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Early climate models successfully predicted global warming

Climate models published between 1970 and 2007 provided accurate forecasts of subsequently observed global surface warming. This finding shows the value of using global observations to vet climate models as the planet warms.

Jennifer E. Kay

Climate models are equations that describe climatically relevant processes and are solved on supercomputers. In addition to being invaluable tools for testing scientific hypotheses, these models have long provided societally important forecasts. The first climate models to numerically describe an evolving and interacting atmosphere, ocean and land surface on a grid covering the entire Earth date back to the 1970s (for example, refs 1–3). Since then, the planet's surface has warmed, in large part because of increased emissions of greenhouse gases. [Writing in *Geophysical Research Letters*](#), Hausfather *et al.*⁴ retrospectively assessed the forecasting skill of climate models published between 1970 and 2007. Their results show that the physics in these early models was accurate in predicting subsequently observed global surface warming.

A key point emphasized by the authors is that the forecasting ability of climate models is limited by unknowable future climate drivers. Many major drivers, such as increased concentrations of carbon dioxide in the atmosphere caused by the burning of fossil fuels, result from human activities and decisions. Early climate modellers included estimates for future climate drivers in their forecasts. However, they could not know, for example, how the world would industrialize or the associated emissions of CO₂ that would result.

Hausfather and colleagues developed a method for evaluating the forecasts of early climate models without penalizing the models for their inaccurate estimates of unknowable future climate drivers. The

authors examined 17 projections of global mean surface temperature (GMST) from 14 models. Before applying their method, they found that 10 projections were consistent with observations. But when inaccuracies in the estimates of climate drivers were taken into account, the authors discovered that 14 projections agreed with the data. Of the three that did not, two predicted higher-than-observed surface warming and one predicted lower-than-observed warming.

Developing credible climate models through an understanding of climatically relevant processes, observations and well-formulated equations is a considerable scientific and computational challenge.

The equations that describe climate are complex and require substantial computing power to solve. As a result, climate models have always been run on the fastest supercomputers available. It is especially impressive that the earliest models assessed by Hausfather *et al.* produced accurate GMST forecasts, given the extremely limited computing power available then compared with that used today (Fig. 1).



Figure 1 | A Univac 1108 computer, from 1972. Hausfather *et al.*⁴ demonstrate that climate models published over the past five decades accurately predicted subsequently observed changes in Earth's global mean surface temperature. These models include ones reported in the 1970s that used supercomputers, such as the Univac 1108, that had extremely limited power relative to those used today. CSU Archives/Everett Collection/Alamy

Although the authors' findings show that climate models can accurately predict GMST, these forecasts are insufficient for understanding and preparing for the effects of ongoing climate change. For instance, regional climate change is especially subject to unpredictable climate variability, which greatly limits forecasting potential — even on decadal timescales when the climate drivers

are known⁵. Moreover, on the basis of GMST forecasts alone, it is hard to predict, for example: to what extent sea level will rise; how ocean acidification caused by uptake of atmospheric CO₂ will influence marine ecosystems; and the frequency and magnitude of future fires, droughts and floods.

Scientists will have to continue to improve climate modelling and to increase their understanding of the effects of climate change, while keeping in mind the tension between the need for increased model resolution, greater representation of climatically relevant processes, and more simulations to characterize unpredictable climate variability. The successful forecasting of GMST by early climate models is impressive, but leaves much work to be done — as scientists, policymakers and stakeholders are all well aware.

Numerical models based on scientific equations describing the atmosphere are used daily to make decisions that save lives and money. As the climate continues to change owing largely to human activities, scientists need to use, improve and communicate the value of numerical models and the equations and knowledge that underlie them. Hausfather and colleagues' work demonstrates that the physics in climate models has been providing accurate forecasts of GMST under increasing amounts of atmospheric CO₂ for decades. Such predictions are useful for estimating the maximum amount of CO₂ that can be released into the atmosphere over time to keep surface warming to a specified level.

Crucially, the authors' results also show that a major source of uncertainty in GMST forecasts comes from climate drivers. And, of these drivers, it is emissions of greenhouse gases from human activity that will largely determine future surface warming. The findings indicate the usefulness of climate-model predictions of GMST in response to increasing greenhouse-gas emissions, despite unknowable future climate drivers. But scientists must also continue to develop climate models in concert with everything else

available to them, to plan for a changed climate that requires much more than forecasts of surface warming.

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<http://bit.ly/2tB6j5Y>

Showing how the tiniest particles in our universe saved us from complete annihilation

Evidence to prove the theory that life survived the Big Bang because a phase transition allowed neutrino particles to reshuffle matter and anti-matter

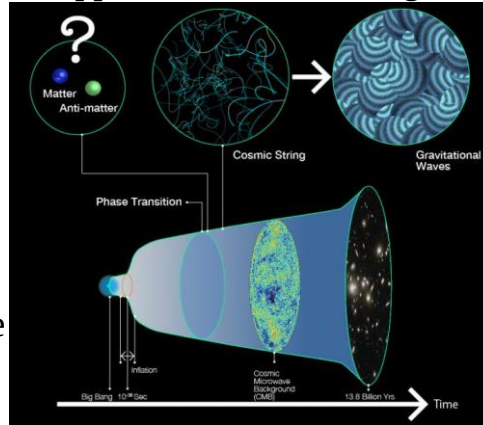
Recently discovered ripples of spacetime called gravitational waves could contain evidence to prove the theory that life survived the Big Bang because of a phase transition that allowed neutrino particles to reshuffle matter and anti-matter, explains a new study by an international team of researchers.

How we were saved from a complete annihilation is not a question in science fiction or a Hollywood movie. According to the Big Bang theory of modern cosmology, matter was created with an equal amount of anti-matter. If it had stayed that way, matter and anti-matter should have eventually met and annihilated one to one, leading up to a complete annihilation.

But our existence contradicts this theory. To overcome a complete annihilation, the Universe must have turned a small amount of anti-matter into matter creating an imbalance between them. The imbalance needed is only a part in a billion. But it has remained a complete mystery when and how the imbalance was created.

"The Universe becomes opaque to light once we look back to around a million years after its birth. This makes the fundamental question of 'why are we here?' difficult to answer," says paper co-author Jeff Dror, postdoctoral fellow at the University of California, Berkeley, and physics researcher at Lawrence Berkeley National Laboratory.

Since matter and anti-matter have the opposite electrical charges, they cannot turn into each other, unless they are electrical neutral. Neutrinos are the only electrical neutral matter particles we know, and they are the strongest contender to do this job. A theory many researchers support is that the Universe went through a phase transition so that neutrinos could reshuffle matter and anti-matter.



Inflation stretched the initial microscopic Universe to a macroscopic size and turned the cosmic energy into matter. However, it likely created an equal amount of matter and anti-matter predicting complete annihilation of our universe. The authors discuss the possibility that a phase transition after inflation led to a tiny imbalance between the amount of matter and anti-matter, so that some matter could survive a near-complete annihilation. Such a phase transition is likely to lead to a network of "rubber-band"-like objects called cosmic strings, that would produce ripples of space-time known as gravitational waves. These propagating waves can get through the hot and dense Universe and reach us today, 13.8 billion years after the phase transition. Such gravitational waves can most likely be discovered by current and future experiments. Credit Original credit: R. Hurt/Caltech-JPL, NASA, and ESA Credit: Kavli IPMU - Kavli IPMU modified this figure based on the image credited by R.Hurt/Caltech-JPL, NASA, and ESA

"A phase transition is like boiling water to vapor, or cooling water to ice. The behavior of matter changes at specific temperatures called critical temperature. When a certain metal is cooled to a low temperature, it loses electrical resistance completely by a phase transition, becoming a superconductor. It is the basis of Magnetic Resonance Imaging (MRI) for cancer diagnosis or maglev technology that floats a train so that it can run at 300 miles an hour without causing dizziness. Just like a superconductor, the phase transition in the early Universe may have created a very thin tube of

magnetic fields called cosmic strings," explains paper co-author Hitoshi Murayama, MacAdams Professor of Physics at the University of California, Berkeley, Principal Investigator at the Kavli Institute for the Physics and Mathematics of the Universe, University of Tokyo, and senior faculty scientist at Lawrence Berkeley National Laboratory.

Dror and Murayama are part of a team of researchers from Japan, US and Canada who believe the cosmic strings then try to simplify themselves, leading up to tiny wobbling of spacetime called gravitational waves. These could be detected by future space-borne observatories such as LISA, BBO (European Space Agency) or DECIGO (Japanese Astronautical Exploration Agency) for nearly all possible critical temperatures.

"The recent discovery of gravitational waves opens up a new opportunity to look back further to a time, as the Universe is transparent to gravity all the way back to the beginning. When the Universe might have been a trillion to a quadrillion times hotter than the hottest place in the Universe today, neutrinos are likely to have behaved in just the way we require to ensure our survival. We demonstrated that they probably also left behind a background of detectable gravitational ripples to let us know," says paper co-author Graham White, a postdoctoral fellow at TRIUMF.

"Cosmic strings used to be popular as a way of creating small variations in mass densities that eventually became stars and galaxies, but it died because recent data excluded this idea. Now with our work, the idea comes back for a different reason. This is exciting!" says Takashi Hiramatsu, a postdoctoral fellow at the Institute for Cosmic Ray Research, University of Tokyo, which runs Japan's gravitational wave detector KAGRA and Hyper-Kamiokande experiments.

"Gravitational wave from cosmic strings has a spectrum very different from astrophysical sources such as merger of black holes.

It is quite plausible that we will be completely convinced the source is indeed cosmic strings," says Kazunori Kohri, Associate Professor at the High Energy Accelerator Research Organization Theory Center in Japan. "It would be really exciting to learn why we exist at all," says Murayama. "This is the ultimate question in science."

The paper was published as an Editor's Suggestion in Physical Review Letters online on 28 January, 2020.

<http://bit.ly/2SnNpIk>

Natural herb kratom may have therapeutic effects and relatively low potential for abuse or harm, according to a user survey

Researchers say findings underscore need for research and regulation, but not an outright ban on sales

Using results of a survey of more than 2,700 self-reported users of the herbal supplement kratom, sold online and in smoke shops around the U.S., Johns Hopkins Medicine researchers conclude that the psychoactive compound somewhat similar to opioids likely has a lower rate of harm than prescription opioids for treating pain, anxiety, depression and addiction.

In a report on the findings, published in the Feb. 3 issue of *Drug and Alcohol Dependence*, the researchers caution that while self-reporting surveys aren't always entirely reliable, they confirmed that kratom is not regulated or approved by the U.S. Food and Drug Administration (FDA), and that scientific studies have not been done to formally establish safety and benefits. They say that U.S. drug agencies should seek to study and regulate rather than ban kratom sales outright because of its seemingly safe therapeutic potential, and as a possible alternative to opioid use.

The American Kratom Association (AKA), a consumer advocacy group, estimates that 5 million people in the U.S. regularly use kratom by either eating its ground leaves in food or brewing them in tea. Kratom is a tropical plant related to coffee trees, and grown

mainly in Southeast Asia. It contains a chemical called mitragynine, an alkaloid that acts on the brain opiate receptors and alters mood. In Asia, where use has long been widespread, people use it in small doses as an energy and mood booster, similar to coffee use in the West. They use larger amounts for pain, or recreationally like beer and wine.

Kratom products are unregulated and nonstandardized, and reports - although sparse - have linked its use to hallucinations, seizures and liver damage, when combined with alcohol or other drugs. In 2016, the U.S. Drug Enforcement Agency (DEA) proposed banning commercial sale and use, and the FDA has advised categorizing it as a Schedule I drug, meaning it has no proven medical application and has a high risk of abuse. These agencies were met with public and supplement industry pushback, and no action was taken. A salmonella contamination outbreak in 2018 among users increased concerns.

This is a [survey of adult kratom users](#) in the US. Credit: Johns Hopkins Medicine

However, says [Albert Garcia-Romeu, Ph.D.](#), instructor of psychiatry and behavioral sciences at the Johns Hopkins University School of Medicine, the new survey findings "suggest that kratom doesn't belong in the category of a Schedule I drug, because there seems to be relatively low rate of abuse potential, and there may be medical applications to explore, including as a possible treatment for pain and opioid use disorder."

"There has been a bit of fearmongering," he adds, "because kratom is opioidlike, and because of the toll of our current opioid epidemic."



A 2015 study in Thailand that reported that people in Asia have been using kratom successfully to treat opioid addiction for decades renewed interest among researchers in the U.S.

For the current survey, Garcia-Romeu says, he and his team enrolled 2,798 people to complete an online survey on their use of kratom. They recruited participants online and through social media, as well as through the AKA. Overall, users were mostly white, educated and middle-aged. Some 61% of users were women, and 90% were white. About 6% reported being multiracial, 1.5% reported being Native American or Hawaiian, 0.5% reported being Asian and 0.4% said they were African American. Participants were an average age of 40. About 84% of participants reported having at least some college education.

Of these participants, 91% reported taking kratom to alleviate pain on average a couple times a day for back, shoulder and knee pain, 67% for anxiety and 65% for depression. About 41% of survey responders said they took kratom to treat opioid withdrawal, and of those people who took it for opioid withdrawal, 35% reported going more than a year without taking prescription opioids or heroin.

As part of the survey, participants completed a Substance Use Disorder Symptom checklist to assess whether their use qualified as a substance use disorder according to the American Psychiatric Association Diagnostic and Statistical Manual of Mental Disorders, Fifth Edition guidelines. Fewer than 3% of responses met the criteria for moderate or severe substance use disorder for abusing kratom, but about 13% met some criteria for kratom-related substance use disorder. This is comparable to about 8%-12% of people prescribed opioid medications who became dependent, according to statistics from the U.S. National Institute for Drug Abuse (NIDA).

"Both prescription and illicit opioids carry the risk of lethal overdose as evidenced by the more than 47,000 opioid overdose

deaths in the U.S. in 2017," says Garcia-Romeu. "Notably there's been fewer than 100 kratom-related deaths reported in a comparable period, and most of these involved mixing with other drugs or in combination with preexisting health conditions."

A third of the survey participants reported having mild unpleasant side effects from kratom, such as constipation, upset stomach or lethargy, which mostly resolved within a day. Only 1.9% reported that side effects were severe enough for them to seek medical treatment, such as feeling withdrawal symptoms such as anxiety, irritability, depression or insomnia when the kratom wore off. Fewer than 10% of participants reported notable kratom-related withdrawal symptoms.

"Although our findings show kratom to be relatively safe according to these self-reports, unregulated medicinal supplements raise concerns with respect to contamination or higher doses of the active chemicals, which could increase negative side effects and harmful responses," says Garcia-Romeu. "This is why we advocate for the FDA to regulate kratom, which would require testing for impurities and maintaining safe levels of the active chemicals. Otherwise, unregulated products run the risk of unsafe additives and dosing problems, which could be like getting a shot of grain alcohol when you were trying to order a beer."

Garcia-Romeu adds that data is scant on whether one can overdose on kratom alone, or how it interacts with alcohol or other drugs. The researchers also say rigorous clinical research needs to be done to test kratom for its potential therapeutic benefits, for behavioral intoxication effects and adverse side effects to further help inform government policy and regulation. They also suggest that people err on the side of caution and not mix kratom with any other drugs or medications, and to always talk with their health care provider before taking any supplement.

Aside from Garcia-Romeu, authors on the study include David Cox, Kelly Dunn and Roland Griffiths of Johns Hopkins and Kirsten Smith of NIDA.

Support for this study was provided in part by grants from NIDA (R01DA003889 and R01DA035246). The authors don't have any conflicts to report.

<http://bit.ly/2OwYOEa>

Flickering light mobilizes brain chemistry that may fight Alzheimer's

For over a century, Alzheimer's disease has confounded all attempts to treat it. But in recent years, perplexing experiments using flickering light have shown promise.

Now, researchers have tapped into how the flicker may work. They discovered in the lab that the exposure to light pulsing at 40 hertz - 40 beats per second - causes brains to release a surge of signaling chemicals that may help fight the disease.

Though conducted on healthy mice, this new study is directly connected to human trials, in which Alzheimer's patients are exposed to 40 Hz light and sound. Insights gained in mice at the Georgia Institute of Technology are informing the human trials in collaboration with Emory University.

"I'll be running samples from mice in the lab, and around the same time, a colleague will be doing a strikingly similar analysis on patient fluid samples," said Kristie Garza, the study's first author. Garza is a graduate research assistant in the lab of Annabelle Singer at Georgia Tech and also a member of Emory's neuroscience program.

One of the surging signaling molecules, in particular, is associated with the activation of brain immune cells called microglia, which purge an Alzheimer's hallmark - amyloid beta plaque, junk protein that accumulates between brain cells.

Immune signaling

In 2016, researchers discovered that light flickering at 40 Hz mobilized microglia in mice afflicted with Alzheimer's to clean up that junk. The new study looked for brain chemistry that connects

the flicker with microglial and other immune activation in mice and exposed a surge of 20 cytokines - small proteins secreted externally by cells and which signal to other cells. Accompanying the cytokine release, internal cell chemistry - the activation of proteins by phosphate groups - left behind a strong calling card.

"The phosphoproteins showed up first. It looked as though they were leading, and our hypothesis is that they triggered the release of the cytokines," said Singer, who co-led the new study and is an assistant professor in the Wallace H. Coulter Department of Biomedical Engineering at Georgia Tech and Emory.

"Beyond cytokines that may be signaling to microglia, a number of factors that we identified have the potential to support neural health," said Levi Wood, who co-led the study with Singer and is an assistant professor in Georgia Tech's George W. Woodruff School of Mechanical Engineering.

The team [publishes its findings in the Journal of Neuroscience](#) on February 5, 2020. (There is no embargo. Pre-publication appeared in December but did not yet contain all edits and elements.) The research was funded by the National Institute of Neurological Disorders and Stroke at the National Institutes of Health, and by the Packard Foundation. Singer was co-first author on the original 2016 study at the Massachusetts Institute of Technology, in which the therapeutic effects of 40 Hz were first discovered in mice.

Sci-fi surrealness

Alzheimer's strikes, with few exceptions, late in life. It destroys up to 30% of a brain's mass, carving out ravines and depositing piles of amyloid plaque, which builds up outside of neurons. Inside neurons, phosphorylated tau protein forms similar junk known as neurofibrillary tangles suspected of destroying mental functions and neurons. After many decades of failed Alzheimer's drug trials costing billions, flickering light as a potentially successful Alzheimer's therapy seems surreal even to the researchers.

"Sometimes it does feel like science fiction," Singer said.

The 40 Hz frequency stems from the observation that brains of Alzheimer's patients suffer early on from a lack of what is called gamma, moments of gentle, constant brain waves acting like a dance beat for neuron activity. Its most common frequency is right around 40 Hz, and exposing mice to light flickering at that frequency restored gamma and also appears to have prevented heavy Alzheimer's brain damage.

Adding to the surrealness, gamma has also been associated with esoteric mind expansion practices, in which practitioners perform light and sound meditation. Then, in 2016, research connected gamma to working memory, a function key to train of thought.

Cytokine bonanza

In the current study, the surging cytokines hinted at a connection with microglial activity, and in particular, the cytokine Macrophage Colony-Stimulating Factor (M-CSF). "M-CSF was the thing that yelled, 'Microglia activation!'" Singer said.

The researchers will look for a causal connection to microglia activation in an upcoming study, but the overall surge of cytokines was a good sign in general, they said.

"The vast majority of cytokines went up, some anti-inflammatory and some inflammatory, and it was a transient response," Wood said. "Often, a transient inflammatory response can promote pathogen clearance; it can promote repair."

"Generally, you think of an inflammatory response as being bad if it's chronic, and this was rapid and then dropped off, so we think that was probably beneficial," Singer added.

Chemical timing

The 40 Hz stimulation did not need long to trigger the cytokine surge. "We found an increase in cytokines after an hour of stimulation," Garza said. "We saw phosphoprotein signals after about 15 minutes of flickering."

Perhaps about 15 minutes was enough to start processes inside of cells and about 45 more minutes were needed for the cells to secrete cytokines. It is too early to know.

20 Hz bombshell

As controls, the researchers applied three additional light stimuli, and to their astonishment, all three had some effect on cytokines. But stimulating with 20 Hz stole the show.

"At 20 Hz, cytokine levels were way down. That could be useful, too. There may be circumstances where you want to suppress cytokines," Singer said. "We're thinking different kinds of stimulation could potentially become a platform of tools in a variety of contexts like Parkinson's or schizophrenia. Many neurological disorders are associated with immune response."

The research team warns against people improvising light therapies on their own, since more data is needed to thoroughly establish effects on humans, and getting frequencies wrong could possibly even do damage.

Lu Zhang and Ben Borron from the Wallace H. Coulter Department of Biomedical Engineering at Georgia Tech and Emory University co-authored the study. The research was funded by the National Institute of Neurological Disorders and Stroke at the National Institutes of Health (grants NIH R01-NS109226 and R01-NS109226-01S1), by the Packard Foundation, the Friends and Alumni of Georgia Tech, and by the Lane family. Any findings, conclusions, and recommendations are those of the authors and not necessarily of the sponsors.

<http://bit.ly/2H4BEkJ>

Novel compound is promising drug candidate for Alzheimer's disease

New gamma secretase inhibitor blocks only amyloid production, no other functions

TROY, N.Y. -- A newly identified compound is a promising candidate for inhibiting the production of amyloids, the abnormal proteins that form toxic clumps, called fibrils, inside the brains of patients with Alzheimer's disease. As published today in the Royal Society

of Chemistry's *Chemical Communications*, the compound -- known as "C1" -- uses a novel mechanism to efficiently prevent the enzyme gamma-secretase from producing amyloids.

Amyloid fibrils are largely composed of the peptide Amyloid beta, which is produced when enzymes, including gamma secretase, make cuts to the amyloid precursor protein found in high concentrations the membrane of brain cells. C1 is a covalent gamma-secretase inhibitor that blocks the active site on the precursor protein where gamma-secretase would bind to transform it into amyloids, rather than - as traditional enzyme inhibitors do - blocking the active site on gamma-secretase itself.

"Historically, drug trials for gamma secretase inhibitors failed because traditional enzyme inhibitors have severe side effects. They stopped all of the normal functions of gamma secretase," said Chunyu Wang, a professor of biological sciences and member of the Center for Biotechnology and Interdisciplinary Studies (CBIS) at Rensselaer Polytechnic Institute. "Our compound binds to the cleavage site of the precursor protein instead of the enzyme itself, which may avoid many problems associated with traditional enzyme inhibitors."

In 2018, with support from the Warren Alpert Foundation, Wang began screening drugs to identify a compound that targets the amyloid precursor protein substrate, which would block the activity of gamma secretase involved in amyloid production while allowing all other functions. He began the search with "in silico screening," using computer modeling to test tens of millions of compounds.

C1 was one of several candidates to emerge from that screening. As described in the paper, C1 blocks amyloid production with high efficiency when present at micromolar concentrations, both in test tubes and in cell culture. The research is patent pending.

C1 is a covalent inhibitor, meaning it forms a chemical bond with its target. Wang said that because of their permanent bond, covalent

inhibitors are more durable than their non-covalent counterparts. Covalent inhibitors make up about one-third of the drug market, even though they have traditionally been viewed as having a higher risk of causing immune reactivity. In recent years, there is surge in the development of covalent inhibitors, as more highly specific covalent inhibitors showed excellent efficacy towards challenging drug targets.

"With a new approach to tackling the principal pathology of Alzheimer's disease, Chunyu's work is generating a fresh roster of drug candidates with enormous promise," said Deepak Vashishta, the director of CBIS. "His works speaks to the power of the interdisciplinary culture of research at CBIS, and we are pleased with this early result."

"Substrate Interaction Inhibits gamma-secretase Production of Amyloid-B peptides." At Rensselaer Wang was joined on the research by Jonathan Dordick, Jing Zhao, Yuanyuan Xiao, and Xinyue Liu, with additional collaborators from the Icahn School of Medicine at Mount Sinai, Memorial Sloan Kettering Cancer Center, Shandong University, and New York University.

<http://bit.ly/2H4apqw>

Genetic variants reduce risk of Alzheimer's disease

A DNA study of over 10,000 people by UCL scientists has identified a class of gene variants that appear to protect against Alzheimer's disease.

The findings, [published in *Annals of Human Genetics*](#), suggest these naturally occurring gene variants reduce the functioning of proteins called tyrosine phosphatases, which are known to impair the activity of a cell signalling pathway known as PI3K/Akt/GSK-3 β . This pathway is important for cell survival.

The research builds on previous studies in mice and rats, which suggested inhibiting the function of these proteins might be protective against Alzheimer's disease, but this is the first time such an effect has been demonstrated in people.

Researchers believe the PI3K/Akt/GSK-3 β signalling pathway could be a key target for therapeutic drugs and the findings also strengthen evidence that other genes could be linked to either elevated or reduced risk of Alzheimer's disease.

"These results are quite encouraging. It looks as though when naturally-occurring genetic variants reduce the activity of tyrosine phosphatases then this makes Alzheimer's disease less likely to develop, suggesting that drugs which have the same effect might also be protective," said the study's lead author, Professor David Curtis (UCL Genetics Institute).

In this study, scientists analysed DNA from 10,000 people: half with Alzheimer's disease and half without.

In total, researchers examined all DNA sequence variants in over 15,000 genes, including over one million individual variants, in order to identify genes in which damaging variants were more common in people with or without Alzheimer's disease.

Researchers found that Alzheimer's disease risk is lower in people with damaging variants in a particular class of genes, which code for tyrosine phosphatases. The researchers say the findings suggest that drugs which have the same effect might also be able to reduce the risk of Alzheimer's. Professor Curtis points out there are already some drugs which act on tyrosine phosphatases but they have not yet been tested in clinical trials.

"Here's a natural experiment in people that helps us understand how Alzheimer's disease develops: as some people have these genetic variants and some don't, we can see that the impact of having particular variants is a reduced likelihood of developing Alzheimer's disease," Professor Curtis added.

The researchers also found suggestive evidence that if there are genetic variants which damage the gene for the PI3K protein, then the risk of Alzheimer's increases.

"There is a consistent story in our results that the activity of the PI3K/Akt/GSK-3 β signalling pathway is protective, which is exactly in line with findings from animal studies," said Professor Curtis.

The study also found suggestive evidence to implicate a gene not previously known to affect Alzheimer's risk, called C1R. The gene is known to affect periodontal Ehlers-Danlos syndrome, a disease involving chronic gum inflammation. Some previous research suggests that gum infections may increase the risk of Alzheimer's disease, so Professor Curtis speculates there may be a mechanism whereby genetic variants in C1R lead to some degree of gum disease, which in turn predisposes to Alzheimer's disease.

This study builds on a major 2019 study involving UCL researchers that identified five new risk genes for Alzheimer's disease, adding to UCL's record of world-leading research in dementia and genetics. "Finding DNA variants which modify the risk of Alzheimer's disease is useful as it may help us develop drugs which target the same proteins. Simultaneously, researchers at UCL and across the globe are finding ways to detect the earliest stages of Alzheimer's disease, before it causes any problems. As our understanding improves, there may be opportunities to intervene with treatments to prevent the disease from progressing," Professor Curtis said.

Professor Curtis, honorary professor at the UCL Genetics Institute and at Queen Mary University London, conducted the study with a team of undergraduate students in the UCL Genetics Institute. The data was generated by an international collaboration, the Alzheimer's Disease Sequencing Project.

<http://bit.ly/2UAP4Nd>

U-M researchers identify unique neuron that computes like a compass

Part of the brain called the retrosplenial cortex, a key region involved in the organ's inner compass

ANN ARBOR--It's 5 p.m. as you leave the parking garage at work, but you realize you have no idea which way to turn to travel home. You know where you are and what street your house is on--it's just that you can't remember how to get there.

This is what happens to patients with damage to a part of their brain called the retrosplenial cortex, a key region involved in the organ's inner compass. Despite its importance for navigation, the neurons and circuits it uses to help get people from the office to home remain understudied.

By recording signals from individual neurons in the mouse brain, researchers at the University of Michigan have identified a distinct excitatory neuron in the retrosplenial cortex. The properties of this neuron are ideally suited to encode direction-related information over long durations, like a compass.

"Regular neurons in the cortex are good at encoding directional information only when you are moving your head, but what happens when your head is still? You still need to know what direction you are facing so that you can use this information to plan your route," said Omar Ahmed, assistant professor of psychology, neuroscience and biomedical engineering, and lead author of the study published in the journal *Cell Reports*.

"You ideally need another kind of neuron--a neuron that can continuously encode your orientation over long durations even when your head is not moving."

Typical excitatory neurons slow down their firing rather quickly. In contrast, the newly identified neurons can continue firing their signals at high rates for extended periods of time--they are persistent and fast.

A second difference lies in their capacity to respond to inputs--these unique neurons, called low rheobase neurons--are hyperexcitable, which means they need little input to be activated.

"A simpler name for this small yet tenacious little neuron, as suggested by my classmate, would be 'The Little Neuron That Could,'" said Ellen Brennan, the graduate student who identified these unique neurons. "It's the perfect name because it highlights the persistence that makes them optimally suited to code continued direction. In comparison, the other typical excitatory neurons here are slow and stubborn."

"So the question was, can these low rheobase neurons process directional information better than typical excitatory neurons?" said Shyam Sudhakar, a postdoctoral fellow in the Ahmed lab who created computer models of these neurons to show that the answer is "yes."

"It's important for my brain to know when I change direction, but it's not good if all my brain detects is change," Brennan said. "A compass always has to know which way is north. It wouldn't be useful without that persistent sense of direction. That is exactly what the low rheobase neurons can provide."

Ahmed's lab is now focused on understanding how these unique neurons are altered in Alzheimer's model mice.

"The retrosplenial cortex is critical for spatial orientation, but is one of the earliest brain regions to show dysfunctional activity in Alzheimer's patients," Ahmed said. "This is probably why the vast majority of Alzheimer's patients suffer from spatial disorientation and get lost easily--because their retrosplenial cells are not working as they should. "By understanding how retrosplenial cells encode compass-like information in healthy versus Alzheimer's brains, we hope to start working towards novel therapies."

Other study co-authors include Izabela Jedrasiak-Cape and Tibin John, both members of Ahmed's lab.

Study: [Hyperexcitable Neurons Enable Precise and Persistent Information Encoding in the Superficial Retrosplenial Cortex](#) [Omar Ahmed](#) Video: <https://youtu.be/Z1Sl49OMbfs>

<https://wb.md/2UvCK0D>

ACIP Releases 2020 Child and Adolescent Vaccine Schedule

Changes reflected in this year's child and adolescent vaccine schedule include guidance that a [hepatitis A](#) catch-up vaccination is now recommended for anyone who was not vaccinated as a child.

Marcia Frellick

The 2020 Childhood and Adolescent Immunization Schedules were [published online](#) today in *Pediatrics* and on the Centers for Disease Control and Prevention (CDC) website.

Sean O'Leary, MD, MPH, a member of the American Academy of Pediatrics (AAP) Committee on Infectious Diseases, told *Medscape Medical News* that, in the past, if a child presented at a doctor's office without any record of the hepatitis A vaccine as an infant, there was no recommendation to give the vaccine. Now that guidance is there.

The 2020 schedule was approved by the AAP, CDC's Advisory Committee on Immunization Practices (ACIP), the American Academy of Family Physicians, the American College of Obstetricians and Gynecologists, and the American College of Nurse-Midwives.

Which Oral Poliovaccine Doses Count

Information was also added regarding which doses of trivalent oral poliovaccine (OPV) count as valid. This pertains to children coming from countries that still use oral poliovirus vaccine.

Doses of OPV administered before April 1, 2016 should be counted (unless specifically noted as administered during a campaign). Doses of the oral vaccine given on or after April 1, 2016 should not be counted. Parts of the world where the oral vaccine was still in use switched on April 1, 2016 from trivalent to bivalent vaccine.

In the United States, the trivalent inactivated poliovirus vaccine is recommended for routine vaccination.

Clarification for Meningococcal B

A terminology change was made that mainly pertains to the [meningococcal serogroup B vaccines](#), O'Leary pointed out. Instead of deciding use of the vaccine by "clinical discretion," the recommendation is now for "shared clinical decision-making."

"Guidance is being developed for what that means," he said. "The idea is that the provider is supposed to have a conversation with the parent or patient about the pros and cons of getting the vaccine in a given situation."

Clarifications Regarding the DTaP Vaccine

Regarding the [diphtheria-tetanus-acellular pertussis \(DTaP\) vaccine](#), authors of the report clarified in the catch-up recommendation that the fifth dose is not necessary if the fourth dose was given when the child was at least 4 years old and it was given at least 6 months after the third dose.

New advice was also given on DTaP given inadvertently after the child's seventh birthday. That is not recommended because it tends to cause local reactions, O'Leary said. If DTaP was given from age 7 to 9 years, it may count in the catch-up series. Routine tetanus toxoid-reduced diphtheria toxoid-acellular pertussis adsorbed (Tdap vaccine) should then be given at age 11 to 12 years.

If it was given from ages 10 to 18 years, "count the dose of DTaP as the adolescent Tdap booster," the new guidance advises.

Tdap Clarification

The [Tdap vaccine](#) may now be used for booster doses and remaining doses of the catch-up series.

Authors also added guidance for Tdap given at age 7 to 10 years. Children aged 7 to 9 years who get the Tdap vaccine should get the routine Tdap dose at ages 11 to 12, but 10-year-olds do not need to get the routine Tdap dose at age 11 to 12 years.

"Prior guidance had made it look like if you got a dose at 10 years you still needed another at 11 to 12 years and now that's been made clear that you don't," O'Leary said. "A lot of states require Tdap upon entrance to 6th grade when a lot of kids are still only 10. Those kids sometimes would get a second dose of Tdap but that was not the official recommendation, and this clarified they don't need the additional dose."

Nothing has changed this year regarding the live attenuated influenza vaccine (LAIV), O'Leary noted. Both the AAP and ACIP recommended the mist last season as an alternative to inactivated influenza vaccine (IIV), with the same list of exceptions.

The vaccine schedules are revised every year to reflect current recommendations for using vaccines licensed by the US Food and Drug Administration.

The recommendation authors have disclosed no relevant financial relationships.

Pediatrics. Published online February 4, 2020. [Full text](#)

<http://bit.ly/39ql4KE>

Increased traffic injuries are a surprising result of restricting older drivers

Japanese research finds that cognitive tests to remove dangerous older drivers from the road lead to increased injuries as the ex-drivers become unprotected road users

Tsukuba, Japan - If older drivers with cognitive impairment are no longer permitted behind the wheel then accident rates should fall. That seems like common sense, but it seems the logic isn't so simple. Since 2009, when Japan added cognitive tests to its license renewal process for those aged 75+, traffic injuries have actually increased.

It turns out, when older drivers lose their licenses, they often have to resort to bicycling or walking to get around. They become what's known as unprotected road users. A new study by researchers centered at the University of Tsukuba in Japan found increased

traffic injuries among such older people, who lack the protection of a motor vehicle. The findings were [published in the journal Accident Analysis and Prevention](#).

Motor vehicle collisions are increasing among older drivers; this has triggered stricter licensing rules. Cognitive tests in Japan aim to identify drivers with possible dementia and require that they see a physician. Other countries such as Denmark and Canada have introduced similar tests. However, the overall success of such programs remains unclear.

"Some studies found increased injury rates as older drivers were forced into a modal shift from driving to walking or biking," study first author Professor Masao Ichikawa says. "We wanted to see if this was true in Japan, and we wanted a more accurate picture. Rather than just look at pre- and post-test numbers, we used interrupted time-series analysis, which offsets factors that may have confounded the results over the years."

Using reliable national data, they found significant increases in traffic deaths and injuries among unprotected road users aged 75 and up in the period after this same age group became subject to testing.

The increases generally occurred at a later age in men. The researchers suggested this may be because women are more anxious about their driving skills and give up their licenses earlier. The study did, however, find decreases in deaths and injuries for motor vehicle passengers aged 75-79 after cognitive tests began. This may owe to friends and family being more reluctant to ride with drivers after seeing their discouraging test results.

"Our findings suggest that Japan's licensing policies may not adequately consider the dangers facing those who become unprotected when they must start walking or biking after losing their license," Professor Ichikawa says.

The study implies a need to reconsider how cognitive testing is implemented. While the tests aim to remove potentially dangerous drivers from the roads, older people's loss of a main mode of transport may expose them to new risks.

<http://bit.ly/3brKZBd>

Solitary confinement significantly increases post-prison death risk

Even just a few days of solitary confinement may significantly increase inmates' risk of death after serving their sentences.

ITHACA, N.Y. - New research from Christopher Wildeman, professor of policy analysis and management at Cornell University, analyzed the Danish prison system and found that 4.5% of former inmates who had spent time in solitary confinement - most for less than a week - died within five years of being released. That was 60% more than those who were not placed in solitary.

"That's a significant increase in the risk of mortality," Wildeman said. "We think it's a pretty substantial effect."

This study tracked everyone - nearly 14,000 people - who began and ended sentences in Danish prisons or jails over a five-year period between 2006 and 2011.

Of the nearly 1,700 inmates who experienced solitary confinement, the average total stay was nearly nine days, but half spent fewer than five days and two-thirds less than a week.

Understanding the effect of such short exposures is important, Wildeman said, because they are often avoidable.

"For somebody who is in disciplinary segregation for 72 hours because of a specific infraction, there's almost always an alternative that a warden or guard could use that wouldn't involve putting someone in solitary," he said. Alternatives might include a fine, loss of privileges or short increase in sentence length.

The researchers had access to a wealth of data about the former inmates from Danish government registers - not only age, gender,

race, ethnicity and education levels, but also information about their family backgrounds, employment and housing histories and prior contacts with the criminal justice system.

That allowed the study to account for many factors that might have made someone more likely to end up in solitary confinement or to die after being released, while acknowledging some gaps in data concerning potential mental health or addiction issues.

Government registers also confirmed dates and causes of death within five years of release. The study determined that the higher death rates for those who had experienced solitary confinement - generally younger inmates serving longer sentences - was driven primarily by non-natural causes such as accidents, suicides and violence.

The finding that just a day or two in solitary confinement appears linked to a higher risk of death after release is somewhat surprising, Wildeman said. More research is needed to understand exactly what amount of exposure elevates mortality, he said.

The study was published in *The Lancet Public Health*.

<http://bit.ly/3bkDZWw>

Medical students become less empathic toward patients throughout medical school

A key factor of solid patient/doctor relationships is a notion of empathy that drives a feeling of shared humanity.

PHILADELPHIA, PA. - According to the [Mohammadreza Hojat](#), PhD, empathy in the context of patient care is "a cognitive attribute that involves an ability to understand the patient's pain, suffering, and perspective combined with a capability to communicate this understanding and an intention to help."

A newly released [national study](#) - led by Dr. Hojat of the Sidney Kimmel Medical College at Thomas Jefferson University raises some tough questions about the level of empathy amongst medical students, though.

The nationwide, multi-institutional cross-sectional study of students at DO-granting medical schools found that those students - like their peers in MD-granting medical schools - lose empathy as they progress through medical school. However, the DO (or osteopathic) students surveyed lost their empathy to a lesser degree than their MD (doctor of medicine) peers.

For the study, 10,751 students enrolled in 41 of 48 campuses of DO-granting medical schools in the United States completed a web-based survey at the end of the 2017-2018 academic year.

The survey included the Jefferson Scale of Empathy (JSE) and the Infrequency Scale of the [Zuckerman-Kuhlman Personality Questionnaire](#) for measuring "good impression" response bias. Researchers compared JSE empathy scores among students in different years of medical school, as well as with preexisting data from students of U.S. MD-granting medical schools.

What did they find? That empathy levels dropped when students progressed from the preclinical years (years one and two) into the clinical phase (years three and four) of medical school "when empathy is most needed."

"As students progress through medical school, you expect empathic engagement in patient care to improve. Apparently, that's not the case," said [Dr. Hojat](#), a Research Professor in the Department of Psychiatry and Human Behavior and Director of the [Jefferson Longitudinal Study](#) at the Center.

Dr. Hojat said the findings struck him as being emblematic of a field driven by an "over-emphasis on science of medicine, and ignoring the art of medicine." From here, he concluded, it's incumbent upon researchers to figure out what's behind the decline in empathy, while continuing to research the matter.

"It's an important responsibility of medical school to train knowledgeable, technically proficient doctors. They should train physicians who can establish better relationships with the patients,

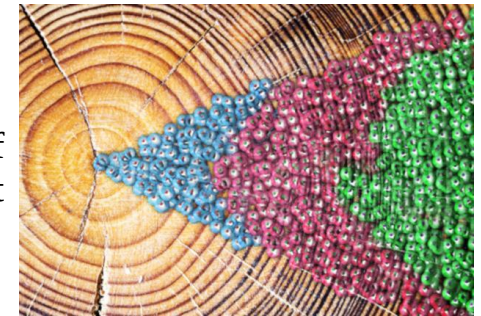
not only doctors who can pass an exam to get license and practice medicine," he said. "You can teach and enhance empathy, but the problem we noticed is that it's not enough, that you have to do additional things to sustain it."

Dr. Mohammadreza Hojat is available for interviews to discuss the findings of this study, potential causes and remedies for the dropoff in empathy levels as DO and MD students progress through medical school. Contact Brian Hickey at 215-951-2718 or brian.hickey@jefferson.edu to schedule an interview, or to get more information about this survey.

<http://bit.ly/2H51u8j>

Cancer mutations occur decades before diagnosis *Analysing the whole genomes of tumours from different cancer types to determine the chronology of genomic changes during cancer development*

Researchers at EMBL's European Bioinformatics Institute (EMBL-EBI) and the Francis Crick Institute have analysed the whole genomes of over 2600 tumours from 38 different cancer types to determine the chronology of genomic changes during cancer development.



Artist's interpretation of pinpointing the onset of cancer progression. Spencer Phillips/EMBL-EBI

Cancer occurs as part of a lifelong process in which our genome changes over time. As we age, our cells cannot maintain the integrity of the genome after cell division without making some errors (mutations). This process can be accelerated by various genetic predispositions and environmental factors, such as smoking. Over our lifetime these mutations build up and cells may be mis-programmed, leading to cancer.

The scientists [published their research in Nature](#) as part of an international collaboration of over 1300 scientists known as the

Pan-Cancer Analysis of Whole Genomes (PCAWG). The project aims to identify and catalogue the underlying patterns of mutation that give rise to many different cancer types. Access to this resource has significant implications for aiding the understanding of tumour progression, as well as opening up possibilities for early diagnosis and clinical intervention.

Calibrating cancer's molecular clock

"We can map out the point mutations arising throughout normal ageing to create a molecular clock for the human genome, akin to tracking the rings of a tree," says Moritz Gerstung, Group Leader at EMBL-EBI. "This provides us with a yardstick to estimate the age of some alterations seen in cancer, and to measure how far a tumour has progressed."

The researchers used data from the Pan-Cancer project and The Cancer Genome Atlas (ICGC) to create tumour development timelines for several cancer types including glioblastoma, and colorectal and ovarian adenocarcinoma. Their findings suggest that tumour development can span the entire lifetime of an individual, so the mutations that initiate cancer progression may arise decades before diagnosis.

"We've observed that changes in chromosome count within tumour cells typically occur late during tumour evolution. However, in some cases, such as in glioblastoma multiforme tumours, these changes can occur decades before diagnosis," says Stefan Dentro, Postdoctoral Fellow at EMBL-EBI. "Typically, cells don't survive for very long with an odd number of chromosomes, but somehow these cells do; possibly founding a tumour that is detected many years later."

Towards early cancer detection

"We've developed the first timelines of genetic mutations across the spectrum of cancer types," says Peter Van Loo, co-lead author and group leader in the Cancer Genomics Laboratory at the Francis

Crick Institute. "For more than 30 cancers, we now know what specific genetic changes are likely to happen, and when these are likely to take place. Unlocking these patterns means it should now be possible to develop new diagnostic tests that pick up signs of cancer much earlier."

Understanding the sequence and chronology of mutations leading to cancer may help clarify the mechanisms of cancer development, which otherwise appear convoluted due to the presence of many alterations in the final cancer cells.

Being able to determine whether a mutation typically occurs early or late during cancer progression may also help to guide early detection. This would make it possible to define the sets of alterations to screen for, to detect pre-cancerous cells at different stages of transformation.

"To a large extent, cancer development is an unfortunate consequence of the normal ageing of our cells," says Moritz Gerstung.

"Fully understanding the molecular progression of the disease is the first step towards identifying targets for early detection and perhaps treatment. The observation that many genetic alterations were already present years before the cancer was diagnosed provides a window of opportunity to detect aberrant cells before they become fully malignant."

The Pan-Cancer project

The Pan-Cancer Analysis of Whole Genomes project is a collaboration involving more than 1300 scientists and clinicians from 37 countries. It involved analysis of more than 2600 genomes of 38 different tumour types, creating a huge resource of primary cancer genomes. This was the starting point for 16 working groups to study multiple aspects of cancer development, causation, progression, and classification.

<http://bit.ly/378zU4x>

Giant, long-lived bacteria could make microbial farms more productive

Bacteria that have been genetically engineered to grow 13 times bigger and live 66% longer than their unmodified cousins could be the stars of future biochemicals factories.

By [Katrina Krämer](#)

Genetically engineered or traditionally bred microorganisms are already used to produce pharmaceuticals like human growth hormone or insulin. But they could also be made to produce more basic chemicals, like fuels and polymers, from renewable feedstocks.

A team of scientists led by [Liming Liu](#) from Jiangnan University in China has now created a strain of giant, long-lived *Escherichia coli*, boosting its ability to produce the biodegradable polymer poly(lactate-co-3-hydroxybutyrate) (PLH) and butyric acid.

E. coli reproduce around every half an hour by dividing symmetrically into two cells.

While this makes the organism essentially immortal, a cell can only stay alive for a set time without dividing. This is called the chronological lifespan. There's also a limit on how many daughter cells it can produce – its replicative lifespan.

Cells that consecutively inherit the oldest tip of the cell, the one opposite the division site, tend to grow slower and accumulate more damaged proteins.

The team increased *E. coli*'s chronological lifespan by 66% while shortening its replicative lifespan. This meant the cells grew to enormous sizes – 13 times larger than ordinary *E. coli* – producing 1.7 times more PLH and 2.6 times more butyric acid.

To achieve this, Liu and colleagues modified genes in *E. coli*'s respiratory chain and the stress response pathway, both of which can alter lifespan.

The former drives the synthesis of the energy-storage molecule [adenosine triphosphate](#) (ATP), but it can also produce cell-damaging superoxide.

The latter activates genes that generate proteins to help the cells cope with heat or cold, acids or starvation.

While this modification hasn't given *E. coli* enough of a boost to meet the demands of industrial production of biopolymers, Liu says that the study provides a proof of concept for the idea of lifespan engineering.

'Despite millions of years of evolution of *E. coli*, its lifespan is remarkably plastic, which is expected to facilitate advances in both metabolic engineering and synthetic biology,' he explains.

Bioengineer [Jixun Zhan](#) from Utah State University, US, believes this is the first time that scientists have modified microbial lifespan and size to increase biochemical production.

'Similar approaches might be applied to different products or different microorganisms,' he says.

But lifespan engineering could also have unintended consequences, says [Cheryl Kerfeld](#), who researches bacterial microcompartments at Lawrence Berkeley National Lab and Michigan State University, US.

While this might mean that engineered bacteria will need go through laboratory evolution to debug any problems, it's also 'a wonderful way to gain biological insight', she says.

'If they're able to build on this, we may even learn some really interesting things about longevity and the implications of lifespan engineering for organisms in general.'

Liu says that his team now plans to alter the lifespan of eukaryotes such as yeast.

References *L Guo et al, Nat. Catal., 2020, DOI: [10.1038/s41929-019-0411-7](https://doi.org/10.1038/s41929-019-0411-7)*

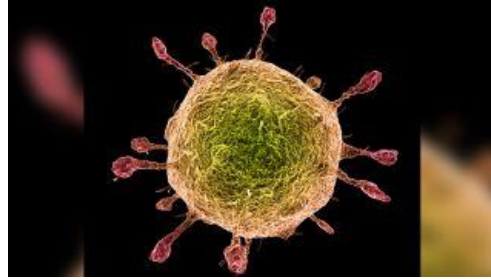
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How does the new coronavirus compare with the flu?

Which one is more worrisome?

By [Rachael Rettner - Senior Writer](#)

The [new coronavirus outbreak](#) has made headlines in recent weeks, but there's another viral epidemic hitting countries around the world: flu season. But how do these viruses compare, and which one is really more worrisome?



The coronavirus particle has a crown of spikes on its surface. (Image: © Alfred Pasiaka/Science Photo Library via Getty Images)

So far, the new coronavirus, dubbed 2019-nCoV, has led to more than 20,000 illnesses and 427 deaths in China, as well as more than 200 illnesses and two deaths outside of mainland China. But that's nothing compared with [the flu](#), also called influenza. In the U.S. alone, the flu has already caused an estimated 19 million illnesses, 180,000 hospitalizations and 10,000 deaths this season, according to the Centers for Disease Control and Prevention (CDC).

That said, scientists have studied seasonal flu for decades. So, despite the danger of it, we know a lot about flu [viruses](#) and what to expect each season. In contrast, very little is known about 2019-nCoV because it's so new. This means 2019-nCoV is something of a wild card in terms of how far it will spread and how many deaths it will cause.

"Despite the morbidity and mortality with influenza, there's a certainty ... of seasonal flu," Dr. Anthony Fauci, director of the National Institute of Allergy and Infectious Diseases, said in a [White House press conference](#) on Jan. 31. "I can tell you all, guaranteed, that as we get into March and April, the flu cases are going to go down. You could predict pretty accurately what the

range of the mortality is and the hospitalizations [will be]," Fauci said. "The issue now with [2019-nCoV] is that there's a lot of unknowns." Scientists are racing to find out more about 2019-nCoV, and our understanding of the virus and the threat it poses may change as new information becomes available. Based on what we know so far, here's how it compares with the flu.

Symptoms and severity

Both seasonal flu viruses (which include influenza A and influenza B viruses) and 2019-nCoV are contagious viruses that cause respiratory illness.

Typical [flu symptoms](#) include fever, cough, sore throat, muscle aches, headaches, runny or stuffy nose, fatigue and, sometimes, vomiting and diarrhea, [according to the CDC](#). Flu symptoms often come on suddenly. Most people who get the flu will recover in less than two weeks. But in some people, the flu causes complications, including [pneumonia](#). So far this flu season, about 1% of people in the United States have developed symptoms severe enough to be hospitalized, which is similar to the rate last season, according to [data from the CDC](#).

With 2019-nCoV, doctors are still trying to understand the full picture of disease symptoms and severity. In a recent study of about 100 people with the virus, published Jan. 30 in the journal [The Lancet](#), the most common symptoms were fever, cough and shortness of breath. Only about 5% of patients in that study reported sore throat and runny nose, and only 1-2% reported [diarrhea](#), nausea and vomiting. Of the more than 20,000 cases reported in China so far, about 14% have been classified as severe, according to [data from the World Health Organization \(WHO\)](#) posted Tuesday (Feb. 4).

It's important to note that, because respiratory viruses cause similar symptoms, it can be difficult to distinguish different respiratory viruses based on symptoms alone, [according to WHO](#).

Death rate

So far this flu season, about 0.05% of people who caught the flu have died from the virus in the U.S., according to CDC data.

The death rate for 2019-nCoV is still unclear, but it appears to be higher than that of the flu. Throughout the outbreak, the death rate for 2019-nCoV has been about 2%. Still, officials note that in the beginning of an outbreak, the initial cases that are identified "skew to the severe," which may make the mortality rate seem higher than it is, Alex Azar, U.S. secretary of the Health and Human Services, said during a news briefing on Jan. 28. The mortality rate may drop as more mild cases are identified, Azar said.

Virus transmission

The measure scientists use to determine how easily a virus spreads is known as the "basic reproduction number," or R0 (pronounced R-nought). This is an estimate of the average number of people who catch the virus from a single infected person, [Live science previously reported](#). The flu has an R0 value of about 1.3, [according to The New York Times](#).

Researchers are still working to determine the R0 for 2019-nCoV. A study published Jan. 29 in the [New England Journal of Medicine](#) (NEJM) estimated an R0 value for the new coronavirus to be 2.2, meaning each infected person has been spreading the virus to an average of 2.2 people.

It's important to note that R0 is not necessarily a constant number. Estimates can vary by location, depending on such factors as how often people come into contact with each other and the efforts taken to reduce viral spread, [Live Science previously reported](#).

Risk of infection

The [CDC estimates](#) that, on average, about 8% of the U.S. population gets sick with the flu each season.

There are currently only 11 cases of 2019-nCoV in the U.S. Still, newly emerged viruses like 2019-nCoV are always of public health

concern, according to the CDC. It's unclear how the situation with this virus in the U.S. will unfold, the agency said. Some people, such as health care workers, are at increased risk for exposure to 2019-nCoV. But for the general American public, the immediate health risk from the virus is low at this time.

Pandemics

It's important to note that seasonal flu, which causes outbreaks every year, should not be confused with [pandemic flu](#), or a global outbreak of a new flu virus that is very different from the strains that typically circulate. This happened in 2009 with the swine flu pandemic, which is estimated to have killed between 151,000 and 575,000 people worldwide, [according to the CDC](#). There is no flu pandemic happening currently.

The 2019-nCoV outbreak has not yet been declared a pandemic, as the majority of cases have occurred in China. But on Jan. 30, the WHO declared the 2019-nCoV outbreak a ["public health emergency of international concern."](#) The declaration was primarily due to concern that the virus could spread to countries with weaker health systems.

Prevention

Unlike seasonal flu, for which there is a [vaccine](#) to protect against infection, there is no vaccine for 2019-nCoV. But researchers at the U.S. National Institutes of Health are in the early stages of developing one. Officials plan to launch a phase 1 clinical trial of a potential vaccine for 2019-nCoV within the next three months.

In general, the CDC recommends the following to prevent the spread of respiratory viruses, which include both coronaviruses and flu viruses: Wash your hands often with soap and water for at least 20 seconds; avoid touching your eyes, nose and mouth with unwashed hands; avoid close contact with people who are sick; stay home when you are sick; and clean and disinfect frequently touched objects and surfaces.

<https://wb.md/2uvIxIX>

Novel Coronavirus: Case Review IDs Clinical Characteristics

A group of physicians in Wuhan, China, who are treating patients with the 2019 novel coronavirus have gone the extra mile to share their clinical experiences with colleagues around the world.

Sharon Worcester

FROM THE LANCET

Nanshan Chen, MD, of Jinyintan Hospital, Wuhan, and his team conducted a retrospective study on 99 cases and, in very short order, published their initial findings in the [Lancet](#) online on Jan. 29. These findings could guide action in other cases and help clinicians all over the world create treatment plans for patients of the 2019-nCoV.

The findings show that older men and patients with comorbidities appear most likely to develop pneumonia associated with the 2019 novel coronavirus (2019-nCoV), and characteristics of those with fatal infections align with the MuLBSTA score — an early warning model for predicting viral pneumonia-related mortality, according to a case review.

Of 99 patients who presented with 2019-nCoV pneumonia at Jinyintan Hospital between Jan. 1 and Jan. 20, 67 were men, the mean age was 55.5 years, and 50 patients had chronic diseases.

"All the data of included cases have been shared with [the World Health Organization]. The study was approved by Jinyintan Hospital Ethics Committee and written informed consent was obtained from patients involved before enrollment when data were collected retrospectively," the researchers noted.

Nearly half of the patients (49%) lived or worked near a specific seafood market, suggesting disease clustering.

Clinical manifestations affecting the majority of patients included fever and cough in 83% and 82% of patients, respectively. Other

symptoms included shortness of breath in 31%, muscle aches in 11%, confusion in 9%, [headache](#) in 8%, sore throat in 5%, and rhinorrhea, chest pain, [diarrhea](#), and nausea and vomiting in 1%-4% of patients, the investigators found.

Imaging showed bilateral pneumonia in 75% of cases, multiple mottling and ground-glass opacity in 14%, and pneumothorax in 1%. Organ function damage was present in a third of patients at admission: 17% had [acute respiratory distress syndrome](#) (ARDS) — including 11 patients who worsened quickly and died of [multiple organ failure](#). Eight percent had acute respiratory injury, 3% had acute renal injury, 4% had [septic shock](#), and 1% had [ventilator-associated pneumonia](#), they said, noting that all cases were confirmed by real-time polymerase chain reaction.

A notable laboratory finding was reduced absolute lymphocyte counts in most patients, the investigators said.

All patients were treated in isolation and 76% received antiviral treatment with [oseltamivir](#), [ganciclovir](#), lopinavir, or [ritonavir](#) for 3-14 days (median, 3 days). Most patients also received antibiotic treatment, including a single antibiotic in 25% of cases and combination therapy in 45%, with most antibiotics used to cover "common pathogens and some atypical pathogens," they said, adding that "when secondary bacterial infection occurred, medication was administered according to the results of bacterial culture and drug sensitivity."

Cephalosporins, quinolones, carbapenems, [tigecycline](#) against methicillin-resistant *Staphylococcus aureus*, [linezolid](#), and antifungal drugs were used, and duration ranged from 3 to 17 days (median, 5 days).

Nineteen patients also received steroid treatments.

As of Jan. 25, 31 patients had been discharged and 57 remained hospitalized. Of the 11 who died, the first 2 were a 61-year-old man and a 69-year-old man, each diagnosed with severe pneumonia and

ARDS. The first experienced sudden cardiac arrest and died on admission day 11, and the second died of severe pneumonia, septic shock, and respiratory failure on admission day 9. Neither had underlying disease, but both had a long history of smoking, the investigators noted.

"The deaths of these two patients were consistent with the [MuLBSTA score](#)," they wrote, explaining that the scoring system takes into account multilobular infiltration, lymphopenia, bacterial coinfection, smoking history, [hypertension](#), and age.

Eight of the nine other patients who died had lymphopenia, seven had bilateral pneumonia, five were over age 60 years, three had hypertension, and one was a heavy smoker, they added.

Most coronavirus infections cause mild symptoms and have good prognosis, but some patients with the 2019-nCoV, which was identified Jan. 7 following the development of several cases of pneumonia of unknown etiology in Wuhan, develop fatal disease. The paucity of data regarding epidemiology and clinical features of pneumonia associated with 2019-nCoV prompted the current retrospective study at the center where the first cases were admitted, the investigators explained.

They noted that the sequence of 2019-nCoV "is relatively different from the six other coronavirus subtypes, including the highly pathogenic [severe acute respiratory syndrome](#) (SARS)-CoV and Middle East Respiratory Syndrome (MERS)-CoV, as well as the human coronaviruses (HCoV)-OC43, -229E, -NL63, and -HKU1 that induce mild upper respiratory disease, but can be classified as a betacoronavirus with evidence of human-to-human transmission.

Mortality associated with SARS-CoV and MERS-CoV have been reported as more than 10% and more than 35%, respectively; at data cutoff for the current study, mortality among the 99 included cases was 11%, which is similar to that in another recent 2019-nCoV [report](#), they said.

The finding of greater risk among older men also has been seen with SARS-CoV and MERS-CoV, and the high rate among individuals with chronic diseases, mainly cerebrovascular disease, cardiovascular disease, and diabetes, also has been reported with MERS-CoV, they added.

"Our results suggest that 2019-nCoV is more likely to infect older adult males with chronic comorbidities as a result of the weaker immune functions of these patients," they wrote.

Coinfection with bacteria and fungi occurred in some patients, particularly those with severe illness, and cultures most often showed *A. baumannii*, *K. pneumoniae*, *A. flavus*, *C. glabrata*, and *C. albicans*, and the findings of reduced absolute lymphocyte values in most patients suggests that "2019-nCoV might mainly act on lymphocytes, especially T lymphocytes, as does SARS-CoV," they noted.

Given the rapid progression with ARDS and septic shock in some patients in this review, "early identification and timely treatment of critical cases is of crucial importance," they said.

"Use of [intravenous immunoglobulin](#) is recommended to enhance the ability of anti-infection for severely ill patients, and steroids (methylprednisolone 1-2 mg/kg per day) are recommended for patients with ARDS, for as short a duration of treatment as possible," they added.

Further, since some studies suggest that a substantial decrease in lymphocyte count indicates consumption of many immune cells by coronavirus, thereby inhibiting cellular immune function, damage to T lymphocytes might be "an important factor leading to exacerbations of patients," they wrote, adding that "[t]he low absolute value of lymphocytes could be used as a reference index in the diagnosis of new coronavirus infections in the clinic."

The MuLBSTA score also should be investigated to determine its applicability for predicting mortality risk in patients with 2019-nCoV infection, they added.

The current study is limited by its small sample size; additional studies are needed to include "as many patients as possible in Wuhan, in other cities in China, and even in other countries to get a more comprehensive understanding of 2019-nCoV," they said.

The National Key R&D Program of China funded the study. The authors reported having no conflicts of interest.

SOURCE: Chen N et al. Lancet. 2020 Jan 29. doi: 10.1016/S0140-6736(20)30211-7. This story originally appeared on MDedge.com.

<https://go.nature.com/2OGExMC>

The mammals that most freely share dangerous microbes with humans

Scientists identify two primate species as hosts of a high number of pathogens that can jump to Homo sapiens.

The mammals that are most likely to pass diseases to humans are those that easily share their bacteria and viruses across species boundaries.

Disease-causing microbes that have jumped from animals to humans include Ebola virus and the coronavirus behind the 2020 epidemic in China. Maya Wardeh at the University of Liverpool, UK, and her colleagues collected information on 1,560 mammalian species, including their geographical ranges, their interactions with humans and their pathogens. Using machine-learning software, the researchers organized the animals into a network that revealed how the species share 3,986 pathogens with one another.



A model projects that the rhesus macaque, which lives across Asia, harbours a large array of microbes that could infect people. Credit: Magnus

Lundgren/Wild Wonders of China/NPL

Mammals that share pathogens with many other species are more likely to serve as reservoirs for human diseases, the researchers found. Among the species predicted to harbour the highest number of potential human pathogens are chimpanzees (*Pan troglodytes*), rhesus macaques (*Macaca mulatta*) and red foxes (*Vulpes vulpes*). The researchers say that the findings could help to identify how bacteria, viruses and other infectious agents jump to humans.

[Proc. R. Soc. B \(2020\)](http://Proc.R.Soc.B(2020))

<http://bit.ly/2umCE0X>

Static electricity as strong as lightning can be saved in a battery

Can we collect static electricity for use? The answer is yes.

Static electricity shock which occurs more often in winter is unpleasant. When two different objects are in repeated contact, it causes friction which then creates static electricity.

This can be found easily in our everyday actions and it is very annoying even between the lovers. In fact, there is no electric current flowing in static electricity but tens of thousands of volts occurs, equal to the power of lightning. Then, can we collect static electricity for use? The answer is yes.

Prof. Dong Sung Kim and his PhD candidate student, Donghyeon Yoo from POSTECH Mechanical Engineering Department and Prof. Jae-Yoon Sim and his PhD student Seoulmin Lee from POSTECH Department of Electronic and Electrical Engineering jointly with the research teams of Prof. Woonbong Hwang of POSTECH and Dongwhi Choi of Kyung Hee University developed a new technology to increase the total amount of energy generated by a 'triboelectric nanogenerator' which [can convert static electricity into power](#). In the meantime, they also succeeded in developing an integrated circuit that makes this energy into practical electric energy.

Energy harvesting is a technology that harvests and converts energies, which occur in everyday life such as human actions, light, heat, vibration of an object and electromagnetic wave and disappear quickly, into usable energies. Among many of the energy harvesting technologies, a triboelectric nanogenerator is a device that obtains static electricity, which can be found when two different materials are in contact and detached.

So far, there have been many studies on triboelectric nanogenerator, however, it has been difficult to commercialize because of its limitations such as small quantity of energy converted from harvested static electricity and that power is only generated when there is friction.

The joint research team fabricated the nano surface structure by using nanoimprinting process to intensify friction under same contact and separate condition. They also used poling process to produce more static electricity under the same given frictional condition due to ease of electron transfer between two objects.

Nanoimprinting process is a method that forms nano surface structures in thermoplastic polymer by stacking nano molds with the polymer films, and then heating under a certain pressure. Poling process is a method that rearranges molecular structures orderly by changing directions of dipoles of the materials in contact and by applying high voltage.

In the meantime, the joint research team successfully invented an integrated circuit that converted temporary and unstable electric energy generated by a triboelectric nanogenerator into reliable power source. They demonstrated that even when 2.5 μW of energy was input, the conversion efficiency recorded over 70%. It was the first time the team verified that stable power of 1.8V was obtained without external power supply when this newly developed integrated circuit was used. This amount of power was enough to

operate sensors of thermo and humidity meters, a calculator and more.

This research was the first demonstration of a triboelectric nanogenerator fabricated by nanoimprinting process using heat and pressure and poling process simultaneously. By using these newly introduced triboelectric nanogenerator and integrated circuit, it is possible to increase the total amount of electric energy produced by obtained static electricity and to convert it into reliable energy. It is expected that this technology can be a reference for future development of a self-powered system which operates sensors without external power source.

Prof. Dong Sung Kim said, "The conventional triboelectric nanogenerators faced challenges in obtaining reliable electric power because it used an auxiliary power source to operate commercial integrated circuit or to operate itself independently. However, our findings can overcome these limitations by converting static electricity into reliable power which can be used instantly. It is also meaningful in a way this research was conducted jointly with colleagues from various fields of academic discipline."

The research was supported by Agency of Defense Development and National Research Foundation of Korea. The research paper was recently posted on the website of Nano Energy, one of the prestigious journals in physics and chemistry.

<http://bit.ly/2w2Unec>

Sugar ants' preference for pee may reduce greenhouse gas emissions

An unlikely penchant for pee is putting a common sugar ant on the map, as new research from the University of South Australia shows their taste for urine could play a role in reducing greenhouse gases.

Led by wildlife ecologist Associate Professor Topa Petit, the Kangaroo Island-based research found that sugar ants prefer urine over sugar - the food source after which they're named - nocturnally

foraging on it to extract nitrogen molecules, some of which could end up in the greenhouse gas, nitrous oxide.

The Australian-first study compared the behaviours of sugar ants (*Camponotus terebrans*) as they were exposed to different concentrations of urine (human and kangaroo ~ 2.5 per cent urea), sugar water (20 per cent and 40 per cent), and urea in water (at 2.5 per cent; 3.5 per cent; 7 per cent and 10 per cent), finding that sugar ants were most attracted to higher concentrations of urea, mining them for long periods within a dry sand substrate.

While other ants are known to be attracted to urine, this is the first time that ants have been observed mining dry urine from sand, and for a long period of time.

Assoc Prof Petit says [the curious discovery could play a role in nitrogen cycling](#).



Sugar ants mining urine in sand on Kangaroo Island UniSA / Sophie Petit

"When I first noticed the ants swarming to scavenge urine, it was purely by accident. But under research conditions we found that the ants determinedly mined urea patches night after night with greater numbers of ants drawn to higher urea concentrations," Assoc Prof Petit says. "Camponotus terebrans are undoubtedly looking for urea in urine because, similar to certain other ant species, a bacterium in their digestive tract allows them to process urea to get nitrogen for protein.

"This remarkable ability to extract urea from dry sand not only shows how sugar ants can survive in arid conditions, but also, how they might reduce the release of ammonia from urine, which leads to the production of nitrous oxide, a highly active greenhouse gas." Nitrous oxide (NO₂) is a greenhouse gas 300 times more potent than carbon dioxide. And while less abundant than carbon dioxide emissions, its presence in the atmosphere has increased

substantially over the past decade, accelerated mostly by the widespread use of fertilisers.

Assoc Prof Petit says that while there is still a lot to learn about the foraging behaviours of sugar ants, the study shows a symbiotic relationship between ants and vertebrates such as kangaroos in dry environments, and evidence of the nitrogen cycle at work.

"The ability of sugar ants to thrive in dry, sandy environments and use sources of nitrogen that may not be available to other species is impressive. It may give them a competitive advantage by allowing them to feed more offspring and therefore increase their numbers," Assoc Prof Petit says.

"Researchers working on ants as bio-indicators on grazed and ungrazed lands should take ants' ability to process urea into account, because large amounts of urine will probably affect the assortment of ant species in the area. It would also be interesting to investigate how much ants may modify the urine ammonia volatilises from paddocks.

"This is not the last we will hear about these sugar ants - they could open up a whole new field of research."

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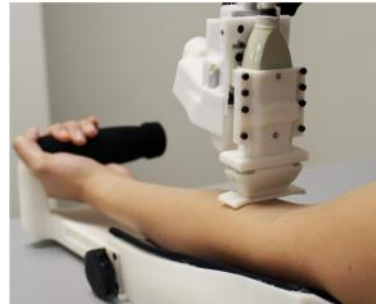
New robot does superior job sampling blood ***First clinical trial of an automated blood drawing and testing device***

In the future, robots could take blood samples, benefiting patients and healthcare workers alike.

A Rutgers-led team has created a blood-sampling robot that performed as well or better than people, according to the first human clinical trial of an automated blood drawing and testing device. The device provides quick results and would allow healthcare professionals to spend more time treating patients in hospitals and other settings.

The results, [published in the journal *Technology*](#), were comparable to or exceeded clinical standards, with an overall success rate of 87% for the 31 participants whose blood was drawn. For the 25 people whose veins were easy to access, the success rate was 97%.

The device includes an ultrasound image-guided robot that draws blood from veins. A fully integrated device, which includes a module that handles samples and a centrifuge-based blood analyzer, could be used at bedsides and in ambulances, emergency rooms, clinics, doctors' offices and hospitals.



This is a prototype of an automated blood drawing and testing device. Unnati Chauhan

Venipuncture, which involves inserting a needle into a vein to get a blood sample or perform IV therapy, is the world's most common clinical procedure, with more than 1.4 billion performed yearly in the United States. But clinicians fail in 27% of patients without visible veins, 40% of patients without palpable veins and 60% of emaciated patients, according to previous studies.

Repeated failures to start an IV line boost the likelihood of phlebitis, thrombosis and infections, and may require targeting large veins in the body or arteries - at much greater cost and risk. As a result, venipuncture is among the leading causes of injury to patients and clinicians. Moreover, a hard time accessing veins can increase procedure time by up to an hour, requires more staff and costs more than \$4 billion a year in the United States, according to estimates.

"A device like ours could help clinicians get blood samples quickly, safely and reliably, preventing unnecessary complications and pain in patients from multiple needle insertion attempts," said lead author [Josh Leipheimer](#), a biomedical engineering doctoral student

in the Yarmush lab in the [biomedical engineering department](#) in the [School of Engineering](#) at [Rutgers University-New Brunswick](#).

In the future, the device could be used in such procedures as IV catheterization, central venous access, dialysis and placing arterial lines. Next steps include refining the device to improve success rates in patients with difficult veins to access. Data from this study will be used to enhance artificial intelligence in the robot to improve its performance.

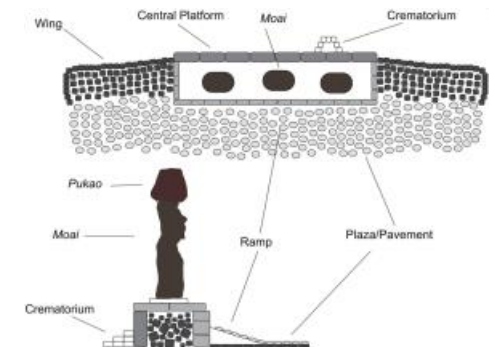
Rutgers co-authors include Max L. Balter and Alvin I. Chen, who both graduated with doctorates; [Enrique J. Pantin](#) at Rutgers Robert Wood Johnson Medical School; [Professor Kristen S. Labazzo](#); and principal investigator [Martin L. Yarmush](#), the Paul and Mary Monroe Endowed Chair and Distinguished Professor in the [Department of Biomedical Engineering](#). A researcher at Icahn School of Medicine at Mount Sinai Hospital also contributed to the study.

<http://bit.ly/2Sf4uFv>

Easter Island society did not collapse prior to European contact, new research shows

Rapa Nui society thrived, continued to build moai statues, despite impact of European arrival

BINGHAMTON, N.Y. - [Easter Island society did not collapse prior to European](#) contact and its people continued to build its iconic moai statues for much longer than previously believed, according to a team of researchers including faculty at Binghamton University, State University of New York.



Schematic of a typical platform ahu showing a plan view (top) and cross-section (bottom). Figure adapted from Martinsson-Wallin (1994) and Skjølsvold (1994). *Journal of Archaeological Science*

The island of Rapa Nui is well-known for its elaborate ritual architecture, particularly its numerous statues (moai) and the monumental platforms that supported them (ahu). A widely-held

narrative posits that construction of these monuments ceased sometime around 1600, following a major societal collapse.

"Our research flies in the face of this narrative," said Carl Lipo, an anthropologist at Binghamton University. "We know, of course, that if we are right, we really need to challenge ourselves (and the archaeological record) to validate our arguments. In this case, we thought to look carefully at the tempo of construction events associated with large platforms."

The researchers, led by the University of Oregon's Robert J. DiNapoli, examined radiocarbon dates, relative architectural stratigraphy and ethnohistoric accounts to quantify the onset, rate and end of monument construction as a means of testing the collapse hypothesis.

"Archaeologists assign ages to the archaeological record by getting what are known as radiocarbon dates," said Lipo. "These dates represent the amount of time since some organisms (a bush, tree, etc.) died. Assembling groups of these dates together to look at patterns requires some sophisticated statistical analyses that have only recently been available to archaeologists. In this paper, we use these tools to provide the first-ever look at the history of platform construction on Easter Island." The researchers found that construction of these statues began soon after colonization and increased rapidly, sometime between the early-14th and mid-15th centuries, with a steady rate of construction events that continued beyond European contact in 1722.

"What we found is that once people started to build monuments shortly after arrival to the island, they continued this construction well into the period after Europeans arrived," said Lipo. "This would not have been the case had there been some pre-contact 'collapse'-- indeed, we should have seen all construction stop well before 1722. The lack of such a pattern supports our claims and

directly falsifies those who continue to support the 'collapse' account.

"Once Europeans arrive on the island, there are many documented tragic events due to disease, murder, slave raiding and other conflicts," he added. "These events are entirely extrinsic to the islanders and have, undoubtedly, devastating effects. Yet, the Rapa Nui people -- following practices that provided them great stability and success over hundreds of years -- continued their traditions in the face of tremendous odds. The degree to which their cultural heritage was passed on - and is still present today through language, arts and cultural practices -- is quite notable and impressive. I think this degree of resilience has been overlooked due to the "collapse" narrative, and deserves recognition."

The researchers believe that their model-based approach to test hypotheses regarding the chronology of collapse can be extended to other case studies around the world where similar debates remain difficult to resolve.

Also contributing to this research were Timothy M. Rieth (International Archaeological Research Institute) and Terry Hunt (University of Arizona).

The paper, "A model-based approach to the tempo of collapse: The case of Rapa Nui (Easter Island)," was [published in the Journal of Archaeological Science](http://bit.ly/2OGZDKV).

<http://bit.ly/2OGZDKV>

Portable lab you plug into your phone can diagnose illnesses like coronavirus

Smartphone lab delivers test results in 'spit' second

Engineers with the University of Cincinnati have created a tiny portable lab that plugs into your phone, connecting it automatically to a doctor's office through a custom app UC developed.

The lab the size of a credit card can diagnose infectious diseases such as coronavirus, malaria, HIV or Lyme disease or countless other health conditions like depression and anxiety.

The patient simply puts a single-use plastic lab chip into his or her mouth then plugs that into a slot in the box to test the saliva.

The device automatically transmits results to the patient's doctor through a custom app UC created for nearly instant results.

UC professor Chong Ahn and his research team used the smartphone device to test for malaria. But the device could be used for smart point of care testing for countless chronic or infectious diseases or to measure hormones related to stress.

"Right now it takes several hours or even days to diagnose in a lab, even when people are showing symptoms. The disease can spread," Ahn said.



University of Cincinnati professor Chong Ahn developed a portable lab that plugs into your smartphone to diagnose diseases like malaria or coronavirus.

The results are transmitted to your doctor over a custom app UC developed.

Joseph Fuqua II/UC Creative Services

The study was [published in the Nature journal Microsystems & Nanoengineering](#).

His research team created a novel lab chip that uses natural capillary action, the tendency for a liquid to adhere to a surface, to draw a sample down two channels called a "microchannel capillary flow assay." One channel mixes the sample with freeze-dried detection antibodies. The other contains a freeze-dried luminescent material to read the results when the split samples combine again on three sensors.

Ahn said the device is accurate, simple to use and inexpensive.

"The performance is comparable to laboratory tests. The cost is cheaper. And it's user-friendly," Ahn said. "We wanted to make it simple so anyone could use it without training or support."

UC doctoral student Sthitodhi Ghosh, the study's lead author, said the biggest advancement in the device is in the novel design of its tiny channels that naturally draw the sample through the sensor

arrays using capillary flow. Ahn is Ghosh's Ph.D. advisor. "The entire test takes place on the chip automatically. You don't have to do anything. This is the future of personal healthcare," Ghosh said. While the device has applications for diagnosing or monitoring viruses or other diseases, Ahn said he sees potential in the field of mental health, where doctors already utilize smartphones to help track the wellness of patients.

<http://bit.ly/2H5GZbh>

What can a primate tell us about cat allergies?

Its venom points to a feline defence mechanism, research suggests.

By Amelia Nichele

The toxin from the world's only venomous primate appears to have given researchers an unexpected insight into the origins of cat allergies.



The slow loris knows what cats are up to. The University of Queensland. An international team led by the University of Queensland, Australia, made the link after studying the venom of the [slow loris](#) (genus *Nycticebus*) from Indonesia, which induces an allergy-like reaction in humans.

"We analysed the DNA sequence of the protein in slow loris venom, discovering that it's virtually identical to the allergenic protein on cats," says lead researcher Bryan Fry. "Cats secrete and coat themselves with this protein, and that's what you react to if you're allergic to them."

Generally, slow lorises only use their venom to fight other slow lorises. When humans are bitten, Fry says, they display similar symptoms to that of an allergic shock. That led him and his colleagues to suggest that when people are "allergic" to cats they are in fact responding to a defence mechanism.

"Our theory is that since this protein is being used as a defensive weapon in slow lorises, it makes sense that cats may be using the

allergen as a defensive weapon too,” he says. “Your pet cat wouldn’t know it, but it may have evolved a toxic defence to keep predators as far away from it as possible.”

That raises more questions, however.

“Similarly, this line of research opens up other fascinating research areas, such as the allergies to ants and bees also being something that has been selected for by evolution – where the victim’s immune system is being hijacked,” says Fry.

“This study is a great example of what makes science so wonderful, where every answer spawns several new and interesting questions”.

The [research](#) is published in the journal *Toxins*.

<https://go.nature.com/39sos5r>

Did pangolins spread the China coronavirus to people?

Genetic sequences of viruses isolated from the scaly animals are 99% similar to that of the circulating virus — but the work is yet to be formally published.

[David Cyranoski](#)

Researchers in Guangzhou, China, have suggested that pangolins

— long-snouted, ant-eating mammals often used in traditional Chinese medicine — are the probable animal source of the coronavirus outbreak that has [infected more than 30,000 people and is wreaking havoc worldwide](#).



Pangolins are scaly creatures often used in traditional Chinese medicine.

Frans Lanting/National Geographic

Scientists say that the suggestion, based on a genetic analysis, seems plausible — but caution that the researchers’ work is yet to be published in full. “This is an extremely interesting observation. Although we need to see more details, it does make sense as there are now some other data emerging that pangolins carry viruses that

are closely related to 2019-nCoV,” says Edward Holmes, an evolutionary virologist at the University of Sydney, Australia.

The identity of the animal source of the coronavirus, named nCoV-2019, has been one of the [key questions that researchers have been racing to answer](#). Coronaviruses are known to circulate in mammals and birds, and scientists have already suggested that nCoV-2019 originally came from bats, a proposal based on the similarity of its genetic sequence to those of other known coronaviruses. But the virus was probably transmitted to humans by another animal. The coronavirus that caused severe acute respiratory syndrome, or SARS, [spread from bats to civet cats to humans](#).

Now, the South China Agricultural University in Guangzhou [says](#) that two of its researchers, Shen Yongyi and Xiao Lihua, have identified the pangolin as the potential source of nCoV-2019 on the basis of a genetic comparison of coronaviruses taken from the animals and from humans infected in the outbreak and other findings. The sequences are 99% similar, the researchers reported at press conference on 7 February.

A good candidate

Previously, researchers have noted that coronaviruses are a possible cause of death in pangolins¹, and that nCoV-2019 and coronaviruses from pangolins use receptors with similar molecular structures to infect cells.

Even before today’s announcement, pangolins were a good candidate for being an intermediate species for the virus, so it’s very interesting that the researchers have found such a close sequence, says David Robertson, a computational virologist at the University of Glasgow, UK.

Pangolins are protected animals, but illegal trafficking is widespread, and some species are critically endangered. They are sold, controversially, for their meat and scales, and for use in traditional Chinese medicine, in which parts of the animal are used

to treat ailments such as skin diseases, menstrual disorders and arthritis. Chinese law states that people selling pangolins can be punished by 10 years or more in prison.

The coronavirus emerged in the Chinese city of Wuhan in December, and is thought to have leapt to humans at a seafood and wild-animal market, where many of the first people to become infected worked. Pangolins were not listed on an inventory of items sold at the market — although the illegality of trading pangolins could explain this omission.

Last month, scientists in Beijing claimed that [snakes were the source of nCoV-2019](#), but that theory was dismissed by other researchers.

Shen and Xiao did not immediately respond to *Nature's* requests for comment, but Liu Yahong, president of the South China Agricultural University, told the press conference that the results would be published soon to help efforts to control the coronavirus.

Scientists hope that the paper will offer details including where the team found the pangolins with the similar virus. Arinjay Banerjee, a coronavirus researcher at McMaster University in Hamilton, Canada, says that another crucial detail is where in pangolins the researchers found the virus — for example, whether it was isolated from blood samples or rectal swabs. This will help to determine how it might have been passed to humans and how such transmission could be prevented in the future.

“I can definitely believe it could be true,” says Kristian Andersen, an immunologist and computational biologist at Scripps Research in La Jolla, California. Andersen says he has compared publicly available sequences of pangolin viruses and found that they are similar to that of nCoV-2019. “I look forward to the published report and data.”

doi: 10.1038/d41586-020-00364-2

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<http://bit.ly/3bh8mNL>

How long coronaviruses persist on surfaces and how to inactivate them

The novel coronavirus 2019-nCoV is making headlines worldwide.

Since there is no specific therapy against it, the prevention of infection is of particular importance in order to stem the epidemic. Like all droplet infections, the virus can spread via hands and surfaces that are frequently touched. "In hospitals, these can be door handles, for example, but also call buttons, bedside tables, bed frames and other objects in the direct vicinity of patients, which are often made of metal or plastic," explains Professor Günter Kampf from the Institute of Hygiene and Environmental Medicine at the Greifswald University Hospital.

Together with Professor Eike Steinmann, head of the Department for Molecular and Medical Virology at Ruhr-Universität Bochum (RUB), he has compiled comprehensive findings from 22 studies on coronaviruses and their inactivation for a future textbook. "Under the circumstances, the best approach was to publish these verified scientific facts in advance, in order to make all information available at a glance," says Eike Steinmann.

Infectious on surfaces for up to nine days

The evaluated studies, which focus on the pathogens Sars coronavirus and Mers coronavirus, showed, for example, that the viruses can persist on surfaces and remain infectious at room temperature for up to nine days. On average, they survive between four and five days. "Low temperature and high air humidity further increase their lifespan," points out Kampf.

Tests with various disinfection solutions showed that agents based on ethanol, hydrogen peroxide or sodium hypochlorite are effective against coronaviruses. If these agents are applied in appropriate concentrations, they reduce the number of infectious coronaviruses by four so-called log steps within one minute: this means, for

example, from one million to only 100 pathogenic particles. If preparations based on other active ingredients are used, the product should be proven to be at least effective against enveloped viruses ("limited virucidal activity"). "As a rule, this is sufficient to significantly reduce the risk of infection," explains Günter Kampf.

Findings should be transferable to 2019-CoV

The experts assume that the results from the analyses of other coronaviruses are transferable to the novel virus. "Different coronaviruses were analysed, and the results were all similar," concludes Eike Steinmann.

Original publication

Günter Kampf, Daniel Todt, Stephanie Pfaender, Eike Steinmann: Persistence of coronaviruses on inanimate surfaces and its inactivation with biocidal agents, in: Journal of Hospital Infection, 2020, DOI: 10.1016/j.jhin.2020.01.022

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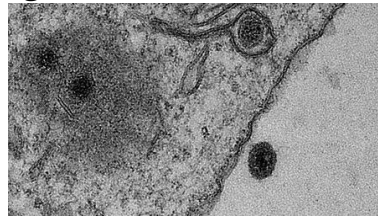
Scientists discover virus with no recognizable genes

Scientists have discovered a virus with no recognizable genes, making it among the strangest known

By [Elizabeth Pennisi](#)

Viruses are some of the most mysterious organisms on Earth.

They're among the world's tiniest lifeforms, and because none can survive and reproduce without a host, some scientists have questioned whether they should even be considered living things.



The Yaravirus (dark smudges) infects amoebae and has all novel genes. J. Abrahão and B. La Scola/IHU-Marseille/Microscopy Center UFMG-Belo Horizonte

Now, scientists have discovered one that has no recognizable genes, making it among the strangest of all known viruses. But how many viruses do we really know? Another group has just discovered thousands of new viruses hiding out in the tissues of dozens of animals.

The finds speak to "how much we still need to understand" about viruses, says one of the researchers, Jônatas Abrahão, a virologist at the Federal University of Minas Gerais, Belo Horizonte.

Abrahão made his discovery while hunting down [giant viruses](#). These microbes—some the size of bacteria—were first discovered in amoebae in 2003. In a local artificial lake, he and his colleagues found not only new giant viruses, but also a virus that—because of its small size—was unlike most that infect in amoebae. They named it Yaravirus. (Yara is the "mother of waters" according to Indigenous Tupi-Guarani mythology.)

Yaravirus's size wasn't the only thing weird about it. When the team sequenced its genome, [none of its genes matched any scientists had come across before](#), the group reports on the bioRxiv preprint server.

Viral novelty doesn't surprise Elodie Ghedin of New York University, who looks for viruses in wastewater and in respiratory systems. More than 95% of the viruses in sewage data have "no matches to reference genomes [in databases]," she says. Like Abrahão, she says, "We seem to be discovering new viruses all the time."

Some of Yaravirus's genes look like those in a giant virus, but it's still unclear how the two are related, Abrahão says. He and his colleagues are still investigating other aspects of the novel virus's lifestyle.

While Abrahão was chasing down viruses one at a time, Christopher Buck and graduate student Michael Tisza, virologists at the National Cancer Institute, were casting a much wider net. They were searching broadly in animal tissues for viruses that keep their genetic material in a circle. The so-called circular viruses include papillomaviruses, one of which, human papillomavirus, can cause cervical cancer, and another virus that's usually harmless to people.

But Buck has evidence the latter may be linked to bladder cancer in patients with kidney transplants and in other people.

To find these viruses, the researchers isolated viral particles from dozens of tissue samples from humans and other animals and screened them for circular genomes. The group confirmed that the DNA belonged to viruses by looking for a gene that codes for a virus's shell. These gene sequences are often unrecognizable, but Tisza wrote a computer program that predicted which genes were most likely to code for the distinctive folds of these shells.

In all, the team discovered approximately 2500 circular viruses, about [600 of which are new to science](#). It's still unclear what impact, if any, these microbes have on human health, the team reports in *eLife*. But Buck says the data should allow doctors and scientists to begin to make those connections. The approach "is an important tool to learn the distribution of hundreds or thousands of viral genomes," Abrahão says.

The new studies have implications beyond figuring out which viruses cause disease. Some viruses that live in the human body [may help keep us healthy](#), and others are essential for keeping ecosystems running smoothly by helping to recycle essential nutrients. "We could not survive without [them]," says Curtis Suttle, an environmental virologist at the University of British Columbia, Vancouver, who was not involved with either study. "There are enormous benefits to the discovery and characterization of viruses."

<https://nyti.ms/2SbFChG>

New Report on 138 Coronavirus Cases Reveals

Disturbing Details

A highly contagious patient, virus transmission inside a hospital and unexpected turns for the worse have emerged as part of the epidemic in China.

By [Denise Grady](#)

One patient, admitted to a hospital in Wuhan, China, infected at least 10 health care workers and four other patients with the coronavirus that has sickened more than 34,000 people, killed 700 and reached two dozen other countries.

The case was just one disturbing detail in a new report on 138 patients in Wuhan that helps explain how the illness progresses and how it spreads.

The report, one of two [published on Friday by JAMA](#), is among the most comprehensive articles to date about people infected with the newly identified virus.

The patients ranged in age from 22 to 92, with a median of 56 years, and were admitted to Zhongnan Hospital of Wuhan University from Jan. 1 to Jan 28. Many of them — 41 percent — were presumed to have caught the virus in the hospital, including 17 people who had been admitted for other illnesses, and 40 health care workers.

The patient who infected so many health workers had been placed in a surgical ward because of abdominal symptoms, and the coronavirus was not initially suspected. Four other patients in that ward also contracted the disease, presumably from the first patient.

The incident was a chilling reminder of the "super-spreaders" in outbreaks of other coronavirus diseases, SARS and MERS — patients who infected huge numbers of other people, sometimes dozens. The phenomenon is poorly understood and unpredictable, an epidemiologist's nightmare. Super-spreaders led to considerable transmission of MERS and SARS inside hospitals.

[Reporting on Friday in JAMA](#), the authors said their data suggested that rapid person-to-person spread of the virus had occurred among their cases. That was in part because of patients like the one admitted to the surgical department, whose symptoms misled doctors into suspecting other illnesses and failing to take precautions to prevent spread of the virus until it was too late.

About 10 percent of the patients did not initially have the usual symptoms, cough and fever, but instead had diarrhea and nausea first. Other uncommon symptoms included headache, dizziness and abdominal pain.

Another cause for concern was that some patients who at first appeared mildly or moderately ill then took a turn for the worse several days or even a week into their illness. The median time from their first symptoms to when they became short of breath was five days; to hospitalization, seven days; and to severe breathing trouble, eight days. Experts say that pattern means patients must be carefully monitored, and it is not safe to assume that someone who seems to be doing well early on is out of the woods.

The finding is a “heads up” to doctors to keep an eye on these patients, Dr. Anthony Fauci, director of the National Institute of Allergy and Infectious Diseases, said in [a recorded interview posted by JAMA](#).

Like previous reports on coronavirus patients, this one found that older people and those with underlying health problems like diabetes, heart disease or cancer tended to become more severely ill than younger, healthier patients.

Over all, about 26 percent of the 138 patients needed intensive care; their median age was 66, compared with a median of 51 years for those who did not require intensive care.

For this series of patients, the death rate was 4.3 percent, which is higher than the estimates coming from other parts of China. The reason is not known, and the figures may change as more information is gathered. Unlike some earlier reports, the new one did not find many more men than women to be infected: 54 percent of the patients were male.

The data on the patients shows that the illness caused pneumonia and a systemic viral infection that set off a powerful inflammatory response in the body, Dr. William Schaffner, an infectious disease

expert at Vanderbilt University, said in an interview. “There are biochemical indicators that a number of the body’s organ systems are likely affected and you have an inflammatory response that is disrupting their function to some extent,” Dr. Schaffner said.

The lungs, heart, liver, kidneys and the systems that control blood clotting are all affected, Dr. Schaffner said, though it is not clear that the virus itself infects organs other than the lungs.

The inflammatory response is a hallmark of a serious viral disease, he said, adding that in recent years it has become apparent that heightened inflammation from diseases like the flu can persist for a month or so after the acute illness is gone, and can increase the risk of heart attacks and strokes in older people.

The [second JAMA report](#) concerns 13 patients treated in three hospitals in Beijing from Jan. 16 to Jan. 29. They were younger than the Wuhan group, with a median age of 34, and no underlying diseases. Only one was over 50. The youngest was a 2-year-old. They did not become as ill as the Wuhan patients, and none died.

The cases, mostly in healthy, young adults, should dispel the notion that only older people contract the illness.

“It can take a young, healthy person and make them sick,” Dr. Schaffner said. “That’s clear from the health care workers and the young people in this paper.”

<https://nyti.ms/38c073y>

Antarctica Sets Record High Temperature: 64.9 Degrees

“This is the foreshadowing of what is to come,” a researcher said. “It’s exactly in line of what we’ve been seeing for decades.”

By [Derrick Bryson Taylor](#)

Antarctica, the coldest, windiest and driest continent on Earth, set a record high temperature on Thursday, underscoring the global warming trend, researchers said.

Esperanza, Argentina's research station on the northern tip of the Antarctic Peninsula, reached 64.9 degrees Fahrenheit, or 18.2 degrees Celsius, breaking the previous record of 63.5 degrees set on March 24, 2015, according to Argentina's [National Meteorological Service](#). The station has been recording temperatures since 1961.

The temperature at Esperanza, where it is summer, was comparable to the weather in Los Angeles and Huntsville, Ala., where the high temperatures were 64 on Thursday, according to the National Weather Service.

The Weather and Climate Extremes Archive, a committee of the [World Meteorological Organization](#), will verify the temperature, the organization said in a news release.

"Everything we have seen thus far indicates a likely legitimate record," Randall Cerveny, an organization official, said.

The record high appears to be associated with a regional "foehn," described as a rapid warming of air coming down a slope or mountain, Mr. Cerveny said.

Temperatures on the continent range on average from 14 degrees Fahrenheit (minus 10 degrees Celsius) on the Antarctic coast, to minus 76 degrees Fahrenheit (minus 60 degrees Celsius) at higher elevations of the interior, the meteorological organization said.

Its ice sheet, which is nearly three miles thick, contains 90 percent of the world's fresh water.

The Antarctic Peninsula, the northwest tip near South America, is among the fastest warming regions of the planet, the meteorological organization said. Antarctica is about the size of the United States and Mexico combined, [according to NASA](#).

The high temperature is in keeping with the earth's overall warming trend, which is in large part caused by [emissions of greenhouse gases](#).

Experts say that warming trend is affecting other parts of Antarctica, including the large West Antarctic Ice Sheet.

"I think of the warming of the atmosphere as like preheating an oven and the polar ice sheets are like a frozen lasagna that you put into the oven and now even the frozen lasagna is starting to defrost at high polar latitude," Maureen Raymo, a research professor in the department of earth and environmental sciences at Columbia University, said on Saturday.

When the ice sheets melt, the water has nowhere to go but into the ocean and will affect shorelines around the world, Professor Raymo said.

"I think this is the tip of the iceberg, so to speak," she said. "This is the foreshadowing of what is to come. It's exactly in line of what we've been seeing for decades" — that air temperature records are increasingly broken.

Last month was the fifth-warmest January in the United States in 126 years of record-keeping, according to the [National Oceanic and Atmosphere Administration](#). The lower 48 states had an average temperature of 35.5 degrees and they all saw above- to much-above-average temperatures last month, it said.

The last decade was [the hottest on record](#) and 2019 was the second-warmest year, according to researchers.

Global average surface temperatures last year were nearly 1.8 degrees Fahrenheit (1 degree Celsius) higher than the average from the middle of the last century, caused by emissions of carbon dioxide and other heat-trapping gases from the burning of fossil fuels.

Henry Fountain contributed reporting.