http://bit.ly/2GdffkP

Tuberculosis bacteria survive in amoebae found in soil

Bacterium which causes bovine TB can survive and grow in small, single-celled organisms found in soil and dung.

Scientists from the University of Surrey and University of Geneva have discovered that the bacterium which causes bovine TB can survive and grow in small, single-celled organisms found in soil and dung. It is believed that originally the bacterium evolved to survive in these single-celled organisms known as amoebae and in time progressed to infect and cause TB in larger animals such as cattle.

During the study, published in the *ISME Journal*, scientists sought to understand more about the bacterium Mycobacterium bovis (M. bovis), which causes bovine TB, and how it can survive in different environments. To do this scientists infected a type of amoebae known as Dictyostelium discoideum with M. bovis. Unlike other bacterium which were digested and used as a food source by the amoebae, M. bovis was unharmed and continued to survive for two days. In-depth analysis showed that the bacterium uses the same genes to escape from amoebae that it uses to avoid being killed by immune cells in larger animals such as cattle and humans.

Scientists also discovered that M. bovis remained metabolically active and continued to grow, although at a slower pace, at lower temperatures than expected. Previously it was thought the bacterium could only replicate at 37˚C, the body temperature of cattle and humans; however, replication of the bacterium was identified at 25 ˚C. Researchers believe that the bacterium's ability to adapt to ambient temperatures and survive in amoebae may partially explain high transmission rates of the bacterium between animals.

Bovine TB is a hugely underestimated problem worldwide and England has the highest incidence of infection in Europe. Cattle found to have bovine TB are legally required to be slaughtered due to the high risk of the disease entering the food chain and spreading to humans. 32,793 cattle were slaughtered in England in 2018 in a bid to curtail the spread of the disease.

Lead author Professor Graham Stewart, Head of the Department of Microbial Sciences at the University of Surrey, said: "Despite implementation of control measures, bovine TB continues to be a major threat to cattle and has an enormous impact on the rural economy. Understanding the biology behind the TB disease and how it spreads is crucial for a balanced discussion on this devastating problem and to developing preventative measures to stop its spread. "An important additional benefit is that our research shows the potential for carrying out at least some future TB research in amoebae rather than in large animals."

More information: *Rachel E Butler et al. Mycobacterium bovis uses the ESX-1 Type VII secretion system to escape predation by the soil-dwelling amoeba Dictyostelium discoideum, The ISME Journal (2020). DOI: 10.1038/s41396-019-0572-z*

https://wb.md/2RM8Q5t

Moderate Alcohol Intake Linked to Lower Risk of Kidney Disease

People who consume up to a limit of 20 drinks per week, have a lower risk of developing chronic kidney disease

Pam Harrison

People who consume either modest, or what some may even consider not-so-modest, amounts of alcohol every week have a lower risk of developing chronic kidney disease (CKD) compared with never drinkers, and higher levels of alcohol consumption are associated with greater protection up to a limit of 20 drinks per week, according to a new analysis of the Atherosclerosis Risk in Communities (ARIC) study.

"Modest alcohol consumption has been found to be associated with lower risk of coronary heart disease (CHD) and myocardial

infarction, which share similar risk factors and pathophysiology with CKD," lead author Emily Hu, MHS, Johns Hopkins University, Baltimore, Maryland, and colleagues observe.

"Our large prospective cohort study of 12,692 blacks and whites in the United States found a significant and consistent inverse association between alcohol consumption and incident CKD...[although] for alcohol consumption > 20 drinks per week, the association was no longer statistically significant," they add.

The study was published in the January issue of the *Journal of Renal Nutrition*.

Lengthy Follow-up of the ARIC Study

The ARIC study was a community-based cohort of middle-aged black and white men and women between the ages of 45 and 64 years at study enrollment. "Alcohol consumption was assessed at visit 1 (1987-1989)," investigators note. People were asked if they currently drank alcohol and, if so, how often.

Four ounces of wine, 12 ounces of beer, or 1.5 ounces of hard liquor counted as a single drink. Current drinkers were categorized as drinking 1 or fewer drinks per week, 2 to 7 drinks per week, 8 to 14 drinks per week, or 15 or more drinks per week.

Incident CKD was defined as an estimated glomerular filtration rate (eGFR) of less than 60 mL/min/1.73m^2 accompanied by a 25% or greater decline in eGFR, kidney disease-related hospitalization or death, or development of end-stage renal disease.

Over a median follow-up of 24 years, 3664 cases of incident CKD were documented among the cohort.

In all three models used to analyze the effect that alcohol might have on CKD risk, "participants who drank alcohol had significantly lower risks of CKD compared with never drinkers," investigators report.

No significant association was observed between CKD risk and former drinkers, they add.

In their main model, adjusted for total energy intake, age, sex, race, income, education level, health insurance, smoking, and physical activity, participants who drank 1 or fewer drinks per week had a 12% lower risk of developing CKD compared with never drinkers, while those who drank 2 to 7 drinks per week had a 20% lower risk of CKD than the same comparator group.

Participants who consumed 8 to 14 drinks per week had a 29% lower CKD risk compared with never drinkers, while those who consumed 15 drinks or more per week had a 23% lower risk of CKD, again compared with never drinkers.

Additional adjustments for potential mediators of CKD risk including diabetes, high blood pressure, body mass index, and baseline eGFR did not appreciably change these estimates, the researchers add. In fact, "the risk of CKD per each additional drink per day after accounting for the competing risk of non-CKD death was similar to the main results," they note.

Gender did not appear to affect the findings but the association between alcohol consumption and CKD risk appeared to be stronger among smokers than nonsmokers.

"We found that alcohol consumption ranging from 1 drink per week to 15 drinks per week was associated with lower risk of incident CKD compared with never drinkers after adjusting for confounders," the authors emphasize.

"Moderate Consumption of Alcohol May Not Be Harmful to Kidneys"

As the authors suggest, the possible ways in which alcohol might affect CKD risk may be similar to the effect alcohol has on the risk of CHD as the two share similar pathophysiological pathways.

For example, the prevalence of diabetes was lower among current drinkers in the current study relative to never drinkers.

"Thus, because diabetes is a major risk factor for CKD, alcohol may...lower the risk of diabetic nephropathy and arteriosclerosis associated with type 2 diabetes," the researchers hypothesize.

They note that alcohol consumption was self-reported so weekly drinking levels in the study may have been under-reported.

"Drinking habits may [also] have changed over time," they acknowledge. Still, they conclude that "moderate consumption of alcohol may not likely be harmful to the kidneys."

However, they stress that the Global Burden of Disease Study suggests even low alcohol consumption may be associated with an increased global disease burden.

"Therefore, our findings must be considered in the context of all the potential benefits and harms of alcohol," they conclude.

The authors have reported no relevant financial relationships.

J Ren Nutr. 2020;30:22-30. Abstract

http://bit.ly/2RKuze1

The unexpected diversity of pain

It comes in many types that each require specialized treatment. Scientists are starting to learn how to diagnose the different varieties.

By Amber Dance

The first squeeze of my left thumb is gentle, almost reassuring. I rate it as 0 out of 100 on the pain scale.

But as a technician ramps up pressure on the custom-made thumb-squeezing device, it becomes less pleasant. I give ratings of 2, 6 … then 36. A few squeezes later, I'm at 79.

At 84, I'm glad the test is over as I put my tender thumb to my lips.

I've offered myself up for a pain study at the University of Michigan, in a long, low-slung building northeast of the university's main campus in Ann Arbor. As the day wears on, I'll undergo needle pokes, leg squeezes and an MRI scan — all part of a grand bid to better understand the root cause of an individual's pain, and point to the best solutions.

It's an understanding that's sorely needed. Lucky for me, I'm just a control in this experiment, and I can cry for mercy whenever I want. That's not the case for the multitudes of people — 50 million in the US alone — who have ongoing, chronic pain, for whom the medical pause buttons are far from adequate.

The thumb pressure test, in which participants rate their pain level on a scale from 0 to 100 as their thumbs are subjected to increasing pressure, is one of several ways that clinicians and researchers can evaluate a person's pain responses. Since people's thresholds to pain in tests like this vary according to pain syndrome, such tests can help with diagnosis. **Amber Dance**

"Our treatments for chronic pain are very bad," says Richard E. Harris, a neuroscientist at the University of Michigan's Chronic Pain and Fatigue Research Center and a co-researcher on the study, which should ultimately help to improve diagnoses and therapies. Today, doctors mostly define pain by where it is: the abdomen, the lower back, the joints. Then they offer up treatments, usually anti-inflammatories or opioids, that too often do nothing to the cells and molecules causing a person to hurt. A recent analysis in the *Journal of the American Medical Association* found that opioids reduced pain by an average of less than one point on a 10-point scale, across a variety of chronic conditions.

As part of the precision medicine movement and thanks to modern brain-imaging technology, scientists are starting to puzzle out the different types of pain: what causes them, how to diagnose them and how to prescribe treatments to match. It's an area that is far from settled. As recently as 2017, the International Association for the Study of Pain defined a new pain type, called nociplastic. It's

characterized by the absence of any nerve or tissue damage in the parts that hurt.

Dan Clauw, director of the Michigan pain center, is passionate about helping people with this kind of long-misunderstood pain, which could underpin chronic conditions, such as fibromyalgia, that afflict millions. His blue eyes flash behind spectacles as he describes crisscrossing the globe to educate other physicians about nociplastic pain. He's wearing a navy blazer and slacks when we meet for lunch between my testing sessions, because he's just returned from giving a presentation about marijuana and pain. He jokes that his colleagues won't recognize him out of his usual jeans.

Imaging the brain, along with doing prodding and poking tests of the type I endured, is beginning to point to signatures that explain the problem and suggest solutions. Eventually, this knowledge will help scientists to develop more targeted therapies, so doctors can treat patients better.

Taxonomy of pain

In broad strokes, pain falls into three categories: nociceptive, neuropathic and nociplastic. ("Noci-" is from the Latin for "to do harm.")

Nociceptive pain results from inflammation or direct damage to tissues. When that torture device squeezes my thumb, for example, pain-sensing nerves notice the pressure and spring into action. They transmit messages to my spinal cord, which sends them on to my brain, telling me "Ouch!"

This kind of discomfort is often short-lived; mine dissipates after I've sucked on my thumb for a few moments. Nociceptive pain can also be chronic, though — for example in osteoarthritis, where the cartilage in joints wears away and causes stretching of tendons and ligaments, or through the ongoing inflammation of rheumatoid arthritis.

Neuropathic pain, in contrast, happens when the pain-sensing nerves themselves are damaged or irritated, so that they send inappropriate "Ow!" signals to the brain. It typically results from some injury or disease, such as diabetes or shingles. It can also happen when a nerve is pinched, as in the case of carpal tunnel syndrome, when a nerve in the wrist gets squeezed. It's often long-lasting, unless the damage is repaired.

And ***nociplastic***, the newly named type, results from no obvious inflammation or injury. Rather, it's as if the volume knob for pain is turned up way too high, not at the pain site itself but further afield. Nociplastic pain seems to arise in parts of the central nervous system — the brain or spinal cord — that receive, transmit, or process those "Ouch!" signals. These nerves misfire, creating a sensation of pain even though nothing may be wrong. The location of the problem, the central nervous system, is why Clauw prefers to call it "central sensitization." The classic example is fibromyalgia, which causes pain that seems to stem from muscles, tendons and joints, despite the real problem's lying in the brain or spinal cord.

http://bit.ly/30Nc4d4

Mosquitoes are drawn to flowers as much as people -- and now scientists know why

Scientists know little about the scents that draw mosquitoes toward certain flowers, or repel them from others

Without their keen sense of smell, mosquitoes wouldn't get very far. They rely on this sense to find a host to bite and spots to lay eggs.

And without that sense of smell, mosquitoes could not locate their dominant source of food: nectar from flowers.

"Nectar is an important source of food for all mosquitoes," said Jeffrey Riffell, a professor of biology at the University of Washington. "For male mosquitoes, nectar is their only food source, and female mosquitoes feed on nectar for all but a few days of their lives."

Yet scientists know little about the scents that draw mosquitoes toward certain flowers, or repel them from others. This information could help develop less toxic and better repellents, more effective traps and understand how the mosquito brain responds to sensory information -- including the cues that, on occasion, lead a female mosquito to bite one of us.

Aedes mosquitoes feeding from Platanthera flowers. **Kiley Riffell**

Riffell's team, which includes researchers at the UW, Virginia Tech and UC San Diego, has discovered the chemical cues that lead mosquitoes to pollinate a particularly irresistible species of orchid. As they report in a paper published online Dec. 23 in the *Proceedings of the National Academy of Sciences*, the orchid produces a finely balanced bouquet of chemical compounds that stimulate mosquitoes' sense of smell. On their own, some of these chemicals have either attractive or repressive effects on the mosquito brain. When combined in the same ratio as they're found in the orchid, they draw in mosquitoes as effectively as a real flower. Riffell's team also showed that one of the scent chemicals that repels mosquitoes lights up the same region of the mosquito brain as DEET, a common and controversial mosquito repellant.

Their findings show how environmental cues from flowers can stimulate the mosquito brain as much as a warm-blooded host -- and can draw the mosquito toward a target or send it flying the other direction, said Riffell, who is the senior author of the study.

The blunt-leaf orchid, or Platanthera obtusata, grows in cool, high-latitude climates across the Northern Hemisphere. From field stations in the Okanogan-Wenatchee National Forest in Washington state, Riffell's team verified past research showing that local mosquitoes pollinate this species, but not its close relatives that grow in the same habitat. When researchers covered the flowers with bags -- depriving the mosquitoes of a visual cue for the flower -- the mosquitoes would still land on the bagged flowers and attempt to feed through the canvas. Orchid scent obviously attracted the mosquitoes. To find out why, Riffell's team turned to the individual chemicals that make up the blunt-leaf orchid's scent.

"We often describe 'scent' as if it's one thing -- like the scent of a flower, or the scent of a person," said Riffell. "Scent is actually a complex combination of chemicals -- the scent of a rose consists of more than 300 -- and mosquitoes can detect the individual types of chemicals that make up a scent."

Riffell describes the blunt-leaf orchid's scent as a grassy or musky odor, while its close relatives have a sweeter fragrance. The team used gas chromatography and mass spectroscopy to identify dozens of chemicals in the scents of the Platanthera species. Compared to its relatives, the blunt-leaf orchid's scent contained high amounts of a compound called nonanal, and smaller amounts of another chemical, lilac aldehyde.

Riffell's team also recorded the electrical activity in mosquito antennae, which detect scents. Both nonanal and lilac aldehyde stimulated antennae of mosquitoes that are native to the blunt-leaf orchid's habitat. But these compounds also stimulated the antennae of mosquitoes from other regions, including *Anopheles stephensi*, which spreads malaria, and *Aedes aegypti*, which spreads dengue, yellow fever, Zika and other diseases.

Experiments of mosquito behavior showed that both native and non-native mosquitoes preferred a solution of nonanal and lilac aldehyde mixed in the same ratio as found in blunt-leaf flowers. If the researchers omitted lilac aldehyde from the recipe, mosquitoes lost interest. If they added more lilac aldehyde -- at levels found in the blunt-leaf orchid's close relatives -- mosquitoes were indifferent or repelled by the scent.

Using techniques developed in Riffell's lab, they also peered directly into the brains of Aedes increpitus mosquitoes, which overlap with blunt-leaf orchids, and a genetically modified strain of *Aedes aegypti* previously developed by Riffell and co-author Omar Akbari, an associate professor at UC San Diego. They imaged calcium ions -- signatures of actively firing neurons -- in the antenna lobe, the region of the mosquito brain that processes signals from the antennae.

These brain imaging experiments revealed that nonanal and lilac aldehyde stimulate different parts of the antenna lobe -- and even compete with one another when stimulated: The region that responds to nonanal can suppress activity in the region that responds to lilac aldehyde, and vice versa. Whether this "cross talk" makes a flower attractive or repelling to the mosquito likely depends on the amounts of nonanal and lilac aldehyde in the original scent. Blunt-leaf orchids have a ratio that attracts mosquitoes, while closely related species do not, according to Riffell.

"Mosquitoes are processing the ratio of chemicals, not just the presence or absence of them," said Riffell. "This isn't just important for flower discrimination -- it's also important for how mosquitoes discern between you and I. Human scent is very complex, and what is probably important for attracting or repelling mosquitoes is the ratio of particular chemicals. We know that some people get bit more than others, and maybe a difference in ratio explains why."

The team also discovered that lilac aldehyde stimulates the same region of the antenna lobe as DEET. That region may process "repressive" scents, though further research would need to verify this, said Riffell. It's too soon to tell if lilac aldehyde may someday be an effective mosquito repellant. But if it is, there is an added bonus.

"It smells wonderful," said Riffell.

Lead author is Chloé Lahondère, who conducted the research as a UW postdoctoral fellow and is now a research assistant professor at Virginia Tech. Additional co-authors are Clément Vinauger, a former UW postdoctoral researcher and current assistant professor at Virginia Tech; UW biology graduate students Ryo Okubo and Jeremy Chan; and UW postdoctoral researcher Gabriella Wolff. The research was funded by the National Institutes of Health, the Air Force Office of Scientific Research and the University of Washington.

For more information, contact Riffell at 206-685-2573 or jriffell@uw.edu.

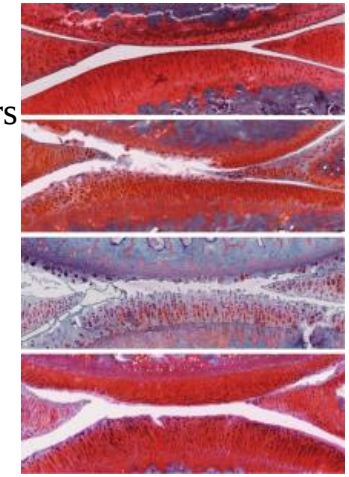
Grant numbers: RO1-DC013693, R21-AI137947, FA9550-14-1-0398, FA9550-16-1-0167

Link to full release with images:
https://www.washington.edu/news/2020/01/21/mosquitoes-flowers/

http://bit.ly/2sPXvsu

Drug combo reverses arthritis in rats

A combination of two previously studied osteoarthritis drugs works better than either drug alone, Salk researchers discovered



LA JOLLA--(January 21, 2020) People with osteoarthritis, or "wear and tear" arthritis, have limited treatment options: pain relievers or joint replacement surgery. Now, Salk researchers have discovered that a powerful combination of two experimental drugs reverses the cellular and molecular signs of osteoarthritis in rats as well as in isolated human cartilage cells. Their results were published in the journal *Protein & Cell* on January 16, 2020.

***The top image shows a knee joint in a healthy rat. (White indicates cartilage.) The second image from top shows a joint with grade 2 untreated osteoarthritis. The third image shows a joint with osteoarthritis that has worsened from grade 2 to grade 4 after six weeks of placebo therapy. The bottom image shows a joint with osteoarthritis that improved from grade 2 to grade 1 (mild) after six weeks of combination therapy with alphaKlotho and sTGFbR2.* Credit: Salk Institute**

"What's really exciting is that this is potentially a therapy that can be translated to the clinic quite easily," says Juan Carlos Izpisua Belmonte, lead author and a professor in Salk's Gene Expression

Laboratory. "We are excited to continue refining this promising combination therapy for human use."

Affecting 30 million adults, osteoarthritis is the most common joint disorder in the United States and its prevalence is expected to rise in coming years due to the aging population and increasing rate of obesity. The disease is caused by gradual changes to cartilage that cushions bones and joints. During aging and repetitive stress, molecules and genes in the cells of this articular cartilage change, eventually leading to the breakdown of the cartilage and the overgrowth of underlying bone, causing chronic pain and stiffness.

Previous research had pinpointed two molecules, alpha-KLOTHO and TGF beta receptor 2 (TGFβR2), as potential drugs to treat osteoarthritis. αKLOTHO acts on the mesh of molecules surrounding articular cartilage cells, keeping this extra-cellular matrix from degrading. TGFβR2 acts more directly on cartilage cells, stimulating their proliferation and preventing their breakdown. While each drug alone had only moderately curbed osteoarthritis in animal models of the disease, Izpisua Belmonte and his colleagues wondered if the two drugs would act more effectively in concert.

"We thought that by mixing these two molecules that work in different ways, maybe we could make something better," says Paloma Martinez-Redondo, a Salk postdoctoral fellow and co-first author of the new study.

The researchers treated young, otherwise healthy rats with osteoarthritis with viral particles containing the DNA instructions for making αKLOTHO and TGFβR2.

Six weeks after the treatment, rats that had received control particles had more severe osteoarthritis in their knees, with the disease progressing from stage 2 to stage 4. However, rats that had received particles containing αKLOTHO and TGFβR2 DNA showed recovery of their cartilage: the cartilage was thicker, fewer cells were dying, and actively proliferating cells were present. These animals' disease improved from stage 2 to stage 1, a mild form of osteoarthritis, and no negative side effects were observed.

"From the very first time we tested this drug combination on just a few animals, we saw a huge improvement," says Isabel Guillen-Guillen, the paper's co-first author. "We kept checking more animals and seeing the same encouraging results."

Further experiments revealed 136 genes that were more active and 18 genes that were less active in the cartilage cells of treated rats compared to control rats. Among those were genes involved in inflammation and immune responses, suggesting some pathways by which the combination treatment works.

To test the applicability of the drug combination to humans, the team treated isolated human articular cartilage cells with αKLOTHO and TGFβR2. Levels of molecules involved in cell proliferation, extra-cellular matrix formation and cartilage cell identity all increased.

"That's not the same as showing how these drugs affect the knee joint in humans, but we think it's a good sign that this could potentially work for patients," says Martinez-Redondo.

The research team plans to develop the treatment further, including investigating whether soluble molecules of the αKLOTHO and TGFβR2 proteins can be taken directly, rather than administered through viral particles. They also will study whether the combination of drugs can prevent the development of osteoarthritis before symptoms develop. "We think that this could be a viable treatment for osteoarthritis in humans," says Pedro Guillen, director of the Clinica CEMTRO and co-corresponding author.

Other authors were Isabel Guillen-Guillen, Chao Wang, Javier Prieto, Masakazu Kurita, Fumiyuki Hatanaka, Cuiqing Zhong, Reyna Hernandez-Benitez, Tomoaki Hishida, Takashi Lezaki, Akihisa Sakamoto, Amy Nemeth, Yuriko Hishida, Concepcion Rodriguez Esteban, Kensaku Shojima, Pradeep Reddy, Ling Huang and Maxim Shokhirev of Salk; Noah Davidson and George Church of Harvard University; Estrella Nuñez-Delicado of Universidad Católica San Antonio de Murcia; Josep Campistol of Hospital Clinic of Barcelona; Isabel Guillen-Vicente, Elena Rodriguez-Iñigo, Juan Manuel Lopez-Alcorocho,

Marta Guillen-Vicente and Pedro Guillen-Garcia of Clinica CEMTRO; and Guang-Hui Liu of Chinese Academy of Sciences.

http://bit.ly/2uwAStF

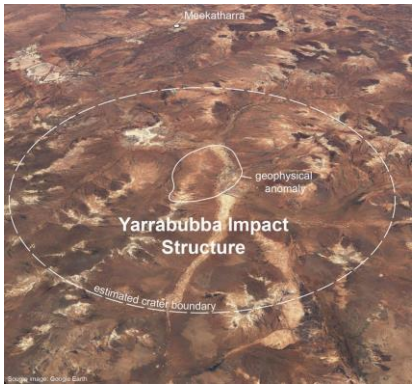
Yarrabubba is Earth's oldest known impact structure

Geological dating provides precise age for event that helped change our climate.

By Natalie Parletta

Evidence that the 70-kilometre wide Yarrabubba crater in outback Western Australia may be the Earth's oldest known meteorite impact structure has been presented in the journal *Nature Communications.*

Dated at 2.229 billion years, 200 million years older than the next known asteroid strike at Vredefort Dome in South Africa, the impact coincides with the end of a deep freeze known as early Snowball Earth and could have contributed to the ice thawing.



After this time period there are no rock records of large glacial deposits for 400 million years, says lead author Timmons Erickson from NASA Johnson Space Centre, Houston, US.

"Because of this, we were interested in seeing the role that an impact crater could have had during a time of global glaciations and whether an impact could release enough water vapour, a strong greenhouse gas, to significantly warm the planet."

Calculating the impact of the meteorite on an icy continent, they found that it could have sent half a trillion tonnes of water vapour into the atmosphere, thereby contributing to the global ice melt. This highlights why the timing of "extraterrestrial bombardment" is important, as the authors write, so its effects on the Earth's environment can be understood.

To date, the historical impact record is fragmented, making it hard to understand how meteorites affect the planet – apart from the Chicxulub asteroid that triggered the last mass extinction and could explain the ocean's acidification.

"There are still lots of gaps in the terrestrial impact record; while we know of thousands of impact craters on the Earth's moon, there are only about 190 recognised impact structures on Earth," says Erickson.

Craters gradually disappear with time through erosion and tectonic movements, making it challenging to find old craters at all, says co-author Aaron Cavosie from Curtin University, Western Australia.

This is the case with Yarrabubba, he adds. "The landscape is barren, but not empty. Bits of rocks exposed near the centre of the formerly giant crater hold the microscopic clues to the past violence that occurred 2.229 billion years ago."

Added to that, geoscience relies heavily on fieldwork, he says, "where observations are made standing in the burning sun, flies buzzing in your ears, dust on your boots.

"The analytical firepower is what delivers the result, but it starts with a geologist who says, 'hey, that rock looks interesting'."

Once the rocks are selected, advanced lab methodologies are applied – in this case, Cavosie says, "electron backscatter diffraction was used to identify the specific crystals that had been age-reset through analysis of their microscopic orientation".

Then they used mass spectrometry to measure "isotopic clocks" contained by uranium and lead in the rocks.

Trace amounts of uranium decays to lead over time at a known rate, Cavosie explains, so their disruption by a meteorite helps to pinpoint the time it struck.

"When a giant impact forms, rocks in the centre get hot enough to cause the atomic bonds in the mineral to break open and reform.

This process evacuates the accumulated lead. After the impact, lead starts collecting again."

The breakthrough at Yarrabubba, part of Western Australia's rich geological heritage, is a "once-in-a-generation type of discovery," says Cavosie, the last dating being the 2.02 billion-year-old Vredefort impact 25 years ago.

"What the Yarrabubba discovery shows clearly is that it is worth the effort to continue to search the geological record for old craters.

"It helps planetary scientists recreate the formative years of Earth's history and write some of the earliest pages in the history book."

http://bit.ly/38Ea61b

Self-destructing dark matter may be flooding the sky with gamma-rays, study suggests

Can the most energetic light in the universe point to the most elusive substance in the universe? A new study thinks so.

By Brandon Specktor - Senior Writer

Gamma-rays — the brightest, most powerful light in the universe — sail across the sky invisible to human eyes. These exceptionally energetic bursts of radiation flash out of supernova explosions, spark off of colliding neutron stars, and spew forth from the hungriest black holes.

When astronomers can catch them with gamma-ray telescopes, these invisible fireworks point toward some of the universe's most explosive structures. Now, an international team of researchers hopes that those all-powerful rays could also lead to something far stranger and more elusive — the invisible substance known as dark matter.

In a new study accepted for publication in the journal Physical Review Letters, and detailed on the preprint database arXiv, the researchers looked at what they call the "unresolved gamma-ray background" — that is, all of the faint and mysterious gamma-ray signals that are left over after known sources like black holes and supernovas are accounted for. When the team compared a map of unresolved gamma-rays with a map of matter density in the same section of the universe, they found that the rays aligned precisely with gravitationally massive areas where dark matter was predicted to hide out.

According to study co-author Daniel Gruen, this correlation suggests that dark matter may be largely responsible for the universe's faint gamma-ray background. If that's the case, it could give astronomers some vital clues about the mysterious substance's properties.

"Dark matter could decay like a radioactive nucleus, producing gamma rays as it does," Gruen, an astrophysicist at the Department of Energy's SLAC National Accelerator Laboratory at Stanford University in California, told Live Science. "Or perhaps multiple dark matter particles are colliding, producing gamma-rays as they interact."

Ripples in the dark

Dark matter is thought to make up about 85% of the universe's mass, though researchers still aren't positive what or where it is. Totally invisible to modern scientific instruments, the stuff has never been successfully detected.

"We do know some of dark matter's properties though," Gruen said. "We know that it's very common, and we know that it has mass that interacts gravitationally with other mass."

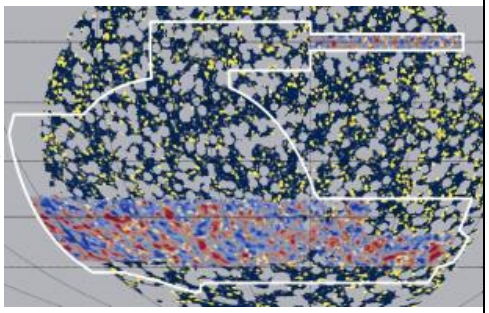
In other words, even though dark matter is invisible, it makes a visible impact on the universe through its powerful gravity. One of those impacts is known as gravitational lensing — essentially, how light from distant galaxies is warped by the gravity of the massive objects it passes on its way toward Earth.

For the new study, the researchers looked at a map of gravitational lensing in a particular chunk of the universe, compiled by a project called the Dark Energy Survey (DES). Mounted on a giant

telescope in Chile, the survey's dedicated camera spent a year snapping high-definition images of hundreds of millions of galaxies, focusing on where distant light is most misshapen by pockets of intense gravity. While some of the most massive regions on the resulting map correspond to known galaxies, other hefty pockets likely show the hidden influence of dark matter at work, Gruen said.

To better understand what that influence might look like, the researchers compared this mass map with a map of gamma-ray emissions detected in the same region by NASA's Fermi gamma-ray telescope over the past nine years. Using a mathematical model, the team removed all radiation that could be definitively tied to "mundane" sources like black holes and supernovas, based on their energy output, distance and various other factors.

Now, left with only the mysterious "unresolved" gamma-ray sources, the team compared both maps. They saw a clear overlap between regions of high gamma-ray radiation and regions with lots of mass.



Here are the team's two maps aligned. Dark matter density (red) overlaps astonishingly well with regions of high gamma-ray activity (yellow). **(Image credit: Daniel Gruen/SLAC/Stanford, Chihway Chang/University of Chicago, Alex Drlica-Wagner/Fermilab)**

"This is the first study where we've been sure that, where there are a lot of gamma rays, there's also a lot of dark matter," Gruen said.

If dark matter truly is emitting gamma rays, that could seriously narrow down how it's detected and what it's actually made of. However, it's still possible that the faint gamma-ray background on the Fermi map has nothing to do with dark matter, Gruen said. The mathematical model that the researchers used to weed out those "mundane" sources of gamma-ray emissions (such as black holes) is based on some assumptions about those objects' properties.If those assumptions are wrong, distant black holes could be responsible for much more of the mysterious gamma-ray background than the researchers accounted for.

"Maybe that model is incomplete, and maybe we're actually learning something about these gamma-ray-emitting black holes," Gruen said. "Perhaps, these black holes are living in more massive galaxies than we thought."

More data on both gamma rays and gravitational lensing will help the team hone their model and better interpret their maps of the universe. Since the study's conclusion, the DES has collected six times more information on the universe's mass distribution, and the FERMI satellite remains one of many telescopes tracking gamma-ray explosions. A follow-up study showing even clearer results should follow in the next few years, Gruen said.

https://nyti.ms/2GtXcGV

Ancient DNA from West Africa Adds to Picture of Humans' Rise

From a burial site in Cameroon, archaeologists recovered human genetic material dating as far back as 8,000 years.

By Carl Zimmer

In October 2015, scientists reconstructed the genome of a 4,500-year-old man who lived in Ethiopia. It was the first time that anyone had created a complete genetic snapshot of an African from an ancient skeleton.

Since then, other researchers have recovered DNA from skeletons unearthed in other regions of the continent. Now researchers have found the first genetic material from West Africa. On Wednesday a team reported that they had recovered DNA from four individuals in Cameroon, dating back as far as 8,000 years.

These ancient genomes contain vital clues to the history of the continent that have largely disappeared in the past few thousand

years. Taken together, they are giving scientists a new vision of our species since it arose in Africa.

In the new study, published in Nature, the researchers reported that modern humans diverged into four major populations between 200,000 and 250,000 years ago. One of those populations is new to scientists; few traces of it remain in the DNA of living Africans.

***The Shum Laka rock shelter in Cameroon, where the remains of two 8,000-year-old boys were discovered in 1994. Scientists recently recovered ancient DNA from the two individuals and from another pair of children buried 5,000 years later.*Credit...Isabelle Ribot**

The vanished population may have consisted of bands of hunter-gatherers who lived south of the Sahara from Mali to Sudan until just a few thousand years ago.

"We are so limited by the information we can get from living people," said Jessica Thompson, an archaeologist at Yale University who was not involved in the new study. "It's pretty clear that there's been a huge transformation in the genetic landscape in Africa just recently."

Scientists have been studying the genetic diversity of living Africans since the 1970s. As it became possible to sequence more DNA, the additional data revealed that the genetic variation among living Africans was much greater than that among the rest of the world combined.

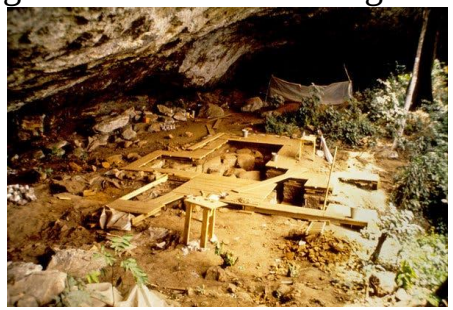
This insight made it clear that our species arose in Africa and stayed there for most of its history. Small groups of people expanded out to give rise to non-African populations.

But scientists have struggled to draw the older branches of the human family tree with much precision. Looking for fresh clues, they tried drilling into ancient bones. The odds seemed low. Many researchers assumed that ancient, fragile DNA molecules would not have survived the hot climate across much of Africa.

The discovery in 2015 of Mota, an Ethiopian skeleton with DNA to offer, proved otherwise. Geneticists and archaeologists began investigating other skeletons from across Africa, and found a few that still contained genetic material.

Mary Prendergast, an archaeologist at Saint Louis University in Madrid, considered the skeletons found at Shum Laka, a rock shelter in Cameroon, among the top candidates to test for DNA. "People working all over the continent are aware of this site," she said.

Archaeologists have dug into the floor of Shum Laka since the 1980s, and have found layers of human remains as old as 30,000 years. The surrounding region has long been viewed as the origin of one of the most important expansions in African history. About 4,000 years ago, the Bantu people started farming oil palm and grains. They later expanded for thousands of miles to the east and south, across a vast swath of Africa.



***A view of the Shum Laka excavation site in 1994. The ancient individuals buried here shared little in common genetically with present-day Bantu-speaking people in the area.*Credit...Pierre de Maret**

Dr. Prendergast wondered if DNA from Shum Laka would show a kinship with living Bantu people. But finding that genetic material would be a long shot, she knew: Shum Laka is close to the Equator and has a heavy rainy season each year. "My hopes were not high at all," she said. "I went into this project thinking, 'Will this work?'"

In the end, it did. The researchers recovered abundant DNA from four individuals, two of whom were buried in the rock shelter 8,000 years ago, and another pair 3,000 years ago.

One of the 8,000-year-old skeletons was especially rich with human DNA. “It’s of a quality of a modern medical genome,” said David Reich, a Harvard Medical School geneticist and a co-author with Dr. Prendergast.

To Dr. Prendergast’s surprise, none of the people at Shum Laka were closely related to Bantu speakers at all. In fact, they had a strong kinship to the Aka, a group of hunter-gatherers with a pygmy body type who live today in rain forests 1,000 miles to the east.

To make sense of this paradox, the researchers carried out a large-scale comparison of all the ancient African DNA gathered so far, along with living people from across Africa and beyond. The team found a scenario that best explains how different groups of Africans ended up with their particular combinations of DNA.

Dr. Reich and his colleagues can trace the major lineages of people back to common ancestors who lived in Africa between 200,000 and 250,000 years ago.

“It seems we have four lineages splitting at the same time,” said Mark Lipson, a postdoctoral researcher at Harvard and an author of the new study.

One lineage passed down their DNA to living hunter-gatherers in southern Africa. A second group were ancestors of the Aka and other central African hunter-gatherers.

A third group became hunter-gatherers in East Africa, as evidenced by the fact that many living Africans in that region have inherited some of that DNA.

The fourth group, which Dr. Reich and his colleagues call “Ghost Modern,” is far more mysterious.

The ancient Shum Laka people have a substantial amount of Ghost Modern ancestry. So does the ancient Mota man from Ethiopia. But ancient remains from Morocco and South Africa had none. Today some people in Sierra Leone have a tiny trace of Ghost Modern ancestry, the researchers found.

It’s possible that the Ghost Moderns were hunter-gatherers who lived across the southern edge of the Sahara. They remained isolated from other Africans for tens of thousands of years. Later, they bred with people from other groups at the eastern and western edges of their range.

Most people in Africa — and the rest of the planet — can trace much of their ancestry to the East African hunter-gatherers. Less than 100,000 years ago, this group split into new lineages.

One group gave rise to many of today’s East African tribes. Another group included the Mota man. They were closely related to the people who expanded east out of East Africa and into the rest of the world.

A separate group of East Africans moved west, encountering and mixing with Central African hunter-gatherers and eventually becoming the first West Africans. The people of Shum Laka may be the descendants of this group.

Many thousands of years passed before a different group of the West Africans gave rise to the Bantu people. Their population discovered agriculture, grew and took over larger areas of land.

But the Bantu farmers didn’t swiftly drive hunter-gatherers to oblivion. The Shum Laka people survived for at least 1,000 years in the heart of Bantu country.

But after a couple thousand years, the society reached a tipping point, and the hunter-gatherers were marginalized. East African tribes that also began farming and grazing livestock applied additional pressure. It’s possible that this pressure brought an end to many groups of hunter-gatherers, including the Mota and the Shum Laka — perhaps even the ancient Ghost Modern people.

The surviving hunter-gatherers interbred with neighboring farmers. The new study finds that the Aka, for instance, can trace 59 percent of their ancestry to the Bantu. “Their results have some big implications for us archaeologists,” Dr. Thompson said.

It's conceivable that researchers could find skeletons of Ghost Modern individual in areas those people once lived. The bones might even hold some DNA that could confirm the hypothesis.

"If we could get really old samples from there, that would be amazing," Dr. Lipson said.

http://bit.ly/2tSEaHJ

Snakes Could Be the Original Source of the New Coronavirus Outbreak in China

A study of the virus's genetic sequence suggests similarities to that seen in snakes, but the origin must still be verified

By Haitao Guo, Guangxiang "George" Luo, Shou-Jiang Gao, The Conversation US

The following essay is reprinted with permission from The Conversation, an online publication covering the latest research.

Snakes—the Chinese krait and the Chinese cobra—may be the original source of the newly discovered coronavirus that has triggered an outbreak of a deadly infectious respiratory illness in China this winter.

The illness was first reported in late December 2019 in Wuhan, a major city in central China, and has been rapidly spreading. Since then, sick travelers from Wuhan have infected people in China and other countries, including the United States.

Using samples of the virus isolated from patients, scientists in China have determined the genetic code of the virus and used microscopes to photograph it. The pathogen responsible for this pandemic is a new coronavirus. It's in the same family of viruses as the well-known severe acute respiratory syndrome coronavirus (SARS-CoV) and Middle East respiratory syndrome coronavirus (MERS-CoV), which have killed hundreds of people in the past 17 years. The World Health Organization (WHO) has named the new coronavirus 2019-nCoV.

We are virologists and journal editors and are closely following this outbreak because there are many questions that need to be answered to curb the spread of this public health threat.

What is a coronavirus?

The name of coronavirus comes from its shape, which resembles a crown or solar corona when imaged using an electron microscope.

Coronavirus is transmitted through the air and primarily infects the upper respiratory and gastrointestinal tract of mammals and birds. Though most of the members of the coronavirus family only cause mild flu-like symptoms during infection, SARS-CoV and MERS-CoV can infect both upper and lower airways and cause severe respiratory illness and other complications in humans.

This new 2019-nCoV causes similar symptoms to SARS-CoV and MERS-CoV. People infected with these coronaviruses suffer a severe inflammatory response.

Unfortunately, there is no approved vaccine or antiviral treatment available for coronavirus infection. A better understanding of the life cycle of 2019-nCoV, including the source of the virus, how it is transmitted and how it replicates are needed to both prevent and treat the disease.

Zoonotic transmission

Both SARS and MERS are classified as zoonotic viral diseases, meaning the first patients who were infected acquired these viruses directly from animals. This was possible because while in the animal host, the virus had acquired a series of genetic mutations that allowed it to infect and multiply inside humans.

Now these viruses can be transmitted from person to person. Field studies have revealed that the original source of SARS-CoV and MERS-CoV is the bat, and that the masked palm civets (a mammal native to Asia and Africa) and camels, respectively, served as intermediate hosts between bats and humans.

In the case of this 2019 coronavirus outbreak, reports state that most of the first group of patients hospitalized were workers or customers at a local seafood wholesale market which also sold processed meats and live consumable animals including poultry, donkeys, sheep, pigs, camels, foxes, badgers, bamboo rats, hedgehogs and reptiles. However, since no one has ever reported finding a coronavirus infecting aquatic animals, it is plausible that the coronavirus may have originated from other animals sold in that market.

The hypothesis that the 2019-nCoV jumped from an animal at the market is strongly supported by a new publication in the Journal of Medical Virology. The scientists conducted an analysis and compared the genetic sequences of 2019-nCoV and all other known coronaviruses.

The study of the genetic code of 2019-nCoV reveals that the new virus is most closely related to two bat SARS-like coronavirus samples from China, initially suggesting that, like SARS and MERS, the bat might also be the origin of 2019-nCoV. The authors further found that the DNA coding sequence of 2019-nCoV spike protein, which forms the "crown" of the virus particle that recognizes the receptor on a host cell, indicates that the bat virus might have mutated before infecting people.

But when the researchers performed a more detailed bioinformatics analysis of the sequence of 2019-nCoV, it suggests that this coronavirus might come from snakes.

From bats to snakes

The researchers used an analysis of the protein codes favored by the new coronavirus and compared it to the protein codes from coronaviruses found in different animal hosts, like birds, snakes, marmots, hedgehogs, manis, bats and humans. Surprisingly, they found that the protein codes in the 2019-nCoV are most similar to those used in snakes.

Snakes often hunt for bats in wild. Reports indicate that snakes were sold in the local seafood market in Wuhan, raising the possibility that the 2019-nCoV might have jumped from the host species—bats—to snakes and then to humans at the beginning of this coronavirus outbreak. However, how the virus could adapt to both the cold-blooded and warm-blooded hosts remains a mystery.

The authors of the report and other researchers must verify the origin of the virus through laboratory experiments. Searching for the 2019-nCoV sequence in snakes would be the first thing to do. However, since the outbreak, the seafood market has been disinfected and shut down, which makes it challenging to trace the new virus' source animal.

Sampling DNA from animals sold at the market and from wild snakes and bats is needed to confirm the origin of the virus. Nonetheless, the reported findings will also provide insights for developing prevention and treatment protocols. The 2019-nCoV outbreak is another reminder that people should limit the consumption of wild animals to prevent zoonotic infections.

This article was originally published on The Conversation. Read the original article.

https://go.nature.com/37uIZpp

Why snakes probably aren't spreading the new China virus

One genetic analysis suggests reptilian reservoir — but researchers doubt that the coronavirus could have originated in animals other than birds or mammals.

Ewen Callaway & David Cyranoski

As human cases rise in a mysterious viral outbreak that originated in China, scientists are rushing to identify the animals, where they suspect the epidemic began. In a controversial study published last night, a team of researchers in China claimed to have an answer: snakes.

But other scientists say there is no proof that viruses such as those behind the outbreak can infect species other than mammals and birds. “Nothing supports snakes being involved,” says David Robertson, a virologist at the University of Glasgow, UK.

The pathogen responsible for the outbreak belongs to a large family called coronaviruses, which includes the viruses that cause severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS), as well as those behind the common cold. The latest virus — currently known as 2019-nCoV — is most closely related to SARS and related viruses that circulate in bats. But these can also infect other animals that can pass the virus to humans. Many scientists suspect that an unknown animal carrying 2019-nCoV spread the virus to humans at a live seafood and wild animal market in Wuhan, where the first cases were documented in December.

“The intermediate host is the missing piece of the puzzle: how have all these people got infected?” says Robertson.

Hedgehogs, chickens and bats

A team led by Wei Ji, a microbiologist at Peking University Health Science Center School of Basic Medical Sciences in Beijing, looked for a sign that 2019-nCoV had adapted to any specific animal host.

***A team of researchers pointed to the many-banded krait snake as one possible source of the coronavirus that originated in Asia.*Credit: Alamy**

Most amino acids are encoded by multiple codons — sequences of three DNA or RNA nucleotide triplets that encode amino acids. One way that viruses adapt is by encoding proteins using the same choice of codons as their host. Wei’s team compared the codons favoured by 2019-nCoV with those preferred by potential hosts including hedgehogs, pangolins, bats, chickens, humans and snakes. The team reported that 2019-nCoV’s choice of codons was most similar to those used by two snakes: *Bungarus multicinctus* (the many-banded krait) and *Naja atra* (the Chinese cobra). Snakes were sold at the Wuhan seafood and animal market, the researchers note.

“Taken together, snakes could be the most likely wildlife animal reservoir for the 2019-nCoV,” they write in a paper published on 22 January in the *Journal of Medical Virology*[1]. Robertson says it’s unlikely that 2019-nCoV has infected any secondary animal host for long enough to alter its genome significantly. “It takes a long time for such a process to play out,” he says.

Evidence gap

“They have no evidence snakes can be infected by this new coronavirus and serve as a host for it,” says Paulo Eduardo Brandão, a virologist at the University of São Paulo who is investigating whether coronaviruses can infect snakes at all. “There’s no consistent evidence of coronaviruses in hosts other than mammals and Aves (birds).”

Wei’s team has not yet responded to e-mails from *Nature*’s news team seeking comment on the paper and the criticism it has received. Many researchers are sceptical that the animal host or hosts of 2019-nCoV can be identified without further field and laboratory work. Many hope that genetic tests of animals or environmental sources, such as cages and containers, from the Wuhan market will turn up clues.

A mammal is the most likely candidate, says Cui Jie, a virologist at the Pasteur Institute of Shanghai who was part of a team that identified SARS-related viruses in bats from a cave in Yunnan province in southwestern China in 2017[2]. SARS and 2019-nCoV are part of a virus subgroup known as betacoronaviruses. Fieldwork in the wake of the 2002–03 SARS outbreak has found such viruses only in mammals, Cui says. “Clearly this 2019-nCoV is a mammalian virus.”

doi: 10.1038/d41586-020-00180-8

References

1. Ji, W., Wang, W., Zhao, X., Zai, J. & Li, X. J. Med. Virol. https://doi.org/10.1002/jmv.25682 (2020). PubMed Article Google Scholar

*2. Hu, B. et al. PLoS Pathog. **13**, e1006698 (2017). PubMed Article Google Scholar*

http://bit.ly/2uAoUiG

Researchers regrow damaged nerves with polymer and protein

Can regenerate long sections of damaged nerves, without the need for transplanting stem cells or a donor nerve.

PITTSBURGH - University of Pittsburgh School of Medicine researchers have created a biodegradable nerve guide -- a polymer tube -- filled with growth-promoting protein that can regenerate long sections of damaged nerves, without the need for transplanting stem cells or a donor nerve. So far, the technology has been tested in monkeys, and the results of those experiments appeared today in *Science Translational Medicine*.

"We're the first to show a nerve guide without any cells was able to bridge a large, 2-inch gap between the nerve stump and its target muscle," said senior author Kacey Marra, Ph.D., professor of plastic surgery at Pitt and core faculty at the McGowan Institute for Regenerative Medicine. "Our guide was comparable to, and in some ways better than, a nerve graft."

Half of wounded American soldiers return home with injuries to their arms and legs, which aren't well protected by body armor, often resulting in damaged nerves and disability. Among civilians, car crashes, machinery accidents, cancer treatment, diabetes and even birth trauma can cause significant nerve damage, affecting more than 20 million Americans.

Peripheral nerves can regrow up to a third of an inch on their own, but if the damaged section is longer than that, the nerve can't find its target. Often, the disoriented nerve gets knotted into a painful ball called a neuroma.

The most common treatment for longer segments of nerve damage is to remove a skinny sensory nerve at the back of the leg -- which causes numbness in the leg and other complications, but has the least chance of being missed -- chop it into thirds, bundle the pieces together and then sew them to the end of the damaged motor nerve, usually in the arm. But only about 40 to 60% of the motor function typically returns.

"It's like you're replacing a piece of linguini with a bundle of angel hair pasta," Marra said. "It just doesn't work as well."

Marra's nerve guide returned about 80% of fine motor control in the thumbs of four monkeys, each with a 2-inch nerve gap in the forearm. The guide is made of the same material as dissolvable sutures and peppered with a growth-promoting protein -- the same one delivered to the brain in a recent Parkinson's trial -- which releases slowly over the course of months.

The experiment had two controls: an empty polymer tube and a nerve graft. Since monkeys' legs are relatively short, the usual clinical procedure of removing and dicing a leg nerve wouldn't work. So, the scientists removed a 2-inch segment of nerve from the forearm, flipped it around and sewed it into place, replacing linguini with linguini, and setting a high bar for the nerve guide to match.

Functional recovery was just as good with Marra's guide as it was with this best-case-scenario graft, and the guide outperformed the graft when it came to restoring nerve conduction and replenishing Schwann cells -- the insulating layer around nerves that boosts electrical signals and supports regeneration. In both scenarios, it took a year for the nerve to regrow. The empty guide performed significantly worse all around.

With these promising results in monkeys, Marra wants to bring her nerve guide to human patients. She's working with the Food and

Drug Administration (FDA) on a first-in-human clinical trial and spinning out a startup company, AxoMax Technologies Inc.

"There are no hollow tubes on the market that are approved by the FDA for nerve gaps greater than an inch. Once you get past that, no off-the-shelf tube has been shown to work," Marra said. "That's what's amazing here."

Additional authors on the study include Neil Fadia, Jacqueline Bliley, Gabriella DiBernardo, Donald Crammond, Ph.D., Benjamin Schilling, Wesley Sivak, M.D., Ph.D., Alexander Spiess, M.D., Kia Washington, M.D., Matthias Waldner, M.D., Liao Han Tsung, Ph.D., Isaac James, M.D., Danielle Minteer, Ph.D., Casey Tompkins-Rhoades, Deok-Yeol Kim, Riccardo Schweizer, M.D., Debra Bourne, M.D., Adam Cottrill, George Panagis, Asher Schusterman, M.D., Francesco Egro, M.D., Insiyah Campwala, Tyler Simpson, M.S., Douglas Weber, Ph.D., Trent Gause, M.D., Jack Brooker, Tvisha Josyula, Astrid Guevara, Alexander Repko and Christopher Mahoney, all of Pitt.

This study was funded by the Armed Forces Institute of Regenerative Medicine (award number W81XWH-14-2-0003). MedGenesis Therapeutix Inc. supplied the growth-promoting protein. Axomax Technologies was formed after the experiments were completed.

http://bit.ly/38Dw3NO

Researchers May Have Solved Mystery of Akrotiri's Monkey Frescoes

Archaeologists had assumed the monkeys were an African species, which the Aegeans probably came into contact with via Egypt.

The blue monkeys painted on the walls of **Akrotiri** on the Greek island of **Santorini** are among many animals found in the frescoes of this 3,600-year-old city.

Historians have studied the murals for decades since they were unearthed in the 1960s and 1970s on the island, which was once known as Thera. But when we and a team of other primatologists recently examined the paintings, we **realized** the monkeys could provide a clue that the Bronze Age world was much more globalized than previously thought.

Archaeologists had assumed the monkeys were an African species, with which the Aegean people that built Akrotiri probably came into contact via trade links with Egypt.

But we think the paintings actually depict Hanuman langurs (genus *Semnopithecus*), monkeys from the Indian subcontinent.

This suggests the Aegean people, who came from Crete and the Cycladic islands in the Aegean Sea, may have had trade routes that reached over 2,500 miles.

The wall paintings of Akrotiri were preserved by ash from a volcano that destroyed the city some time in the 16th or 15th century BCE and offer an incredible glimpse of an early civilization in Europe.

Monkeys fresco on the north wall of Room 6 of Building Complex Beta at Akrotiri, Thera. **Image credit: Thera Akrotiri Excavations.**

We haven't been able to translate the earliest Aegean writing, but the paintings suggest just how developed these people's society, economy and culture were.

Much animal art from this period is generalized, meaning it's hard to confidently identify individual species.

In the case of the monkeys, we also don't have any physical remains from Aegean settlements to provide additional evidence of which species are depicted.

The reason why archaeologists and art historians have assumed they came from Egypt is because that was the nearest location with an indigenous monkey population that had known trade links with the Aegean.

As a result, the Akrotiri monkeys have been variously identified as baboons, vervets and grivet monkeys, all African species that live across a wide area.

Marie Pareja decided to take a different approach, gathering a team of primatologists who study apes, monkeys, and lemurs, including renowned taxonomic illustrator Stephen Nash.

Together, we examined photos of the art and discussed the animals depicted, considering not only fur color and pattern but also body size, limb proportions, sitting and standing postures, and tail position.

While we all agreed that some of the animals depicted were baboons, as previously thought, we began to debate the identification of the animals from one particular scene.

***Southern plains gray langurs (*Semnopithecus dussumieri*) in northern India.* Image credit: Thomas Schoch / CC-BY-SA-3.0.**

Identifying the langurs

The monkeys in the paintings are gray-blue. But although some living monkeys have small patches of blue skin — the blue on a mandrill's face, for example — none have blue fur.

There is an African forest monkey called the blue monkey, but it is mainly olive or dark gray, and the face patterns don't match those in the paintings. So we needed to use other characteristics to identify them.

They were previously believed to be vervets or grivets, small monkeys weighing between 3kg and 8kg (roughly the size of a housecat) that are found in the savannas of north and east Africa. Despite their silvery white fur, they also have dark-colored hands and feet and an overall look that matches the depictions in the paintings.

However, Hanuman langurs, which weigh a more substantial 11 to 18 kg, have a similar look. They also move quite differently, and this was crucial to the identification.

Both primates primarily live on the ground (as opposed to in trees) and have long limbs and tails. But the langurs tend to carry their tail upward, as an S- or C-shape or curving towards the head, while vervet monkeys carry their tail in a straight line or arcing downward. This tail position, repeated across multiple images, was a key factor in identifying the monkeys as Hanuman langurs.

International links

We know from archaeological evidence that Aegean peoples had access to minerals such as tin, lapis lazuli and carnelian that came from beyond the Zagros mountains on the western border of modern Iran.

But the artistic detail of the Akrotiri paintings, compared to other monkey art of the period, suggests that the artists had seen live animals, perhaps while traveling abroad.

It's understandable that earlier scholars thought the monkeys were African since relations between the Aegean and Egypt were already well known and supported by archaeological evidence. If you expect to find an African monkey, you will only look at African animals for possible explanations.

But as primatologists, we were able to bring a fresh look at the evidence without preconceived notions of ancient peoples or trade routes, and consider species living further afield.

This study is an excellent example of the importance of academics from different disciplines working together. Without the expertise of primatologists, it may not have been possibly to confidently identify these animals. Conversely, primatologists may not have considered these ancient human-primate interactions without a prompt from archaeologists.

M.N. Pareja et al. *A new identification of the monkeys depicted in a Bronze Age wall painting from Akrotiri, Thera.* Primates, *published online December 5, 2019; doi: 10.1007/s10329-019-00778-1*

Authors: Tracie McKinney, senior lecturer in human biology at the University of South Wales, & Marie Nicole Pareja Cummings, consulting scholar in the Museum of Archaeology and Anthropology at the University of Pennsylvania.

This article was originally published on The Conversation.

http://bit.ly/2uzzRBe

One immune cell type appears to attack any type of cancer

We don't know enough to know whether this is useful yet.

John Timmer

While cancerous cells look a lot like normal human cells, they're still different enough that the immune system regularly attacks them. Obviously, this attack sometimes bogs down, allowing cancer to thrive and spread. Figuring out how to get the immune system back on track has been a major focus of research, and success in the area has been honored with a Nobel Prize.

Despite these successes, many patients aren't helped by the newer immune-focused therapies, raising questions of what else we still need to figure out to help cancer patients. A new paper highlights something we may have missed: a class of immune cells that appears to be primed specifically to attack cancer. But the finding raises questions about what it is on cancer cells that the immune cells are recognizing and why they fail to keep cancer in check.

Finding cancer killers

The start of this work was pretty simple: a large international team of researchers grew a mix of immune cells called "T cells" in the presence of cancerous cells and looked for cells that grew rapidly. This rapid growth is typically a sign that the immune cells have been activated by something they recognize—in this case, the cancer. They identified one particular lineage of T cells that grew well and named it MC.7.G5, confirming yet again that most scientists don't belong in the creative industries.

One notable thing about the MC.7.G5 cells quickly became apparent: MC.7.G5 didn't simply grow well in the presence of cancer cells; it killed them. So, the authors tested a variety of different cancer types (lung cancer, melanoma, colon, breast, and more). These cells don't have much in common. They're activated by different mutations, start out with different populations of proteins on their surface, and have many other differences from one another. So it wasn't clear what the T cells could possibly be recognizing on their surfaces in order to attack them. Yet attack them they did.

To find out, the researchers did an experiment that wouldn't have been possible just a decade earlier: they used a gene-editing construct to eliminate every single protein-coding gene that we know of in the genome. Lots of individual populations of a cancer-cell line had a single gene knocked out and then were tested to see whether the MC.7.G5 immune cells could still kill them. If any cancer cells were left alive, then the gene edited in them would be essential for producing the molecule used by the immune cells to recognize cancer.

The experiment identified a series of genes involved in putting a single protein on the surface. But, of course, that protein is also present on normal cells. How could it possibly be responsible for the cancer cells being recognized as distinct?

Fortunately, we know a lot about the family of molecules that the protein, MR1, belongs to, as well as a bit about MR1 itself. The larger family includes the molecules that help the immune system recognize self from non-self by binding to bits of the cell's proteins and presenting them on the cell's surface for the immune system to check out. If either these molecules or the proteins they present look different, the immune system attacks. So, that makes a degree of sense as something that can trigger the immune system to go after the cancer cells.

MR1, however, doesn't work like that. Instead, it brings some of the cell's metabolites to the surface. And the researchers confirmed that it has to bind to something in order to make it to the surface. They hypothesize that it's a metabolite that's specific to cancer cells, but they have no idea what it might be.

Stay on target

While there are still some question marks about what causes these immune cells to pick out cancerous cells, there's no shortage of evidence that they do so effectively.

The researchers tested the immune cells against resting and dividing normal cells and got no response. MC.7.G5 didn't kill healthy cells that were stressed or damaged. So, there's no indication that the immune cells accidentally go off target and kill healthy cells.

The researchers also confirmed that the cancer-killing T cells are defined by the standard receptor that T cells normally use to recognize infected cells. They made a copy of this receptor's genes and inserted them into T cells from an unrelated individual. They also killed cancerous cells from at least two different sources.

Finally, the authors injected lymphoma cells into immune-compromised mice, then added the cancer-killing T cells. In control mice without the cancer-killing cells, the lymphoma took over the bone marrow, eventually accounting for about 80 percent of the cells there.

With the cancer-killing cells injected at the same time, the bone marrow in the mice consistently had far fewer cancer cells (consistently less than 10 percent of the total cells). This indicates that the immune cells can help keep cancer in check but may not be able to consistently eradicate it.

Does that mean, as the BBC has claimed, that these cells "May treat all cancer"? Well, to begin with, the T cells were seemingly unable to eliminate cancer in mice. That's more significant than it seems, in that lots of potential treatments seem to work well in mice, but few ever advance to the point of clinical trials in humans, much less end up being used as treatments. This is a case when mouse assays are helpful for knowing what deserves a closer look but far from the last word on a topic.

Do we all have cancer killers?

These cancer-killing immune cells were also obtained from at least two individuals, suggesting that they may be present in all humans. Yet humans regularly suffer from cancer, so there's clearly something that keeps them from doing their job. At this point, we don't have the slightest clue as to what that something might be.

Then there's the issue of what the cells are recognizing that allows them to identify cancer cells. Whatever it is, it's not widely present on healthy cells. But the body has a dizzying number of specialized cell types, so we've barely scratched the surface of testing whether these cells might attack some healthy cell types. However, if the authors are right about a couple of things, there's a very good chance the cells might.

The authors suggest that the target of the cancer-killing cells is a metabolite presented on the surface by the protein MR1. And, because the gene-editing screen didn't pull out any metabolic enzymes, they suspect that the metabolite is essential for cancer cell viability. It's difficult to understand how something central to cancer cell viability, produced using the same genes found in normal cells, isn't ever produced by normal cells.

None of this is to say that this discovery won't end up being important. But we really need much more information before we're in a position to judge whether it is or not.

Nature Immunology, 2020. DOI: 10.1038/s41590-019-0578-8 (About DOIs).

http://bit.ly/2GrSmKp

The easy route the easy way: New chip calculates the shortest distance in an instant

Scientists have developed the world's first fully coupled AI chip that can solve the traveling salesman problem for 22 cities instantly, something that would take about 1,200 years for a high-performance von Neumann CPU

How would you go about returning books to the correct shelves in a large library with the least amount of walking? How would you determine the shortest route for a truck that has to deliver many packages to multiple cities? These are some examples of the "traveling salesman problem", a type of "combinatorial optimization" problem, which frequently arises in everyday situations. Solving the traveling salesman problem involves searching for the most efficient of all possible routes. To do this easily, we require the help of low-power, high-performance artificial intelligence.

To solve this conundrum, scientists are actively exploring the use of integrated circuits. In this method, each state in a traveling salesman problem (for example, each possible route in the delivery truck) is represented by "spin cells", each having one of two states. Using a circuit which can store the strength of one spin cell state over another, the relationship between these states (or to use our analogy, the distance between two cities for the delivery truck) can be obtained. Using a large system containing the same number of spin cells and circuits as the components (or the cities and routes for the delivery truck) in the problem, we can identify the state requiring the least energy, or the route covering the least distance, thus solving the traveling salesman problem, or any other type of combinatorial optimization problem.

However, a major drawback of the conventional way of using integrated circuits is that it requires pre-processing, and the number of components and time required to input the data increase as the scale of the problem increases. For this reason, this technology has only been able to solve the traveling salesman problem involving a maximum of 16 states, or cities.

A group of researchers led by Professor Takayuki Kawahara of the Department of Electrical Engineering at Tokyo University of Science aimed to overcome this issue. They observed that the interactions between each spin cell is linear, which ensured that the spin cells could only interact with the cells near them, prolonging the processing time. "We decided to arrange the cells slightly differently to ensure that all spin cells could be connected," Prof Kawahara explains.

To do this, they first arranged the circuits in a two-dimensional array, and the spin cells separately in a one-dimensional arrangement. The circuits would then read the data and an aggregate of this data was used to switch the states of the spin cells. This would mean that the number of spin cells required and the time needed for processing were drastically reduced.

The authors have presented their findings at the IEEE 18th World Symposium on Applied Machine Intelligence and Informatics (SAMI 2020). "Our new technique thus represents a fully coupled method," remarks Prof Kawahara, "and has the potential to solve a traveling salesman problem involving up to 22 cities." The authors are hopeful that this technology will have future applications as a high-performance system with low power requirements for office equipment and tablet terminals for finding easily find optimal solutions from large numbers of combinations.

Part of this article is based on results obtained from a project commissioned by the New Energy and Industrial Technology Development Organization (NEDO), METI, Japan.

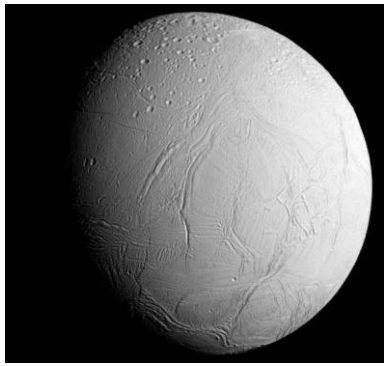
http://bit.ly/2RukFOy

Geochemical Model Reveals Inner Complexity of Enceladus

New geochemical model that reveals that carbon dioxide in the moon's ocean may be controlled by chemical reactions at its seafloor.

Enceladus, an ocean-harboring moon of Saturn, **erupts** a **plume** that contains gases and frozen sea spray into space. By understanding the composition of the plume, planetary scientists can learn about what the **ocean** is like, how it got to be this way,

and whether it provides environments where Earth-like life could survive. Now, a research team at the Southwest Research Institute has developed a new geochemical model that reveals that **carbon dioxide** in the moon's ocean may be controlled by chemical reactions at its seafloor.



"We came up with a new technique for analyzing the plume composition to estimate the concentration of dissolved carbon dioxide in the ocean," said lead author Dr. Christopher Glein, a researcher in the Space Science and Engineering Division at the Southwest Research Institute.

***Cassini captured this image of Enceladus as it neared the moon for its closest-ever dive past the moon's active south polar region. The image was taken in visible light with the spacecraft's narrow-angle camera on October 28, 2015. The image shows heavily cratered northern latitudes at top, transitioning to fractured, wrinkled terrain in the middle and southern latitudes. The wavy boundary of the moon's active south polar region is visible at bottom, where it disappears into wintry darkness. This view looks towards the Saturn-facing side of Enceladus. The image was taken at a distance of approximately 60,000 miles (96,000 km) from Enceladus and at a Sun-Enceladus-spacecraft, or phase, angle of 45 degrees.* Image credit: NASA / JPL-Caltech / Space Science Institute.**

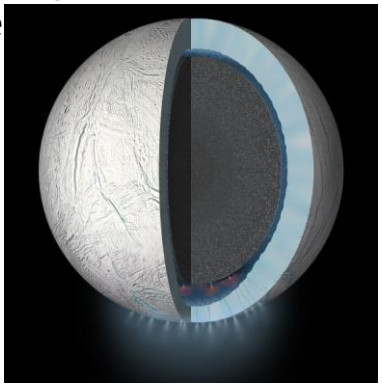
"This enabled modeling to probe deeper interior processes."

The analysis of mass spectrometry data from NASA's Cassini spacecraft indicates that the abundance of carbon dioxide is best explained by geochemical reactions between the moon's rocky core and liquid water from its subsurface ocean.

Integrating this information with Cassini/Ion Neutral Mass Spectrometer's previous discoveries of silica and molecular hydrogen — two chemicals that are considered to be markers for hydrothermal processes — points to a more complex, geochemically diverse core.

"Based on our findings, Enceladus appears to demonstrate a massive carbon sequestration experiment," Dr. Glein said.

"On Earth, climate scientists are exploring whether a similar process can be utilized to mitigate industrial emissions of carbon dioxide."



"Using two different data sets, we derived carbon dioxide concentration ranges that are intriguingly similar to what would be expected from the dissolution and formation of certain mixtures of silicon- and carbon-bearing minerals at the seafloor."

***This artist's rendering showing a cutaway view into the interior of Enceladus. A plume of ice particles, water vapor and organic molecules sprays from fractures in the moon's south polar region.* Image credit: NASA / JPL-Caltech.**

Another phenomenon that contributes to this complexity is the likely presence of hydrothermal vents inside Enceladus.

"The dynamic interface of a complex core and seawater could potentially create energy sources that might support life," said co-author Dr. Hunter Waite, also from the Space Science and Engineering Division at the Southwest Research Institute.

"While we have not found evidence of the presence of microbial life in the ocean of Enceladus, the growing evidence for chemical disequilibrium offers a tantalizing hint that habitable conditions could exist beneath the moon's icy crust."

"Distinct sources of observed carbon dioxide, silica and hydrogen imply mineralogically and thermally diverse environments in a heterogeneous rocky core," Dr. Glein added.

"We suggest that the core is composed of a carbonated upper layer and a serpentinized interior."

Carbonates commonly occur as sedimentary rocks such as limestone on Earth, while serpentine minerals are formed from igneous seafloor rocks that are rich in magnesium and iron.

It is proposed that hydrothermal oxidation of reduced iron deep in the core creates hydrogen, while hydrothermal activity intersecting quartz-bearing carbonated rocks produces silica-rich fluids.

Such rocks also have potential to influence the carbon dioxide chemistry of the ocean via low-temperature reactions involving silicates and carbonates at the seafloor.

"The implications for possible life enabled by a heterogeneous core structure are intriguing," Dr. Glein said. "This model could explain how planetary differentiation and alteration processes create chemical (energy) gradients needed by subsurface life."

The study was published in the journal *Geophysical Research Letters*.

Christopher R. Glein & J. Hunter Waite. The carbonate geochemistry of Enceladus' ocean. Geophysical Research Letters, *published online January 22, 2020; doi: 10.1029/2019GL085885*

http://bit.ly/37BXJms

Sick of Big Pharma's pricing, health insurers pledge $55M for cheap generics

Blue Cross and Blue Shield companies partner with Civica to make cheaper generics.

Beth Mole - 1/24/2020, 4:25 AM

Fed up with the exorbitant price tags on old, off-patent medications, 18 Blue Cross and Blue Shield companies are partnering with a nonprofit dedicated to manufacturing and selling affordably priced generic drugs. The BCBS companies are providing $55 million in their new partnership with nonprofit Civica Rx, the two organizations announced.

Like the new venture, Civica was born out of frustration with the pharmaceutical industry's steep price increases as well as perilous shortages of essential drugs. In 2018, numerous health care organizations banded together with three philanthropies to manufacture their own brand of generic drugs, forming Civica and thwarting the generic industry. Their aim was to provide hospitals with injectable generic medications in steady supplies at affordable prices.

The health care organizations involved in Civica now represent over 1,200 hospitals in 46 states. Last October, Civica delivered its first drugs to a hospital in Utah and is now producing and distributing several drugs.

With the new partnership with BCBS companies, Civica will expand out of just hospital medications. Specifically, the deal will create a subsidiary that will either make drugs or partner with manufacturers to offer more affordably priced generic versions of select drugs in exchange for aggregate, multi-year purchasing commitments.

The partners were mum on which drugs they will select but said that they will first focus on ones "identified as having high potential for savings" that currently have little competition. They also encouraged others, including "other health plans, employers, retail partners, and health care innovators" to join their effort.

In an interview with The New York Times, Civica board chairman Dan Liljenquist said that the new venture "will not solve all the problems of the world, but we do know that 90 percent of prescriptions are generic, and there are certain parts of the generic markets that are not functioning like competitive markets should. And we intend to compete in those markets."

In recent years, generic drug makers have been accused of price gouging and being involved in price-fixing schemes. Additionally, brand-name drug makers have been accused of offering faux-generic drugs—sometimes called "authorized" generics—in order to keep drug prices high and stymie competition.

Civica and the BCBS companies aren't the only ones looking to get around the generic market. California Gov. Gavin Newsom proposed earlier this month having the state make its own brand of generic drugs to reduce healthcare costs. Sen. Elizabeth Warren (D-Mass.) and Rep. Jan Schakowsky (D-Ill.) have proposed a similar measure at the federal level.

https://nyti.ms/2Gq3V51

Coronavirus Deaths Are So Far Mostly Older Men, Many With Previous Health Issues

As China released details about the first 17 people who have died in the outbreak, a well-known SARS expert raised an alarm about the virus's spread, saying he felt "powerless."

By Austin Ramzy

HONG KONG — When the man finally went to a hospital, he had been sick for a week. It was Dec. 26, and Mr. Zeng, 61, was weak with a cough. He got worse. A day later he was transferred to intensive care, and on Dec. 30 he was put on a ventilator to try to keep him alive.

He was moved to another hospital and attached to another machine that oxygenated his blood. Still, he got worse, and on Jan. 9 his heart stopped.

Mr. Zeng, whom the authorities have identified only by his surname, became the first confirmed death from the new coronavirus that emerged in the central city of Wuhan and has since spread around the country and beyond.

China's health commission, which has tightly controlled news about the toll of the outbreak, on Thursday released details about the first 17 confirmed deaths from the disease. (Several more deaths were announced early Friday, bringing the death toll to 25.)

The detailed information was released as the authorities canceled transportation within Wuhan and several nearby cities and largely blocked residents from leaving. Medical experts have questioned whether the measures in Wuhan have come too late to prevent the spread of the coronavirus, which has been found in infected travelers in Washington State, Japan, South Korea, Thailand and Taiwan.

Dr. Guan Yi, a professor of infectious diseases at the University of Hong Kong who visited Wuhan this week, warned that there was a potential for the virus to spread rapidly despite the controls put in place on Thursday morning.

"We have a chance to have a pandemic outbreak," said Dr. Guan, who was part of the team that identified the coronavirus that caused the deadly SARS outbreak in 2002 and 2003. SARS infected more than 8,000 people and killed nearly 800.

Dr. Guan also told Caixin, an influential Chinese magazine known for investigative reports, that he had traveled to Wuhan hoping to help track the virus's animal source and control the epidemic. But he left, he said, feeling "powerless, very angry."

Dr. W. Ian Lipkin, an epidemiologist at Columbia University who advised the Chinese government and the World Health Organization during the SARS outbreak, said that infected people outside Wuhan would continue to spread the disease.

"The horse is already out of the barn," he said.

An examination of the information provided by the government about the initial deaths show a disease that has thus far largely killed older men, many of who had underlying health problems.

Most had gone to the hospital with a fever and a cough, though at least three did not have fevers when they were admitted, according to the health commission's statement.

Among the first 17 victims were 13 men and four women. All were identified only by their last names. The youngest was a 48-year-old woman, Yin, who died on Monday, more than a month after her symptoms were first recorded. The oldest cases were two 89-year-old men who died on Saturday and Sunday. The median age was 75.

Many had underlying conditions like cirrhosis of the liver, hypertension, diabetes and Parkinson's disease. Most spent more than a week in hospitals, with some undergoing treatment for a month or longer. But two died just four days after they were admitted.

While much about the virus remains unknown, medical experts found some positive signs in the fact that the disease did not appear to be killing young and otherwise healthy people.

It was a somewhat reassuring sign, Dr. Lipkin wrote, that "the majority of fatal cases are elderly and/or have a chronic disease that would increase their susceptibility to infectious diseases."

The Chinese health commission said more than 570 cases had been confirmed in the country by the end of Wednesday, with 95 in grave condition. The outbreak has happened as China was preparing for the Lunar New Year holiday, the biggest travel period of the year, increasing the likelihood of the coronavirus circulating further beyond Wuhan.

Dr. Guan, in his interview with Caixin, was critical of the local government, saying it had not done enough earlier this week to stop the coronavirus in Wuhan.

"Even though the central authorities have said in the past two days they were attaching a high degree of importance, local health protections had not been upgraded at all," he said. "At the time I thought this was going to be a 'state of war.' Why hadn't the alarm been sounded?"

Dr. Guan said he was disturbed by the lack of safety measures being put in place. At the airport he saw no disinfection being carried out and only a few random places like a Starbucks had put out liquid hand sanitizer dispensers.

The situation was so surprising, "my jaw dropped," he said.

He said he continually ran into obstacles when trying to find researchers to work with on tracing the source of the virus. The seafood and poultry market believed to the source had been thoroughly cleaned, he complained, preventing any effective investigation. "There's no crime scene," he said.

The path of the coronavirus could prove harder to trace and control than SARS, when a small number of highly infectious superspreaders helped transmit the disease to a large number of people, Dr. Guan said.

"I've experienced a lot, and I've never felt scared, most of these are controllable," he said, citing previous battles with SARS, avian influenza and other outbreaks. "But this time I'm scared."

Javier Hernández contributed reporting from Beijing, and Amber Wang contributed research.

http://bit.ly/38MqGfz

The 'place' of emotions

A study of the IMT School for Advanced Studies Lucca describes how affective states are mapped in the brain

The entire set of our emotions is topographically represented in a small region of the brain, a 3 centimeters area of the cortex, report scientists in a study conducted at the IMT School for Advanced Studies Lucca, Italy. The discovery of this "map" of emotions comes from a work conducted by the Molecular Mind Laboratory (MoMiLab) directed by Professor **Pietro Pietrini**, and recently published in **Nature Communications**.

To investigate how the brain processes the distinct basic component of emotional states, the IMT School researchers asked a group of 15 volunteers enrolled in the study to express, define and rate their emotions while watching the iconic 1994 American movie Forrest Gump. For the entire length of the film, in fact, the 15 volunteers reported scene by scene their feelings and their respective strength on a scale from 1 to 100. Their answers were then compared to those of 15 other persons who had watched the same movie during a functional magnetic resonance imaging (fMRI) study conducted

in Germany. The imaging data were obtained through "open science", a platform where scientists from different laboratories can share their data, so that anyone can replicate their findings or use the data for novel experiments, as in this case.

To unveil cortical regions involved in emotion processing, the "emotional ratings" were used by scientists for predicting the fMRI response of the brain. The correspondence between functional characteristics and the relative spatial arrangement of distinct patches of cortex was then used to test the topography of affective states.

As researchers found out, the activation of temporo-parietal brain regions was associated to the affective states we feel in an exact moment, providing us with the map of our emotional experience.

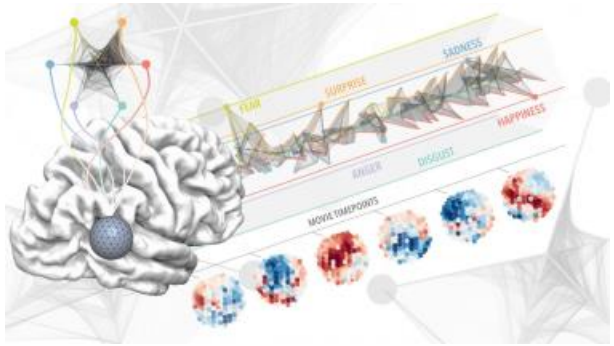


Illustration of how emotions are represented in the brain according to the findings of the study. Results revealed the existence of an "emotionotopic" mapping in the right temporo-parietal territories, associated to the the complex and multifaceted subjective emotional experience elicited by watching the Forrest Gump movie. **Credit Luca Cecchetti, IMT School for Advanced Studies Lucca**

The analysis of the data by **Giada Lettieri**, first author of the study along with Giacomo Handjaras, both PhD students at the IMT School, and their collaborators shows that the polarity, complexity and intensity of emotional experiences are represented by smooth transitions in right temporo-parietal territories. The spatial arrangement allows the brain to map a variety of affective states within a single patch of cortex.

To summarize, the right temporo-parietal junction can topographically represent the variety of the affective states that we experience: which emotions we feel in a specific moment, and how much we perceive them. The process resembles the way senses, like sight or hearing, are represented in the brain. For this reason, the researchers proposed the definition emotionotopy as a principle of emotion coding.

Historically, emotions have often been considered a "separate" human faculty, well distinct from cognition. As a matter of fact, this point of view has been recently challenged by various studies showing how much affective responses can influence cognitive processes, such as decision-making and memory. The IMT School study adds new details to this more recent view that the principles responsible for the representation of sensory stimuli are also responsible for the mapping of emotions.

"This study is also an interesting example of open science and sharing data initiatives in neuroscience", said **Luca Cecchetti**, senior author of the paper and Assistant Professor at the IMT School. "The fMRI data were collected by Michael Hanke and colleagues at Otto von Guericke University Magdeburg and publicly released at studyforrest.org. This allowed us to exploit high-quality neuroimaging data, at the same time saving resources and time. Following the same principle, we released data and code at https://osf.io/tzpdf/".

"Dissecting the brain correlates of elementary factors that modulate intensity and quality of our emotions has major implications to understand what happens when emotions get sick, as in case of depression and phobia. These studies are getting psychiatry closer to other fields of medicine in finding objective biological correlates of feelings, which are subjective states", commented Professor **Pietro Pietrini**, psychiatrist and co-author of the research, director of MoMiLab at the IMT School.

Emotionotopy in the Human Right Temporo-Parietal Cortex

Giada Lettieri, Giacomo Handjaras, Emiliano Ricciardi, Andrea Leo, Paolo Papale, Monica Betta, Pietro Pietrini and Luca Cecchetti - doi: 10.1038/s41467-019-13599-z.

http://bit.ly/2GssSws

Can lithium halt progression of Alzheimer's disease?

McGill researchers' findings show that may be the case

There remains a controversy in scientific circles today regarding the value of lithium therapy in treating Alzheimer's disease. Much of this stems from the fact that because the information gathered to date has been obtained using a multitude of differential approaches, conditions, formulations, timing and dosages of treatment, results are difficult to compare. In addition, continued treatments with high dosage of lithium render a number of serious adverse effects making this approach impracticable for long term treatments especially in the elderly.

In a new study, however, a team of researchers at McGill University led by Dr. Claudio Cuello of the Department of Pharmacology and Therapeutics, has shown that, when given in a formulation that facilitates passage to the brain, lithium in doses up to 400 times lower than what is currently being prescribed for mood disorders is capable of both halting signs of advanced Alzheimer's pathology such as amyloid plaques and of recovering lost cognitive abilities. The findings are published in the most recent edition of the Journal of Alzheimer's Disease.

Building on their previous work

"The recruitment of Edward Wilson, a graduate student with a solid background in psychology, made all the difference," explains Dr. Cuello, the study's senior author, reflecting on the origins of this work. With Wilson, they first investigated the conventional lithium formulation and applied it initially in rats at a dosage similar to that used in clinical practice for mood disorders. The results of the initial tentative studies with conventional lithium formulations and dosage were disappointing however, as the rats rapidly displayed a number of adverse effects. The research avenue was interrupted but renewed when an encapsulated lithium formulation was identified that was reported to have some beneficial effects in a Huntington disease mouse model.

The new lithium formulation was then applied to a rat transgenic model expressing human mutated proteins causative of Alzheimer's, an animal model they had created and characterized. This rat develops features of the human Alzheimer's disease, including a progressive accumulation of amyloid plaques in the brain and concurrent cognitive deficits.

"Microdoses of lithium at concentrations hundreds of times lower than applied in the clinic for mood disorders were administered at early amyloid pathology stages in the Alzheimer's-like transgenic rat. These results were remarkably positive and were published in 2017 in Translational Psychiatry and they stimulated us to continue working with this approach on a more advanced pathology," notes Dr. Cuello.

Encouraged by these earlier results, the researchers set out to apply the same lithium formulation at later stages of the disease to their transgenic rat modelling neuropathological aspects of Alzheimer's disease. This study found that beneficial outcomes in diminishing pathology and improving cognition can also be achieved at more advanced stages, akin to late preclinical stages of the disease, when amyloid plaques are already present in the brain and when cognition starts to decline.

"From a practical point of view our findings show that microdoses of lithium in formulations such as the one we used, which facilitates passage to the brain through the brain-blood barrier while minimizing levels of lithium in the blood, sparing individuals from adverse effects, should find immediate therapeutic applications," says Dr. Cuello. "While it is unlikely that any medication will revert the irreversible brain damage at the clinical stages of Alzheimer's it is very likely that a treatment with microdoses of

encapsulated lithium should have tangible beneficial effects at early, preclinical stages of the disease."

Moving forward

Dr. Cuello sees two avenues to build further on these most recent findings. The first involves investigating combination therapies using this lithium formulation in concert with other interesting drug candidates. To that end he is pursuing opportunities working with Dr. Sonia Do Carmo, the Charles E. Frosst-Merck Research Associate in his lab.

He also believes that there is an excellent opportunity to launch initial clinical trials of this formulation with populations with detectable preclinical Alzheimer's pathology or with populations genetically predisposed to Alzheimer's, such as adult individuals with Down Syndrome.

While many pharmaceutical companies have moved away from these types of trials, Dr. Cuello is hopeful of finding industrial or financial partners to make this happen, and, ultimately, provide a glimmer of hope for an effective treatment for those suffering from Alzheimer's disease.

"NP03, a Microdose Lithium Formulation, Blunts Early Amyloid Post-Plaque Neuropathology in McGill-R-Thy1-APP Alzheimer-Like Transgenic Rats," by Wilson, Do Carmo, Cuello, et al. was published online on December 16, 2019 in the Journal of Alzheimer's disease. *doi: 10.3233/JAD-190862*

http://bit.ly/2O28B4W

Patients suffer invasive treatments for harmless cancers

Increasingly being diagnosed with cancers that will do them no harm if left undetected or untreated

Australians are increasingly being diagnosed with cancers that will do them no harm if left undetected or untreated, exposing them to unnecessary surgeries and chemotherapy, says a new study published online today in the *Medical Journal of Australia*.

The research, led by Professor Paul Glasziou, the Director of the Institute for Evidence-Based Healthcare at Bond University, drew on data from the Australian Institute of Health and Welfare to compare how the lifetime risk of five cancers had changed between 1982 and 2012.

The study shows compared to 30 years ago, Australians are much more likely to experience a cancer diagnosis in their lifetime.

The figures suggest that in 2012 24 percent of cancers or carcinomas in men were overdiagnosed.

These included 42 percent of prostate cancers, 42 percent of renal cancers, 73 percent of thyroid cancers and 58 percent of melanomas.

For women, 18 percent of cancers or carcinomas were overdiagnosed, including 22 percent of breast cancers, 58 percent of renal cancers, 73 percent of thyroid cancers and 58 percent of melanomas.

The figures are significant because of the harm that can occur from cancer treatment of patients who would never have had symptoms in their lifetime.

"Cancer treatments such as surgery, radiotherapy, endocrine and chemotherapy carry risks of physical harms," the authors of the study reported.

"In the absence of overdiagnosis, these harms are generally considered acceptable.

"In the context of overdiagnosed cancers, however, affected individuals cannot benefit but can only be harmed by these treatments."

The authors also refer to separate studies showing overdiagnosis could be linked to psychological problems.

"For example, men's risk of suicide appears to increase in the year after receiving a prostate cancer diagnosis."

The new study, which was led by Professor Glasziou in conjunction with co-authors Professor Alexandra Barratt and Associate Professor Katy Bell of University of Sydney, Associate Professor Mark Jones of Bond University, and Dr Thanya Pathirana of

Griffith University, calls for urgent policy changes to address overdiagnosis.

Professor Glasziou said increasing rates of diagnosis were a result of improvements and wider use of testing and screening.

"The problem is that some screening identifies abnormal cells that look like cancer but don't behave like cancer. However, reducing that problem is not easy, as some types of screening are important".

Professor Glasziou said the best option to reducing melanoma deaths may not be ever-more screening "but applying daily sunscreen" and research on better treatments.

"While much of the overdiagnosis is due to screening, many overdiagnosed cancer cases are incidental findings, that is, the patient is being tested for something else when the cancer is detected," Professor Glasziou said.

"Getting the balance right between too little and too much screening and testing will not be easy, but this is an important step.

It is the first time that the risk of overdiagnosis has been quantified across five cancers, anywhere in the world."

Associate Professor Bell said that the findings also suggest an important role for health services such as the Australian Institute of Health and Welfare, in detecting potential overdiagnosis and alerting health policy decision makers to the problem early on.

"Patterns of increased test use, cancer incidence, or treatment rates, without corresponding rises in mortality could indicate emerging areas of overdiagnosis," she said.

"People still need to remain vigilant when it comes to early detection of cancers, however they need to be informed and engage in shared decision making with their medical professionals about the harms of cancer screening and other associated procedures."

Declaration: The researchers received funding from the Australian National Health and Medical Research Council.

http://bit.ly/2tS7uxW

Wuhan seafood market may not be source of novel virus spreading globally

A description of the first clinical cases published in The Lancet on Friday challenges that hypothesis.

By Jon Cohen

As confirmed cases of a novel virus surge around the world with worrisome speed, all eyes have so far focused on a seafood market in Wuhan, China, as the origin of the outbreak. But a description of the first clinical cases published in *The Lancet* on Friday challenges that hypothesis.

The paper, written by a large group of Chinese researchers from several institutions, offers details about the first 41 hospitalized patients who had confirmed infections with what has been dubbed 2019-novel coronavirus (2019-nCoV). The earliest case became ill on 1 December and had no reported link to the seafood market, the authors report. “No epidemiological link was found between the first patient and later cases,” they state. Their data also show that in total, 13 of the 41 cases had no link to the marketplace either. “That’s a big number, 13, with no link,” says Daniel Lucey, an infectious disease specialist at the University of Georgetown

Earlier reports from Chinese health authorities and the World Health Organization said the first patient had onset of symptoms on 8 December—and those reports simply said “most” cases had links to the seafood market, which was closed on 1 January.

Lucey says if the new data are accurate, the first human infections must have occurred in November—if not earlier—because there is an incubation time between infection and symptoms surfacing. If so, the virus possibly spread silently between people in Wuhan and perhaps elsewhere before the cluster of cases from the city’s now infamous Huanan Seafood Wholesale Market was discovered in

late December. “The virus came into that marketplace before it came out of that marketplace,” Lucey asserts.

The Lancet paper’s data also raises questions about the accuracy of the initial information China provided, says Lucey. At the beginning of the outbreak, the main official source of public information was notices from the Wuhan Municipal Health Commission. Its notices on 11 January started to refer to the 41 patients as the only confirmed cases and the count remained the same until 18 January. The notices did not state that the seafood market was the source, but repeatedly noted that there was no evidence of human-to-human transmission and that most cases linked to the market. Because the Wuhan Municipal Health Commission noted that diagnostic tests had confirmed these 41 cases by January 10 and officials presumably knew the case histories of each patient, “China must have realized the epidemic did not originate in that Wuhan Huanan seafood market,” Lucey tells *ScienceInsider*. (Lucey also spoke about his concerns in an interview published online yesterday by Science Speaks, a project of the Infectious Disease Society of America.) Kristian Anderson, an evolutionary biologist at the Scripps Research Institute in San Diego who has analyzed sequences of 2019-nCoV to try to clarify its origin, says the 1 December timing of the first confirmed case was “an interesting tidbit” in *The Lancet* paper. “The scenario of somebody being infected outside the market and then later bringing it to the market is one of the three scenarios we have considered that is still consistent with the data, he says. “It’s entirely plausible given our current data and knowledge.” The other two scenarios are that the origin was a group of infected animals or a single animal that came into that marketplace.

Anderson on 25 January posted on a virology research website his analysis of 27 available genomes of 2019-nCoV. It suggests they had a “most recent common ancestor”—meaning a common source—as early as 1 October.

Bin Cao of Capital Medical University in Beijing, the corresponding author of the Lancet article and a pulmonary specialist, wrote Science in an e-mail that he and his co-authors “appreciate the criticism” from Lucey.. “Now It seems clear that [the] seafood market is not the only origin of the virus,” he wrote in an e-mail to ScienceInsider. “But to be honest, we still do not know where the virus came from now.”

Lucey notes that the discovery of the coronavirus that causes Middle East Respiratory Syndrome (MERS), a sometimes fatal disease that occurs sporadically, came from a patient in Saudi Arabia in June 2012 but later studies traced it back to an earlier hospital outbreak of unexplained pneumonia in Jordan in April of that year. Stored samples from two people who died in Jordan confirmed that they had been infected with the virus. Retrospective analyses of blood samples in China from people and animals—including vendors from other animal markets--may reveal a clear picture of where the 2019-nCoV originated, he suggests. “There might be a clear signal among the noise,” he says.

http://bit.ly/2GqhFwD

How smart were our ancestors? Turns out the answer isn’t in brain size, but blood flow

Rate of blood flow to the brain may be a better indication of cognitive ability than brain size alone.

Roger S. Seymour

How did human intelligence evolve? Anthropologists have studied this question for decades by looking at tools found in archaeological digs, evidence of the use of fire and so on, and changes in brain size measured from fossil skulls.

However, working with colleagues at the Evolutionary Studies Institute of the University of the Witwatersrand in South Africa, we have found a new way to estimate the intelligence of our ancestors.

By studying fossil skulls, we determined how much blood – and how much energy – the brains of ancient hominins required to keep running.

This energy use gives us a measure of how much thinking they did. We found the rate of blood flow to the brain may be a better indication of cognitive ability than brain size alone.

The brain as a supercomputer

Researchers have often assumed increases in intelligence in human ancestors (hominins) occurred as brains grew larger.

This is not an unreasonable assumption; for living primates, the number of nerve cells in the brain is almost proportional to the brain's volume. Other studies of mammals in general indicate the brain's metabolic rate – how much energy it needs to run – is nearly proportional to its size.

Information processing in the brain involves nerve cells (neurons) and the connections between them (synapses). The synapses are the sites of information processing, much like the transistor switches of a computer.

The human brain contains more than 80 billion neurons and up to 1,000 trillion synapses. Although it occupies only 2% of the body, the brain uses about 20% of the energy of a resting person.

Some 70% of that energy is used by the synapses to produce neurochemicals that transfer information between neurons.

To understand how much energy the brains of our ancestors used, we focused on the rate of blood flow to the brain. Because blood supplies essential oxygen to the brain, it's closely related to synaptic energy use.

The human brain requires about 10 mL of blood every second. This changes remarkably little, whether a person is awake, asleep, exercising or solving tricky maths problems.

In this regard, we can view the brain as a rather energy-expensive supercomputer. The greater a computer's capacity, the more power it needs to stay running – and the bigger its electrical supply cables need to be. It is the same with the brain: the higher the cognitive function, the higher the metabolic rate, the greater the blood flow and the larger the arteries that supply the blood.

Measuring artery size from skulls

The blood flow to the cognitive part of the brain, the cerebrum, comes through two internal carotid arteries. The size of these arteries is related to the rate of blood flow through them.

Just as a plumber would install larger water pipes to accommodate a higher flow rate to a larger building, the circulatory system adjusts the sizes of blood vessels to match the rate of blood flow in them. The rate of flow is in turn related to how much oxygen an organ requires.

We initially established the relationship between blood flow rate and artery size from 50 studies involving ultrasound or magnetic resonance imaging of mammals. The size of the internal carotid arteries can be found by measuring the size of the holes that allow them through the base of the skull.

Next, we measured these holes in the skulls of 96 modern great apes, including chimpanzees, orangutans, gorillas. We compared the skulls to 11 from *Australopithecus* hominins that lived approximately 3 million years ago.

Chimpanzee and orangutan brains are approximately 350 mL in volume, while gorilla and *Australopithecus* are a little larger at 500 mL. Conventional wisdom suggests *Australopithecus* should be at least as intelligent as the others.

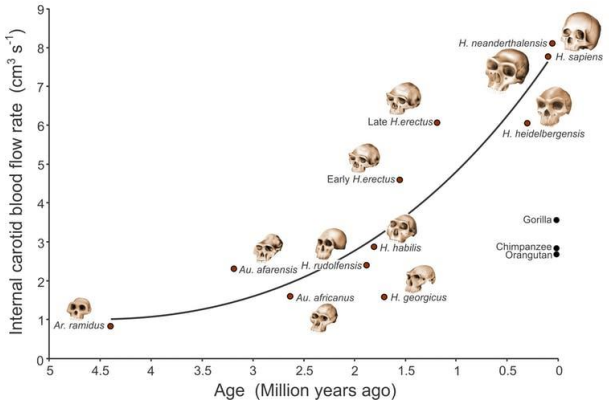
However, our study showed an *Australopithecus* brain had only two thirds the blood flow of a chimp or orangutan, and half the flow of a gorilla.

Anthropologists have often placed *Australopithecus* between apes and humans in terms of intelligence, but we think this is likely wrong.

The unique trajectory of human brain evolution

In humans and many other living primates, the rate of internal carotid artery blood flow appears to be directly proportional to brain size. This means if the size of the brain doubles, the rate of blood flow also doubles.

This is unexpected because the metabolic rate of most organs increases more slowly with organ size. In mammals, doubling the size of an organ will normally increase its metabolic rate only by a factor of about 1.7.



Over time, the brains of our ancestors required more and more energy. **Roger Seymour, Author provided**

This suggests the metabolic intensity of primate brains – the amount of energy each gram of brain matter consumes each second – increased faster than expected as brain size increased. For hominins, the growth was even quicker than in other primates.

Between the 4.4 million year old *Ardipithecus* and *Homo sapiens*, brains became almost five times larger, but blood flow rate grew more than nine times larger. This indicates each gram of brain matter was using almost twice as much energy, evidently due to greater synaptic activity and information processing.

The rate of blood flow to the brain appears to have increased over time in all primate lineages. But in the hominin lineage, it increased much more quickly than in other primates. This acceleration went side by side with the development of tools, the use of fire and undoubtedly communication within small groups.

Professor Emeritus of Physiology, University of Adelaide

Disclosure statement

Roger S. Seymour receives funding from The Australian Research Council.

http://bit.ly/30UK3QS

Scientists are moving at record speed to create new coronavirus vaccines—but they may come too late

In the stock pandemic movie, scientists are frantically working on concoctions to stop the spread of a newly emerging virus—and by the end, voila, they succeed and save the world.

By Jon CohenJan. 27, 2020 , 6:32 AM

In the real world, vaccines played limited, if any, roles in slowing the Zika epidemic that walloped Latin America in 2016, the devastating 2014-2016 West African Ebola epidemic, and the pandemic flu that began circulating in 2009. The shots just weren't ready in time.

This time, with infections of a novel coronavirus exploding in China—case numbers soared to over 2700 the past 24 hours—and racing around the world, scientists contend they are better prepared than ever to produce a vaccine at Hollywood speed. Of course, the 2019-novel coronavirus (2019-nCoV), as it is now dubbed, has a solid lead in the race, and by the time a vaccine proves its worth in a clinical trial and manufacturers scale up production, it once again may be too late to make a significant dent in the course of the epidemic. But scientists hope they can make a difference.

One sign of the breakneck pace was the announcement on 23 January by the Coalition for Epidemic Preparedness Innovations (CEPI) that it will give three companies a total of $12.5 million to

develop 2019-CoV vaccines. A nonprofit formed in 2016 solely to fund and shepherd the development of new vaccines against emerging infectious diseases, CEPI is trying to have vaccines developed and tested faster than any previous effort, anywhere, ever. "This is what CEPI was created to do," says CEO Richard Hatchett.

Each of the three efforts that CEPI supports began within hours after Chinese researchers first posted a sequence of 2019-CoV in a public database. That happened on Friday evening, 10 January, in Bethesda, Maryland, home of the U.S. National Institute of Allergy and Infectious Diseases (NIAID). Barney Graham, deputy director of NIAID's Vaccine Research Center, began analyzing the sequence with his team on Saturday morning. The following Monday, Graham discussed his findings with researchers at Moderna, a vaccine maker in Cambridge, Massachusetts. On Tuesday, they signed a deal to collaborate.

Moderna makes vaccines by converting viral sequences into messenger RNA (mRNA). When injected into the body, the mRNA causes the body to produce a viral protein that can trigger the desired immune response. Moderna already has nine vaccines in clinical trials that use the mRNA "platform," says Stéphane Bancel, the company's CEO. "It was a really, really hard scientific challenge to make the first one, but once you get the first one working, the next one becomes really easy: You get the sequence, and this is just another one," says Bancel. "It's the same manufacturing process by the same group in the same room."

One of the nine vaccines, also co-developed with NIAID, targets MERS, a disease caused by a different but similar coronavirus that occasionally infects people in the Middle East. Tested only in animals so far, the MERS vaccine relies on a protein on the viral surface called the spike. In theory, all the team needs to do is swap in the genetic sequence for 2019-nCoV's spike to make the new product. "We have a lot of information about how to make [the spike]," says Graham. The MERS spike protein produces stronger immune responses when it's in a "stabilized" confirmation, and so his team has tweaked the mRNA accordingly. They hope to apply the same trick to 2019-nCoV.

Philadelphia-based Inovio, another company working on a 2019-nCoV vaccine with help from CEPI, began its project that same Saturday morning. Inovio produces vaccines made of DNA. It also has a MERS vaccine—which is further along than Moderna, already having entered human trials—that also relies on the spike protein. "Our team worked around the clock and was able to design a spike-focused vaccine by that Sunday night," says Joseph Kim, Inovio's CEO.

Both Moderna and Inovio say they could have enough vaccine produced one month from now to begin animal testing. Kim says he's looking forward to the race. "We're starting at the exact same time and this is a great opportunity for us to go *mano a mano* with Moderna," says Kim. "I like our chances."

CEPI's third grant is going to researchers at the University of Queensland (UQ) in Australia. They are developing a vaccine consisting of viral proteins produced in cell cultures, an older technology. UQ molecular virologist Keith Chappell, one of the project's leaders, says the "aspirational goal" is to have a candidate vaccine ready for human tests 16 weeks from now. "This is incredibly ambitious and we can provide no guarantee that we can meet this target," says Chappell. "Our team is working as hard and fast as we possibly can. It is reassuring to us that we are not the only team tasked with a response."

Once candidate vaccines are available, researchers will test them in animals to see if they are safe and produce an immune response. If so, companies will have to receive regulatory approvals to launch phase I human trials, which test safety and immune responses in small numbers of volunteers who are not at risk of the disease. In

the case of the U.S. Food and Drug Administration, approval typically takes one month. NIAID already has a vaccine trials network in place that plans to stage the phase I study of the Moderna vaccine; NIAID director Anthony Fauci expects the trial could start within three months.

In parallel to the human trials, researchers will want to test the vaccine's ability to protect animals intentionally exposed to the virus. That will require engineering a mouse model or finding another animal species—likely monkeys—that scientists can reliably infect with 2019-nCoV. "We're building the airplane as we're flying," says Inovio's Kim.

In the best-case scenario, Graham says, the Moderna vaccine will perform well in phase I studies and be ready for larger, real-world efficacy tests in humans by summertime. But previous efforts to race forward new vaccines during epidemics have hit unanticipated speed bumps. "I'm a little more circumspect about the timeline," says CEPI's Hatchett.

Even when experimental vaccines work in clinical trials, mass-producing them quickly is inevitably a huge challenge. If Moderna devoted all of its vaccine manufacturing capabilities to one product, it could make 100 million doses in a year, says Bancel. Inovio can currently only produce 100,000 doses a year, but is "actively speaking with a larger manufacturer," says Kim, which could increase their output to "multimillion" doses. The UQ teams says it could make 200,000 doses in six months.

None of that comes even close to what might be needed to protect the world's population in the worst-case scenario. But if the new coronavirus is seasonal in nature, as many respiratory viruses are, time might be on the vaccine makers' side. Influenza, for instance, in most of the world typically transmits in winter and disappears in summer. "If [nCoV-2019] behaves anything like flu, there will be seasonal transmission and then it will go down and there will be a recrudescence in the fall," says Hatchett. "So it could be even one year down the road before we see a large wave of disease. And it could be that a vaccine then plays a role in a timely fashion." Widespread infection in populations—which may be happening in Wuhan now—can also lead to lasting immunity in many people, reducing the need for vaccine.

Moderna's Bancel says the preparation of the vaccine ultimately is a precautionary measure. "Nobody knows what's going to happen," he says. "We're all hoping we'll never need this vaccine."

http://bit.ly/2Gvr45K

Towering dinosaur with radioactive skull identified in Utah

The 155-million-year-old specimen was headless until a radiation detector located the skeleton's skull.

By Laura Geggel - Associate Editor

Paleontologists have discovered the skeleton and radioactive skull of a previously unknown species of *Allosaurus*. The fearsome two-legged dinosaur sported 80 sharp teeth and horns over its eyes when it lived about 155 million years ago in what is now Utah.

This illustration shows a pack of the newly discovered Allosaurus jimmadseni attacking a young sauropod. **(Image: © Todd Marshall)**

But researchers didn't know any of these details at first; originally, they found only the dinosaur's skeleton but not the head. Even so, the block of rock that encased the skeleton was so massive — it weighed 6,000 lbs. (2,700 kilograms) — that paleontologists had to use explosives to remove the fossils and a helicopter to transport it.

It wasn't until six years later, in 1996, that the headless body and its skull were reunited.

That happy reunion was made possible by Ramal Jones, a retired University of Utah radiologist. Armed with a radiation detector, he located the radioactive skull not far from its body. It's not uncommon for dinosaur bones to be radioactive, as radioactive elements can leach into the bones over time from the surrounding sediment. Later, teams from Dinosaur National Monument excavated the dinosaur's head, which helped researchers identify the remains as a newfound dinosaur species.

Scientists named the beast *Allosaurus jimmadseni*, after paleontologist James Madsen Jr. (1932-2009), recognizing him for his "herculean efforts of protecting, excavating, preparing and curating of many thousands of *Allosaurus* bones," the researchers wrote in the study.

During the late Jurassic period, *A. jimmadseni* lived on the semiarid flood plains of western North America. This dinosaur is the oldest species of *Allosaurus*, outdating Utah's better-known *Allosaurus fragilis*, which helped make the *Allosaurus* the state's official fossil.

This illustration shows all of the bumps and dips on the fearsome face of Allosaurus jimmadseni. **(Image credit: Andrey Atuchin)**

"Previously, paleontologists thought there was only one species of *Allosaurus* in Jurassic North America, but this study shows there were two species — the newly described *Allosaurus jimmadseni* evolved at least 5 million years earlier than its younger cousin, *Allosaurus fragilis*," study co-lead researcher Mark Loewen said in a statement. Loewen is a research associate at the Natural History Museum of Utah and an associate professor in the Department of Geology and Geophysics at the University of Utah.

This dinosaur was a big carnivore, measuring up to 29 feet (9 meters) long and weighing about 4,000 lbs. (1.8 metric tons). It had a narrow skull, horns in front of its eyes and a crest that ran from those horns to its nose. Each of the dinosaur's long arms ended with three sharp claws.

"The skull of *Allosaurus jimmadseni* is more lightly built than its later relative *Allosaurus fragilis*, suggesting a different feeding behavior between the two," Loewen noted.

Loewen and co-researcher Daniel Chure, a retired paleontologist at Dinosaur National Monument, detailed the study online Friday (Jan. 24) in the journal PeerJ.