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We Finally Have The First-Ever Analysis of Stardust Retrieved From The Ryugu Asteroid

We're finally getting a more detailed glimpse of what makes up asteroid Ryugu

Michelle Starr

It's been over a year since the Hayabusa2 probe delivered its precious cargo of dust from an alien space rock, and we're finally getting a more detailed glimpse of what makes up asteroid Ryugu.

In two papers published today, international teams of scientists have revealed that, in accordance with analyses conducted by the probe while at the asteroid, Ryugu is very dark, very porous, and some of the most primitive Solar System material we've ever had access to here on Earth.

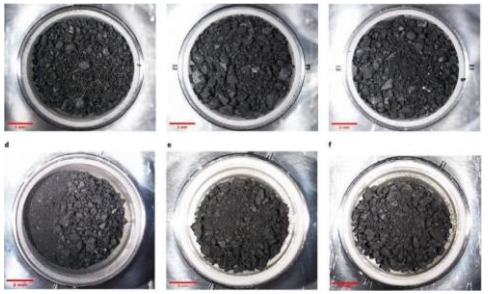
Although not unexpected, the results are very cool. Since the asteroid has remained more or less unchanged since the formation of the Solar System 4.5 billion years ago, the sample is one of our best tools yet for understanding the composition of the dust from which the inner Solar System objects coalesced.

"The Hayabusa2 returned samples … appear to be among the most primordial materials available in our laboratories," wrote one of the teams in their paper. "The samples constitute a uniquely precious collection, which may contribute to revisiting the paradigms of Solar System origin and evolution."

Asteroid Ryugu, formerly known as 1999 JU3, is only the second asteroid from which a sample return mission has been conducted. The first was Itokawa, whose sample return mechanism failed, resulting in only a minute amount of dust finally reaching Earth in 2010.

Ryugu is about a kilometer (0.62 miles) across, with a ridge around its equator; it travels an elliptical orbit that carries it just inside Earth's orbital path around the Sun, then out almost as far as Mars's orbit. The mission to get to the asteroid, touch down on it twice, then return any dust retrieved to Earth took a deeply impressive level of skill and planning.

But it worked, and 5.4 grams of precious asteroid dust were returned and duly analyzed, while Hayabusa2 sailed off for a series of rendezvous with other asteroids over the coming years.



Ryugu samples returned by the Hayabusa2 probe. **(Yada et. al., Nat. Astron., 2021)**

Based on remote sensing and on-asteroid measurements, we already know Ryugu is what we call a C-type asteroid, the most common type of asteroid in the Solar System. These rocks are rich in carbon, which makes them very dark; they also have lots of volatile elements.

In the first paper, led by astronomer Toru Yada of the Japan Aerospace Exploration Agency (JAXA), an analysis of a Ryugu sample reveals that the asteroid is extremely dark. Typically, C-type asteroids have an albedo (that's the measure of how much solar radiation a body reflects) of 0.03 to 0.09. Asphalt has an albedo of 0.04. Ryugu's albedo is 0.02. That means it reflects just 2 percent of the solar radiation that hits it.

The asteroid is also, the researchers determined, extremely porous. According to their measurements, Ryugu has a porosity of 46 percent. That's more porous than any carbonaceous meteorite we've ever had the opportunity to study, although we have seen more porous asteroids. This is consistent with the asteroid's porosity as measured by remote thermal imaging, and measurements conducted on the asteroid itself.

In the second paper, a team led by astronomer Cédric Pilorget of the Université Paris-Saclay in France analyzed the composition of the

dust. They detected that the asteroid seems to consist of an extremely dark matrix, possibly dominated by phyllosilicates, or clay-like minerals, although there was a lack of a clear hydration signature.

In this matrix, they identified inclusions of other minerals, such as carbonates, iron, and volatile compounds.

Both of these papers agree that, in porosity and composition, Ryugu seems most similar to a type of meteorite classed as "CI chondrites". That means the meteorite is carbonaceous, and similar to the Ivuna meteorite. These meteorites have, compared to other meteorites, a composition very similar to that of the solar photosphere, suggesting they are the most primitive of all known space rocks.

More in-depth analyses will no doubt be on the way to try to discover more – not just about Ryugu, but what our Solar System was like as it was forming from the Sun's leftover dust.

"Our initial observations in the laboratory for the entire set of returned samples demonstrate that Hayabusa2 retrieved a representative and unprocessed (albeit slightly fragmented) sample from Ryugu," Yada's team wrote in their paper.

"Our data support and extend remote-sensing observations that suggested that Ryugu is dominated by hydrous carbonaceous chondrite-like materials, similar to CI chondrites, but with a darker, more porous and more fragile nature. This inference should be further corroborated by in-depth investigations hereafter by state-of-the-art analytical methods with higher resolution and precision."

The two papers have been published in *Nature Astronomy*. They can be found here and here.

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Your Likely Order of COVID-19 Symptoms Depends on the Variant

Order of symptoms that COVID-19 patients experience is different for different variants of the virus

The most likely order of symptoms that COVID-19 patients experience is different for different variants of the virus, according to a new study published on December 16th, 2021, in *PLOS Computational Biology* by Peter Kuhn of the University of Southern California and colleagues.

The researchers previously developed a mathematical model predicting the order of COVID-19 symptoms based on data from the initial outbreak in China in early 2020. In the new work, they wanted to know whether the order of symptoms varied in patients from different geographical regions or with various patient characteristics. They used their modeling approach to predict symptom order in a set of 373,883 cases in the USA between January and May 2020.

Surprisingly, the most likely symptom order differed between the initial outbreak in China—where fever most often preceded cough, and nausea/vomiting was a common third symptom—and the subsequent spread to the USA, where cough was most likely to be the first symptom, and diarrhea was a more common third symptom. By analyzing additional data from Brazil, Hong Kong and Japan, the team showed that the different orders of symptoms were associated not with geographic region, weather, or patient characteristics, but with SARS-CoV-2 variants. The presence of the D614G variant in an area—which was predominant in the USA in early 2020—was associated with a higher likelihood of cough being the first COVID-19 symptom experienced by patients. As Japan shifted from the original Wuhan reference strain to the D614G variant, symptom order shifted as well. The increased transmission of D614G could be linked to the symptom order, the authors hypothesize.

“These findings indicate that symptom order can change with mutation in viral disease and raise the possibility that D614G variant is more transmissible because infected people are more

likely to cough in public before being incapacitated with fever," they say.

For more on this study, see Researchers May Have Discovered Why First COVID-19 Wave Spread So Fast in US and Europe.

Reference: "Modeling the onset of symptoms of COVID-19: Effects of SARS-CoV-2 variant" by Joseph R. Larsen, Margaret R. Martin, John D. Martin, James B. Hicks and Peter Kuhn, 16 December 2021, PLOS Computational Biology.
DOI: 10.1371/journal.pcbi.1009629

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https://bit.ly/3mybSKM

Early humans hunted the largest available animals to extinction for 1.5 million years

The largest animals available in their surroundings provided the greatest quantities of food in return for a unit of effort

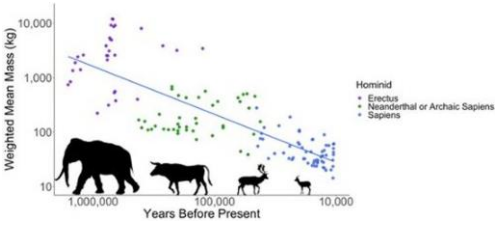
A groundbreaking study by researchers from Tel Aviv University tracks the development of early humans' hunting practices over the last 1.5 million years—as reflected in the animals they hunted and consumed. The researchers claim that at any given time early humans preferred to hunt the largest animals available in their surroundings, which provided the greatest quantities of food in return for a unit of effort.

In this way, according to the researchers, early humans repeatedly overhunted large animals to extinction (or until they became so rare that they disappeared from the archaeological record) and then went on to the next in size—improving their hunting technologies to meet the new challenge. The researchers also claim that about 10,000 years ago, when animals larger than deer became extinct, humans began to domesticate plants and animals to supply their needs, and this may be why the agricultural revolution began in the Levant at precisely that time.

The study was conducted by Prof. Ran Barkai and Dr. Miki Ben-Dor of the Jacob M. Alkow Department of Archaeology and Ancient Near Eastern Cultures, Prof. Shai Meiri of the School of Zoology and Steinhardt Museum of Natural History, and Jacob Dembitzer, a research student of Prof. Barkai and Prof. Meiri, who led the project. The paper was published in the journal *Quaternary Science Reviews*.

The study, unprecedented in both scope and timespan, presents a comprehensive analysis of data on animal bones discovered at dozens of prehistoric sites in and around Israel. Findings indicate a continual decline in the size of game hunted by humans as their main food source—from giant elephants 1-1.5 million years ago down to gazelles 10,000 years ago.

According to the researchers, these findings paint an illuminating picture of the interaction between humans and the animals around them over the last 1.5 million years.



Linear regression of log10 transformed weighted mean body mass (in kg) per stratigraphic layer as a function of time (log10 years before present). **Credit: Tel Aviv University**

Prof. Barkai notes two major issues presently addressed by prehistorians worldwide: What caused the mass extinction of large animals over the past hundreds of thousands of years—overhunting by humans or perhaps recurring climate changes? And what were the driving forces behind great changes in humankind—both physical and cultural—throughout its evolution?

Prof. Barkai says that "in light of previous studies, our team proposed an original hypothesis that links the two questions: We think that large animals went extinct due to overhunting by humans, and that the change in diet and the need to hunt progressively smaller animals may have propelled the changes in humankind. In

this study we tested our hypotheses in light of data from excavations in the Southern Levant covering several human species over a period of 1.5 million years."

Jacob Dembitzer adds that "we considered the Southern Levant (Israel, the Palestinian Authority, Southwest Syria, Jordan, and Lebanon) to be an 'archaeological laboratory' due to the density and continuity of prehistoric findings covering such a long period of time over a relatively small area—a unique database unavailable anywhere else in the world. Excavations, which began 150 years ago, have produced evidence for the presence of humans, beginning with Homo erectus who arrived 1.5 million years ago, through the neandertals who lived here from an unknown time until they disappeared about 45,000 years ago, to modern humans (namely, ourselves) who came from Africa in several waves, starting around 180,000 years ago."

The researchers collected all data available in the literature on animal bones found at prehistoric sites in the Southern Levant, mostly in Israel. These excavations, conducted from 1932 until today, provide a unique sequence of findings from different types of humans over a period of 1.5 million years. With some sites comprising several stratigraphic layers, sometimes thousands of years apart, the study covered a total of 133 layers from 58 prehistoric sites, in which thousands of bones belonging to 83 animal species had been identified. Based on these remains, the researchers calculated the weighted mean size of the animals in each layer at every site.

Prof. Meiri says that "Our study tracked changes at a much higher resolution over a considerably longer period of time compared to previous research. The results were illuminating: we found a continual, and very significant, decline in the size of animals hunted by humans over 1.5 million years. For example, a third of the bones left behind by Homo erectus at sites dated to about a million years ago, belonged to elephants that weighed up to 13 tons (more than twice the weight of the modern African elephant) and provided humans with 90% of their food. The mean weight of all animals hunted by humans at that time was 3 tons, and elephant bones were found at nearly all sites up to 500,000 years ago."

"Starting about 400,000 years ago, the humans who lived in our region—early ancestors of the Neandertals and Homo sapiens, appear to have hunted mainly deer, along with some larger animals weighing almost a ton, such as wild cattle and horses. Finally, in sites inhabited by modern humans, from about 50,000 to 10,000 years ago, approximately 70% of the bones belong to gazelles—an animal that weighs no more than 20-30kg. Other remains found at these later sites came mostly from fallow deer (about 20%), as well as smaller animals such as hares and turtles."

Jacob Dembitzer says that "our next question was: What caused the disappearance of the large animals? A widely accepted theory attributes the extinction of large species to climate changes through the ages. To test this, we collected climatic and environmental data for the entire period, covering more than a dozen cycles of glacial and interglacial periods. This data included temperatures based on levels of the oxygen 18 isotope, and rainfall and vegetation evidenced by values of carbon 13 from the local Soreq Cave. A range of statistical analyses correlating between animal size and climate, precipitation, and environment, revealed that climate, and climate change, had little, if any, impact on animal extinction."

Dr. Ben-Dor says that "our findings enable us to propose a fascinating hypothesis on the development of humankind: humans always preferred to hunt the largest animals available in their environment, until these became very rare or extinct, forcing the prehistoric hunters to seek the next in size. As a result, to obtain the same amount of food, every human species appearing in the Southern Levant was compelled to hunt smaller animals than its

predecessor, and consequently had to develop more advanced and effective technologies. Thus, for example, while spears were sufficient for Homo erectus to kill elephants at close range, modern humans developed the bow and arrow to kill fast-running gazelles from a distance."

Prof. Barkai concludes that "we believe that our model is relevant to human cultures everywhere. Moreover, for the first time, we argue that the driving force behind the constant improvement in human technology is the continual decline in the size of game. Ultimately, it may well be that 10,000 years ago in the Southern Levant, animals became too small or too rare to provide humans with sufficient food, and this could be related to the advent of agriculture. In addition, we confirmed the hypothesis that the extinction of large animals was caused by humans—who time and time again destroyed their own livelihood through overhunting. We may therefore conclude that humans have always ravaged their environment but were usually clever enough to find solutions for the problems they had created—from the bow and arrow to the agricultural revolution. The environment, however, always paid a devastating price."

More information: *Jacob Dembitzer et al, Levantine overkill: 1.5 million years of hunting down the body size distribution, Quaternary Science Reviews (2021). DOI: 10.1016/j.quascirev.2021.107316*

https://wb.md/33NS934

Convalescent Plasma Cuts COVID-19 Hospitalizations in Half: Study

Can cut hospital admissions for COVID-19 by 54% if therapy is administered within 8 days of symptom onset

Damian McNamara, MA

A "definitive study" from Johns Hopkins University researchers and others shows that convalescent plasma can cut hospital admissions for COVID-19 by 54% if therapy is administered within 8 days of symptom onset.

In the study of 1181 adults randomly assigned to high-titer convalescent plasma or placebo, 2.9% of people receiving the therapy were hospitalized compared to 6.3% who received placebo control plasma. This translates to a 54% risk reduction for hospitalization with convalescent plasma.

"We have a clear difference," principal investigator David Sullivan, MD, a professor at Johns Hopkins Bloomberg School of Public Health in Baltimore, said during a a Tuesday media briefing.

"This is very good news since we are in the midst of the Omicron surge, which has defeated [some of] our major monocular antibody therapies," said Arturo Casadevall, MD, chair of the Department of Molecular Microbiology and Immunology at Johns Hopkins.

"So we have a new tool to keep people from progressing in their disease and to reduce progression or hospitalization," Casadevall said. The findings were published as a preprint study Tuesday on *medRxiv*. The study has not yet been peer reviewed.

Whereas many convalescent plasma studies were done in hospitalized patients, this is one of only a handful performed in outpatients, the researchers note.

There is a regulatory catch. The FDA restricted emergency use authorization (EUA) for convalescent plasma in February 2021 to include only high-dose titer plasma and to limit the therapy to hospitalized patients with early disease or for immunocompromised people who cannot mount an adequate antibody response.

Sullivan and colleagues hope their findings will prompt the FDA to expand the EUA to include outpatients.

"We have shared this data with both the World Health Organization and the FDA," study co-author Kelly Gebo, MD, MPH, said during the media briefing. "We do believe that this could be scaled up quickly," added Gebo, professor of medicine at Johns Hopkins University School of Medicine. Convalescent plasma "could be

used as a potential treatment as variants continue to evolve, such as we've seen with Omicron."

Pre-Omicron Results

The study was conducted at Johns Hopkins University and 23 other sites nationwide between June 2020 and October 2021. This means researchers enrolled symptomatic adults during circulation of the SARS-CoV-2 ancestral strain and the Alpha and Delta variants.

However, Sullivan said, "We think that...plasma with high levels of antibodies can adapt faster to Omicron, although it will take us longer to get an Omicron-specific supply."

Because of the timing of the study, 80% of participants were unvaccinated. Mean age was 44 years and 57% were women. Black and Hispanic participants each accounted for more than 12% of the study population. On average, participants received a transfusion within 6 days of the start of symptoms. In the study, 37 people out of 589 control group participants were hospitalized, compared to 17 of the 592 who received the convalescent plasma.

"We know antibodies work against SARS-CoV-2. The vaccines have been spectacular — producing antibodies that reduce hospitalizations and prevent transmission," Sullivan said. "Convalescent plasma provides much of the same antibodies instantly."

Convalescent and Controversial

Convalescent plasma has been one of the controversial treatments for people with COVID-19 — with studies going back and forth on the potential benefits and efficacy. An NIH-funded study published in August 2021, for example, showed no significant benefit.

"As you know, convalescent plasma has had a rocky ride," Casadevall said. "It was deployed with great excitement in the terrible, early days of the pandemic. Unfortunately, the early excitement and optimism was dampened with some of the randomized control trials appearing to show no benefit in reducing mortality and hospitalized patients," he added.

In contrast, the current study shows "where convalescent plasma works using the latest. most rigorous clinical investigation tools available: a double-blinded, randomized, placebo-control trial," Casadevall said.

Why a Preprint, and Why Now?

The researchers decided to release their data today in recognition of the lag time between reporting of COVID-19 cases and hospitalizations, Sullivan said. "That's part of the reason we decided to act now with this knowledge — that it does take a couple of weeks — with cases of Omicron going up." Furthermore, "We thought this was actionable data for decision-makers," he added.

A reporter asked why the Johns Hopkins researchers chose to hold a media briefing for a preprint study.

A preprint is "not so unusual given the SARS-CoV-2 pandemic," said study senior author Daniel Hanley, MD, division director of brain injury outcomes at Johns Hopkins University School of Medicine.

"The data are the data," Casadevall added. "This is not going to change from peer review." Peer review may change some of the wording of the manuscript, but not the numbers, he added.

"Now with the Omicron crisis and the fact that we have lost some more main monoclonal antibodies, it is essential to get this information out," Casadevall said.

Plasma Therapy Nothing New

Donation and transfusion of convalescent plasma is highly regulated with strict criteria, said Evan Bloch, MBChB, associate director of the Transfusion Medicine Division at Johns Hopkins University School of Medicine.

If the FDA opts to expand the EUA based on this or other evidence, administration of convalescent plasma could be rolled out fairly quickly, the researchers note.

Plasma transfusion takes place in hospitals and at infusion centers every day. The infrastructure is in place in many countries, even low- and middle-resource nations, around the world to provide convalescent plasma therapy. The major difference between traditional plasma and SARS-CoV-2 convalescent plasma is the indication, Bloch added.

In addition, convalescent plasma has a polyclonal composition — a benefit compared to monoclonal antibodies, he added. "It's more durable or adaptive [compared to] some of the targeted therapies, such as monoclonal antibodies, where we've witnessed this diminished efficacy with viral evolution."

medRxiv. Published online December 21, 2021. Full text

https://bit.ly/3mB3YjE

More Than 10,000 Studies Debunk Outdated Biological 'Explanation' For Male Success

Idea there's some kind of 'superdiversity' among male brains has been repeatedly cited in the scientific literature

Mike Mcrae

From world politics to top-ranking businesses, to the upper rungs of academia and even Nobel laureates, men outnumber women by a significant margin.

One claim to such disparity has been attributed to biology. The idea there's some kind of 'superdiversity' among male brains has been repeatedly cited in the scientific literature in recent decades; but according to a newly published meta-analysis, this argument for male success is entirely unsupported by evidence.

"Based on our data, if we assume that humans are like other animals, there is equal chance of having a similar number of high-achieving women as there are high-achieving men in this world," says biologist and lead author Lauren Harrison from the Australian National University (ANU).

"Based on this logic, there is also just as great a chance of having a similar number of men and women that are low achievers."

Most research on diversity within various species tends to focus on differences between the sexes. It's not hard to find numerous and extreme examples of dimorphism; even within our own species, contrasts in sex chromosomes are responsible for exaggerating a litany of anatomical characteristics, such as beards or boobs.

Since the late 19th century, with the writings of the famous English sexologist Havelock Ellis, the assumption that larger male brains equal greater potential for cognitive prowess has been used to explain why men 'deserve' positions of influence and command.

Much has since been written on whether statistical differences across the sex divide translate into anything truly significant (short answer - they don't), but few studies have looked into whether anatomical diversity within one sex provides for a greater spectrum of behavior.

Generalizing the assertion towards non-human animals, in this new meta-analysis the team investigated whether equivalents of our own personality traits across 220 species varied to any great extent within either of the sexes.

In spite of a thorough search of some 10,000 studies, the team couldn't find any compelling evidence demonstrating greater richness of variability within the personality traits of males or females of any of the species included.

That's not to say there were no differences across species as a whole. Some select characteristics, such as immunity or certain morphological traits, were also found to vary considerably within sexes in particular species.

But if we're to use nature as a proxy for our own expanse of variation within male brains as suggested in the past, we can only conclude the rich landscape of female brains provides just as much opportunity for genius (and nonsense) as the male's. "If males are more variable than females, it would mean there are more men than

women with either very low or very high IQs," says one of the authors, evolutionary biologist Michael Jennions from ANU.

"But our research in over 200 animal species shows variation in male and female behavior is very similar. Therefore, there is no reason to invoke this argument based on biology to explain why more men than women are Nobel laureates, for example, which we associate with high IQ."

A lack of evidence in favor of behavioral variation among men doesn't rule out other biological explanations for the shatter-proof glass ceiling that permeates so much of modern society.

It does, however, limit arguments for that ceiling being a result of our biological wiring, and thus being something that we can't – or shouldn't – do anything about. Dismantling notions that male merit is cemented in biology might even help to break down the social structures that are actually responsible for gender biases.

"Instead of using biology to explain why there are more male CEOs or professors, we have to ask what role culture and upbringing play in pushing men and women down different pathways," says Harrison. This research was published in *Biological Reviews*.

https://bit.ly/3qj6hJm

Woolly mammoths survived on mainland North America until 5,000 years ago, DNA reveals

Environmental reconstructions reveal that mammoths persisted long after they disappeared from the fossil record.

By Cameron Duke

Woolly mammoths may have survived in North America thousands of years longer than scientists previously thought, vials of Alaskan permafrost reveal.

The hairy beasts might have persisted in what is now the Yukon, in Canada, until around 5,000 years ago — 5,000 years longer than experts previously estimated, a new study suggests. That conclusion comes from snippets of mammoth DNA that were found in vials of frozen dirt that had been stored and forgotten in a laboratory freezer for a decade.

"Organisms are constantly shedding cells throughout their life," said study lead author Tyler Murchie, a postdoctoral researcher in the Department of Anthropology at McMaster University in Ontario. For instance, He explained that a person sheds roughly 40,000 skin cells per hour, on average, meaning we are constantly ejecting bits of our DNA into our surroundings.

An artist's illustration of woolly mammoths. Scientists have discovered that woolly mammoths coexisted with humans in North America for thousands of years longer than previously believed. **(Image credit: Daniel Eskridge via Getty Images)**

That's also true of other life-forms; nonhuman animals, plants, fungi, and microbes are constantly leaving microscopic breadcrumb trails everywhere. Most of this genetic detritus doesn't linger in the environment, though. Soon after being discarded, the vast majority of the DNA bits are consumed by microbes, Murchie said. The fraction of the shed DNA that does remain might bind to a small bit of mineral sediment and be preserved. Though only a tiny proportion of what was initially shed remains centuries later, it can nevertheless provide a window into a vanished world teeming with strange creatures. "In a tiny fleck of dirt," Murchie told Live Science, "is DNA from full ecosystems."

Murchie analyzed soil samples taken from permafrost in the central Yukon. Many of the samples dated to the Pleistocene-Holocene transition (14,000-11,000 years ago), a period marked by rapidly changing climatic conditions in which many large mammals — such as saber-toothed cats, mammoths and mastodons — vanished from the fossil record.

The DNA fragments in Murchie's samples were small — often no larger than 50 letters, or base pairs. However, on average, he was able to isolate roughly 2 million DNA fragments per sample. By analyzing DNA from soil samples of known ages, he indirectly observed the evolution of ancient ecosystems over this turbulent period.

The main advantage to studying ancient DNA is that researchers can observe organisms that tended not to fossilize well. "An animal has only one body," said Murchie, and the odds of it fossilizing are not that great. On top of that, you have to find it. But that same animal constantly ejected innumerable amounts of DNA into the environment throughout its lifetime.

The soil samples — which span a period of time from 30,000 years ago to 5,000 years ago — revealed that mammoths and horses likely persisted in this Arctic environment much longer than previously thought. Mammoths and horses were in steep decline by the Pleistocene-Holocene transition, the DNA data suggest, but they didn't disappear all at once due to changes in climate or overhunting. An earlier study, published in October in the journal Nature, suggested that some mammoths survived on isolated islands away from human contact until 4,000 years ago. However, the new study is the first to determine that small populations of mammoths coexisted with humans on the mainland of North America well into the Holocene, as recently as 5,000 years ago.

. Megafauna extinctions from this era have largely been blamed on one of two explanations: human paleo-hunters or climate catastrophe, said lead author Hendrik Poinar, an evolutionary geneticist and director of the McMaster Ancient DNA Centre.

However, the new study "changes the focus away from this two-pitted debate that has plagued [paleontology] for so long," Poinar said.

The team's research provides evidence that the extinction of North American megafauna is much more nuanced, he said. There's no doubt that the animals were under pressure from both human hunters and a rapidly changing climate. The question is, "how much were they hunted and whether or not that was truly the tipping point," Poinar told Live Science.

Analyzing ancient DNA from dirt has the potential to tell us a lot about ancient life; Poinar and Murchie said Arctic permafrost is ideal for these types of ancient DNA studies because freezing preserves ancient DNA very well. But that might not be possible forever: As ice in the Arctic melts due to rapid increases in temperature, "we're going to lose a lot of that life history data," Murchie said. "It's just going to fall away before anyone gets a chance to study it." This study was published Dec. 8 in the journal Nature Communications.

https://bit.ly/3409DcL

New grafting technique could combat the disease threatening Cavendish bananas

Scientists have found a novel way to combine two species of grass-like plant including banana, rice and wheat, using embryonic tissue from their seeds.

The technique allows beneficial characteristics, such as disease resistance or stress tolerance, to be added to the plants.

Grafting is the technique of joining the shoot of one plant with the root of another, so they continue to grow together as one. Until now it was thought impossible to graft grass-like plants in the group known as monocotyledons because they lack a specific tissue type, called the vascular cambium, in their stem.

Researchers at the University of Cambridge have discovered that root and shoot tissues taken from the seeds of monocotyledonous grasses—representing their earliest embryonic stages—fuse efficiently. Their results are published today in the journal *Nature*.

An estimated 60,000 plants are monocotyledons; many are crops

that are cultivated at enormous scale, for example rice, wheat and barley.

The finding has implications for the control of serious soil-borne pathogens including Panama Disease, or 'Tropical Race 4', which has been destroying banana plantations for over 30 years. A recent acceleration in the spread of this disease has prompted fears of global banana shortages.

"We've achieved something that everyone said was impossible. Grafting embryonic tissue holds real potential across a range of grass-like species. We found that even distantly related species, separated by deep evolutionary time, are graft compatible," said Professor Julian Hibberd in the University of Cambridge's Department of Plant Sciences, senior author of the report.

The technique allows monocotyledons of the same species, and of two different species, to be grafted effectively. Grafting genetically different root and shoot tissues can result in a plant with new traits—ranging from dwarf shoots, to pest and disease resistance.

The scientists found that the technique was effective in a range of monocotyledonous crop plants including pineapple, banana, onion, tequila agave and date palm. This was confirmed through various tests, including the injection of fluorescent dye into the plant roots—from where it was seen to move up the plant and across the graft junction.

"I read back over decades of research papers on grafting and everybody said that it couldn't be done in monocots. I was stubborn enough to keep going—for years—until I proved them wrong," said Dr. Greg Reeves, a Gates Cambridge Scholar in the University of Cambridge Department of Plant Sciences, and first author of the paper.

He added: "It's an urgent challenge to make important food crops resistant to the diseases that are destroying them. Our technique allows us to add disease resistance, or other beneficial properties like salt-tolerance, to grass-like plants without resorting to genetic modification or lengthy breeding programs."

The world's banana industry is based on a single variety, called the Cavendish banana—a clone that can withstand long-distance transportation. With no genetic diversity between plants, the crop has little disease-resilience. And Cavendish bananas are sterile, so disease resistance can't be bred into future generations of the plant. Research groups around the world are trying to find a way to stop Panama Disease before it becomes even more widespread.

Grafting has been used widely since antiquity in another plant group called the dicotyledons. Dicotyledonous orchard crops including apples and cherries, and high value annual crops including tomatoes and cucumbers, are routinely produced on grafted plants because the process confers beneficial properties—such as disease resistance or earlier flowering.

The researchers have filed a patent for their grafting technique through Cambridge Enterprise. They have also received funding from Ceres Agri-Tech, a knowledge exchange partnership between five leading UK universities and three renowned agricultural research institutes.

"Panama disease is a huge problem threatening bananas across the world. It's fantastic that the University of Cambridge has the opportunity to play a role in saving such an important food crop," said Dr. Louise Sutherland, Director Ceres Agri-Tech.

Ceres Agri-Tech, led by the University of Cambridge, was created and managed by Cambridge Enterprise. It has provided translational funding as well as commercialisation expertise and support to the project, to scale up the technique and improve its efficiency.

More information: *Julian Hibberd, Monocotyledonous plants graft at the embryonic root–shoot interface, Nature (2021). DOI: 10.1038/s41586-021-04247-y. www.nature.com/articles/s41586-021-04247-y*

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FDA greenlights Pfizer's oral COVID-19 drug

Paxlovid, which slashes hospitalizations and deaths in high-risk patients, could help blunt Omicron's impact

The U.S. Food and Drug Administration (FDA) has granted an emergency use authorization for the potent oral antiviral regimen developed by Pfizer to treat COVID-19, making it just the second such drug to receive a regulatory greenlight by any country. Last month, the United Kingdom authorized the use of a Merck-made pill that appears much less effective than the Pfizer drug.

Today's authorization of Pfizer's candidate, dubbed Paxlovid, is "a major step forward in the fight against this global pandemic," says Patrizia Cavazzoni, director of FDA's Center for Drug Evaluation and Research." It's "outstanding news," tweeted Leana Wen, a public health policy expert at George Washington University. Paxlovid "can be of great help to reduce the growing strain on hospitals," she wrote.

In the final analysis of a clinical trial, Pfizer reported its therapy reduced hospitalizations and deaths by 88% in unvaccinated patients with at least one risk factor for severe disease, such as diabetes or obesity. The Merck drug, molnupiravir, cut those numbers by about 30%. It also comes with more safety concerns.

Paxlovid combines two pills designed to be taken over a period of 5 days, starting within 5 days of the onset of COVID-19 symptoms. Following in the footsteps of revolutionary treatments for HIV/AIDS and hepatitis, one oral compound, nirmatrelvir, inhibits the main protease of SARS-CoV-2. When the virus replicates, it initially produces two long "polyproteins," which are then cut into smaller functional proteins that carry out a host of key viral functions. SARS-CoV-2's main protease makes 11 of those cuts; by inhibiting the enzyme, nirmatrelvir blocks the virus from replicating.

The second compound is another protease inhibitor called ritonavir. Originally developed to tackle HIV's protease, it also slows down metabolism of other drugs in the liver, allowing nirmatrelvir to remain in the body for longer periods of time.

Pfizer scientists originally designed a coronavirus protease inhibitor in 2003 to treat severe acute respiratory syndrome (SARS), the deadly viral disease that emerged in China and caused a worldwide outbreak that year. But it was shelved when the SARS epidemic ended. Company scientists resurrected the drug when SARS-CoV-2 broke out, and quickly showed that it blocked the new virus in cell culture and animals. But the drug had to be given by infusion, so company scientists tweaked its structure to make it more soluble, which means it can be packaged as a pill.

FDA has authorized Paxlovid for use by adults and children 12 years of age and older who have tested positive for SARS-CoV-2 and are at high risk of developing severe symptoms. Pfizer is also continuing clinical trials for use of the drug regimen on COVID-19 patients at standard risk of developing severe disease and, prophylactically, for people who had contact with infected individuals.

All these uses will likely increase demand for COVID-19 tests. And that has Wen and other public health officials worried this could exacerbate testing shortages that have arisen as Omicron cases have exploded.

Antiviral pills are not expected to have an immediate impact on the spread of COVID-19. But by preventing many hospitalizations and deaths, they could relieve the pressure on health systems and change the course of the pandemic, provided they're made widely available at reasonable prices. (*Science*'s news team made oral COVID-19 treatments a runner-up for the magazine's Breakthrough of the Year.)

In November, President Joe Biden's administration announced it

planned to purchase 10 million courses of Paxlovid for more than $5 billion. Pfizer says it expects to produce up to 80 million treatment courses by the end of 2022, with 30 million courses available in the first half of the year. In a conference call today, Jeffrey Zients, White House COVID-19 response coordinator, said 265,000 courses of Paxlovid will be available in the United States in January 2022. But because manufacturing of the drug can take up to 8 months, the full 10 million treatment courses ordered by the Biden administration won't be available until late summer of 2022.

The company says it is working to ensure access around the world and will offer the drug to low-income countries at a discount. Pfizer has also signed a voluntary license agreement with the Medicines Patent Pool to facilitate access to the drug in 95 low- and middle-income countries that account for approximately 53% of the world's population. Some public health advocates have said this deal leaves out many millions of people, however.

FDA authorized Pfizer's pill regimen without holding an advisory committee meeting, perhaps a reflection of the enormous pressure the Omicron surge is expected to place on the U.S. hospital system. The European Medicines Agency (EMA) is still reviewing Paxlovid, but in an unusual move told countries on 16 December that the drug nevertheless "can be used" in patients at high risk—another indicator of the high hopes that the drug can blunt the impact of the Omicron wave. EMA suggested countries could use Paxlovid "for example in emergency use settings, in the light of rising rates of infection and deaths due to COVID-19 across the EU."

FDA has not authorized molnupiravir yet, although some outsiders expect it will do so very soon. Merck's drug had an advisory panel meeting on 30 November, at which members expressed significant reservations about its modest effectiveness and possible dangers. Molnupiravir induces mutations in the virus' genome during replication, which some panelists think could facilitate the emergence of new virus variants; others feared it could lead to cancer-causing mutations in patients. Both concerns remain theoretical, however, and some scientists suggest the two drugs should be combined in a cocktail to reduce the risk of SARS-CoV-2 developing resistance to either drug.

doi: 10.1126/science.acz9906

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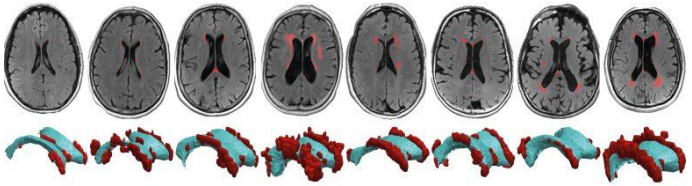
Wear and Tear in Vulnerable Brain Areas Lead to Lesions Linked to Cognitive Decline in Aging

Researchers at Stevens Institute of Technology show that strain on ventricular walls explains where lesions develop in the aging brain.

As our brains age, small lesions begin to pop up in the bundles of white matter that carry messages between our neurons. The lesions can damage this white matter and lead to cognitive deficits.

Now, researchers at Stevens Institute of Technology and colleagues not only provide an explanation for the location of these lesions but also how they develop in the first place.



Lesions (red) occur near areas that must stretch more to accommodate pressure changes of the circulating cerebrospinal fluid. When the walls of the CSF-filled ventricle (black) wear thin, CSF leaks into the brain tissue (grey) and creates lesions. **Credit: Stevens Institute of Technology**

The work, led by Johannes Weickenmeier, an assistant professor of mechanical engineering at Stevens, highlights the importance of viewing the brain as more than neural circuitry that underpins how thoughts are formed, and memories created. It's also a physical object that's prone to glitches and mechanical failures. "The brain is susceptible to wear and tear in vulnerable areas," Weickenmeier

said. “Especially in an aging brain, we need to look at its biomechanical properties to better understand how things can start to go wrong.”

These lesions — known as deep and periventricular white matter hyperintensities because they show up as bright white patches on MRI scans — are poorly understood. But they are not uncommon: most people have some by the time they reach their 60s, and changes only increase with age. The more lesions that accumulate and the faster they grow, the more prone we become to cognitive impairments ranging from memory problems to motor disorders.

Using MRI scans from eight healthy subjects, Weickenmeier worked with Valery Visser, now a doctorate student at the University of Zurich, and Henry Rusinek, a radiologist at NYU Grossman School of Medicine, to develop an individualized computer model of each subject’s brain. The team mapped the strain placed on ventricular walls, the linings of fluid-filled chambers deep in the brain, as waves of pressure pulse through the subject’s cerebral spinal fluid, or CSF. They found that hyperintensities tend to occur near areas that must stretch more to accommodate pressure changes of the circulating CSF because, as such areas wear thin, CSF can leak into the brain and cause lesions.

“The cell wall that lines the ventricles wears out over time, like a balloon that’s repeatedly blown up and deflated,” said Weickenmeier. “And the stresses aren’t uniform — they’re defined by the geometry of the ventricle, so we can predict where these failures will occur.”

The model provides a simple, physics-based explanation for the locations of these lesions, revealing that mechanical loads “must be a major contributor to the onset of disease,” said Weickenmeier.

The team’s research, published recently in *Scientific Reports*, used 2D imaging showing a cross-section of the brain, but Weickenmeier’s team has since expanded its research to a full 3D model of the brain. Next, Weickenmeier hopes to use advanced MRI technologies developed at Stevens to study the movement of the ventricle wall directly.

In the long term, the team’s findings might enable the development of new treatments for lesions. Ordinarily, pharmaceutical treatments struggle to cross the blood-brain barrier and reach affected areas, but the new research suggests that it might be possible to channel drugs to lesions directly through leaks in the ventricular wall. “That’s still a long way off, and we didn’t study it directly,” Weickenmeier cautioned. “But it’s an intriguing possibility.”

The broader takeaway from the team’s research, explained Weickenmeier, is that the brain’s aging process is mediated by physical processes, including the pressure of circulating blood and CSF. That underscores the need for healthy behaviors — such as getting enough exercise and avoiding harmful substances — that can reduce those strains on the brain.

Reference: “Peak ependymal cell stretch overlaps with the onset locations of periventricular white matter lesions” by Valery L. Visser, Henry Rusinek and Johannes Weickenmeier, 9 November 2021, Scientific Reports. DOI: 10.1038/s41598-021-00610-1

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Flecks of silver in poop of ancient Cambrian creature baffle scientists

How did metal get into this worm's poop 500 million years ago?

By Harry Baker

Researchers were baffled when they found shiny specks of silver in fossilized worm poop, because there is no known explanation for how the wiggly creatures could have made it.

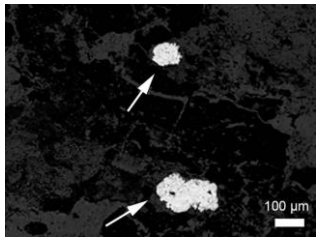
The silver specks were found in coprolites, or fossilized feces, that were embedded in a lagerstätte — a deposit of exceptionally preserved fossils that sometimes includes fossilized soft tissues — in the Mackenzie Mountains in Canada. The ancient dung was produced by tiny worms that lived below the seafloor when the

region was covered by an ocean during the Cambrian period, between 543 million years to 490 million years ago.

The largest of the silver specks was around 300 micrometers wide (for comparison, a human hair is between 17 and 180 micrometers wide) — sizable for the excrement of such a small creature, according to a statement..

The discovery of silver inside coprolites was "very surprising," lead researcher Julien Kimmig, an assistant research professor at the Earth and Environmental Systems Institute at PennState, told Live Science. "It's the first time we've ever seen this."

The researchers were initially confused as to which animal the coprolites belonged to. But after slicing through the rock samples, they came across fossilized worms still in their burrows, which would have been built below the seafloor.



***A scanning electron microscope micrograph of two smaller silver accumulations in a coprolite*. (Image credit: Julien Kimmig)**

"We got lucky that we found one of the worms still in the burrow," Kimmig said. "While it is not uncommon to find coprolites in the fossil record, it is very rare that we can assign the producer to them."

However, the researchers do not believe the worms were responsible for the silver specks in the poop. The worms would only have been able to obtain the silver from the surrounding seafloor. But after analyzing the surrounding sediment, the researchers found that there were not sufficient concentrations of silver to explain the sizable chunks in the coprolites. Silver was also thought to be toxic to small invertebrates such as worms, but this idea has not been tested properly, according to the statement.

Instead, the culprit is a "microbial colony that likely extracted it out of the water column," Kimmig said. These microbes, most likely bacteria, then deposited the silver inside the worm feces before it fossilized, Kimmig said. This could explain the uniform distribution of the metal throughout the coprolites, he added.

For Kimmig, the most exciting part of the discovery was that microbes have been "mining" metals for so long.

"It is fascinating to see what bacteria can do with metals, and we know that nowadays, they can extract many different ones from mining waste, for example," Kimmig said. "But seeing that this was likely already a well-developed trade over 500 million years ago is just fascinating."

The study was published online earlier this year in the Canadian Journal of Earth Sciences.

https://bit.ly/3et94KC

Darkness caused by dino-killing asteroid snuffed out life on Earth in 9 months

As sunlight dimmed, plants and animals died.

By Mindy Weisberger

The years following the asteroid impact that wiped out non-avian dinosaurs were dark times — literally. Soot from raging wildfires filled the sky and blocked the sun, directly contributing to the wave of extinctions that followed, new research has found.

After the asteroid struck, around 66 million years ago, the cataclysm extinguished many forms of life instantly. But the impact also caused environmental changes leading to mass extinctions that played out over time. One such extinction trigger may have been the dense clouds of ash and particles that spewed into the atmosphere and spread over the planet, which would have enveloped parts of Earth in darkness that could have persisted for up to two years.

During that time photosynthesis would have failed, leading to ecosystem collapse. And even after sunlight returned, this decline could have persisted for decades more, according to research

presented Dec. 16 at the annual meeting of the American Geophysical Union (AGU), held in New Orleans and online.

The Cretaceous period (145 million to 66 million years ago) ended with a bang when an asteroid traveling at approximately 27,000 mph (43,000 km/h) slammed into Earth. It measured about 7.5 miles (12 kilometers) in diameter, and left behind a scar known as the Chicxulub crater, which lies underwater in the Gulf of Mexico near the Yucatán Peninsula and spans at least 90 miles (150 km) in diameter. The impact eventually snuffed out at least 75% of life on Earth, including all non-avian dinosaurs (the lineage that produced modern birds is the only branch of the dinosaur family tree that weathered the extinction).

Clouds of pulverized rock and sulfuric acid from the crash would have darkened skies, cooled global temperatures, produced acid rain and sparked wildfires, Live Science previously reported. Scientists first proposed the post-asteroid "nuclear winter scenario" in the 1980s; this hypothesis suggested that darkness played a part in the mass extinctions after the Cretaceous impact, said Peter Roopnarine, a curator of geology in the Department of Invertebrate Zoology and Geology at California Academy of Sciences, and a presenter at the AGU meeting.

However, it's only in the past decade or so that researchers developed models showing how that darkness may have impacted life, Roopnarine told Live Science in an email.

"The common thinking now is that global wildfires would have been the main source of fine soot that would have been suspended into the upper atmosphere," Roopnarine said. "The concentration of soot within the first several days to weeks of the fires would have been high enough to reduce the amount of incoming sunlight to a level low enough to prevent photosynthesis."

Dark days

The team studied the impact of this long-term darkness by reconstructing ecological communities that would have existed at the time of the asteroid impact. They used 300 species known from the Hell Creek Formation, a fossil-rich expanse of shale and sandstone that dates to the latter part of the Cretaceous and extends over parts of Montana, North Dakota, South Dakota and Wyoming.

"We focused on that region because the fossil record is well-sampled and well-understood ecologically, so we could reconstruct the paleocommunity reliably," Roopnarine said.

They then created simulations that exposed their communities to periods of darkness lasting from between 100 and 700 days, to see which intervals would produce the rate of vertebrate extinction that was preserved in the fossil record — about 73%, according to the presentation. The onset of post-impact darkness would have been rapid, reaching its maximum in just a few weeks, Roopnarine said in the email.

The researchers found that ecosystems could recover after a period of darkness that lasted up to 150 days. But after 200 days, that same community reached a critical tipping point, where "some species went extinct and patterns of dominance shifted," the scientists reported. In the simulations where darkness lasted for the maximum duration, extinctions spiked dramatically. During a darkness interval of 650 to 700 days, extinction levels reached 65% to 81%, suggesting that the Hell Creek communities experienced about two years of darkness, according to the models.

"Conditions varied across the globe because of atmospheric flow and temperature variation, but we estimated that the darkness could have persisted in the Hell Creek area for up to two years," Roopnarine said, adding that these findings are preliminary and

Once an ecosystem reached that tipping point, it could eventually rebound with a new distribution of species; however, that process would have taken decades, the researchers found. Extended stimulations of Hell Creek communities that went dark for 700 days

showed that after the darkness lifted, it took 40 years for conditions in the ecosystem to start to rebound, the scientists reported at the conference.

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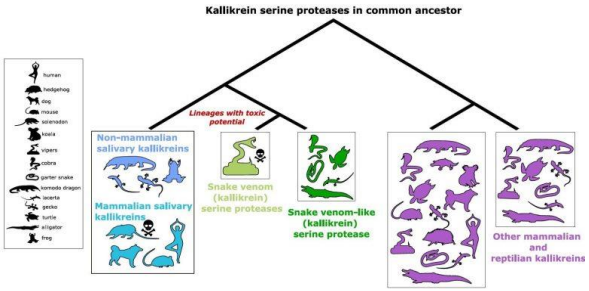
Common Origin: Venoms in Snakes and Salivary Protein in Mammals Evolved From the Same Ancestral Gene

A new study has found that a class of toxins found in snake and mammalian venom evolved from the same ancestral gene.

Snakes, some lizards, and even a few mammals can have a venomous bite. Although these lineages split more than 300 million years ago, their venoms have evolved from the same ancestral salivary protein, reported scientists today (December 22, 2021) in *BMC Biology*.

Researchers from the Okinawa Institute of Science and Technology Graduate University (OIST) in Japan and the Australian National University focused on a class of toxins found in most snake venoms and all other reptile and mammalian venoms called kallikrein serine proteases and traced their origins to a gene found in a common ancestor.



Salivary kallikreins, like those found in mice, humans, and venomous mammals like shrews and solenodons, are closely related to toxic serine protease kallikreins found in venomous snakes. **Credit: OIST**

"Venoms are cocktails of toxic proteins that have evolved across the whole animal kingdom, typically as a method of killing or immobilizing prey," explained Agneesh Barua, co-first author and PhD student at OIST.

"The oral venom systems found in snakes are particularly complex, and the origin of their venoms is still unclear."

In a previous paper, Barua and his colleagues found that the mammal salivary gland and snake venom gland share a similar pattern of activity in a group of regulatory genes, suggesting that the foundation needed for venom to evolve exists in both snakes and mammals.

"In that paper, we hypothesized that in the ancestor of snakes and mammals, there was a common group of genes that had a toxic potential," said Barua.

"Snakes and mammals then took different evolutionary paths, with snake lineages evolving diverse and increasingly toxic concoctions, while in mammals, venom did evolve, but to a much lesser degree. But what we wanted to know is whether the toxins within mammal and snake venom evolved from a common ancestral gene."

Kallikrein serine proteases are a kind of protein-degrading enzyme, which play a key role in regulating blood pressure. Mammal saliva contains small quantities of these proteins, although their function remains unclear to this day. But in venomous snakes and mammals, like shrews and solenodons, these proteins have evolved toxicity. When injected in high amounts, they drastically reduce blood pressure, potentially causing unconsciousness and even death.

Early on, researchers noticed biochemical similarities between kallikrein serine proteases in snake venoms and those in mammal saliva, but scientists did not know until now whether they were, in fact, related.

"There are so many different serine proteases that have a high degree of similarity, that until now, it was too difficult to isolate the right genes needed to determine the evolutionary history," said Barua.

With recent advances in genomic methods, the research group were able to identify and compare all the kallikrein genes in reptiles, amphibians, fishes and mammals to create an evolutionary tree.

Excitingly, they found that snake venom kallikrein serine proteases and mammal salivary kallikreins did evolve from the same ancestral gene.

“This is really strong evidence for our hypothesis that venom evolved from a common group of genes in an ancestor that had a toxic potential,” said Barua. “But the most surprising thing was that non-toxic salivary kallikreins, like those found in humans and mice, also evolved from the same ancestral gene.”

In fact, the researchers found that the non-toxic kallikreins in mammal saliva were more closely related to the venomous toxins found in snakes than to other kallikreins found within mammals.

Overall, this evidence suggests that salivary kallikrein proteins in mammals, including humans, also have the evolutionary potential to become toxic.

But, Barua quickly added, there is a caveat. “Just because we have the building blocks to evolve venom doesn’t mean this will occur. Venom is really energetically expensive to make, so there had to be a strong ecological pressure for it, which humans, and most mammals don’t have.”

But what this does tell us, he said, is that the line between venomous and non-venomous mammals is blurrier than previously thought.

Reference: “Co-option of the same ancestral gene family gave rise to mammalian and reptilian toxins” 22 December 2021, BMC Biology. DOI: 10.1186/s12915-021-01191-1

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Scientists Just Identified a Brand New Muscle Layer in The Human Jaw

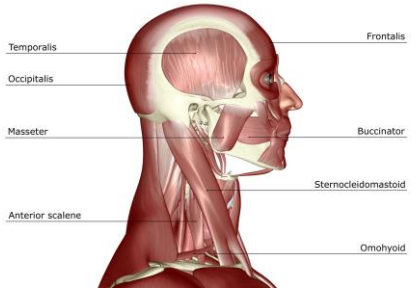
Researchers have confirmed the existence of a layer of muscle in the human jaw that has until now eluded anatomists

David Nield

It turns out there are still exciting new discoveries to be made in a field as well-studied as human anatomy: researchers have confirmed the existence of a layer of muscle in the human jaw that has until now eluded anatomists.

This new muscle is a deeper, third section of the masseter muscle. It's the most prominent jaw muscle: press your hand against the back of your jaw while you chew and you'll feel it moving.

Typically represented as having just two layers, there has been suspicions based on animal studies that there is more to its structure. However until now, attempts to describe it have been contradictory and confusing.

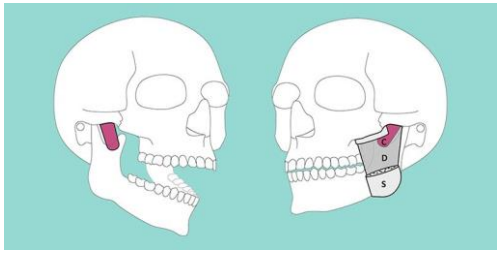


(MedicalRF.com/Getty Images)

Through an analysis of more than two dozen human heads – including one living subject and 12 heads preserved in formaldehyde – it's been established through a new study that the masseter muscle does indeed have three distinct sections, not two.

"This deep section of the masseter muscle is clearly distinguishable from the two other layers in terms of its course and function," says Szilvia Mezey, from the Department of Biomedicine at the University of Basel in Switzerland.

The name *Musculus masseter pars coronidea*, or the coronoid section of the masseter, has been proposed for the new muscle layer by the researchers, because it attaches to the muscular (coronoid) process of the lower jaw – the mandible bone.



***The masseter muscle has a superficial (S), a deep (D), and a deeper layer (C = coronoid).* (Jens C. Türp, UZB)**

The way the muscle fibers in *Musculus masseter pars coronidea* are arranged suggest that the newly discovered piece of anatomy plays

an important role in keeping the lower jaw stable. It sits higher up against the jaw and closer to it than the other two layers, and is smaller in size as well.

While this third section has occasionally been discussed as a possibility before, here the team was looking specifically for it, and was able to identify it as a separate entity. Previous studies had been inconsistent in their observations and conclusions.

"In view of these contradictory descriptions, we wanted to examine the structure of the masseter muscle again comprehensively," says Jens Christoph Türp, from the University Center for Dental Medicine at the University of Basel.

A comprehensive combination of techniques – including detailed dissection (for the heads left to medical science) and MRI scans (for the heads still attached to a living person) was used to outline the position and probable function of the muscle layer. In all cases studied, the coronoid part of the masseter could be identified.

While other mammals also have more than two layers to this muscle group, it's not clear whether any are equivalent to the *Musculus masseter pars coronidea*.

Just to add to the mystery, it appears to be missing in chimpanzees, making it possible that it's a human thing. This is something that might be investigated in the future, the researchers suggest.

And the discovery means more than just an update to anatomical records: after further study, the identification of this muscle layer could help with all kinds of surgical procedures and therapy treatments involving the lower jaw.

"Although it's generally assumed that anatomical research in the last 100 years has left no stone unturned, our finding is a bit like zoologists discovering a new species of vertebrate," says Türp.

The research has been published in *Annals of Anatomy*.

https://bit.ly/344oWBn

Tsunamis' Magnetic Fields Can Be Detected Before Sea Levels Change

Warning sign that can be detected even earlier than sea level rises

David Nield

Seconds count when it comes to tsunami alerts, and scientists may have found a warning sign that can be detected even earlier than sea level rises: the magnetic fields created by these gigantic rushes of waves.

Even though the difference might only be a minute or two, that can save lives. Magnetic field data could be incorporated into tsunami prediction and warning systems in the future, giving communities in danger more time to prepare and take evasive action.

While scientists have previously predicted that magnetic field disruption might be a useful factor in tsunami warning systems through the use of simulations, this disruption hasn't been measured alongside sea level increases during real world tsunami events.

"It is very exciting because in previous studies we didn't have the observation [of] sea level change," says geophysicist Zhiheng Lin, from Kyoto University in Japan.

"We have observations [of] sea level change, and we find that the observation agrees with our magnetic data as well as theoretical simulation."

The team looked at the collected data from two tsunamis: a tsunami in Samoa in 2009, and a tsunami in Chile in 2010.

The numbers confirmed that the magnetic field generated by the conductive waves of a tsunami arrives before the waves themselves, and that the field can be used to predict wave height.

How much earlier the magnetic field can be detected depends on the water depth, the researchers found: with a 4,800-meter (3-mile) deep sea, it's about a minute. Changes in wave height of just a few centimeters can be detected, the researchers report.

Both the vertical and horizontal variations in the tsunami magnetic field can inform predictions of sea level change, according to the study. However, the underlying models need to have good estimates of ocean depths and the electrical structure below the sea floor, which will affect the field readings.

"I think the practical goal would be if your ability to model tsunamis is so improved... you could come up with much better predictions of what areas might need to be warned [and] how badly it might hit certain places," says Neesha Schnepf, a researcher of geomagnetics at the University of Colorado, Boulder, who wasn't involved in the study.

There is a problem though – not many observation stations are set up to record this type of magnetic field data. What's more, the readings only work in deep sea environments – where there's less background environmental noise – rather than in coastal regions.

The team behind the findings say that the additional information gleaned from more sophisticated observation stations, and more observation stations in general, would be worth the extra investment considering the devastation that tsunamis can cause.

What the findings give us is another tool in planning for and minimizing the disruption of natural disasters – and we already know the terrible consequences that can result when unstoppable waves of water hit the shore without warning.

"They did something that basically needed to be done," says Schnepf. "We've needed a study that compared the magnetic field data with the sea level change from the pressure data, and I'm pretty sure they're the first to really compare how well the sea level from magnetic field matches the sea level from pressure, so that's definitely very useful."

The research has been published in the *Journal of Geophysical Research: Solid Earth*.

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Could Fabkin Hormonal Complex Spell the End of Diabetes?

Could be a novel target to treat both type 1 and type 2 diabetes and also potentially prevent their development in the first place

Liam Davenport

A hitherto unknown hormonal complex that regulates extracellular energy production in pancreatic islet (beta) cells could be a novel target to not only treat both type 1 and type 2 diabetes but also potentially to prevent their development in the first place, suggests basic science research led by US investigators.

Fatty-acid-binding protein 4 (FABP4), a recently identified hormone, was known to be elevated in type 2 diabetes, but the researchers now show that it is not only increased in type 1 diabetes but also that those increases predate its development.

They also show that antibodies against the hormone in mice models prevent type 1 diabetes and improve glycemic control in type 2 disease.

Moreover, it forms a complex with two other proteins that the researchers termed "Fabkin."

The research, published in *Nature* this month, indicates that increased levels of the complex blunts beta cell function, while antibody treatment improves beta cell function.

"For many decades, we have been searching for the signal that communicates the status of energy reserves in adipocytes (fat cells) to generate appropriate endocrine responses, such as the insulin production from pancreatic beta cells," said senior author Gökhan S. Hotamisligil, MD, PhD, in a press release.

"We now have identified Fabkin as a novel hormone that controls this critical function through a very unusual molecular mechanism."

Still a Long Way to Go

Speaking to *Medscape Medical News*, Hotamisligil, who is director

of the Sabri Ülker Center for Metabolic Research at Harvard T. H. Chan School of Public Health, Boston, Massachusetts, explained that taking the findings to the clinic entails answering a number of questions. "That will keep us busy for a long time, and there are also translational questions, which are extremely exciting," but the team is very "optimistic" that the findings will transfer well into humans, he said.

One reason is that in mice and humans with type 1 and type 2 diabetes, "we see exactly the same pattern of regulation" of Fabkin levels and that, "equally importantly," sustained high levels of the hormone "correlate with poor diabetes control" in type 1 diabetes and disease severity in type 2 disease.

"This is the first strong indication that it will translate well, and the second is that, if we take human islets...and then apply this hormone into those islets, we see the same suppression of insulin secretion and viability that we see in mice islets."

Moreover, blocking the hormone prevents the "negative effects" that we see on the islets, which is a "really critical" factor in suggesting that Fabkin could be a viable treatment target in humans, Hotamisligil explained.

He continued that, encouragingly, "nature has done some experiments in humans" with Fabkin, showing that "you can have a safe and healthy life with a mutation in the components of this complex...that reduces levels of the hormone.

"These individuals have a greatly reduced risk for both diabetes and cardiovascular disease, so this tells us that, if we can establish a safe agent that can be used in humans, this will be well-tolerated for life, and it will have beneficial effects."

Lastly, Hotamisligil said that such an agent already exists, "so it's really just a matter of making it suitable for human use and taking it through the testing procedures."

He cautioned, however, that "these are important pillars" for translational research "that we rarely, if ever, find in many of our projects," and there is still a long way to go.

Study Details: FABP4 Levels Associated With Glycemic Control

The team says the research was "inspired" by previous studies showing that *Fabp4* knockout mice had higher beta-cell mass in the pancreas and significantly increased glucose-stimulated insulin secretion.

While it is "well established" that FABP4 is increased in type 2 diabetes, they initially examined whether levels are also regulated in type 1 diabetes, independently of adiposity and insulin resistance.

Looking at serum samples from normoglycemic individuals and those with new-onset type 1 diabetes in the BABYDIAB and DiMELLI cohorts, they found that FABP4 was increased approximately 1.6-fold in the latter. In another cohort of older patients with type 1 diabetes of variation durations, serum FABP4 levels were correlated with A1c levels (P = .005), "which suggests that FABP4 is associated with glycemic control."

Mouse studies indicate that FABP4 levels are increased both shortly before and during new-onset type 1 diabetes, implying that the hormone "may have a role in beta-cell failure and pathogenesis" in both type 1 and type 2 diabetes.

Antibody targeting of FABP4 levels in mice also revealed that treatment from 10 weeks of age protected against the development of type 1 diabetes, while antibody-treated mice with diabetes had significantly reduced blood glucose and increased plasma insulin levels vs mice given control antibodies.

This, the team says, "suggests that these mice had a less severe diabetes phenotype" with the protection against type 1 diabetes similar to that seen in *Fabp4* knockout mice. Mice with diet-induced obesity and non-obese mice with diabetes treated with anti-FABP4 antibodies had improved glucose tolerance tests and a

significant increase in islet number and beta cell mass vs controls.

Further work enabled the team to identify a complex formed by circulating FABP4–adenosine kinase (ADK)–and nucleoside diphosphate kinase (NDPK), which could be targeted by anti-FABP4 antibodies via both FABP4 and NPDK.

"We propose the name Fabkin for this new hormone complex formed by NDPK to indicate its unique constitution of a fatty-acid-binding protein and kinases," the researchers write.

The team then found that the Fabkin complex alters calcium homeostasis in the endoplasmic reticulum (ER).

This, "results in ER dysfunction, increased sensitivity to environmental stress and potentiation of beta-cell death *in vitro*," which are mechanisms "critical" to the pathogenesis of both type 1 and 2 diabetes.

Finally, they showed that targeting Fabkin with anti-FABP4 antibodies "preserves beta-cell mass and enhances beta-cell function to protect against diabetes in multiple models."

Funding for this study came from National Institutes of Health and Juvenile Diabetes Research Foundation grants. The Hotamisligil Lab has generated intellectual property (assigned to Harvard University) related to hormonal FABP4 and its therapeutic targeting and receives funding for this project from Lab1636, LLC, an affiliate of Deerfield Management. Gökhan S. Hotamisligil is on the Scientific Advisory Board of Crescenta Pharmaceuticals and holds equity. Other authors have no conflicts of interest to declare.

Nature. 2021. doi: 10.1038/s41586-021-04137-3. Abstract

https://bit.ly/3mA5vGP

Recently Evolved Region of the "Dark Genome" Offers Clues to Treatment of Schizophrenia and Bipolar Disorder

Scientists investigating the DNA outside our genes — the 'dark genome' — have discovered recently evolved regions that code for proteins associated with schizophrenia and bipolar disorder.

They say these new proteins can be used as biological indicators to distinguish between the two conditions, and to identify patients more prone to psychosis or suicide.

Schizophrenia and bipolar disorder are debilitating mental disorders that are hard to diagnose and treat. Despite being amongst the most heritable mental health disorders, very few clues to their cause have been found in the sections of our DNA known as genes.

The scientists think that hotspots in the 'dark genome' associated with the disorders may have evolved because they have beneficial functions in human development, but their disruption by environmental factors leads to susceptibility to, or development of, schizophrenia or bipolar disorder.

The results are published today (December 23, 2021) in the journal *Molecular Psychiatry*.

"By scanning through the entire genome we've found regions, not classed as genes in the traditional sense, which create proteins that appear to be associated with schizophrenia and bipolar disorder," said Dr Sudhakaran Prabakaran, who was based in the University of Cambridge's Department of Genetics when he conducted the research, and is senior author of the report.

He added: "This opens up huge potential for new druggable targets. It's really exciting because nobody has ever looked beyond the genes for clues to understanding and treating these conditions before."

The researchers think that these genomic components of schizophrenia and bipolar disorder are specific to humans — the newly discovered regions are not found in the genomes of other vertebrates. It is likely that the regions evolved quickly in humans as our cognitive abilities developed, but they are easily disrupted — resulting in the two conditions.

"The traditional definition of a gene is too conservative, and it has diverted scientists away from exploring the function of the rest of the genome," said Chaitanya Erady, a researcher in the University

of Cambridge's Department of Genetics and first author of the study.

She added: "When we look outside the regions of DNA classed as genes, we see that the entire human genome has the ability to make proteins, not just the genes. We've found new proteins that are involved in biological processes and are dysfunctional in disorders like schizophrenia and bipolar disorder."

The majority of currently available drugs are designed to target proteins coded by genes. The new finding helps to explain why schizophrenia and bipolar disorder are heritable conditions, and could provide new targets for future treatments.

Schizophrenia is a severe, long-term mental health condition that may result in hallucinations, delusions, and disordered thinking and behavior, while bipolar disorder causes extreme mood swings ranging from mania to depression. The symptoms sometimes make the two disorders difficult to tell apart.

Prabakaran left his University position earlier this year to create the company NonExomics, in order to commercialize this and other discoveries. Cambridge Enterprise, the commercialization arm of the University of Cambridge, has assisted NonExomics by licensing the intellectual property. Prabakaran has raised seed funding to develop new therapeutics that will target the proteins implicated in schizophrenia and bipolar disorder, and other diseases.

His team has now discovered 248,000 regions of DNA outside of the regions conventionally defined as genes, which code for new proteins that are disrupted in disease.

Reference: "Novel open reading frames in human accelerated regions and transposable elements reveal new leads to understand schizophrenia and bipolar disorder" by Chaitanya Erady, Krishna Amin, Temiloluwa O. A. E. Onilogbo, Jakub Tomasik, Rebekah Jukes-Jones, Yagnesh Umrania, Sabine Bahn and Sudhakaran Prabakaran, 23 December 2021, Molecular Psychiatry.
DOI: 10.1038/s41380-021-01405-6

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Active COVID-19 Infection – By at Least Three Virus Variants – *Detected in Wild Deer in 6 Ohio Locations - Scientists unsure if wild deer could be SARS-CoV-2 virus reservoir.*

Scientists have detected infection by at least three variants of the virus that causes COVID-19 in free-ranging white-tailed deer in six northeast Ohio locations, the research team has reported.

Previous research led by the U.S. Department of Agriculture had shown evidence of antibodies in wild deer. This study, published today (December. 23, 2021) in *Nature*, details the first report of active COVID-19 infection in white-tailed deer supported by the growth of viral isolates in the lab, indicating researchers had recovered viable samples of the SARS-CoV-2 virus and not only its genetic traces.

Based on genomic sequencing of the samples collected between January and March 2021, researchers determined that variants infecting wild deer matched strains of the SARS-CoV-2 virus that had been prevalent in Ohio COVID-19 patients at the time. Sample collection occurred *before the Delta variant was widespread*, and that variant was not detected in these deer. The team is testing more samples to check for new variants as well as older variants, whose continued presence would suggest the virus can set up shop and survive in this species.

The fact that wild deer can become infected "leads toward the idea that we might actually have established a new maintenance host outside humans," said Andrew Bowman, associate professor of veterinary preventive medicine at The Ohio State University and senior author of the paper.

"Based on evidence from other studies, we knew they were being exposed in the wild and that in the lab we could infect them and the virus could transmit from deer to deer. Here, we're saying that in

the wild, they are infected," Bowman said. "And if they can maintain it, we have a new potential source of SARS-CoV-2 coming in to humans. That would mean that beyond tracking what's in people, we'll need to know what's in the deer, too.

"It could complicate future mitigation and control plans for COVID-19."

A lot of unknowns remain: how the deer got infected, whether they can infect humans and other species, how the virus behaves in the animals' body, and whether it's a transient or long-term infection.

The research team took nasal swabs from 360 white-tailed deer in nine northeast Ohio locations. Using PCR testing methods, the scientists detected genetic material from at least three different strains of the virus in 129 (35.8%) of the deer sampled.

The analysis showed that B.1.2 viruses dominant in Ohio in the early months of 2021 spilled over multiple times into deer populations in different locations.

"The working theory based on our sequences is that humans are giving it to deer, and apparently we gave it to them several times," Bowman said. "We have evidence of six different viral introductions into those deer populations. It's not that a single population got it once and it spread."

Each site was sampled between one and three times, adding up to a total of 18 sample collection dates. Based on the findings, researchers estimated the prevalence of infection varied from 13.5% to 70% across the nine sites, with the highest prevalence observed in four sites that were surrounded by more densely populated neighborhoods.

White-tailed deer functioning as a viral reservoir of SARS-CoV-2 would likely result in one of two outcomes, Bowman said. The virus could mutate in deer, potentially facilitating transmission of new strains to other species, including humans, or the virus could survive in deer unmutated while it simultaneously continues to evolve in humans, and at some point when humans don't have immunity to the strains infecting deer, those variants could come spilling back to humans.

How transmission happened initially in these deer, and how it could happen across species, are among the pending questions related to these findings. The research team speculated that white-tailed deer were infected through an environmental pathway – possibly by drinking contaminated water. Research has shown that the virus is shed in human stool and detectable in wastewater.

The white-tailed deer tested for this study were part of a population control initiative, so they are not a transmission threat.

Though there are an estimated 600,000 white-tailed deer in Ohio and 30 million in the United States, Bowman said this sampling focused on locations close to dense human populations and is not representative of all free-ranging deer.

Reference: 23 December 2021, Nature. DOI: 10.1038/s41586-021-04353-x

This work was supported by the Ohio State Infectious Diseases Institute and the National Institute of Allergy and Infectious Diseases. In addition to USDA, NIAID, Ohio Wildlife Center and Cleveland Metroparks contributors, Ohio State co-authors include Vanessa Hale, Patricia Dennis, Dillon McBride, Jacqueline Nolting, Christopher Madden, Devra Huey, Margot Ehrlich, Jenessa Winston, Dubraska Diaz-Campos, Page Yaxley, Alexis McLaine, Risa Pesapane, Mark Flint, Jaylene Flint, Anastasia Vlasova, Scott Kenney, Qiuhong Wang, Linda Saif and Seth Faith.

https://nyti.ms/3EvrftD

This Sea Lizard Had a Grand Piano-Size Head and a Big Appetite

Scientists have described a giant new species of ichthyosaur that evolved its 55-foot-long body size only a few million years after the lizards returned to the seas.

By Sabrina Imbler

About 246 million years ago, a sea lizard with a skull the size of a grand piano died in the ancient ocean that is now Nevada. It was an ichthyosaur, and its body was most likely the size of a modern sperm whale.

Although ichthyosaurs and whales are separated by a few hundred million years, they have a lot in common. Both descend from lineages of animals that returned to the sea after stints on land. Both evolved giant bodies that made them the largest creatures in the seas when they lived. Both birthed live young.

***Lars Schmitz, a paleontologist at the Claremont Colleges in California and an author of a new paper describing Cymbospondylus youngorum, a giant sea lizard that lived 246 million years ago.*Credit...Martin Sander**

But it took whales 45 million years of living in the ocean to evolve their most giant body sizes. This new species of giant ichthyosaur appeared only three million years after the first ichthyosaurs took to the seas, suggesting the sea lizards evolved big bodies at a breakneck speed. This early giant lived before small dinosaurs were common on land; the terrestrial world would not see a giant this size for about 40 million more years, with the emergence of sauropods in the Jurassic.

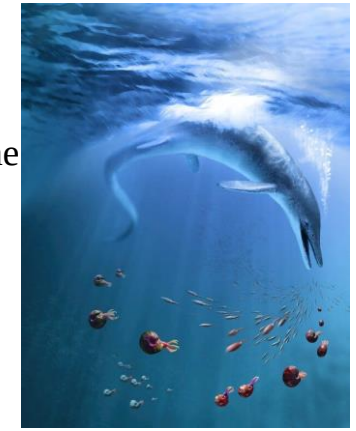
A group of scientists describe the new ichthyosaur, which they named Cymbospondylus youngorum, and reconstructed its food webs in a paper published on Thursday in the journal Science.

"It is definitely a surprise," said Benjamin C. Moon, an ichthyosaurus researcher at the University of Bristol in England who was not involved with the research. "It's not a long time to go from pretty much just in the water to suddenly dominating in such massive sizes."

The ichthyosaur was first discovered in 1998 in Fossil Hill, Nev. But excavations did not begin until 2011 because the bones rested in steep mountains, making it difficult to transport equipment to the site, said Lars Schmitz, a paleontologist at Scripps College in California and an author of the paper. "It's very strenuous," Dr. Schmitz said. "It was a huge effort to get it out of the field."

To Dr. Schmitz, the fossil's large size was humbling, even half-buried — the reptile's humerus dwarfed his rock hammer. "It makes you feel very small," he said.

In 2015, the researchers finished excavating all that remained of the ichthyosaur — its skull, shoulder and arm bones — and sent the fossil to be prepared at the Natural History Museum of Los Angeles County. "It was mind-blowing seeing it," said Jorge Velez-Juarbe, an associate curator of marine mammals at the museum and another author of the paper.



***An artist's reconstruction of Cymbospondylus youngorum in the Triassic ocean, present-day Nevada.*Credit...Stephanie Abramowicz/Natural History Museum of Los Angeles County**

Based on the size of its skull, the authors estimate the ichthyosaur very likely grew as long as 55 feet. Dr. Moon said this might be a slight overestimate and suggested a more conservative 45 to 50 feet. "The same ballpark of modern day whales," they said. "There was nothing else as big as these things around."

The ichthyosaur swam in the seas of the Triassic Era shortly after the most severe mass extinction in Earth's history, which killed off 81 percent of marine life. The researchers had one question: "How did it become so big?" Dr. Schmitz said.

In modern oceans, many giant whales are filter feeders, straining krill and other plankton through the plates of their mouths. But this abundance of modern plankton, which enabled whales to become so large, did not exist when the ichthyosaurs lived, which might suggest those ancient oceans did not have enough energy to support such a large predator.

Eva Maria Griebeler, an evolutionary ecologist at Johannes

Gutenberg University Mainz in Germany and an author of the paper, examined fossils gathered from the Nevada site to reconstruct the food webs of the ichthyosaur's ancient seas. She and other researchers consulted teeth and stomach content, as well as size differences between food web members, to understand who ate whom, Dr. Griebeler said. The ichthyosaur's bluntly pointed teeth suggest it fed on fish and squid, and perhaps even smaller marine reptiles.

"Count the number and size of the predators at the top, and the number and sizes of their prey and see whether these numbers add up," Dr. Moon said, explaining the model.

Dr. Griebeler's model found that the abundance of ammonites alone provided enough energy to support the giants. They did not feed directly on the ammonites, but they ate other creatures that crushed the shelled cephalopods: a shorter, less diverse food web that still offered the same energy input as modern oceans. "It's this astonishing thing," Dr. Griebeler said. "This food web has a completely different structure than extant ones."

Lene Liebe Delsett, a paleontologist at the Smithsonian National Museum of Natural History who was not involved with the research, praised the study's food web model as a "first step" toward understanding the Triassic ocean environment. "There's still so much we don't know about these early ecosystems," she said.

And how did ichthyosaurs manage to balloon in a paltry three million years when whales took 45 million years? Dr. Velez-Juarbe said he could not think of any other marine vertebrates that evolved large body sizes as quickly as the ichthyosaurs did. But the authors offer a number of possible explanations, including that the reptiles' large eyes and endothermy may have made them better hunters. Or perhaps the mass extinction offered life an opportunity to diversify, reducing the number of competing predators.

Dr. Delsett, who wrote a perspective in Science accompanying the new paper with Nick Pyenson, also a paleontologist at the Smithsonian, believes research on extinct marine giants can offer insight into the conservation of whales.

"They lived through one mass extinction and survived; they lived through climate change," Dr. Delsett said of the ichthyosaurs. "If you can understand marine evolution, it is easier to take better care of the oceans today."

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Yamagata University finds drug effective in treating ALS

Drug being developed for the treatment of Alzheimer's is also effective in treating amyotrophic lateral sclerosis

Yamagata University said Friday it has found that a drug being developed for the treatment of Alzheimer's is also effective in treating amyotrophic lateral sclerosis, more commonly known as Lou Gehrig's disease.

The drug has been found capable of curbing the abnormal agglomeration of protein that causes the progressive neurodegenerative disease, the state-run university in northeastern Japan said.

People with ALS lose their ability to walk, talk, eat and eventually breathe as the disease kills motor neurons, causing muscles to weaken and eventually paralyze.

There are currently drugs that can slow the progress of the disease, but the new medicine under development will be the first of its kind to work on protein accumulated in the brain and spinal cord, according to Takeo Kato, chief of the Yamagata National Hospital's ALS treatment research center.

The fatal disease is characterized by the aggregation of ubiquitinated proteins in affected motor neurons, but the research team was successful in curbing the aggregation of proteins in mice with lab-grown ALS by administering the drug candidate.

Since the experiment was conducted on mice suffering familial ALS, the less common type, researchers will now carry out experiments on mice with the more common sporadic or non-inherited ALS. The research team aims to start clinical trials involving human patients in 2024.

There are about 10,000 people in Japan who suffer from ALS, with about 1,000 to 2,000 people being newly diagnosed with the disease every year, according to Mitsubishi Tanabe Pharma Corp.

Alzheimer's disease, the most common cause of dementia, is thought to be caused by deposits of a protein fragment called beta-amyloid and twisted fibers of another protein called tau building up in the brain, according to the Alzheimer's Association.

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Omicron may cause milder disease. A lab study hints at why.

Omicron appears to be less efficient at entering lung cells.

By Nicoletta Lanese

The omicron variant of SARS-CoV-2 may be less efficient at infiltrating the lungs and spreading from cell to cell, compared with other versions of the coronavirus, early studies of human cells in a lab dish suggest.

This may help explain why some early data from countries such as South Africa and England suggest the strain causes less severe disease. But although omicron may not invade lung cells efficiently, the new study, posted Tuesday (Dec. 21) to the preprint database bioRxiv, confirmed that the variant dodges most of the antibodies made by fully vaccinated individuals.

And similar to other research, the team showed a "booster" dose of the Pfizer vaccine significantly increased the neutralization power of vaccinated people's antibodies, "though we'd still expect a waning in immunity to occur over time," senior author Ravindra Gupta, a professor of clinical microbiology at the Cambridge Institute for Therapeutic Immunology and Infectious Diseases, said in a statement.

The research has not yet been peer-reviewed or published in a scientific journal, but the findings hint "that omicron's mutations present the virus with a double-edged sword: it's got better at evading the immune system, but it might have lost some of its ability to cause severe disease," Gupta said. That said, scientists still need to confirm that these results from experiments in lab dishes match what happens in human patients, and that omicron's mutations actually influence the severity of infection.

Data from South Africa, England and other countries suggest that omicron infections might be less severe, on average, but background levels of immunity from natural infection and vaccination make these results tricky to interpret, NPR reported.

Omicron has more than 30 mutations in the genes that code for its spike protein, the part of the virus that plugs into cells to trigger infection, Live Science previously reported. Of those, 10 code for parts of the "receptor binding domain" (RBD), or the specific portion of the spike protein that latches onto cells.

To probe how these spike mutations might change how the virus interacts with cells, the researchers engineered synthetic viruses, called pseudoviruses, that carry the omicron spike protein. For comparison, they also generated pseudoviruses with the delta spike protein and some with the Wuhan-1 spike, or that of the original SARS-CoV-2 virus.

The team wanted to understand how three omicron-specific mutations in the so-called polybasic cleavage site (PBCS) affect the virus's ability to enter cells. After the spike protein plugs into a cell, the PBCS cleaves, or splits open, to allow genetic material from the virus to enter the host cell; the alpha and delta variants carry PBCS mutations that help them enter cells more easily, according to a previous study by the researchers, published June 8 in the journal

Cell Reports.

Omicron carries similar mutations in its PBCS genes, so the team predicted that it might slip into cells as easily as alpha and delta do. They tested this theory by using their pseudoviruses to infect human lung cells in lab dishes, as well as lung organoids — 3D clusters of cells made to mimic features of full-size lungs. They found that, despite its concerning PBCS mutations, omicron entered the lung cells and organoids less efficiently than delta and instead more closely resembled Wuhan-1.

Delta also outperformed omicron in a second experiment. Upon entering a cell, the delta pseudoviruses triggered cell fusion, a phenomenon that sticks neighboring cells together and allows the virus to quickly spread between them. Widespread cell-cell fusion in the lungs is often seen in the context of severe COVID-19, the researchers noted in their report. However, in their experiments, omicron initiated cell fusion less efficiently than delta, and this seemed to hinder the virus's ability to replicate in lung cells.

(A separate study, also not peer reviewed, found that omicron replicated much more efficiently than delta in upper airway cells, but less efficiently than even the original strain of SARS-CoV-2 in lung cells.)

"We speculate that the more efficient the virus is at infecting our cells, the more severe the disease might be," Gupta said in the statement. "The fact that omicron is not so good at entering lung cells and that it causes fewer fused cells with lower infection levels in the lab suggests this new variant may cause less severe lung-associated disease."

Future studies will need to confirm that these experiments in lab dishes translate to the human body. In the meantime, the team's experiments with antibodies affirm that to achieve maximum protection against the variant, people should get booster shots ASAP, Gupta said in the statement.

"Individuals who have only received two doses of the vaccine — or worse, none at all — are still at significant risk of COVID-19, and some will develop severe disease," he said. "The sheer number of new cases we are seeing every day reinforces the need for everyone to get their boosters as quickly as possible."

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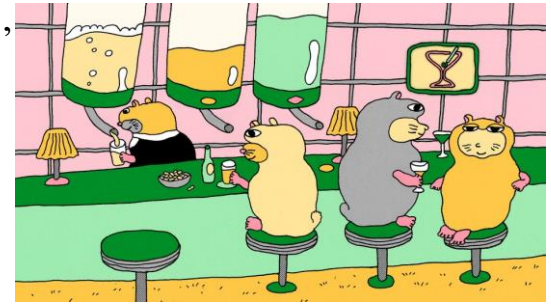
You Have No Idea How Hard It Is to Get a Hamster Drunk

"You just put a bottle of unsweetened Everclear on the cage and they love it."

By Sarah Zhang

The heaviest drinkers in the animal kingdom are punier than you might expect. Elephants, for example, are massive, but they are relative lightweights—they lack a gene for alcohol metabolism. Humans actually rank pretty highly, thanks to our ancestors' propensity for picking fermented fruit off the ground. But to find the real champs, you have to think smaller. Think hoarder. Think hamster.



Tom Bingham

"You just put a bottle of unsweetened Everclear on the cage and they love it," says Gwen Lupfer, a psychologist at the University of Alaska Anchorage who has studied alcohol consumption in hamsters. They regularly down 18 grams per kilogram of body weight a day, the alcoholic equivalent of a human drinking a liter and a half of 190-proof Everclear. In the wild, hamsters hoard ryegrass seeds and fruit in their burrows, and they eat this fermenting store as it becomes more and more alcoholic over the winter. In the lab, well, they're pretty happy with Everclear. Given

the choice between water and alcohol, they go for the booze.

Humans have known about hamsters' affinity for alcohol since at least the 1950s, when scientists in Texas found that hamsters could outdrink the common lab rat. Rats can be made to drink alcohol—either by selectively breeding genetic lines or by feeding them a mix of sugar and ethanol until they develop a taste for the latter. (Ethanol is the specific type of alcohol found in alcoholic drinks.) But with hamsters, "you could take a hamster right from the pet store and give it grain alcohol," says Danielle Gulick, an addiction researcher at the University of Florida. "It would happily drink."

And they can drink a lot before getting drunk. When Lupfer was studying dwarf hamsters, she and her students rated the animals' drunkenness on a literal wobbling scale. They scored the hamsters from zero, for "no visible wobbling," to four, for "falls onto side and does not right self." (They had previously, unsuccessfully, tried to track the hamsters' walking by dipping their paws in watercolor—they couldn't tell the drunk and sober hamsters' paw prints apart.) The hamsters never averaged above 0.5 on the wobbling scale—even at the highest oral doses. But when Lupfer and her team instead injected the ethanol directly into the hamsters' abdomens, the animals didn't do so well. They started wobbling and falling over at much, much lower doses.

Consumed orally, Lupfer explains, alcohol goes straight from the gut to the liver, which starts breaking down the mind-altering toxin that is ethanol. Hamster livers are "so efficient" at processing ethanol that very little ends up in their blood, says Tom Lawton, a critical-care doctor in Bradford, England. But when the hamsters got injected with ethanol, the substance could bypass the liver and go into their bloodstream and then their brain—hence much wobbling and falling over. Hamsters' alcohol tolerance is likely an adaptation to their hoarding lifestyle. (Other animal hoarders might have evolved a similar tolerance, but they haven't been as easy to study in a lab.) They would have a tough time getting through the winter, Lupfer told me, if they "didn't like their own food that they'd hoarded or if they got sick from the alcohol in it."

Hamsters don't just tolerate alcohol, though; they prefer it to water—and that might be because they're drinking for the calories. (Alcohol has seven calories per gram, almost as many as does fat, which clocks in at nine.) Gulick has found that giving hamsters sucrose water can suppress their boozing, but calorie-free sucrose water cannot. And in the '90s, scientists investigating whether hamsters could be a good model for alcoholism studies decided to test ethanol against carefully calorie-matched offerings of tomato juice, peach juice, mango juice, sugar water, and a chocolate Ensure Plus nutrition shake. The hamsters indeed started drinking less alcohol when given sweet, calorie-rich alternatives. Chocolate Ensure Plus worked the best, which the researchers chalked up to a preference for its taste.

Lawton, who recently tweeted about hamsters and alcohol in a delightful thread, told me that he bred hamsters in his youth in Yorkshire. He did not learn until medical school that very serious scientists had studied hamsters' alcoholic preferences. But as a teenager, he made a related discovery of his own. When his house got so cold that the hamsters would start hibernating, a spot of brandy would perk them right back up. Cheers.