Neanderthals prior to the evolutionary split between Neanderthals and humans, roughly 500,000 years ago. They used the algorithm to analyze 279 modern human genomes, two Neanderthal genomes and one genome from Denisovans, another group of archaic humans.

They found that just 1.5% to 7% of the human genome is unique to *Homo sapiens*, free from signs of interbreeding or ancestral variants. Green described the 7% value as the portion of the human genome where humans are more closely related to each other than to Neanderthals or Denisovans. The 1.5% value is the portion that includes gene variants that all humans have but no Neanderthal or Denisovan had.

Green said he and his colleagues were surprised by their findings. "It seems like not a lot of the genome is uniquely human," he said. They were also surprised that most of the genes within that 1.5% to 7% portion were "genes that we know and recognize," — largely coding for proteins known to be involved in brain development and function — rather than genetic material that isn't known to have a specific function.

The researchers also found that the human-specific mutations arose through two distinct "bursts" of adaptive genetic changes that occurred around 600,000 years ago and 200,000 years ago, the authors said. Exactly why the genetic changes occurred at those times — or what might have been going on in the environment to trigger those changes — is unknown.

Focusing on these mutations, and understanding exactly what they do in the brain, may help researchers understand how humans and Neanderthals differed cognitively and biologically.

For example, researchers may be able to take cells in a lab dish and genetically edit the human-specific genes to "flip them back" to the Neanderthal version, Green said. It wouldn't be the same as having an actual Neanderthal around to study, Green added, but "it could give you a molecular idea of what that change did in human history."

https://bit.ly/3ky76g0

Expert panel says new $56K Alzheimer's drug is unproven—and worth $8,400 max

A Biogen rep said assessing its drug requires "innovative thinking."

Beth Mole

Biogen's new Alzheimer's drug Aduhelm continues to face opposition after its contentious approval by the Food and Drug Administration last month—which the FDA now says should be independently investigated. Some insurers say they won't pay for the drug, some hospitals say they won't administer it, and yet more experts say it has no proven benefit and is dramatically overpriced at $56,000 for a year's supply.

On Thursday, a panel of medical experts convened by the nonprofit Institute for Clinical and Economic Review (ICER) voted 15 to 0 to say that there is no evidence that Aduhelm provides clinical benefit to patients. The unanimous vote echoes another one from a panel of expert advisors for the Food and Drug Administration who voted last November against FDA approval. Eleven of ten advisors voted that data collected in two identical Phase III clinical trials failed to show that the drug is effective, with the remaining advisor voting "uncertain."

The FDA nevertheless approved the drug on June 7, sparking a firestorm of criticism. In an unprecedented move last week, the FDA updated its recommendation for who should receive the drug, significantly narrowing the pool from all Alzheimer's patients to only those with mild disease. It's unusual for the FDA to make such a modification so soon after an initial decision and without fresh data to back a change.

Things got weirder when Acting FDA Commissioner Janet Woodcock announced that she was calling for the Office of the Inspector General to independently investigate if any FDA officials involved in the decision got too cozy with Biogen prior to the approval. Ongoing concern over the FDA's relationship with Biogen could "undermine the public's confidence in the FDA's decision," she wrote in a letter to acting Inspector General Christi Grimm. The House Committee on Oversight and Reform had already opened a similar investigation of its own.

But doctors, hospitals, and insurers aren't waiting to hear the outcomes of any investigations. The Cleveland Clinic and Mount Sinai's Health System in New York City have both already announced that they will not administer the drug, the New York Times reported. Six affiliates of Blue Cross and Blue Shield in Florida, New York, Michigan, North Carolina, and Pennsylvania have said they will not cover the drug because they consider it "investigational" or "experimental," the Boston Globe reported.

Other insurers are holding off on decisions until Medicare weighs in. On Monday, Medicare opened a National Coverage Determination analysis to determine its coverage policy. Some early analyses have estimated that Medicare could end up paying billions of dollars if even a sliver of Medicare-eligible Alzheimer's patients ends up taking the drug.

Last month, the ICER reported that its latest cost-effectiveness analysis for Aduhelm set its price at $3,000 to $8,400 per year. That would represent an 85 percent to 95 percent discount from its

current list price of $56,000 per year.

At the ICER meeting Thursday, Biogen's top medical officer, Maha Radhakrishnan, told the panel that the company "regret[s] that the ICER assessment missed the mark," on evaluating the drug, according to FiercePharma. Radhakrishnan argued that assessing Aduhelm requires "innovative thinking" and a new framework.

https://bit.ly/3hO6W2e

Do you need a COVID-19 booster vaccine to prevent delta variant?

Current evidence suggests the COVID-19 vaccines administered in the U.S. are still highly effective against the delta variant.

By Yasemin Saplakoglu - Staff Writer

People who are fully vaccinated against COVID-19 in the U.S. are strongly protected against the highly transmissible delta variant of the coronavirus, and do not need booster shots yet, according to experts. "Americans who have been fully vaccinated do not need a booster shot at this time," according to a joint statement from the Centers for Disease Control and Prevention (CDC) and Food and Drug Administration (FDA). "We continue to review any new data as it becomes available and will keep the public informed."

The statement came after Pfizer-BioNTech announced plans to seek authorization for a booster shot for its COVID-19 vaccine. Though all the vaccine manufacturers have been studying booster shots just in case they would be needed, Pfizer's decision to seek authorization so soon took experts by surprise, and many of them criticized the announcement, The New York Times reported.

Current evidence suggests the Pfizer, Moderna and Johnson & Johnson's COVID-19 vaccines — the three that are being administered in the U.S. — are all strongly protective against the delta variant, according to the Times. The European Medicines Agency (the European counterpart to the FDA) said it was too early to tell whether more than two shots of COVID-19 vaccines will be necessary, according to Reuters.

The delta variant, or B.1.617.2, was first identified in India in October 2020 and the World Health Organization designated it a "variant of concern" in May 2021, Live Science previously reported. The delta variant is thought to be 60% more transmissible than the alpha variant, the previous dominant variant in the U.S., according to the report. The delta variant currently makes up nearly 58% of new cases in the U.S., according to the CDC.

A study conducted by Public Health England found that Pfizer's COVID-19 vaccine was 88% effective against symptomatic disease caused by the delta variant, Live Science reported. Other studies from Scotland and Canada also found that the vaccine was 79% and 87% effective, respectively, at preventing symptomatic disease from that variant, according to the Times.

But a preliminary study conducted in Israel, which hasn't yet been peer-reviewed, found that the vaccine was only about 64% effective in preventing symptomatic illness but 93% effective in preventing serious illness from delta, according to a statement. Pfizer said its own findings from Israel were similar to these results, according to the Times.

Johnson & Johnson recently said that its single-shot COVID-19 vaccine was also protective against the delta variant, Live Science previously reported. Moderna has also said that blood sample tests from vaccinated people have shown the delta variant was highly effective in producing antibodies against the delta variant, according to the Times. Experts say that the vast majority of people who develop severe COVID-19 disease are not vaccinated.

"Preliminary data from several states over the last few months suggest that 99.5% of deaths from COVID-19 in the United States were in unvaccinated people," Rochelle Walensky, CDC director, said on July 8 during a press briefing. "Those deaths were preventable with a simple, safe shot."

Because the vaccines seem to protect people against catching the delta variant, and especially from developing severe disease and death from it, boosters aren't needed at this time, experts told Buzzfeed News. "The dam is still holding, even if there has been some splashing going on," immunologist E. John Wherry, director of the Penn Institute of Immunology told Buzzfeed News. "We are prepared for booster doses if and when the science demonstrates that they are needed," the CDC and FDA statement said.

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With call for 'raw data' and lab audits, WHO chief pressures China on pandemic origin probe

Tedros Adhanom Ghebreyesus, is urging China to increase its transparency about the early days of the COVID-19 pandemic

By Jon Cohen

In a sharp tightening of the diplomatic screws, the director of the World Health Organization (WHO), Tedros Adhanom Ghebreyesus, is urging China to increase its transparency about the early days of the COVID-19 pandemic and allow greater access to its labs to help resolve the origin of SARS-CoV-2.

Tedros, as he prefers to be called, also says WHO will create a new body to conduct the next phase of studies into the emergence of the virus, an unexpected move that concerns some scientists, including at least one member of an existing mission that the agency organized to study COVID-19's origin. "I'm worried about delays and of course it's a bit strange," says virologist and veterinarian Marion Koopmans of Erasmus University. "We're losing valuable time."

At a press conference on 15 July and in a statement made yesterday at an information session on the pandemic's origin, Tedros called for more aggressively probing the two leading theories of how SARS-CoV-2 first infected humans and then emerged in Wuhan in December 2019: that the virus made a natural "zoonotic" jump from an unknown animal species into humans or, more controversially, that it first infected a human during laboratory or field studies of coronaviruses found in animals. (An even more contentious theory suggests the virus was genetically engineered in a Wuhan lab.)

Tedros, who has been accused of being too deferential to Chinese President Xi Jinping, said China has not shared "raw data" from the early days of the pandemic and called for "audits of relevant laboratories and research institutions operating in the area of the initial human cases identified in December 2019."

The Wuhan Institute of Virology is world famous for its study of bat coronaviruses, and an outpost of the country's Center for Disease Control and Prevention also has a lab in the city that does similar work.

Researchers who have been critical of WHO's handling of the origin issue welcome Tedros' tougher tone. "It's a sign that the WHO might be able to do more credible or balanced investigation," says Alina Chan, a gene therapy researcher at the Broad Institute, who with 17 other scientists co-authored a 14 May letter in *Science* that argued the lab theory deserves a more balanced assessment. But Chan doubts that China will agree to audits of its labs. "Right now, the lack of clarity is in China's interest," she says .

Another author of the *Science* letter, microbiome researcher David Relman of Stanford University, wished Tedros had owned up to past WHO "missteps." "I don't think he can simply just take the next step and not worry about what's happened so far."

But other researchers think Tedros has been caught up in what Gerald Keusch, associate director of the National Emerging Infectious Diseases Laboratory Institute at Boston University, calls "the barrage of media and political commentary"-- particularly sharp in the United States, WHO's largest funder—about a potential lab leak.

The Biden administration, which recently rejoined WHO after former president Donald Trump's rift with the agency, has launched its own inquiry in the origins of the pandemic, including a possible lab leak. "I think he's under enormous pressure, and he's capitulated," says Keusch, who co-authored two letters in the *Lancet* that favor the natural origin theory and criticize the "conspiracy theories" and speculation that fuel some lab-origin arguments. "It's sad." (Tedros declined an interview request.)

Earlier this year, the WHO sent a team of international scientists to China to work with colleagues there on a joint mission to study the origin of SARS-CoV-2.

The team was not explicitly asked to examine the lab origin hypothesis, yet it did discuss that scenario at length with researchers at the Wuhan Institute of Virology. The report issued in March by the joint mission, which had just completed the first of two planned phases of studies, then declared the lab origin hypothesis "extremely unlikely" and favored the zoonotic theory.

That sparked controversy, and even Tedros was chagrined. At the press conference Thursday he said it was "premature" to discount the lab theory. "As you know, I was a lab technician myself, an immunologist, and have worked in the lab. And lab accidents happen. It's common."

China's Foreign Ministry Spokesperson Zhao Lijian pushed back on Tedros' remarks at a press conference yesterday, stressing that the joint mission report reached "important conclusions." Zhao, who repeated the Chinese government's frequent claim that SARS-CoV-2 might have first infected a human in another country or even entered China through frozen food, suggested the WHO director was "politicizing the issue." China shared "large amounts of data" with the WHO mission team, he insisted, only holding back information that compromised personal privacy.

International members of the joint mission have previously noted they both lacked a mandate and didn't have the expertise to conduct an independent biosafety audit of the Wuhan labs. Koopmans calls it "logical" to push for lab audits but suggests the demand right now could backfire. "It's not going to be popular with China, so I'm a little bit worried that that will shut the doors to the rest of the studies that we feel are needed," she says, adding that it would make more sense to lobby for audits if the soon-to-be completed investigation by the Biden administration yields any evidence supporting a lab origin.

Tedros' call for more raw data echoes concerns raised by Koopmans and other international researchers on the joint mission. For example, they asked for more data on the first 174 documented COVID-19 cases, a plea Tedros repeated yesterday.

But Koopmans says those data became less important to team members as their work progressed, because they realized that the pandemic predated those cases. A "circular" Tedros presented to member states earlier this week spelled out other data the phase 2 studies should attempt to gather—which the joint mission report describes in great detail—such as testing of captive and wild animals, particularly in regions where SARS-CoV-2 first circulated, and of humans who came in contact with them.

Tedros also told the member states in his remarks this week that he wanted more "studies of animal markets in and around Wuhan, including continuing studies on animals sold at the Huanan wholesale market."

In its final report, the mission had noted that it found "no verified reports of live mammals being sold around 2019" in the Huanan Seafood Market, which was linked to the first cluster of cases, and other Wuhan markets tied to early human infections. Yet a study posted 7 June 2021 in *Scientific Reports* documented that thousands of live mammals were sold between May 2017 and Nov 2019 at the markets, including Huanan, which alone was linked to 28% of the

first 174 COVID-19 cases and also had abundant evidence of SARS-CoV-2 on its floors and in its drains.

Whether Koopmans and other members of the existing joint mission will help conduct those studies is murky. Tedros said a new WHO International Scientific Advisory Group for Origins of Novel Pathogens (SAGO) "will play a vital role in the next phase of studies into the origins of SARS-CoV-2, as well as the origins of future new pathogens."

WHO soon will make an open call for "highly qualified experts" to apply. Koopmans says she would welcome broadening the existing group's expertise, especially to conduct lab audits and to study the blood of more humans who live far from Wuhan and may have been exposed to SARS-CoV-2 before the outbreak even surfaced.

Keusch, however, worries that SAGO will replace the existing origin task force. The current group has highly qualified, diverse experts who worked "diligently" and established important ties to their Chinese colleagues, he says. "I'm very suspicious about dismissing the initial task force and now allowing individuals and governments to nominate themselves, which will result in a partisan, selective process and not lead to the best composition," he says.

Relman, who says he is uncertain whether he will apply for SAGO because of the time commitment, wonders if WHO is the best organization to oversee SARS-CoV-2 origin studies. "They're not a truly independent body," says Relman. "They are the product of a very political world, and what makes their problem 100 times worse is that they don't have the resources to operate independently."

He suggests the United Nations may want to create an entirely new organization along the lines of the International Atomic Energy Agency to study pathogen origins. But he is pleased at WHO's new push for answers. "I really do hope that good science can rule the day."

https://bit.ly/3kx2jLP

Researchers Have Created a Dissolvable Pacemaker

The wireless device is biodegradable and might be a safer alternative to temporary pacemakers.

By Victoria Song

While you might be more familiar with permanent pacemakers, temporary versions of the device are sometimes needed after open-heart surgery, heart attacks, or overdoses. The problem is these devices can cause infections, become dislodged, or introduce other complications like scarring during removal.

But now, researchers from Northwestern and George Washington universities say they've created a temporary, wireless pacemaker that dissolves in the body after use.

Image: Northwestern University/George Washington University

In a study published in *Nature Biotechnology* (via Wired), the researchers describe a teeny device made of thin, flexible, and lightweight biocompatible materials that can be reabsorbed by the body in five to seven weeks. It also doesn't require a battery for power or rigid wires and leads, as it harvests energy using NFC—the same tech used in smartphones for contactless payments. The device is only 250 microns thick and weighs less than half a gram. According to Wired, the big thing here is that silicon can be reabsorbed by the body. That means super-thin silicon can be used to create electronic components that are much thinner than the silicon that powers consumer electronics.

"Instead of using wires that can get infected and dislodged, we can implant this leadless biocompatible pacemaker," Dr. Rishi Arora, the study's co-lead and a cardiologist at Northwestern Medicine, said in a press statement. "The circuitry is implanted directly on the surface of the heart, and we can activate it remotely." Arora went on to say that the device could also potentially be modified so that

doctors may someday implant bioresorbable pacemakers in the leg or arm veins.

The current process for temporary pacemakers involves sewing electrodes onto the heart, with leads that exit the chest and connect to an external box. It's not the most comfortable scenario for patients, as it limits their movements and activities to prevent dislodging. A flexible pacemaker that you can stick onto the heart that then later dissolves would eliminate that problem. The researchers also claim it's possible to tailor the device's thickness and composition to more precisely control how long the device functions before dissolving.

That said, it'll be a while before this sort of technology can be used on humans. The researchers were successful when testing on mice and rabbits, but scaling this sort of treatment to humans requires more clinical testing and trials for both safety and efficacy. According to Wired, clinical trials based on this design might begin in roughly three years. While that seems like a long time, this type of medical technology often has a long lead time due to rigorous testing standards. However, if successful, that could open the door to other types of dissolvable implants for other hard-to-operate on organs.