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An 'Internet apocalypse' could ride to Earth with the next solar storm, new research warns

The underwater cables that connect nations could go offline for months, the study warns.

By Brandon Specktor

The sun is always showering Earth with a mist of magnetized particles known as solar wind. For the most part, our planet's magnetic shield blocks this electric wind from doing any real damage to Earth or its inhabitants, instead sending those particles skittering toward the poles and leaving behind a pleasant aurora in their wake.

But sometimes, every century or so, that wind escalates into a full-blown solar storm — and, as new research presented at the SIGCOMM 2021 data communication conference warns, the results of such extreme space weather could be catastrophic to our modern way of life.

In short, a severe solar storm could plunge the world into an "internet apocalypse" that keeps large swaths of society offline for weeks or months at a time, Sangeetha Abdu Jyothi, an assistant professor at the University of California, Irvine, wrote in the new research paper. (The paper has yet to appear in a peer-reviewed journal).

"What really got me thinking about this is that with the pandemic we saw how unprepared the world was. There was no protocol to deal with it effectively, and it's the same with internet resilience," Abdu Jyothi told WIRED. "Our infrastructure is not prepared for a large-scale solar event."

Part of the problem is that extreme solar storms (also called coronal mass ejections) are relatively rare; scientists estimate the probability of an extreme space weather directly impacting Earth to be between 1.6% to 12% per decade, according to Abdu Jyothi's paper.

In recent history, only two such storms have been recorded — one in 1859 and the other in 1921. The earlier incident, known as the Carrington Event, created such a severe geomagnetic disturbance on Earth that telegraph wires burst into flame, and auroras — usually only visible near the planet's poles — were spotted near equatorial Colombia. Smaller storms can also pack a punch; one in March 1989 blacked out the entire Canadian province of Quebec for nine hours.

Since then, human civilization has become much more reliant on the global internet, and the potential impacts of a massive geomagnetic storm on that new infrastructure remain largely unstudied, Abdu Jyothi said. In her new paper, she tried to pinpoint the greatest vulnerabilities in that infrastructure.

The good news is, local and regional internet connections are likely at low risk of being damaged because fiber-optic cables themselves aren't affected by geomagnetically induced currents, according to the paper.

However, the long undersea internet cables that connect continents are a different story. These cables are equipped with repeaters to boost the optical signal, spaced at intervals of roughly 30 to 90 miles (50 to 150 kilometers). These repeaters are vulnerable to geomagnetic currents, and entire cables could be made useless if even one repeater goes offline, according to the paper.

If enough undersea cables fail in a particular region, then entire continents could be cut off from one another, Abdu Jyothi wrote. What's more, nations at high latitudes — such as the U.S. and the U.K. — are far more susceptible to solar weather than nations at lower latitudes. In the event of a catastrophic geomagnetic storm, it's those high-latitude nations that are most likely to be cut off from the network first. It's hard to predict how long it would take to repair underwater infrastructure, but Abdu Jyothi suggests that

large-scale internet outages that last weeks or months are possible.
In the meantime, millions of people could lose their livelihoods.
"The economic impact of an Internet disruption for a day in the US is estimated to be over $7 billion," Abdu Jyothi wrote in her paper. "What if the network remains non-functional for days or even months?"
If we don't want to find out, then grid operators need to start taking the threat of extreme solar weather seriously as global internet infrastructure inevitably expands. Laying more cables at lower latitudes is a good start, Abdu Jyothi said, as is developing resilience tests that focus on the effects of large-scale network failures.
When the next big solar storm does blast out of our star, people on Earth will have about 13 hours to prepare for its arrival, she added. Let's hope we're ready to make the most of that time when it inevitably arrives.

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Umami Taste Receptor Evolved with Primates' Diets

A study suggests that mutations in the gene that encodes the T1R1/T1R3 taste receptor allowed primates that relied on insects for protein to transition to eating leaves and fruit.

Abby Olena

Most people enjoy umami flavor, which is perceived when a taste receptor called T1R1/T1R3 senses the amino acid glutamate. In some other mammals, such as mice, however, this same receptor is much less sensitive to glutamate. In a new study published August 26 in *Current Biology*, researchers uncover the molecular basis for this difference. They show that the receptor evolved in humans and some other primates away from mostly binding free nucleotides, which are common in insects, to preferentially binding glutamate, which is abundant in leaves.
The authors argue that the change facilitated a major evolutionary shift in these primates toward a plant-heavy diet.
"The question always comes up about the evolution of umami taste: In humans, our receptor is narrowly tuned to glutamate, and we never had a good answer for why," says Maude Baldwin, a sensory biologist at the Max Planck Institute for Ornithology in Germany. She was not involved in the new work, but coauthored a 2014 study with Yasuka Toda, who is also a coauthor on the new paper, showing that the T1R1/T1R3 receptor is responsible for sweet taste in hummingbirds.
In the new study, the authors find "that this narrow tuning has evolved convergently multiple times [and] that it's related to folivory," she says, calling the paper "a hallmark, fantastic study, and one that will become a textbook example of how taste evolution can relate to diet and how to address these types of questions in a rigorous, comprehensive manner."
In 2011, Toda, who was then at the University of Tokyo and now leads a group at Meiji University in Japan, and Takumi Misaka of the University of Tokyo developed a strategy to use cultured cells to analyze the function of taste receptors. They used the technique to tease out the parts of the human T1R1/T1R3 that differed from that of mice and thus underlie the high glutamate sensitivity in the human receptor, work that they published in 2013.
As part of that project, Toda and Misaka also established a collaboration with Takashi Hayakawa, now a group leader at Hokkaido University in Japan, and Hiroo Imai, a biologist at Kyoto University. Both Hayakawa and Imai are affiliated with the Primate Research Institute at Kyoto University and thus have expertise in nonhuman primate biology, as well as access to genomic DNA for further receptor comparisons.
In the 2013 study, the team found that among three nonhuman primates—squirrel monkeys (*Saimiri boliviensis*), baboons (*Papio hamadryas*), and macaques (*Macaca nemestrina*)—only squirrel

monkey T1R1/T1R3 had very low sensitivity to glutamate, just like mouse T1R1/T1R3. "Thus, we hypothesized that the glutamate taste perception has been acquired during primate evolution," Toda writes in an email to *The Scientist.*

In the new *Current Biology* study, Toda and colleagues test that hypothesis. First, they used Toda's cell-culture strategy to make comparisons of glutamate sensitivity among the T1R1/T1R3 receptors from 17 species of primates. The receptors from all but four nonhuman primates—marmosets (*Callithrix jacchus*), tarsiers (*Carlito syrichta*), squirrel monkeys, and greater galagos (*Otolemur crassicaudatus*)—were sensitive to glutamate. These four species primarily rely on insects for protein. In contrast, the receptors from humans and gorillas were much less responsive to the free nucleotides inosine monophosphate and guanosine 5'-monophosphate than were the receptors from the rest of the primates.

The team then identified the protein building blocks responsible for either glutamate or nucleotide recognition by comparing the DNA codes for different species' receptors and constructing chimeras between the spider monkey (*Ateles geoffroyi,* most responsive to glutamate) and squirrel monkey (most responsive to free nucleotides) receptors, which they then tested in cell culture. Substituting just two spider monkey nucleotides for squirrel monkey nucleotides was sufficient to switch the sensitivity from glutamate to free nucleotides, and vice versa.

The authors next explored the relationship between diet and receptor sensitivity. They found that leaves and fruit have a lower concentration of free nucleotides than do insects, and concentrations of glutamate higher than that of free nucleotides. The four nonhuman primates with a taste receptor specialized to detect free nucleotides primarily rely on insects as a protein source, while most of the other primates the researchers studied include leaves and fruit as a large proportion of their diets. In a final test of one species' preferences, the researchers showed that squirrel monkeys prefer to drink water that has added free nucleotides, but show no preference for water with monosodium glutamate added.

The diversity of methods that the authors use to address how the genetic evolution of taste receptors occurred in conjunction with dietary patterns is "impressive," says Addison Kemp, a biological anthropologist at the University of Southern California Keck School of Medicine who did not participate in the study. One open question, she adds, is what patterns of taste receptor sensitivity to glutamate are present in the lineage that includes lemurs and lorises, only one of which—the ring-tailed lemur—was included in the current analysis.

The researchers showed in the study that the ring-tailed lemur T1R1/T1R3 receptor demonstrates affinity for both glutamate and free nucleotides, "but that is their one representative from this really, really diverse clade," Kemp explains. Plus, lemurs and lorises "tend to retain a better sense of smell, as they have a wider range of functional olfactory genes, and the interplay between taste and smell is really important in terms of the ingestive experience," she says, adding that, based on the paper, it sounds like the authors are planning to look at this group in the future. "It will be really interesting to see what kind of patterns they see in terms of taste receptor sensitivity to glutamate within this lineage."

The findings indicate that "sensory systems are very flexible and can evolve new adaptive sensory capabilities," Toda writes. "To use leaves as a new protein source, the ancestors of large primates (including humans) evolved their umami taste receptor as a sensor for glutamate," she explains, adding that this specialization for glutamate may have helped primates overcome bitter and aversive tastes also present in leaves.

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Genetic Analysis Illuminates Origins of Lung Cancer in People With No History of Smoking

Many of these tumors arise from the accumulation of mutations caused by natural processes

A genomic analysis of lung cancer in people with no history of smoking has found that a majority of these tumors arise from the accumulation of mutations caused by natural processes in the body. This study was conducted by an international team led by researchers at the National Cancer Institute (NCI), part of the National Institutes of Health (NIH), and describes for the first time three molecular subtypes of lung cancer in people who have never smoked.

These insights will help unlock the mystery of how lung cancer arises in people who have no history of smoking and may guide the development of more precise clinical treatments. The findings were published today (September 6, 2021) in *Nature Genetics*.

"What we're seeing is that there are different subtypes of lung cancer in never smokers that have distinct molecular characteristics and evolutionary processes," said epidemiologist Maria Teresa Landi, M.D., Ph.D., of the Integrative Tumor Epidemiology Branch in NCI's Division of Cancer Epidemiology and Genetics, who led the study, which was done in collaboration with researchers at the National Institute of Environmental Health Sciences, another part of NIH, and other institutions. "In the future, we may be able to have different treatments based on these subtypes."

Lung cancer is the leading cause of cancer-related deaths worldwide. Every year, more than 2 million people around the world are diagnosed with the disease. Most people who develop lung cancer have a history of tobacco smoking, but 10% to 20% of people who develop lung cancer have never smoked. Lung cancer in never smokers occurs more frequently in women and at an earlier age than lung cancer in smokers.

Environmental risk factors, such as exposure to secondhand tobacco smoke, radon, air pollution, and asbestos, or having had previous lung diseases, may explain some lung cancers among never smokers, but scientists still don't know what causes the majority of these cancers.

In this large epidemiologic study, the researchers used whole-genome sequencing to characterize the genomic changes in tumor tissue and matched normal tissue from 232 never smokers, predominantly of European descent, who had been diagnosed with non-small cell lung cancer. The tumors included 189 adenocarcinomas (the most common type of lung cancer), 36 carcinoids, and seven other tumors of various types. The patients had not yet undergone treatment for their cancer.

The researchers combed the tumor genomes for mutational signatures, which are patterns of mutations associated with specific mutational processes, such as damage from natural activities in the body (for example, faulty DNA repair or oxidative stress) or from exposure to carcinogens. Mutational signatures act like a tumor's archive of activities that led up to the accumulation of mutations, providing clues into what caused the cancer to develop. A catalog of known mutational signatures now exists, although some signatures have no known cause. In this study, the researchers discovered that a majority of the tumor genomes of never smokers bore mutational signatures associated with damage from endogenous processes, that is, natural processes that happen inside the body.

As expected, because the study was limited to never smokers, the researchers did not find any mutational signatures that have previously been associated with direct exposure to tobacco smoking. Nor did they find those signatures among the 62 patients who had been exposed to secondhand tobacco smoke. However, Dr. Landi

cautioned that the sample size was small and the level of exposure highly variable. "We need a larger sample size with detailed information on exposure to really study the impact of secondhand tobacco smoking on the development of lung cancer in never smokers," Dr. Landi said.

The genomic analyses also revealed three novel subtypes of lung cancer in never smokers, to which the researchers assigned musical names based on the level of "noise" (that is, the number of genomic changes) in the tumors. The predominant "piano" subtype had the fewest mutations; it appeared to be associated with the activation of progenitor cells, which are involved in the creation of new cells. This subtype of tumor grows extremely slowly, over many years, and is difficult to treat because it can have many different driver mutations. The "mezzo-forte" subtype had specific chromosomal changes as well as mutations in the growth factor receptor gene *EGFR*, which is commonly altered in lung cancer, and exhibited faster tumor growth. The "forte" subtype exhibited whole-genome doubling, a genomic change that is often seen in lung cancers in smokers. This subtype of tumor also grows quickly.

"We're starting to distinguish subtypes that could potentially have different approaches for prevention and treatment," said Dr. Landi. For example, the slow-growing piano subtype could give clinicians a window of opportunity to detect these tumors earlier when they are less difficult to treat. In contrast, the mezzo-forte and forte subtypes have only a few major driver mutations, suggesting that these tumors could be identified by a single biopsy and could benefit from targeted treatments, she said.

A future direction of this research will be to study people of different ethnic backgrounds and geographic locations, and whose exposure history to lung cancer risk factors is well described.

"We're at the beginning of understanding how these tumors evolve," Dr. Landi said. "This analysis shows that there is heterogeneity, or diversity, in lung cancers in never smokers."

Stephen J. Chanock, M.D., director of NCI's Division of Cancer Epidemiology and Genetics, noted, "We expect this detective-style investigation of genomic tumor characteristics to unlock new avenues of discovery for multiple cancer types."

Reference: "Genomic and evolutionary classification of lung cancer in never smokers" by Tongwu Zhang, Philippe Joubert, Naser Ansari-Pour, Wei Zhao, Phuc H. Hoang, Rachel Lokanga, Aaron L. Moye, Jennifer Rosenbaum, Abel Gonzalez-Perez, Francisco Martínez-Jiménez, Andrea Castro, Lucia Anna Muscarella, Paul Hofman, Dario Consonni, Angela C. Pesatori, Michael Kebede, Mengying Li, Bonnie E. Gould Rothberg, Iliana Peneva, Matthew B. Schabath, Maria Luana Poeta, Manuela Costantini, Daniela Hirsch, Kerstin Heselmeyer-Haddad, Amy Hutchinson, Mary Olanich, Scott M. Lawrence, Petra Lenz, Maire Duggan, Praphulla M. S. Bhawsar, Jian Sang, Jung Kim, Laura Mendoza, Natalie Saini, Leszek J. Klimczak, S. M. Ashiqul Islam, Burcak Otlu, Azhar Khandekar, Nathan Cole, Douglas R. Stewart, Jiyeon Choi, Kevin M. Brown, Neil E. Caporaso, Samuel H. Wilson, Yves Pommier, Qing Lan, Nathaniel Rothman, Jonas S. Almeida, Hannah Carter, Thomas Ried, Carla F. Kim, Nuria Lopez-Bigas, Montserrat Garcia-Closas, Jianxin Shi, Yohan Bossé, Bin Zhu, Dmitry A. Gordenin, Ludmil B. Alexandrov, Stephen J. Chanock, David C. Wedge and Maria Teresa Landi, 6 September 2021, Nature Genetics.
DOI: 10.1038/s41588-021-00920-0
The study was conducted by the Intramural Research Program of NCI and National Institute of Environmental Health Sciences.

https://bit.ly/3yRdjY4

How ancient farmers throttled their immune systems to survive

If COVID-19 had swept Europe before farming, "more people would have died than today"

By Ann Gibbons

When early farmers of the Vinca culture first sowed barley and wheat 7700 years ago in the rich soil of the Danube River and its tributaries, they changed more than their diet: They introduced a new way of life to the region. They crowded together in mud huts, living cheek by rump with aurochs, cows, pigs, and goats—and their poop—in settlements that eventually swelled to thousands of people. Togetherness brought a surge in diseases such as influenza, tuberculosis, and other maladies spread from animals to people and

through early farming communities.

Now a new study of ancient DNA shows how the immune systems of those early farmers responded to this new, pathogen-ridden environment. The Neolithic Revolution was a "turning point" in the evolution of immune responses to infectious disease, according to a paper published today in *eLife*. The study suggests that in Europeans, evolution favored genes that throttled back inflammatory reactions to pathogens like influenza, restraining the hyperalert inflammatory response that can be deadlier than the pathogen itself.

"This study does a great job of showing that our immune system has continued to evolve in response to pathogen pressure," says population geneticist Joseph Lachance of the Georgia Institute of Technology. But he notes that the paper relies on an unproven method of predicting ancient immune responses. "I buy it, but it needs to be studied [more] when we have more ancient DNA."

Researchers have long suspected that early farmers got sick more often than nomadic hunter-gatherers. Studies suggest farmers in large Neolithic sites such as Çatalhöyük in Turkey faced a flurry of new zoonotic diseases such as influenza and salmonella, as well as new animal-borne strains of diseases like malaria and tuberculosis. "If farmers got sick more, how did their immune systems change?" asked infectious disease specialist Mihai Netea of Radboud University Nijmegen Medical Centre, who led the study.

To approach that question, his team first studied genetically based variation in the immune responses of living people. They took blood samples from more than 500 people in the Human Functional Genomics Project (HFGP), a biobank based in Nijmegen, Netherlands, and challenged the samples with various pathogens. Then they measured levels of specific cytokines—immunoregulatory proteins such as interleukin and interferon that are secreted by immune cells—and looked for correlations between those levels and a suite of immune gene variants.

In the new study, the team used those results to come up with what's called a polygenic risk score that predicts the strength of the inflammatory response in the face of specific diseases, based on an individual's immune gene variants. The researchers then applied their technique to the past: From existing databases they downloaded ancient DNA sequences from 827 remains found across Europe, including Vinca farmers from today's Romania. They calculated the cytokine levels ancient people would likely have produced and their polygenic risk scores for inflammation.

The remains dated from between 45,000 and 2000 years ago, enabling the team to look for changes over time. They found that when faced with infections, Europeans who lived after agriculture likely produced dramatically lower levels of systemic cytokines than earlier hunter-gatherers. Those lower levels were likely adaptive, Netea says. "When people first encountered new pathogens, some overreacted and died, like we see with COVID today," he says. "The children of the people who survived didn't produce as many cytokines, so the whole population becomes more resistant."

The study also revealed a flip side: When infected with the fungus *Candida* and *Staphylococcus* bacteria—pathogens that tend to start as localized infections—farmers likely mounted more robust inflammatory responses than earlier hunter-gatherers. A strong inflammatory response can quell a localized infection before it spreads, but a robust systemic response, as sparked by the flu or malaria, can spiral out of control.

The study is exciting because it clearly shows that the population frequencies of genes regulating inflammation "change strongly from the beginning of the Neolithic," says molecular anthropologist Ben Krause-Kyora of Kiel University.

But Lachance questions whether polygenic risk scores developed

for modern people can predict inflammation for people in other places and times. Pathogens have evolved over time, he notes, and modern risk prediction might not apply to ancient disease strains. Population geneticist Luis Barreiro of the University of Chicago, agrees, saying the authors "don't formally demonstrate the predictive value of these polygenic risk scores."

More samples of ancient DNA from people and pathogens, especially on other continents, is needed to test whether evolution scaled back the production of inflammatory cytokines in farmers everywhere. But the study clearly demonstrates that somehow or other, European's inflammatory responses to pathogens did change dramatically during the Neolithic, Lachance says. To Netea, the findings suggest the ancient burst of evolution may have an impact even today: If a coronavirus like SARS-CoV-2 had swept through Europe before agriculture, he says, "more people would have died than today because they produced more proinflammatory cytokines."

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These fridge-free COVID-19 vaccines are grown in plants and bacteria

Nanoengineers at the University of California San Diego have developed COVID-19 vaccine candidates that can take the heat.

Their key ingredients? Viruses from plants or bacteria.

The new fridge-free COVID-19 vaccines are still in the early stage of development. In mice, the vaccine candidates triggered high production of neutralizing antibodies against SARS-CoV-2, the virus that causes COVID-19. If they prove to be safe and effective in people, the vaccines could be a big game changer for global distribution efforts, including those in rural areas or resource-poor communities.

"What's exciting about our vaccine technology is that is thermally stable, so it could easily reach places where setting up ultra-low temperature freezers, or having trucks drive around with these freezers, is not going to be possible," said Nicole Steinmetz, a professor of nanoengineering and the director of the Center for Nano-ImmunoEngineering at the UC San Diego Jacobs School of Engineering.

The vaccines are detailed in a paper published Sept. 7 in the *Journal of the American Chemical Society*.

The researchers created two COVID-19 vaccine candidates. One is made from a plant virus, called cowpea mosaic virus. The other is made from a bacterial virus, or bacteriophage, called Q beta.

Both vaccines were made using similar recipes. The researchers used cowpea plants and *E. coli* bacteria to grow millions of copies of the plant virus and bacteriophage, respectively, in the form of ball-shaped nanoparticles. The researchers harvested these nanoparticles and then attached a small piece of the SARS-CoV-2 spike protein to the surface. The finished products look like an infectious virus so the immune system can recognize them, but they are not infectious in animals and humans. The small piece of the spike protein attached to the surface is what stimulates the body to generate an immune response against the coronavirus.

The researchers note several advantages of using plant viruses and bacteriophages to make their vaccines. For one, they can be easy and inexpensive to produce at large scales. "Growing plants is relatively easy and involves infrastructure that's not too sophisticated," said Steinmetz. "And fermentation using bacteria is already an established process in the biopharmaceutical industry."

Another big advantage is that the plant virus and bacteriophage nanoparticles are extremely stable at high temperatures. As a result, the vaccines can be stored and shipped without needing to be kept cold. They also can be put through fabrication processes that use heat. The team is using such processes to package their vaccines into polymer implants and microneedle patches. These processes

involve mixing the vaccine candidates with polymers and melting them together in an oven at temperatures close to 100 degrees Celsius. Being able to directly mix the plant virus and bacteriophage nanoparticles with the polymers from the start makes it easy and straightforward to create vaccine implants and patches.

The goal is to give people more options for getting a COVID-19 vaccine and making it more accessible. The implants, which are injected underneath the skin and slowly release vaccine over the course of a month, would only need to be administered once. And the microneedle patches, which can be worn on the arm without pain or discomfort, would allow people to self-administer the vaccine.

"Imagine if vaccine patches could be sent to the mailboxes of our most vulnerable people, rather than having them leave their homes and risk exposure," said Jon Pokorski, a professor of nanoengineering at the UC San Diego Jacobs School of Engineering, whose team developed the technology to make the implants and microneedle patches.

"If clinics could offer a one-dose implant to those who would have a really hard time making it out for their second shot, that would offer protection for more of the population and we could have a better chance at stemming transmission," added Pokorski, who is also a founding faculty member of the university's Institute for Materials Discovery and Design.

In tests, the team's COVID-19 vaccine candidates were administered to mice either via implants, microneedle patches, or as a series of two shots. All three methods produced high levels of neutralizing antibodies in the blood against SARS-CoV-2.

Potential pan-coronavirus vaccine

These same antibodies also neutralized against the SARS virus, the researchers found.

It all comes down to the piece of the coronavirus spike protein that is attached to the surface of the nanoparticles. One of these pieces that Steinmetz's team chose, called an epitope, is almost identical between SARS-CoV-2 and the original SARS virus.

"The fact that neutralization is so profound with an epitope that's so well conserved among another deadly coronavirus is remarkable," said co-author Matthew Shin, a nanoengineering Ph.D. student in Steinmetz's lab. "This gives us hope for a potential pan-coronavirus vaccine that could offer protection against future pandemics."

Another advantage of this particular epitope is that it is not affected by any of the SARS-CoV-2 mutations that have so far been reported. That's because this epitope comes from a region of the spike protein that does not directly bind to cells. This is different from the epitopes in the currently administered COVID-19 vaccines, which come from the spike protein's binding region. This is a region where a lot of the mutations have occurred. And some of these mutations have made the virus more contagious.

Epitopes from a nonbinding region are less likely to undergo these mutations, explained Oscar Ortega-Rivera, a postdoctoral researcher in Steinmetz's lab and the study's first author. "Based on our sequence analyses, the epitope that we chose is highly conserved amongst the SARS-CoV-2 variants."

This means that the new COVID-19 vaccines could potentially be effective against the variants of concern, said Ortega-Rivera, and tests are currently underway to see what effect they have against the Delta variant, for example.

Plug and play vaccine

Another thing that gets Steinmetz really excited about this vaccine technology is the versatility it offers to make new vaccines. "Even if this technology does not make an impact for COVID-19, it can be quickly adapted for the next threat, the next virus X," said Steinmetz.

Making these vaccines, she says, is "plug and play:" grow plant

virus or bacteriophage nanoparticles from plants or bacteria, respectively, then attach a piece of the target virus, pathogen, or biomarker to the surface. "We use the same nanoparticles, the same polymers, the same equipment, and the same chemistry to put everything together. The only variable really is the antigen that we stick to the surface," said Steinmetz.

The resulting vaccines do not need to be kept cold. They can be packaged into implants or microneedle patches. Or, they can be directly administered in the traditional way via shots.

Steinmetz and Pokorski's labs have used this recipe in previous studies to make vaccine candidates for diseases like HPV and cholesterol. And now they've shown that it works for making COVID-19 vaccine candidates as well.

Next steps

The vaccines still have a long way to go before they make it into clinical trials. Moving forward, the team will test if the vaccines protect against infection from COVID-19, as well as its variants and other deadly coronaviruses, in vivo.

More information: *Trivalent subunit vaccine candidates for COVID-19 and their delivery devices, Journal of the American Chemical Society (2021). DOI: 10.1021/jacs.1c06600*

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DNA left behind without a touch

The longer someone spends in a room the more likely they are to leave a trace of themselves

A person can leave DNA on a surface without directly touching it, a Flinders University study has found, with the longer someone spends in a room the more likely they are to leave a trace of themselves behind.

Recently published in the journal *Forensic Science International: Genetics* and led by Lucas Puliatti, a Flinders University honors graduate, the study looked at how much DNA was deposited by people across varying distances and time periods.

DNA collection plates were placed around individuals' desks, spaced out between 0.5 to 5 meters, and left for one day to six weeks before being swabbed and profiled.

Without anyone directly touching the collection plates, DNA from multiple people was present after only one day, with the DNA profiles stronger the closer the plates were to an individual and the longer they stayed out.

Co-authors Dr. Oliva Handt from Forensic Science SA and Dr. Duncan Taylor from Flinders University's College of Science and Engineering and Forensic Science SA say that advancements in forensic science have seen DNA profiles able to be generated from very limited samples.

"This brings into question how people's DNA may end up on particular surfaces, a question we have to understand if DNA evidence is going to be useful for police investigating, or courts deliberating over a crime," says Dr. Taylor. "A person may have deposited their DNA by touching something, but our research shows it may also have been deposited by that person merely being in close proximity." The results showed distance and time were the key factors in how much DNA was likely to be found.

The collection plates that sat within two meters of the office desks collected the most DNA, while those beyond four meters were very unlikely to collect any DNA at all.

In terms of time, the study showed the longer a person was in the vicinity of a surface, the more likely their DNA would be detected, with the amount of DNA deposited also increasing over time.

The authors say as well as helping to understand how DNA might become present during a crime, the study shows the importance of avoiding cross contamination.

"It doesn't take much to leave your DNA behind, and this study shows the importance of all the proper personal protective equipment, such as masks and gloves, that are used in forensic

laboratories," says Dr. Taylor.

"The level of DNA an individual transfers to untouched items in their immediate surroundings' by Lucas Puliatti, Oliva Handt and Duncan Taylor is published in the journal *Forensic Science International: Genetics*.

More information: *Lucas Puliatti et al, The level of DNA an individual transfers to untouched items in their immediate surroundings, Forensic Science International: Genetics (2021).* *DOI: 10.1016/j.fsigen.2021.102561*

https://bit.ly/3E0iEQC

Transatlantic slave trade introduced novel pathogenic viruses in the Americas

Slave trade may have introduced new pathogenic viruses from Africa to North America

The transatlantic slave trade may have introduced new pathogenic viruses from Africa to North America that affected Indigenous communities, shows an analysis of ancient DNA published in *eLife*. The findings suggest that European colonists brought new viruses, including smallpox, measles and mumps, to North America, which caused outbreaks that led to major population declines in Native American communities. This discovery adds new information about the legacy of the transatlantic slave trade in North America.

"Multiple outbreaks in what is now Mexico killed millions of Indigenous people, Africans and some Europeans in the 16th century. But the exact pathogens responsible for some of these outbreaks is not currently known," explains first author Axel Guzmán-Solís, a former student at the International Laboratory for Human Genome Research, Universidad Nacional Autónoma de México, Mexico, and who is now a Ph.D. student at the Icahn School of Medicine at Mount Sinai, New York, US. "We wanted to understand what viruses were circulating in Mexico during this period."

To do this, Guzmán-Solís and the team extracted ancient viral DNA from the teeth of probable victims of these outbreaks buried at a Colonial-era hospital and chapel. They included victims who were Indigenous as well as those who were of African descent. The team then used this DNA to reconstruct the genomes of viruses present in those samples. This allowed them to identify ancient human hepatitis B virus and human B19 parvovirus from different individuals. By comparing these virus' genomes to others, they found that the viruses likely originated in Africa.

"Our results suggest that the viruses were introduced to the Americas by colonists engaged in the slave trade," says co-senior author Daniel Blanco-Melo, a former postdoctoral researcher at the Icahn School of Medicine at Mount Sinai in New York who is now an Assistant Professor at the Fred Hutchinson Cancer Research Center in Seattle, U.S. "The cruel, unsanitary and overcrowded conditions on the ships that transported millions of people across the Atlantic was a favorable setting for the spread of infectious diseases. Therefore, this gruesome practice likely introduced new pathogens to Indigenous people who had no immunity to them." He adds that the conditions that colonists forced Africans and Native Americans to live in during this time would have also promoted the spread of the diseases and may have fueled epidemics.

The study is not able to determine whether these individuals were infected in Africa, during the forced transport, or if the viruses occurred after the Africans' arrival in North America. It is also unable to say whether the viruses caused the victims' deaths. But it does provide evidence that these viruses, which can cause serious disease, were circulating in the affected populations.

"Our findings also suggest that multiple, newly introduced viruses were circulating at the same time, which may explain why the epidemics proved so deadly for Indigenous communities," says co-senior author Maria Ávila-Arcos, Principal Investigator at the International Laboratory for Human Genome Research,

Universidad Nacional Autónoma de México. "Together, this work demonstrates how the new field of paleovirology can help us learn more about the possible role of these and other pathogens in colonial epidemics and better understand the role of human actions in spreading them."

More information: *Axel A Guzmán-Solís et al, Ancient viral genomes reveal introduction of human pathogenic viruses into Mexico during the transatlantic slave trade, eLife (2021). DOI: 10.7554/eLife.68612*

https://bit.ly/3l8ADLZ

The Plan to Stop Every Respiratory Virus at Once

The benefits of ventilation reach far beyond the coronavirus. What if we stop taking colds and flus for granted, too?

By Sarah Zhang

When London vanquished cholera in the 19th century, it took not a vaccine, or a drug, but a sewage system. The city's drinking water was intermingling with human waste, spreading bacteria in one deadly outbreak after another. A new comprehensive network of sewers separated the two. London never experienced a major cholera outbreak after 1866. All that was needed was 318 million bricks, 23 million cubic feet of concrete, and a major reengineering of the urban landscape.

The 19th and early 20th century saw a number of ambitious public-health efforts like this. The United States eliminated yellow fever and malaria, for example, with a combination of pesticides, wide-scale landscape management, and window screens that kept mosquitoes at bay. One by one, the diseases that people accepted as inevitable facts in life—dysentery, typhoid, typhus, to name a few more—became unacceptable in the developing world. But after all this success, after all we've done to prevent the spread of disease through water and insects, we seem to have overlooked something. We overlooked air.

This turned out to have devastating consequences for the beginning of the coronavirus pandemic. The original dogma, you might remember, was that the novel coronavirus spread like the flu, through droplets that quickly fell out of the air. We didn't need ventilation or masks; we needed to wash our hands and disinfect everything we touched. But a year and half of evidence has made clear that the tiny virus-laden particles indeed linger in the air of poorly ventilated areas. It explains why outdoors is safer than in, why a single infected person can super-spread to dozens of others without directly speaking to or touching them. If we are to live with this coronavirus forever—as seems very likely—some scientists are now pushing to reimagine building ventilation and clean up indoor air. We don't drink contaminated water. Why do we tolerate breathing contaminated air?

It's not just about COVID-19. The scientists who recognized the threat of airborne coronavirus early did so because they spent years studying evidence that—contrary to conventional wisdom—common respiratory illnesses such as the flu and colds can also spread through the air. We've long accepted colds and flus as inevitable facts of life, but are they? Why not redesign the airflow in our buildings to prevent them, too? What's more, says Raymond Tellier, a microbiologist at McGill University, SARS-CoV-2 is unlikely to be the last airborne pandemic. The same measures that protect us from common viruses might also protect us from the next unknown pathogen.

To understand why pathogens can spread through the air, it helps to understand just how much of it we breathe. "About eight to 10 liters a minute," says Catherine Noakes, who studies indoor air quality at the University of Leeds, in England. Think four or five big soda bottles per minute, multiply that by the number of people in a room, and you can see how we are constantly breathing in one another's lung secretions.

The particles emitted when people cough, talk, or breathe come in a range of sizes. We've all been unwittingly sprayed by large droplets

of saliva from the mouth of an overenthusiastic talker. But smaller particles called aerosols can also form when the vocal cords vibrate to air rushing out from the lungs. And the smallest aerosols come from deep inside the lungs. The process of breathing, says Lidia Morawska, an aerosol scientist at Queensland University of Technology, in Australia, is essentially a process of forcing air through the lungs' moist passages. She compares it to spraying a nebulizer or perfume bottle, in which liquid—lung secretions, in this case—becomes suspended in exhaled air.

Even before SARS-CoV-2, studies of respiratory viruses like the flu and RSV have noted the potential for spread through fine aerosols. The tiny liquid particles seem to carry the most virus, possibly because they come from deepest in the respiratory tract. They remain suspended longest in the air because of their size. And they can travel deeper into *other* people's lungs when breathed in; studies have found that a smaller amount of influenza virus is needed to infect people when inhaled as aerosols rather than sprayed up the nose as droplets. Real-world evidence stretching back decades also has suggested that influenza could spread through the air. In 1977, a single ill passenger transmitted the flu to 72 percent of the people on an Alaska Airlines flight. The plane had been grounded for three hours for repairs and the air-recirculation system had been turned off, so everyone was forced to breathe the same air.

In official public-health guidance, however, the possibility of flu-laden aerosols still barely gets a mention. The CDC and World Health Organization guidelines focus on large droplets that supposedly do not travel beyond six feet or one meter, respectively. (Never mind that scientists who actually study aerosols knew this six-foot rule violated the laws of physics.) The coronavirus should get us to take the airborne spread of flu and colds more seriously too, says Jonathan Samet, a pulmonary physician and epidemiologist at the Colorado School of Public Health. At the very least, it should spur research to establish the relative importance of different routes of transmission. "We had done such limited research before on airborne transmission of common infections," Samet told me. This just wasn't seen as a major problem until now.

At the University of Maryland, Donald Milton—one of the few longtime airborne-transmission researchers—is about to embark on a multiyear, controlled trial aimed at understanding influenza. Flu patients and healthy participants will share a room in this study. And they will take different precautions, such as hand-washing plus face shields or having good ventilation, which would presumably stop either droplet or aerosol transmission. The trial is meant to prove which intervention works the best, and thus which transmission route is dominant. When Milton had managed to get funding for a different aerosol study in the 2000s, he said a public-health official told him, "We're funding you to put the nail in the coffin of the idea that aerosols are important." Now, Milton says, "We'll find out which direction the nail is being driven here."

A virus that lingers in the air is an uncomfortable and inconvenient revelation. Scientists who had pushed the WHO to recognize airborne transmission of COVID-19 last year told me they were baffled by the resistance they encountered, but they could see why their ideas were unwelcome. In those early days when masks were scarce, admitting that a virus was airborne meant admitting that our antivirus measures were not very effective. "We want to feel we're in control. If something is transmitted through your contaminated hands touching your face, you control that," Noakes said. "But if something's transmitted through breathing the same air, that is very, very hard for an individual to manage."

The WHO took until July 2020 to acknowledge that the coronavirus could spread through aerosols in the air. Even now, Morawska says, many public-health guidelines are stuck in a pre-airborne world.

Where she lives in Australia, people are wearing face masks to walk down the street and then taking them off as soon as they sit down at restaurants, which are operating at full capacity. It's like some kind of medieval ritual, she says, with no regard for how the virus actually spreads. In the restaurants, "there's no ventilation," she adds, which she knows because she's the type of scientist who takes an air-quality meter to the restaurant.

Earlier this year, Morawska and dozens of her colleagues in the fields of building science, public health, and medicine published an editorial in *Science* calling for a "paradigm shift" around indoor air. Yes, vaccines and masks work against the coronavirus, but these scientists wanted to think bigger and more ambitious—beyond what any single person can do to protect themselves. If buildings are allowing respiratory viruses to spread by air, we should be able to redesign buildings to prevent that. We just have to reimagine how air flows through all the places we work, learn, play, and breathe.

The pandemic has already prompted, in some schools and workplaces, ad hoc fixes for indoor air: portable HEPA filters, disinfecting UV lights, and even just open windows. But these quick fixes amount to a "Band-Aid" in poorly designed or functioning buildings, says William Bahnfleth, an architectural engineer at Penn State University who is also a co-author of the *Science* editorial. (Tellier, Noakes, and Milton are authors too; the author list is a real who's who of the field.) Modern buildings have sophisticated ventilation systems to keep their temperatures comfortable and their smells pleasant—why not use these systems to keep indoor air free of viruses too?

Indeed, hospitals and laboratories already have HVAC systems designed to minimize the spread of pathogens. No one I spoke with thought an average school or office building has to be as tightly controlled as a biocontainment facility, but if not, then we need a new and different set of minimum standards. A rule of thumb, Noakes suggested, is at least four to six complete air changes an hour in a room, depending on its size and occupancy. But we also need more detailed studies to understand how specific ventilation levels and strategies will actually reduce disease transmission among people. This research can then guide new indoor air-quality standards from the American Society of Heating, Refrigerating and Air-Conditioning Engineers (ASHRAE), which are commonly the basis of local building codes. Changing the building codes, Bahnfleth said, is what will actually get buildings to change their ventilation systems.

The challenge ahead is cost. Piping more outdoor air into a building or adding air filters both require more energy and money to run the HVAC system. (Outdoor air needs to be cooled, heated, humidified, or dehumidified based on the system; adding filters is less energy intensive but it could still require more powerful fans to push the air through.) For decades, engineers have focused on making buildings more energy efficient, and it's "hard to find a lot of professionals who are really pushing indoor air quality," Bahnfleth said. He has been helping set COVID-19 ventilation guidelines as chair of the ASHRAE Epidemic Task Force. The pushback based on energy usage, he said, was immediate. In addition to energy costs, retrofitting existing buildings might require significant modifications. For example, if you add air filters but your fans aren't powerful enough, you're on the hook for replacing the fans too.

The question boils down to: How much disease are we willing to tolerate before we act? When London built its sewage system, its cholera outbreaks were killing thousands of people. What finally spurred Parliament to act was the stench coming off the River Thames during the Great Stink of 1858. At the time, Victorians believed that foul air caused disease, and this was an emergency. (They were wrong about exactly how cholera was spreading from

the river—it was through contaminated water—but they had ironically stumbled upon the right solution.)

COVID-19 does not kill as high a proportion of its victims as cholera did in the 19th century. But it has claimed well over 600,000 lives in the U.S. Even a typical flu season kills 12,000 to 61,000 people every year. Are *these* emergencies? If so, what would it take for us, collectively, to treat them as such? The pandemic has made clear that Americans do not agree on how far they are willing to go to suppress the coronavirus. If we can't get people to accept vaccines and wear masks in a pandemic, how do we get the money and the will to rehaul all our ventilation systems?

"The costs of that kind of large-scale infrastructure remodeling are astronomical, and the tendency is to look for other kinds of fixes," Nancy Tomes, a historian of medicine at Stony Brook University, said. It's also a problem distributed across millions of buildings, each with its own idiosyncrasies in layout and management. Schools, for example, have struggled to get the funds and make the ventilation upgrades in time for the school year.

In their *Science* editorial, Morawska and her co-authors wrote, "While the scale of the changes required is enormous, this is not beyond the capabilities of our society, as has been shown in relation to food and waterborne disease, which have largely been controlled and monitored." Morawska is optimistic, which perhaps you have to be to embark on this endeavor. The changes might take too long to matter for this current pandemic, but there are other viruses that spread through the air, and there *will be* more pandemics. "My whole drive is to do something for the future," she told me.

How much actually changes "depends on the momentum created now," she said. She pointed out that the vaccines looked like they were going to quickly end the pandemic—but then they didn't, as the Delta variant complicated things. The longer this pandemic drags on, the steeper the cost of taking indoor air for granted.

https://bit.ly/3z1fU1q

New Algorithm Can Identify Pre-Alzheimer's Brain Changes With Over 99% Accuracy

New system for detecting potential indicators of Alzheimer's has reached close to 100 percent accuracy.

David Nield

One of the most important ways in which artificial intelligence algorithms are proving beneficial is in diagnosing disease much faster than mere human beings can – and a new system for detecting potential indicators of Alzheimer's has reached close to 100 percent accuracy.

Through an analysis of fMRI brain scan images taken from 138 people, the new algorithm achieved an accuracy rate of over 99 percent. It performed better in terms of accuracy, sensitivity, and specificity than existing methods, the researchers report.

In particular, the method is able to pick out signs of mild cognitive impairment or MCI – which is the step between cognitive decline (as normally associated with aging) and Alzheimer's. Often, MCI won't come with any physical symptoms that can be spotted.

However, it's also important to note that MCI doesn't always necessarily mean Alzheimer's – but it's an important potential indicator of the disease in the future.

While manual analysis of MRI scans for signs of MCI is possible, humans are nowhere near as fast or reliable as deep learning techniques, which learn from vast databases of training data, then apply that knowledge to new data in intelligent ways.

"Modern signal processing allows delegating the image processing to the machine, which can complete it faster and accurately enough," says Rytis Maskeliūnas, an informatics professor from the Kaunas University of Technology (KTU) in Lithuania.

"Of course, we don't dare to suggest that a medical professional should ever rely on any algorithm 100 percent. Think of a machine

as a robot capable of doing the most tedious task of sorting the data and searching for features."

Once the computer software has highlighted potential cases, specialists can then review and confirm them. An earlier diagnosis means earlier treatment, even if we're yet to discover a way of stopping Alzheimer's completely.

The AI model outlined in this new study is based on the existing ResNet18 neural network. The modified system was able to split brain scans into six categories, from healthy to full manifestations of Alzheimer's disease.

"Although this was not the first attempt to diagnose the early onset of Alzheimer's from similar data, our main breakthrough is the accuracy of the algorithm," says Maskeliūnas. "Obviously, such high numbers are not indicators of true real-life performance, but we're working with medical institutions to get more data."

Various methods are used to detect Alzheimer's right now, including eye tracking, voice analysis, and even the installation of sensors in people's homes – but AI methods like the one outlined in this new study promise to be faster and simpler.

More than 78,000 fMRI scans were used to train and validate the model and hit the high accuracy rates, and the researchers say that their model could eventually be used to develop software that incorporates other data, including age and blood pressure.

Alzheimer's disease is the world's most frequent cause of dementia, contributing to some 70 percent of cases worldwide. Around 24 million people are currently thought to be affected globally, and as societies age, that figure is expected to rise sharply.

"Medical professionals all over the world attempt to raise awareness of an early Alzheimer's diagnosis, which provides the affected with a better chance of benefiting from treatment," says Maskeliūnas.

The research has been published in *Diagnostics*.

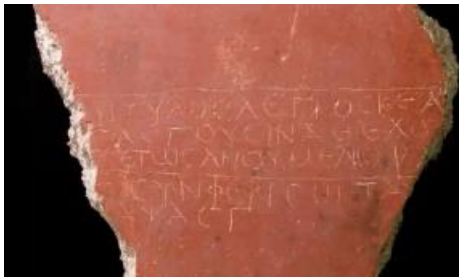
https://bit.ly/3E8NPJI

‘I don’t care’: text shows modern poetry began much earlier than believed

Academic finds that lines widely reproduced in the eastern Roman empire are ‘stressed’ in a way that laid the foundations for what we recognise as poetry

Alison Flood

For Taylor Swift, the “haters gonna hate”, but she’ll just “shake it off”. Now research by a Cambridge academic into a little-known ancient Greek text bearing much the same sentiment – “They say / What they like / Let them say it / I don’t care” – is set to cast a new light on the history of poetry and song.



The poem written in a graffito from Cartagena, Spain in the second to third century. **Photograph: José Miguel Noguera Celdrán**

The anonymous text, which concludes with the lines “Go on, love me / It does you good”, was popular across the eastern Roman empire in the second century, and has been found inscribed on 20 gemstones and as a graffito in Cartagena, Spain.

After comparing all known versions of the text for the first time, classics professor Tim Whitmarsh spotted that it used a different form of metre than usually found in ancient Greek poetry, employing stressed and unstressed syllables. Whitmarsh said that “stressed poetry”, the ancestor of all modern poetry and song, was unknown before the fifth century, when it began to be used in Byzantine Christian hymns. Before the emergence of stressed poetry, poetry was quantitative – based on syllable length.

“We’ve known for a long time that there was popular poetry in ancient Greek, but a lot of what survives takes a similar form to traditional high poetics. This poem, on the other hand, points to a

distinct and thriving culture, primarily oral, which fortunately for us in this case also found its way on to a number of gemstones," said Whitmarsh. "You didn't need specialist poets to create this kind of musicalised language, and the diction is very simple, so this was clearly a democratising form of literature. We're getting an exciting glimpse of a form of oral pop culture that lay under the surface of classical culture."

Whitmarsh believes the verse, with its lines of four syllables, with a strong accent on the first and a weaker on the third, could represent a "missing link" between the lost world of ancient Mediterranean oral poetry and song, and the more modern forms that we know today. It is, he says, so far unparalleled in the classical world.

"Poetry was so important; everyone read Homer and all that sort of thing. But we know that spoken language wasn't really appropriate to that kind of poetry, so at some point people come in with stressed poetry, which is the equivalent of modern poetry. That's the form we use all the time, and it's so natural to us now that it feels as if it's universal, but it's not – it actually occurred in Greek culture at a specific moment. This poem pushes back the earliest appearance of stressed poetry by at least 300 years," he said. "It has this sort of magnetic rhythm to it, four beats to the bar, a stress on the first beat, and weaker stress on the third beat, which is rock'n'roll and pop music as well."

The theme of the poem "also feels preternaturally modern", said Whitmarsh, comparing it to the Sex Pistols line: "We're pretty a-pretty vacant / And we don't care." The poem reads: "Λέγουσιν They say / ἃ θέλουσιν What they like / λεγέτωσαν Let them say it / οὐ μέλι μοι I don't care / σὺ φίλι με Go on, love me / συνφέρι σοι It does you good." "It's the idea of not caring – this strident assertion of your individuality in a world that's demanding things of you," Whitmarsh said.

The gemstones on which the poems were inscribed, the best preserved of which was found around the neck of a young woman buried in a sarcophagus in what is now Hungary, were mass-produced by workshops and distributed from Spain to Mesopotamia.

Whitmash, [whose paper on the text has just been published in the Cambridge Classical Journal], believes they were mostly bought by people from the middle ranks of Roman society.

The poem inscribed on a cameo on a medallion of glass paste found in a sarcophagus in what is now Hungary. **Photograph: Aquincum Museum**

"The closest modern equivalent is probably a quote T-shirt. When you have people across a huge empire eager to buy into things that connect them to centres of fashion and power, you have the conditions for a simple poem to go viral, and that's clearly what happened here," he said. "I think the poem appealed because it allowed people to escape local pigeon-holing, and claim participation in a network of sophisticates who 'got' this kind of playful, sexually charged discourse."

Whitmarsh came across the poem in a collection of inscriptions, digging into its history after a Cambridge colleague, Anna Lefteratou, a native Greek speaker, said it reminded her of some later medieval poetry.

"That prompted me to dig under the surface and once I did that these links to Byzantine poetry became increasingly clear. It was a lockdown project really. I wasn't doing the normal thing of flitting around having a million ideas in my head. I was stuck at home with a limited number of books and rereading obsessively until I realised this was something really special," he said. "The reason no one has thought about it as a poem before is because it's not catalogued alongside works of literature, it's catalogued as an inscription. We've got tens of thousands of inscriptions from antiquity, and I just think people weren't looking for it."

https://wb.md/3C0zHA

Men Prefer Telemedicine; Doctors Should Take Notice: Survey

29% of all men preferred virtual visits, and younger men were more comfortable with virtual visits than in-person visits

Aine Cryts

Twenty-six percent of men of color and 20% of White men said they visit their primary care physician less than once a year or never, according to a national survey from the Cleveland Clinic. Additionally, only 35% of Latino men and 31% of Asian men see their primary care physician more than once a year, according to the survey.

The survey included only male persons. Although the sample size was small — only 1000 persons — physicians say they are seeing the same trends at their practices.

The survey, which was as part of the Cleveland Clinic's annual MENtion It campaign, shows that virtual visits across the Cleveland Clinic's network increased from approximately 37,000 in 2019 to 1.2 million in 2020. Five key findings emerged from the survey:

**** Twenty-nine percent of all men preferred virtual visits, and younger men were more comfortable with virtual visits than in-person visits. Forty-one percent of millennials (persons aged 25 to 40 years), 36% of the Generation Z cohort (aged 18 to 24 years), and 32% of Generation Xers (aged 41 to 56 years) preferred a virtual visit. Only 9% of baby boomer men (aged 57 years of age and older) preferred virtual care.***

**** Forty-four percent of all men preferred to talk about sexual health problems with a physician online or by phone because they were "too embarrassed" to discuss them in person. Of Latino men, 56% reported feeling embarrassed about discussing sexual health problems during an in-person visit.***

**** Nineteen percent of millennial men visit their primary care physician "only when something is wrong."***

**** Older men are more comfortable than younger men when it comes to talking about health issues. For example, 61% of Gen Z, 70% of millennial, and 87% of baby boomer men are "very comfortable" discussing health risks. Regarding talking about sexual issues, 34% of Gen Z, 49% of millennial, and 59% of baby boomer men were "very comfortable."***

**** Younger men are accessing online health sites and online health visits with physicians. Twenty-eight percent of millennial men and 25% of Gen Z men have accessed online services such as Roman or Hims for a personal evaluation or to get a prescription filled; only 6% of baby boomer men use these online tools.***

Younger Men Often Seek "Transactional" Care

Andrew Carroll, MD, a family physician in Chandler, Arizona, said the survey's findings mirror what he sees in his practice. Although his older male patients understand the importance of having a primary care physician to ensure continuity of care, younger male patients are more likely to come in for "transactional" types of care, such as getting stitches or for treatment of a sinus infection.

When men of any age have an established relationship with a physician, they are not as embarrassed by questions regarding their sexual health, either in person or in a virtual setting, he said.

Carroll regards media coverage of actor Chadwick Boseman's death from colon cancer at the age of 43 as a factor in male patients being more inclined to talk about their health. "But again, we want men to know that having a relationship with a physician is good at any life stage," he said.

According to the American Cancer Society, Black patients are disproportionately affected by colorectal cancer. Compared to other ethnic groups, Blacks in the United States are 20% more likely to get colorectal cancer and are approximately 40% more likely to die as a result.

Increasing the Number of Physicians of Color Can Help

Telehealth is an option for many of Ogechika Alozie, MD's, patients. Many of the El Paso, Texas–based infectious disease specialist's patients are men with HIV. Their average age is 35. Approximately 35% of his patients prefer telehealth visits, he said.

The lack of physicians of color has an impact on patients and their ability to build a trusting relationship with healthcare practitioners, said Alozie. "I'm lucky to be Black, and I live in El Paso, so we're kind of the same shade...and I [treat] HIV, so they know we're talking about sex."

In 2019, approximately 1.2 million people in the United States had HIV, according to the US Department of Health and Human Services. That year, the highest rates of HIV infections were among Black persons (42%), followed by Latino persons, at nearly 22%, and people of multiple races, at 18%, according to the agency.

Alozie, who is also chair of the Texas Medical Association's committee on health information technology, advises physicians who are conducting telehealth visits to employ softer backgrounds that feature pictures. Other than the use of backgrounds, Alozie's advice for getting patients to open up during visits is the same for in-person visits:

**** Don't be in a hurry, especially during the first visit.***

**** Ask open-ended questions in which the patient talks and you listen.***

**** Define the visit up front. For example, "We're going to talk about X, Y, and Z. Is that okay? Tell me about X.' " This sets expectations as to what's going to be covered during the visit, he said.***

Alozie calls himself "a hugger." He also likes to shake his patient's hand or put a hand on their shoulder during in-person visits. "There's never going to be a replacement for the in-person visit. Telehealth is about giving our patients an option."

https://bit.ly/3lfo9T0

Combining sunlight and wastewater nitrate to make the world's number 2 chemical

Not only uses wastewater to make ammonia but does so 10 times as efficiently

Engineers at the University of Illinois Chicago have created a solar-powered electrochemical reaction that not only uses wastewater to make ammonia—the second most-produced chemical in the world—but also achieves a solar-to-fuel efficiency that is 10 times better than any other comparable technology.

Their findings are published in *Energy & Environmental Science*, a top journal for research at the intersection of energy delivery and environmental protections.

"This technology and our method have great potential for allowing on-demand synthesis of fertilizers and could have an immense impact on the agricultural and energy sectors in developed and developing countries, and on efforts to reduce greenhouse gases from fossil fuels," said lead researcher Meenesh Singh, assistant professor of chemical engineering at the UIC College of Engineering.

Ammonia, a combination of one nitrogen atom and three hydrogen atoms, is a key compound of fertilizers and many manufactured products, like plastics and pharmaceuticals. Current methods to make ammonia from nitrogen require enormous amounts of heat, generated by burning fossil fuels, to break the strong bonds between nitrogen atoms so they can bind to hydrogen. This century-old process produces a substantial fraction of global greenhouse gas emissions, which are a driving force of climate change.

Previously, Singh and his colleagues developed an environmentally friendly method to make ammonia by filtering pure nitrogen gas through an electrically charged, catalyst-covered mesh screen in a water-based solution. This reaction used only a tiny amount of

fossil fuel energy to electrify the screen, which breaks apart nitrogen atoms, but it produced more hydrogen gas (80%) than ammonia (20%).

Now, the researchers have improved this concept and developed a new method that uses nitrate, one of the most common groundwater contaminants, to supply nitrogen and sunlight to electrify the reaction. The system produces nearly 100% ammonia with nearly zero hydrogen gas side reactions. The reaction needs no fossil fuels and produces no carbon dioxide or other greenhouse gases, and its use of solar power yields an unprecedented solar-to-fuel efficiency, or STF, of 11%, which is 10 times better than any other state-of-the-art system to produce ammonia (about 1% STF).

The new method hinges on a cobalt catalyst, which the researchers describe along with the new process in their paper, "Solar-Driven Electrochemical Synthesis of Ammonia using Nitrate with 11% Solar-to-Fuel Efficiency at Ambient Conditions."

To identify the catalyst, the researchers first applied computational theory to predict which metal would work best. After identifying cobalt through these models, the team experimented with the metal, trying different ways to optimize its activity in the reaction. The researchers found that a rough cobalt surface derived from oxidation worked best to create a reaction that was selective, meaning it converted nearly all the nitrate molecules to ammonia.

"Finding an active, selective, and stable catalyst that worked in a solar-powered system is powerful proof that sustainable synthesis of ammonia at an industrial scale is possible," Singh said.

Not only is the reaction itself carbon-neutral, which is good for the environment, but if the system is developed for industrial use, it may also have an almost net-negative, restorative effect on the environment.

"Using wastewater nitrate means we also have to remove the contaminant from surface and groundwater. Over time, this means the process may simultaneously help correct for industrial waste and runoff water and rebalance the nitrogen cycle, particularly in rural areas which may experience economic disadvantages or bear the greatest risk from high exposure to excess nitrate," Singh said.

High exposure to nitrate through drinking water has been associated with health conditions like cancer, thyroid disease, preterm birth, and low birth weight.

"We are all very thrilled with this achievement, and we are not stopping here. We are hopeful that we will soon have a larger prototype with which we can test a much greater scale," said Singh, who is already collaborating with municipal corporations, wastewater treatment centers, and others in the industry on further developing the system. A patent for the new process has been filed by the UIC Office of Technology Management.

Co-authors of the paper are Nishithan Kani and Aditya Parajapati of UIC, Joseph Gauthier of Texas Tech University, Jane Edgington and Linsey Seitz of Northwestern University, Isha Bordawekar of Warren Township High School, Windom Shields and Mitchell Shields of Worldwide Liquid Sunshine, and Aayush Singh of Dow Inc.

More information: *Nishithan C. Kani et al, Solar-driven electrochemical synthesis of ammonia using nitrate with 11% solar-to-fuel efficiency at ambient conditions, Energy & Environmental Science (2021). DOI: 10.1039/D1EE01879E*

https://bit.ly/3tBihqE

Eating Peanuts May Lower Risk of Cardiovascular Disease and Stroke Among Asians

Asian men and women in Japan who ate peanuts had a lower risk of having an ischemic stroke or a CVD event

Asian men and women living in Japan who ate peanuts (on average 4-5 peanuts/day) had a lower risk of having an ischemic stroke or a cardiovascular disease event compared to those who did not eat peanuts, according to new research published today in *Stroke*, a journal of the American Stroke Association, a division of the American Heart Association.

While previous studies have linked peanut consumption with

improved cardiovascular health among Americans, researchers in this study specifically examined the link between peanut consumption and the incidence of different types of stroke (ischemic and hemorrhagic) and cardiovascular disease events (such as stroke and ischemic heart disease) among Japanese men and women. Eating peanuts may lower risk of ischemic stroke, cardiovascular disease among Asians.

**** Peanut consumption was linked with a lower risk of ischemic stroke and cardiovascular disease in a Japanese population study.***

**** Peanut consumption was not, however, linked to a lower risk of hemorrhagic stroke or ischemic heart disease.***

**** Incorporating even small amounts of peanuts (4-5 peanuts/day) into your diet may be protective for ischemic stroke and cardiovascular disease.***

"We showed for the first time a reduced risk for ischemic stroke incidence associated with higher peanut consumption in an Asian population," said lead study author Satoyo Ikehara, Ph.D., specially appointed associate professor of public health in the department of social medicine at the Osaka University Graduate School of Medicine in Suita, Japan. "Our results suggest that adding peanuts to your diet has a beneficial effect on the prevention of ischemic stroke."

Peanuts are rich in heart-healthy nutrients, such as "monounsaturated fatty acids, polyunsaturated fatty acids, minerals, vitamins and dietary fiber that help lower risk of cardiovascular disease by reducing risk factors, including high blood pressure, high blood levels of 'bad' cholesterol, and chronic inflammation," Ikehara said.

Researchers examined the frequency of how often people reported eating peanuts in relation to stroke occurrence and cardiovascular disease. The analysis includes people who were recruited in two phases, in 1995 and 1998-1999, for a total of more than 74,000 Asian men and women, ages 45 to 74, from the Japan Public Health Center-based Prospective Study. Participants completed a comprehensive lifestyle survey, which included a questionnaire about the frequency of peanut consumption. They were followed for approximately 15 years – through 2009 or 2012, depending on when they were originally enrolled. The incidence of stroke and ischemic heart disease were determined by linking with 78 participating hospitals in the areas included in the study.

Researchers adjusted for other health conditions, smoking, diet, alcohol consumption, and physical activity, as detailed by participants in the questionnaires. According to medical records, researchers noted 3,599 strokes (2,223 ischemic and 1,376 hemorrhagic) and 849 cases of ischemic heart disease developed during the follow-up period.

The levels of peanut consumption were ranked in four quartiles, with 0 peanuts a day as the least intake compared to 4.3 unshelled peanuts a day (median) as the highest. Compared to a peanut-free diet, researchers found eating about 4-5 unshelled peanuts per day was associated with:

**** 20% lower risk of ischemic stroke;***

**** 16% lower risk of total stroke; and***

**** 13% lower risk of having cardiovascular disease (this included both stroke and ischemic heart disease).***

**** A significant association was not found between peanut consumption and a lower risk of hemorrhagic stroke or ischemic heart disease.***

The link between peanut consumption and lowered risk of stroke and cardiovascular disease was consistent in both men and women.

"The beneficial effect of peanut consumption on risk of stroke, especially ischemic stroke was found, despite the small quantity of peanuts eaten by study participants," Ikehara said. "The habit of eating peanuts and tree nuts is still not common in Asian countries.

However, **adding even a small amount** to one's diet could be a simple yet effective approach to help reduce the risk of cardiovascular disease."

The American Heart Association recommends eating about five servings of unsalted nuts per week; one serving is ½ ounce (2 tablespoons) of nuts. Besides peanuts, the Association also says other healthy nut options include unsalted cashews, walnuts, pecans, macadamia nuts and hazelnuts.

Several limitations were noted in the study, including the validity and reliability of peanut consumption measurements in the data collection and analysis. Bias caused by these measurements may lead to errors in the association. However, a measurement error correction analysis was performed, and the associations proved to be accurate.

References:

"Peanut consumption and risk of stroke and ischemic heart disease in Japanese men and women: the JPHC study" 9 September 2021, Stroke.

DOI: 10.1161/STROKEAHA.120.031212 Co-authors are Hiroyasu Iso, M.D., Ph.D.; Yoshihiro Kokubo, M.D., Ph.D., FAHA; Kazumasa Yam

9 September 2021, Stroke. DOI: 10.1161/STROKEAHA.121.036172 Co-authors are Hiroyasu Iso, M.D., Ph.D.; Yoshihiro Kokubo, M.D., Ph.D., FAHA; Kazumasa Yamagishi, M.D., Ph.D.; Isao Saito, M.D., Ph.D.; Hiroshi Yatsuya, M.D., Ph.D.; Takashi Kimura, Ph.D.; Norie Sawada, M.D., Ph.D.; Motoki Iwasaki, M.D., Ph.D.; and Shoichiro Tsugane, M.D., Ph.D.

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https://wb.md/3npGUG3

Walking 7000 Steps per Day May Reduce Mortality Risk

For middle-aged individuals, walking at least 7,000 steps per day may reduce mortality risk up to 70%, based on prospective data from more than 2,000 people.

Will Pass

Findings were consistent regardless of race or sex, and step intensity had no impact on mortality risk, reported lead author Amanda E. Paluch, PhD, of the University of Massachusetts Amherst, and colleagues.

"In response to the need for empirical data on the associations of step volume and intensity with mortality in younger and diverse populations, we conducted a prospective study in middle-aged Black and White adults followed up for mortality for approximately 11 years," the investigators wrote in JAMA Network Open. "The objectives of our study were to examine the associations of step volume and intensity with mortality overall and by race and sex."

Steps per Day Is Easy to Communicate

Paluch noted that steps per day is a "very appealing metric to quantify activity," for both researchers and laypeople.

"Steps per day is simple and easy to communicate in public health and clinical settings," Paluch said in an interview. "Additionally, the dramatic growth of wearable devices measuring steps makes it appealing and broadens the reach of promoting physical activity to many individuals. Walking is an activity that most of the general population can pursue. It can also be accumulated throughout daily living and may seem more achievable to fit into busy lives than a structured exercise session."

The present investigation was conducted as part of the Coronary Artery Risk Development in Young Adults (CARDIA) Study. The dataset included 2,110 participants ranging from 38-50 years of age, with a mean age of 45.2 years. A slightly higher proportion of the subjects were women (57.1%) and White (57.9%).

All participants wore an ActiGraph 7164 accelerometer for 1 week and were then followed for death of any cause, with a mean follow-up of 10.8 years. Multivariable-adjusted Cox proportional hazards models included a range of covariates, such as smoking history, body weight, alcohol intake, blood pressure, total cholesterol, and others. Step counts were grouped into low (less than 7,000 steps per

day), moderate (7,000-9,999), and high (at least 10,000 steps per day) categories.

Compared with individuals who took less than 7,000 steps per day, those who took 7,000-9,000 steps per day had a 72% reduced risk of mortality (hazard ratio, 0.28; 95% confidence interval, 0.15-0.54).

Going beyond 10,000 steps appeared to add no benefit, based on a 55% lower risk of all-cause mortality in the highly active group, compared with those taking less than 7,000 steps per day (HR, 0.45; 95% CI, 0.25-0.81).

Walking faster didn't appear to help either, as stepping intensity was not associated with mortality risk; however, Paluch urged a cautious interpretation of this finding, calling it "inconclusive," and suggesting that more research is needed.

"It is also important to note that this study only looked at premature all-cause mortality, and therefore the results may be different for other health outcomes, such as the risk of cardiovascular disease, or diabetes, cancer, or mental health outcomes," Paluch said.

"The results from our study demonstrated that those who are least active have the most to gain," Paluch said. "Even small incremental increases in steps per day are associated with a lower mortality risk during middle age. A walking plan that gradually works up toward 7,000-10,000 steps per day in middle-aged adults may have health benefits and lower the risk of premature mortality."

Causality Cannot Be Confirmed

According to Raed A. Joundi, MD, DPhil, of the University of Calgary (Alta.), the study size, diverse population, and length of follow-up should increase confidence in the findings, although a causal relationship remains elusive.

"As this study is observational, causality between step count and mortality cannot be confirmed; however, the authors accounted for many factors, and the association was consistent in different analyses and with prior literature," Joundi said in an interview. "The authors did not assess the risk of other important events like stroke and heart attack, and these could be addressed in a future study."

Joundi, who recently published a study linking exercise with a 50% reduction in mortality after stroke, noted that "physical activity has innumerable benefits, and it's important that people engage in activity that can be regular and consistent, regardless of the type or intensity."

To this end, he highlighted the use of "devices capable of monitoring step count, which can be an important motivational tool," and suggested that these findings may bring a sigh of relief to step counters who come up a little short on a common daily goal.

"A target of 10,000 steps is often used for public health promotion, and this study now provides convincing observational evidence that it may be an optimal step count target for mortality reduction," Joundi said. "However, if 10,000 steps per day is not feasible, 7,000 steps seems to be a very reasonable target given its association with markedly lower mortality in this study."

Not All Step Counters Are Equal

Unfortunately, such recommendations are complicated by uncertainty in measurement, as widely used step counting devices, like smart watches, may not yield the same results as research-grade accelerometers, according to Nicole L. Spartano, PhD, of Boston University.

"Many comparison studies have been conducted in laboratory settings among young healthy adults, but these do not necessarily reflect real-life wear experiences that will be generalizable to the population as a whole," Spartano wrote in an accompanying editorial. She called for large-scale comparison studies to compare research-grade and consumer devices.

"The reason for conducting comparison studies is not to develop distinct guidelines for different devices or subgroups of the

population, but rather to understand the variability so that we can develop one clear message that is most appropriate to the public," Spartano wrote. "Some devices may have bias in terms of step measurement at different activity intensity and may not record steps as accurately in older adults or individuals with obesity or mobility disorders. For example, when adults who were obese wore an ActiGraph monitor in a laboratory setting, the device only recorded 80% of steps walked at a moderate pace, while other devices recorded close to 100% of steps walked. If we in the public health community are to move toward using these devices more for physical activity prescription, these details will need to be explored in more depth."

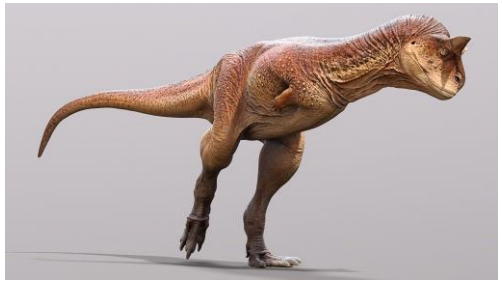
CARDIA was conducted and supported by the National Heart, Lung, and Blood Institute in collaboration with the University of Alabama at Birmingham, Northwestern University, the University of Minnesota, and the Kaiser Foundation Research Institute. Some study authors received grants from the National Institutes of Health and the Kaiser Foundation Research Institute. Spartano disclosed relationships with Novo Nordisk, the American Heart Association, the Alzheimer's Association, and the National Institutes of Health. Joundi and Paluch disclosed no relevant financial relationships.

https://bit.ly/2YQtY1C

Scientists reveal the fossilised skin of a bull-like carnivorous dinosaur

One of the strangest carnivorous dinosaurs ever discovered has been given a makeover by a pair of Belgian and Australian palaeontologists.

The remarkable fossil was discovered in 1984 by celebrated Argentine palaeontologist José Bonaparte who named the animal *Carnotaurus*, which translates as "carnivorous bull" in reference to its strange skull with large horns.



***Artist's reconstruction of Carnotaurus based on the scaly skin of described in the present study.* Credit: Jake Baardse**

The skeleton, which comes from Chubut Province of Patagonia, was preserved along with sheets of its scaly hide. Although scientists at the time knew other types of dinosaurs were scaly, *Carnotaurus* was the first meat-eating dinosaur discovered with skin.

Although a number of scientists had looked at the fossilized skin, no one had studied it in detail. Palaeontologist Dr. Christophe Hendrickx from the Unidad Ejecutora Lillo in San Miguel de Tucumán, who led the present study said, "by looking at the skin from the shoulders, belly and tail regions, we discovered that the skin of this dinosaur was more diverse than previously thought, consisting of large and randomly distributed conical studs surrounded by a network of small elongated, diamond-shaped or subcircular scales."

Hendrickx worked with Dr. Phil Bell, an expert in dinosaur skin, from the University of New England in Australia who pointed out the large studs and small scales of *Carnotaurus* is reminiscent of the thorny devil lizard found in Outback Australia.

Unlike more recent discoveries of feathered dinosaurs, particularly from China, the 8-meter-long *Carnotaurus* was entirely scaly, with no evidence of feathers. As an active predator, the scientists speculate the scales would have been important in regulating the animals body temperature, as they do in modern reptiles.

The study was published in the journal *Cretaceous Research*.

More information: *Christophe Hendrickx et al, The scaly skin of the abelisaurid Carnotaurus sastrei (Theropoda: Ceratosauria) from the Upper Cretaceous of Patagonia, Cretaceous Research (2021). DOI: 10.1016/j.cretres.2021.104994*

https://bit.ly/2Xk3pl1

Gout Medicine Could Also Battle COVID-19 – FDA Approved and Has Potent Antiviral Properties

Hope for a viable therapeutic to combat not only SARS-CoV-2 infection but also other common and deadly respiratory viruses

As COVID-19 cases continue to skyrocket across the U.S. and the world, few options are available for treating patients infected with the SARS-CoV-2.

But new research from the University of Georgia offers hope for a viable therapeutic to combat the disease that has claimed more than 4 million lives worldwide.

Published in Nature's *Scientific Reports*, the study found that probenecid has broad antiviral properties, making it a prime candidate to combat not only SARS-CoV-2 infection but also other common and deadly respiratory viruses like RSV and flu.

Probenecid is an FDA-approved medication that's primarily used to treat gout, and it's already widely available in the U.S. The drug has been on the market for over 40 years and has minimal side effects.

"There's really nothing out there to safely fight these viruses," said Ralph Tripp, lead author of the study and GRA Eminent Scholar of Vaccine and Therapeutic Studies in UGA's College of Veterinary Medicine. "This antiviral works for all RNA respiratory viruses we tested, including SARS-CoV-2. RSV, coronavirus and flu all circulate in the same season. Bottom line is you can potentially reduce infection and disease using this one oral drug."

Blocking viral reproduction

Viruses work by coopting a person's own cells to replicate and produce more of the virus. Probenecid blocks that replication process, keeping the virus from infecting the individual's cells.

In clinical development at the pharmaceutical company TrippBio, Tripp showed the drug works as a prophylactic prior to virus exposure and as a post-exposure treatment in animal models against SARS-CoV-2 and flu. The drug also has proven effective in fighting the RSV in vitro, and in vivo studies are in progress.

Although the drug would primarily be used after a person is positive for the virus, the prophylactic findings mean people with known exposures could also potentially take the drug to prevent getting sick.

COVID-19 treatment options limited

The current go-to treatments for seriously ill COVID-19 patients, remdesivir and monoclonal antibodies, can only be given through an IV. And by the time a COVID patient needs them, it's often too late.

"These treatments have seen some effectiveness against SARS-CoV-2, but they're very expensive and very hard to come by," Tripp said. "In reality, there are only a handful of options that can actually be used because of the cost, restricted IV usage, and lack of access. That's not very useful to the world."

Probenecid, on the other hand, is widely available. Primary care physicians could prescribe a pill to patients, and they could pick it up at their local drugstore.

Repurposing drugs that are already approved to work against one problem is common. For example, remdesivir was originally intended to fight Ebola virus, but when it showed some promise in fighting the coronavirus, it was enlisted to battle COVID-19.

In addition to preventing illness before it starts, probenecid may also potentially increase the efficacy of other treatments. Probenecid is already used to up the potency of some antibiotics, so it's possible the medication could work in conjunction with other COVID-19 treatments as well.

Now the researchers are investigating what dosage of probenecid could have the biggest impact fighting viruses in people. TrippBio is set to begin clinical trials of the medication within the year.

"SARS-CoV-2, RSV and flu have a huge impact on health systems throughout the world," Tripp said. "Probenecid has a potent antiviral effect against these viruses, and it works safely."

Probenecid is already FDA approved and has potent antiviral properties against SARS-CoV-2.

Reference: "Probenecid inhibits SARS-CoV-2 replication in vivo and in vitro" by Jackelyn Murray, Robert J. Hogan, David E. Martin, Kathy Blahunka, Fred D. Sancilio, Rajiv Balyan, Mark Lovern, Richard Still and Ralph A. Tripp, 10 September 2021, Scientific Reports. DOI: 10.1038/s41598-021-97658-w

https://bit.ly/3liPaF6

Mars rocks collected by Perseverance boost case for ancient life

NASA's Perseverance Mars rover has now collected two rock samples, with signs that they were in contact with water for a long period of time boosting the case for ancient life on the Red Planet.

"It looks like our first rocks reveal a potentially habitable sustained environment," said Ken Farley, project scientist for the mission, in a statement Friday. "It's a big deal that the water was there for a long time."

The six-wheeled robot collected its first sample, dubbed "Montdenier" on September 6, and its second, "Montagnac" from the same rock on September 8. Both samples, slightly wider than a pencil in diameter and about six centimeters long, are now stored in sealed tubes in the rover's interior.

A Martian rock dubbed "Rochette" that provided NASA's Perseverance rover its first two samples.

A first attempt at collecting a sample in early August failed after the rock proved too crumbly to withstand Perseverance's drill.

The rover has been operating in a region known as the Jezero Crater, just north of the equator and home to a lake 3.5 billion years ago, when conditions on Mars were much warmer and wetter than today.

The rock that provided the first samples was found to be basaltic in composition and likely the product of lava flows.

Volcanic rocks contain crystalline minerals that are helpful in radiometric dating.

This in turn could help scientists build up a picture of the area's geological history, such as when the crater formed, when the lake appeared and disappeared, and how climate changed over time.

"An interesting thing about these rocks as well is that they show signs for sustained interaction with groundwater," NASA geologist Katie Stack Morgan told a press conference.

The scientists already knew the crater was home to a lake, but couldn't rule out the possibility that it had been a "flash in the pan" with floodwaters filling up the crater for as little as 50 years. Now they are more certain groundwater was present for much longer.

"If these rocks experienced water for long periods of time, there may be habitable niches within these rocks that could have supported ancient microbial life," added Stack Morgan.

The salt minerals in the rock cores may have trapped tiny bubbles of ancient Martian water. "Salts are great minerals for preserving signs of ancient life here on Earth, and we expect the same may be true for rocks on Mars," added Stack Morgan.

NASA is hoping to return the samples to Earth for in depth lab analysis in a joint mission with the European Space Agency sometime in the 2030s.