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Martian life must be rare as free energy source remains untapped

If life still exists on the Red Planet, it must be very rare – or so an unexploited energy source in the atmosphere suggests.

By Bob Holmes

The Martian atmosphere is unusually rich in carbon monoxide, which many microbes here on Earth can convert to carbon dioxide to yield energy for growth.

Does anything call Mars home? **JPL/NASA**

"It's a free lunch, just sitting in the atmosphere, that microbes could be eating," says Steven Sholes, an astrobiologist at the University of Washington. The persistence of that leftover lunch suggests that Martian life must be nonexistent, or at least very rare.

To determine just how rare, Sholes gathered estimates of how quickly solar radiation generates carbon monoxide in the Martian atmosphere, and how fast it diffuses down to the planet's surface and into subsurface rocks, where any Martian life would be sheltering from deadly radiation. Then he used these estimates to calculate the maximum subsurface microbial biomass that could be consuming carbon monoxide, yet still leave the observed amount of leftovers.

Martian microbes?

By this calculation, Mars could harbour no more than one billionth of Earth's biomass, or less than one microbial cell per cubic centimetre of soil, he told the Astrobiology Science Conference in Mesa, Arizona, last week.

His analysis doesn't prove the existence of life on Mars today one way or the other, only that if it is there it is rare. The calculation also only accounts for microbes that metabolise carbon monoxide, he notes. Other microbes, using other metabolic pathways, could be present – though it would be surprising if they didn't adapt to make use of the free lunch, he says.

Even the high end of Sholes's estimate suggests that spacecraft looking for extant life on Mars face a daunting task. The least productive environments on Earth contain 100 times more cells per cubic centimetre as the calculated Martian maximum, says Tori Hoehler, an astrobiologist at NASA Ames Research Center in California.

"It's not easy to find those organisms," says Hoehler, so finding even sparser life on Mars will be even tougher.

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Scientists find new genetic roots for intelligence

52 genes uncovered provide very robust associations with intelligence

Intelligence is one of the most investigated traits in humans and higher intelligence is associated with important economic and health-related life outcomes. Despite high heritability estimates of 45% in childhood and 80% in adulthood, only a handful of genes had previously been associated with intelligence and for most of these genes the findings were not reliable. The study, published in the journal Nature Genetics, uncovered 52 genes for intelligence, of which 40 were completely new discoveries. Most of these genes are predominantly expressed in brain tissue.

"These results are very exciting as they provide very robust associations with intelligence. The genes we detect are involved in the regulation of cell development, and are specifically important in synapse formation, axon guidance and neuronal differentiation. These findings for the first time provide clear clues towards the underlying biological mechanisms of intelligence", says Danielle Posthuma, Principal Investigator of the study.

The study also showed that the genetic influences on intelligence are highly correlated with genetic influences on educational attainment,

and also, albeit less strongly, with smoking cessation, intracranial volume, head circumference in infancy, autism spectrum disorder and height. Inverse genetic correlations were reported with Alzheimer's disease, depressive symptoms, smoking history, schizophrenia, waist-to-hip ratio, body mass index, and waist circumference.

"These genetic correlations shed light on common biological pathways for intelligence and other traits. Seven genes for intelligence are also associated with schizophrenia; nine genes also with body mass index, and four genes were also associated with obesity. These three traits show a negative correlation with intelligence", says Suzanne Sniekers, first author of the study and postdoc in the lab of Posthuma. "So, a variant of gene with a positive effect on intelligence, has a negative effect on schizophrenia, body mass index or obesity."

Future studies will need to clarify the exact role of these genes in intelligence in order to obtain a more complete picture of how genetic differences lead to differences in intelligence. "The current genetic results explain up to 5% of the total variance in intelligence. Although this is quite a large amount of variance for a trait as intelligence, there is still a long road to go: given the high heritability of intelligence, many more genetic effects are expected to be important, and these can only be detected in even larger samples", says Danielle Posthuma.

The study is published in Nature Genetics, May 22, 2017.

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Study redefines HPV-related head and neck cancers

Study concludes much of what was believed about the human papilloma virus in HPV-related head and neck cancers may be wrong

Much of what we thought we knew about the human papilloma virus (HPV) in HPV-related head and neck cancers may be wrong, according to a newly published study by Virginia Commonwealth University (VCU) researchers that analyzed data from The Human Cancer Genome Atlas. Head and neck cancers involving HPV are on the rise, and many experts believe we are seeing the start of an epidemic that will only get worse in the coming years.

The Cancer Genome Atlas is a collaboration between the National Cancer Institute (NCI) and the National Human Genome Research (NHGR) Institute that makes publicly available genomic information on tumor samples from 33 different types of cancers. Its aim is to help the cancer research community improve the prevention, diagnosis and treatment of cancer.

It is thought that there are two main forms of HPV-related cancers, episomal and integrated. In episomal variants, the HPV genome replicates independently. Integrated HPV has become part of the DNA of the host cell and relies on it for replication.

Previously, it was believed that most HPV-related head and neck cancers had integrated HPV, as is what is believed with HPV-related cervical cancers.

However, Windle's study, recently published in the journal Oncotarget, found that HPV DNA is maintained separate from the human genome in the majority of HPV-related head and neck cancers, though, in many cases, the HPV genome can acquire a small piece of human DNA making it look like integrated HPV.

This viral-human hybrid represents a new category of episomal HPV in HPV-related cancers.

"Our work challenges the idea that finding HPV DNA joined to human DNA means that HPV is integrated. With this new view of the state of HPV, we conclude that episomal HPV is the predominant state in HPV-related head and neck cancers," says Brad Windle, member of the Cancer Molecular Genetics research program at VCU Massey Cancer Center, professor at the Philips Institute for Oral Health Research at the VCU School of Dentistry and co-principle investigator on the study. "This is an important distinction because patients with episomal HPV cancer respond better to therapy than patients with integrated HPV cancer."

Windle's team analyzed the genomes of all 520 HNC samples in The Cancer Genome Atlas and found that 72 were HPV positive. The large majority of these cancers had a common type of the virus known as HPV16 present, so they focused on that virus type. The data showed that 75 percent of the HPV16 samples had the HPV genome in the episomal state, and about half of the genomes contained a piece of human DNA within their circular structure.

The researchers also found that 73 percent of the tumor samples were still dependent on proteins known as E1 and E2 for replication. This is important because when the HPV genome integrates with human DNA, expression of the HPV E2 protein--essential for independent replication--is lost. The presence of E2, or lack thereof, in tumor biopsies could be a reliable way for physicians to determine the cancer type and provide a more accurate prognosis.

"Perhaps our most striking outcome is the potential to target the E1 and E2 proteins for diagnosis and treatment," says Windle. With nearly three quarters of these cancers dependent on E1 and E2 for replication, we could develop drugs that target these proteins and promote cell death."

Windle's team plans to continue studying the integration of HPV in HPV-related head and neck cancers, and suggests that viral-human DNA hybrid HPV should be further explored in HPV-related cervical cancers. His team is currently working with Massey clinicians in order to use this information to assess patients' prognosis in the clinic.

Windle collaborated on this research with Iain M. Morgan, director and professor at the Philips Institute for Oral Health Research at the VCU School of Dentistry, member of the Cancer Molecular Genetics research program at Massey and co-principle investigator on this study; Tara J. Nulton, from the Philips Institute for Oral Health Research at the VCU School of Dentistry; Amy L. Olex, from the C. Kenneth and Dianne Wright Center for Clinical and Translational Research at VCU; and Mikhail Dozmorov, Ph.D., from the C. Kenneth and Dianne Wright Center for Clinical and Translational Research and the Department of Biostatistics at VCU.

This study was supported by a grant from the National Institute of Dental and Craniofacial Research, VCU's National Institutes of Health Clinical and Translational Science Awards (CTSA) grant UL1TR000058, and, in part, by VCU Massey Cancer Center's NCI Cancer Center Support Grant P30CA016059.

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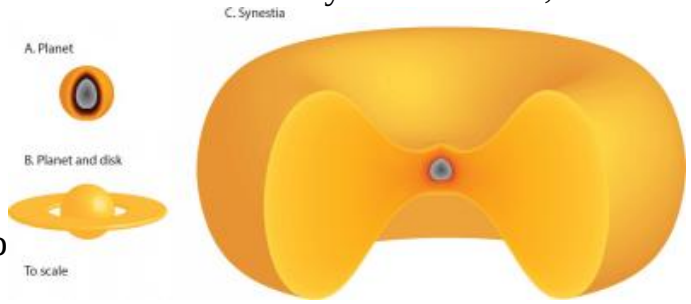
Scientists propose synestia, a new type of planetary object

There's something new to look for in the heavens, and it's called a "synestia"

There's something new to look for in the heavens, and it's called a "synestia," according to planetary scientists Simon Lock at Harvard University and Sarah Stewart at the University of California, Davis. A synestia, they propose, would be a huge, spinning, donut-shaped mass of hot, vaporized rock, formed as planet-sized objects smash into each other.



Rocky planets are thought to form from giant impacts between planet-size bodies. Impacts with high energy and high angular momentum could form a synestia, a rotating mass of vaporized rock, where outer layers of the vaporized planet are in orbit around the rest of the body. Synestias give new insights into how planets and moons form. This figure shows to scale a rocky planet, a molten disk/ring structure, and a synestia all with the same mass (about one Earth mass). **Simon Lock, Harvard University**

And at one point early in its history, the Earth itself was likely a synestia, said Stewart, who is a professor in the Department of Earth and Planetary Sciences at UC Davis. Lock and Stewart describe the new object in a paper published May 22 in the Journal of Geophysical Research: Planets.

Lock, who is a graduate student at Harvard, and Stewart study how planets can form from a series of giant impacts. Current theories of planet formation hold that rocky planets such as the Earth, Mars and Venus formed early in the existence of our solar system as smaller objects collided with each other. These collisions were so violent that the resulting bodies melted and partially vaporized, eventually cooling and solidifying to the (nearly) spherical planets we know today.

Lock and Stewart are particularly interested in collisions between spinning objects. A rotating object has angular momentum, which must be conserved in a collision. Think of a skater spinning on ice: If she extends her arms, she slows her rate of spin, and to spin faster she holds her arms close. Her angular momentum is the same.

Now consider two ice skaters turning on ice: if they catch hold of each other, the angular momentum of each adds together, so their total angular momentum must be the same.

Lock and Stewart modeled what happens when the "ice skaters" are Earth-sized rocky planets colliding with other large objects with both high energy and high angular momentum.

"We looked at the statistics of giant impacts, and we found that they can form a completely new structure," Stewart said.

The researchers found that over a range of high temperatures and high angular momentum, planet-sized bodies could form a new, much larger structure, an indented disk rather like a red blood cell or a donut with the center filled in. The object is mostly vaporized rock, with no solid or liquid surface.

They have dubbed the new object a "synestia," from "syn-," "together" and "Hestia," Greek goddess of architecture and structures.

A new type of structure

The key to synestia formation is that some of the structure's material actually goes into orbit. In a spinning solid sphere, every point from the core to the surface is rotating at the same rate. But in a giant impact, the material of the planet can become molten or gaseous and expands in volume. If it gets big enough and is moving fast enough, parts of the object pass the velocity needed to keep a satellite in orbit, and that's when it forms a huge, disk-shaped synestia.

Previous theories had suggested that giant impacts might cause planets to form a disk of solid or molten material surrounding the planet. But for the same mass of planet, a synestia would be much larger than a solid planet with a disk.

Most planets likely experience collisions that could form a synestia at some point during formation, Stewart said. For an object like the Earth, the synestia would not last very long -- perhaps a hundred years -- before it lost enough heat to condense back into a solid object. But synestias formed from larger or hotter objects such as gas giant planets or stars could potentially last much longer, she said.

The synestia structure also suggests new ways to think about lunar formation, Stewart said. Earth's moon is remarkably similar to Earth in composition, and most current theories about how the moon formed involve a giant impact that threw material into orbit. But such an impact could have instead formed a synestia from which the Earth and moon both condensed. No one has yet observed a synestia directly, but they might be found in other solar systems once astronomers start looking for them alongside rocky planets and gas giants.

The work was supported by NASA and the U.S. Department of Energy.

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Supercomputing helps researchers understand Earth's interior

Geologists create model with potential to predict earthquakes, volcanoes, and other tectonic activity

Contrary to posters you may have seen hanging on the walls in science buildings and classrooms, Lijun Liu, professor of geology at Illinois, knows that Earth's interior is not like an onion.

While most textbooks demonstrate the outer surface of the Earth as the crust, the next inner level as the mantle, and then the most inner layer as the core, Liu said the reality isn't as clear-cut. "It's not just in layers, because the Earth's interior is not stationary," Liu said.

In fact, underneath our feet there's tectonic activity that many scientists have been aware of, but Liu and his team have created a computer model to help better explain it -- a model so effective that researchers believe it has the potential to predict where earthquakes and volcanoes will occur.

Using this model, Liu, along with doctoral student Jiashun Hu, and Manuele Faccenda from the University of Padua in Italy, recently published a research paper in the journal of Earth and Planetary Science Letters that focuses on the deep mantle and its relationship to plate tectonics.

"It's well-known that there are plate tectonics driving the Earth's evolution, but exactly how this process works is not entirely clear," he said.

Liu and Hu looked specifically at the continent of South America to determine which tectonic factors contribute to the deformation, or the evolution, of the mantle.

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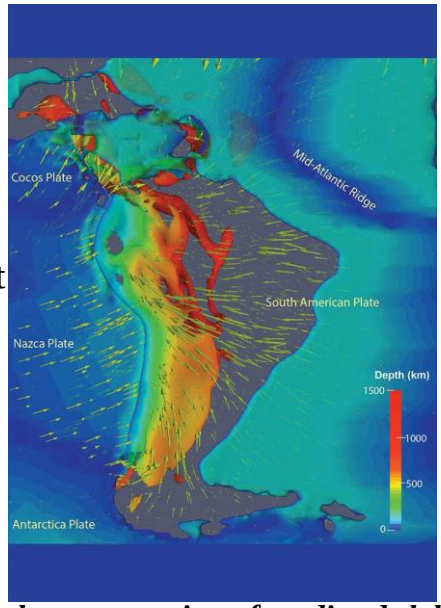

***Researchers created a three-dimensional representation of predicted slab geometry and mantle flow. The image outlines areas with a temperature at 300 degrees Celsius cooler than the surrounding mantle, with different colors representing different depths. Oceanic plates and slabs are semi-transparent, and continents are entirely transparent. Green arrows represent velocity vectors inside the mantle*Lijun Liu, University of Illinois.**

To answer this question, the team created a data-centric model using the Blue Waters supercomputer at the National Center for Supercomputing Applications at Illinois. The sophisticated four-dimensional data-oriented geodynamic models are among the first of their kind.

"We are actually the first ones to use data assimilation models in studying mantle deformation, in an approach similar to weather forecasting," Liu said. "We are trying to produce a system model that simultaneously satisfies all the observations we have. We can then obtain a better understanding about dynamic processes of the Earth evolution."

While there are many debates in regards to how the Earth's internal evolution is driven, the model created by the team seemed to find an answer that better fits available observations and underlying physics. The team found that the subducting slab -- a portion of the oceanic plate that slides beneath a continental plate -- is the dominant driving force behind the deformation of the mantle.

Essentially, the active subduction of the slab determines most other processes that happen as part of a chain reaction. "The result is game-changing. The driving force of mantle flow is actually simpler than people thought," Liu said. "It is the most direct consequence of plate tectonics. When the slab subducts, it naturally controls everything surrounding it. In a way this is elegant, because it's simple."

By understanding this mechanism of Earth evolution, the team can make better predictions regarding the movement of the mantle and the lithosphere, or crust.

The team then evaluated the model's predictions using other data. Hu, the lead author on the paper, said that by comparing the predictions to tectonic activities such as the formation of mountains and volcanoes, a clear consistency emerged. "We think our story is correct," Hu said.

Consequently, the model also provides interesting insight on the evolution of continents as far back as the Jurassic, when dinosaurs roamed the Earth on Pangaea, the only continent at the time. This is still the team's ongoing research.

Liu said that in a separate paper that uses the same simulation, published by Liu and Hu in Earth and Planetary Science Letters in 2016, the model provided an accurate prediction for why earthquakes happen in particular locations below South America. He explained that earthquakes aren't evenly spread within the subducting slab, meaning there are potentially areas where an earthquake is more or less likely to take place.

"We found that whenever you see a lack of earthquakes in a region, it corresponds to a hole in the slab," Liu said. "Because of the missing

slab in the hole, there's no way to generate earthquakes, so we might be able to know where more earthquakes will take place."

The model also explained why certain volcanoes might exist further inland and have different compositions, despite the common thought that volcanoes should exist solely along the coast, as a result of water coming off the down-going slab. As the model helps explain, a volcano can form inland if the slab subducts at a shallower angle, and a hole in the shallow slab allows for a special type of magma to form by melting of the crust.

"Ultimately this model will provide a promising way of solving the question of how and why continents move the way they do," Liu said. "The answer should depend on what the mantle is doing. This is a way to much better understand Earth evolution."

The team is currently expanding the model to analyze the entire globe. "We are looking forward to more exciting results," Liu said.

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3.3-million-year-old fossil reveals the antiquity of the human spine

Portions of human skeletal structure were established millions of years earlier than previously thought, Mizzou researcher finds

For more than 3 million years, Selam lay silent and still. Eager to tell her story, the almost perfect fossil skeleton of a 2 1/2 year-old toddler was discovered at Dikika, Ethiopia -- and she had a lot to say. An international research team slowly chipped away at the sandstone surrounding Selam at the National Museums of Ethiopia to reveal something remarkable -- even though millions of years have passed, she's a lot like us. Selam, which means "peace" in the Ethiopian Amharic language, was an early human relative from the species Australopithecus afarensis -- the same species as the famous Lucy skeleton. The findings, published this week in the Proceedings of the National Academy of Science, indicate that Selam possesses the most complete spinal column of any early fossil human relative, and her vertebral bones, neck and rib cage are mainly intact. This new research demonstrates that portions of the human skeletal structure were established millions of years earlier than previously thought.

The almost perfect fossil skeleton of a 2 1/2 year-old toddler was discovered at Dikika, Ethiopia. **Zeray Alemseged, University of Chicago**

Many features of the human spinal column and rib cage are shared among primates. The human spine reflects the distinctive mode of walking upright on two feet. Among the distinctive features is that humans have fewer rib-bearing vertebrae, bones of the back, than those of our closest relatives, and more vertebrae in the lower back allowing motions for walking effectively. When and how this pattern evolved has been unknown because complete sets of vertebrae are rarely preserved in the fossil record.

"For many years we have known of fragmentary remains of early fossil species that suggest that the shift from rib-bearing, or thoracic, vertebrae to lumbar, or lower back, vertebrae was positioned higher in the spinal column than in living humans, but we have not been able to determine how many vertebrae our early ancestors had," said Carol Ward, a Curators Distinguished Professor of Pathology and Anatomical Sciences in the MU School of Medicine, and lead author on the study. "Selam has provided us the first glimpse into how our early ancestors' spines were organized."

Selam was discovered by Zeresenay Alemseged, a professor in the Department of Organismal Biology and Anatomy at the University of Chicago. The skeleton was surrounded by sandstone, and Alemseged and his team have been preparing the delicate fossil for 13 years at the National Museum of Ethiopia.

"Continued and painstaking research on the Selam shows that the general structure of the human spinal column emerged over 3.3 million years ago, shedding light on one of the hallmarks of human

evolution," Alemseged said. "This type of preservation is unprecedented, particularly in a young individual whose vertebrae are not yet fully fused."

In order to be analyzed, Selam had to take a trip. She traveled to the European Synchrotron Radiation Facility in Grenoble, France, where Alemseged and the research team used high-resolution imaging technology to visualize the bones. Scans were later sent to Ward at MU for further comparative studies.

"This technology provides the opportunity to virtually examine aspects of the vertebrae otherwise unattainable from the original specimen," said coauthor of the study Fred Spoor, a professor of evolutionary anatomy in the Department of Biosciences at the University College London.

Ward says the scans indicated that Selam had the distinctive thoracic-to-lumbar joint transition found in other fossil human relatives, but the specimen is the first to show that, like modern humans, our earliest ancestors had only twelve thoracic vertebrae and twelve pairs of ribs, which is fewer than in most apes.

"This unusual early human configuration may be a key in developing more accurate scenarios concerning the evolution of bipedality and modern human body shape," said Thierra Nalley, an assistant professor of anatomy at Western University of Health Sciences in Pomona, California, also an author of the paper.

The study, "Thoracic Vertebral Count and Thoracolumbar Transition in Australopithecus afarensis" was published in the Proceedings of the National Academy of Science. Funding for the research was provided by Margaret and Will Hearst, the National Science Foundation and the European Synchrotron Radiation Facility. The content is solely the responsibility of the authors and does not necessarily represent the official views of the funding agencies.

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Scientists find 7.2-million-year-old pre-human remains in the Balkans

Fossils indicate great apes and humans split several hundred thousand years earlier than believed, and in the Eastern Mediterranean, not in Africa

The common lineage of great apes and humans split several hundred thousand years earlier than hitherto assumed, according to an international research team headed by Professor Madelaine Böhme from the Senckenberg Centre for Human Evolution and Palaeoenvironment at the University of Tübingen and Professor Nikolai Spassov from the Bulgarian Academy of Sciences. The researchers investigated two fossils of Graecopithecus freybergi with state-of-the-art methods and came to the conclusion that they belong to pre-humans. Their findings, published today in two papers in the journal PLOS ONE, further indicate that the split of the human lineage occurred in the Eastern Mediterranean and not - as customarily assumed - in Africa.

The lower jaw of the 7.175 million year old Graecopithecus freybergi (El Graeco) from Pyrgos Vassilissis, Greece (today in metropolitan Athens).
Wolfgang Gerber, University of Tübingen

Present-day chimpanzees are humans' nearest living relatives. Where the last chimp-human common ancestor lived is a central and highly debated issue in palaeoanthropology. Researchers have assumed up to now that the lineages diverged five to seven million years ago and that the first pre-humans developed in Africa. According to the 1994 theory of French palaeoanthropologist Yves Coppens, climate change in Eastern Africa could have played a crucial role. The two studies of the research team from Germany, Bulgaria, Greece, Canada, France and Australia now outline a new scenario for the beginning of human history.

Dental roots give new evidence

The team analyzed the two known specimens of the fossil hominid Graecopithecus freybergi: a lower jaw from Greece and an upper

premolar from Bulgaria. Using computer tomography, they visualized the internal structures of the fossils and demonstrated that the roots of premolars are widely fused.

"While great apes typically have two or three separate and diverging roots, the roots of Graecopithecus converge and are partially fused - a feature that is characteristic of modern humans, early humans and several pre-humans including Ardipithecus and Australopithecus", said Böhme.

Scientists find 7.2-million-year-old pre-human remains in the Balkans

The lower jaw, nicknamed 'El Graeco' by the scientists, has additional dental root features, suggesting that the species Graecopithecus freybergi might belong to the pre-human lineage. "We were surprised by our results, as pre-humans were previously known only from sub-Saharan Africa," said Jochen Fuss, a Tübingen PhD student who conducted this part of the study.

A 7.24 million year old upper premolar of Graecopithecus from Azmaka, Bulgaria. **Wolfgang Gerber, University of Tübingen**

Furthermore, Graecopithecus is several hundred thousand years older than the oldest potential pre-human from Africa, the six to seven million year old Sahelanthropus from Chad. The research team dated the sedimentary sequence of the Graecopithecus fossil sites in Greece and Bulgaria with physical methods and got a nearly synchronous age for both fossils - 7.24 and 7.175 million years before present. "It is at the beginning of the Messinian, an age that ends with the complete desiccation of the Mediterranean Sea," Böhme said.

Professor David Begun, a University of Toronto paleoanthropologist and co-author of this study, added, "This dating allows us to move the human-chimpanzee split into the Mediterranean area."

Environmental changes as the driving force for divergence

As with the out-of-East-Africa theory, the evolution of pre-humans may have been driven by dramatic environmental changes. The team led by Böhme demonstrated that the North African Sahara desert originated more than seven million years ago. The team concluded this based on geological analyses of the sediments in which the two fossils were found. Although geographically distant from the Sahara, the red-colored silts are very fine-grained and could be classified as desert dust. An analysis of uranium, thorium, and lead isotopes in individual dust particles yields an age between 0.6 and 3 billion years and infers an origin in Northern Africa.

Scientists find 7.2-million-year-old pre-human remains in the Balkans

An electron microscope image of a dust particle rounded by eolian transport. It originated in the Sahara desert and was found in 7.2 million year old sediments in Greece. Credit: Ulf Linnemann, Senckenberg Center for Human Evolution and Palaeoenvironment, University of Tübingen

Moreover, the dusty sediment has a high content of different salts. "These data document for the first time a spreading Sahara 7.2 million years ago, whose desert storms transported red, salty dusts to the north coast of the Mediterranean Sea in its then form," the Tübingen researchers said. This process is also observable today. However, the researchers' modelling shows that, with up to 250 grams per square meter and year, the amount of dust in the past considerably exceeds recent dust loadings in Southern Europe more than tenfold, comparable to the situation in the present-day Sahel zone in Africa.

Fire, grass, and water stress

The researchers further showed that, contemporary to the development of the Sahara in North Africa, a savannah biome formed in Europe. Using a combination of new methodologies, they studied microscopic fragments of charcoal and plant silicate particles, called phytoliths. Many of the phytoliths identified derive from grasses and particularly from those that use the metabolic pathway of C4-photosynthesis, which is common in today's tropical grasslands and savannahs. The

global spread of C4-grasses began eight million years ago on the Indian subcontinent - their presence in Europe was previously unknown.

"The phytolith record provides evidence of severe droughts, and the charcoal analysis indicates recurring vegetation fires," said Böhme. "In summary, we reconstruct a savannah, which fits with the giraffes, gazelles, antelopes, and rhinoceroses that were found together with Graecopithecus," Spassov added

"The incipient formation of a desert in North Africa more than seven million years ago and the spread of savannahs in Southern Europe may have played a central role in the splitting of the human and chimpanzee lineages," said Böhme. She calls this hypothesis the North Side Story, recalling the thesis of Yves Coppens, known as East Side Story.

The findings are described in two studies published in PLOS ONE titled "Potential hominin affinities of Graecopithecus from the late Miocene of Europe" and "Messinian age and savannah environment of the possible hominin Graecopithecus from Europe."

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'Half a glass of wine every day' increases breast cancer risk

Further evidence has emerged of the link between alcohol consumption in women and an increased risk of breast cancer.

According to a report from the World Cancer Research Fund, half a glass of wine or a small beer a day increases the risk of breast cancer.

It also backs up research showing that regular intensive exercise can reduce the risk of the disease.

But is it really that simple?

Breast cancer is by far the most common cancer in women in the UK with one in eight women developing the disease during their lifetime.

But scientists say they can't explain why the cancer occurs in some people and not in others. There are numerous causes and lots of factors to take into account, including lifestyle, hormone levels and other medical conditions. Basically, it's a complex picture and there's no point focusing on one factor only.

So what are the risk factors for breast cancer?

For a start, there are some factors you cannot control such as your sex, age, height, genes and when you started your periods.

Being a woman, over 50 and past the menopause, and having a history of breast cancer in your family, all increase your risk of getting the disease. Being tall and starting periods before the age of 12 are thought to increase the risk too.

Cancer Research UK lists 18 different factors which could cause breast cancer to some degree. Alcohol is only one of them.

What does this report say?

It says there are ways women can lower their risk of breast cancer by focusing on factors they can control, like diet, weight and exercise.

After analysing more than 100 studies that examined the medical history of 12 million women, the report backs up current advice to be aware of alcohol consumption. The report found evidence that drinking an extra small glass of wine every day (10g of alcohol) increases a woman's risk of breast cancer after the menopause by 9%.

What does that really mean?

It means that in a group of 100 women, around 13 would be likely to develop breast cancer anyway. And if they all drank an additional small glass of wine every day, one extra case might develop among the original group.

What about exercise and diet?

When it comes to exercise, the report found that doing more vigorous exercise, like cycling or running, cut the risk of post-menopausal breast cancer by 10% compared to the least active women.

Breastfeeding was also found to lower the risk of the disease before and after the menopause.

And there was limited evidence that eating more leafy vegetables, such as cabbage, spinach and kale, decreased the risk of a less common kind of breast cancer.

We already know that regular physical exercise, eating a balanced diet and maintaining a healthy weight are important for reducing the risk of lots of diseases, including cancers. But scientists say all these factors interact with each other and that makes it difficult to tease out which ones are driving the cancer and to what extent.

What is the recommended advice on alcohol intake?

New guidelines were introduced in 2016 which said that men and women should drink no more than 14 units a week - equivalent to six pints of beer or seven glasses of wine - and some days should be free of alcohol altogether.

The UK's chief medical officers' advice was based on research which showed that any amount of alcohol can increase the risk of cancer.

Pregnant women are advised not to drink at all.

What's been the reaction to this report?

Cancer experts say the findings don't tell us anything new about the link between alcohol and breast cancer, which is already well known.

But if you can, to stack the odds in your favour, they say it is a good idea to have some alcohol-free days during every week and not to increase your drinking.

However, Cancer Research UK says there is no need be alarmed and "go teetotal". It is also important to look at the bigger picture.

Drinking alcohol has a greater effect on the risks of several other cancers - including mouth, liver and bowel - than it does on breast cancer, so there is no reason to become fixated on alcohol.

Kevin McConway, emeritus professor of applied statistics at the Open University, says the risks have "to be set against whatever pleasure women might obtain from their drinking".

The report does not provide absolute risks and as such, Prof Sir David Spiegelhalter, from the University of Cambridge, said it did not seem a good basis for recommending that women give up alcohol completely.

However, Dr Anne McTiernan, lead report author and cancer expert at the Fred Hutchinson Cancer Research Center in Seattle, said the evidence regarding breast cancer was clear. "Having a physically active lifestyle, maintaining a healthy weight throughout life and limiting alcohol are all steps women can take to lower their risk."

http://bit.ly/2qw0yiq

Why our brain cells may prevent us burning fat when we're dieting

A study carried out in mice may help explain why dieting can be an inefficient way to lose weight: key brain cells act as a trigger to prevent us burning calories when food is scarce.

"Weight loss strategies are often inefficient because the body works like a thermostat and couples the amount of calories we burn to the amount of calories we eat," says Dr Clémence Blouet from the Metabolic Research Laboratories at University of Cambridge. "When we eat less, our body compensates and burns fewer calories, which makes losing weight harder. We know that the brain must regulate this caloric thermostat, but how it adjusts calorie burning to the amount of food we've eaten has been something of a mystery."

Now, in research published in the open access journal eLife, a team of researchers has identified a new mechanism through which the body adapts to low caloric intake and limits weight loss in mice. Mice share a number of important biological and physiological similarities with humans and so are a useful model for studying how our bodies work.

The researchers tested the role of a group of neurons in a brain region known as the hypothalamus. These 'agouti-related neuropeptide' (AGRP) neurons are known for their major role in the regulation of appetite: when activated, they make us eat, but when fully inhibited they can lead to almost complete anorexia.

The team used a genetic trick to switch the AGRP neurons 'on' and 'off' in mice so that they could rapidly and reversibly manipulate the neurons' activity. They studied the mice in special chambers than can measure energy expenditure, and implanted them with probes to remotely measure their temperature, a proxy for energy expenditure, in different contexts of food availability.

The researchers demonstrated that AGRP neurons are key contributors to the caloric thermostat that regulates our weight, regulating how many calories we burn. The findings suggest that when activated, these neurons make us hungry and drive us to eat - but when there is no food available, they act to spare energy, limiting the number of calories that we burn and hence our weight loss.

As soon as food becomes available and we start eating, the action of the AGRP neurons is interrupted and our energy expenditure goes back up again to normal levels.

In addition, the researchers also describe a mechanism through which AGRP neurons regulate their activity by detecting how much energy we have on-board and then controlling how many calories we burn.

"Our findings suggest that a group of neurons in the brain coordinate appetite and energy expenditure, and can turn a switch on and off to burn or spare calories depending on what's available in the environment," says Dr Blouet, who led the study. "If food is available, they make us eat, and if food is scarce, they turn our body into saving mode and stop us from burning fat."

"While this mechanism may have evolved to help us cope with famine, nowadays most people only encounter such a situation when they are deliberately dieting to lose weight. Our work helps explain why for these people, dieting has little effect on its own over a long period. Our bodies compensate for the reduction in calories."

Dr Luke Burke, the study's first author, adds: "This study could help in the design of new or improved therapies in future to help reduce overeating and obesity. Until then, best solution for people to lose weight - at least for those who are only moderately overweight - is a combination of exercise and a moderate reduction in caloric intake."

Burke, LK et al. mTORC1 in AGRP neurons integrates exteroceptive and interoceptive food-related cues in the modulation of adaptive energy expenditure in mice. eLife; 23 May 2017; DOI: 10.7554/eLife.22848

http://bit.ly/2r9Hicr

Birds, bees and other critters have scruples, and for good reason

Psychologists find examples of conscientiousness, such as working hard, paying attention to detail and striving to do the right thing, throughout the animal kingdom

Humans are not the only species to show a strong work ethic and scruples. UC Berkeley researchers have found evidence of conscientiousness in insects, reptiles, birds, fish and other critters.

In reviewing nearly 4,000 animal behavior studies, UC Berkeley psychologists Mikel Delgado and Frank Sulloway tracked such attributes as industriousness, neatness, tenacity, cautiousness and self-discipline across a broad range of creatures great and small.

Just as in humans, conscientiousness in animals - which includes working hard, paying attention to detail and striving to do the right thing - has such evolutionary benefits as giving them an edge in hunting and gathering, attracting mates, procreating and fending off predators, according to the review published in the online issue of the journal Psychological Bulletin.

"Honeybees who are more likely to remove bee carcasses from their hive have more offspring, and birds who keep their nests tidier are less susceptible to being preyed on," said Delgado, a UC Berkeley doctoral student in psychology. "Also, for many bird species, mastering song is key to mating success."

And, "in some bird species, females carefully inspect the display nests that are built by males," she added. "Those males that build the best display nests and that have chosen nesting sites that are well hidden from predators, are more likely to be selected as mates."

Delgado and Sulloway divided the conscientious characteristics they found in animals into two main categories: "order and Industriousness," which includes organization and cleanliness, and "achievement striving and competence," which covers mastery and deliberation. Birds and insects tended to fit into the orderliness category, whereas primates and other mammals fit more squarely into the achievement striving box.

Moreover, researchers said, this split is reflected in the "phylogenetic" family tree in which primates and other mammals branched off from birds, reptiles, invertebrates and other species as their personality traits evolved to help them adapt to differing life conditions. "Orderly and industrious tendencies appear to have originated in insects and fish, whereas achievement striving and competence may be more closely related to problem-solving, group living, and the complexity of the environment that those animals inhabit," Delgado said.

Among other tools, researchers tracked animal characteristics using the "Big Five" model, which breaks down personality into the five overarching categories of openness, conscientiousness, extraversion, agreeableness and neuroticism.

While previous research has identified openness, extraversion, agreeableness and neuroticism in animals, this is the first time conscientiousness has been recognized throughout the animal kingdom. That's because previous research defined conscientiousness too narrowly as a human trait based on emotions, intentions and morality, Delgado said.

"We argue for using a more behaviorally based approach in assessing animal personality in future research," Delgado said.

http://bit.ly/2rLlh6m

Alzheimer's, Parkinson's, and Huntington's diseases share common crucial feature

Finding suggests that treatment for one disease could work for the other two

MAYWOOD, IL - A Loyola University Chicago study has found that abnormal proteins found in Alzheimer's disease, Parkinson's disease, and Huntington's disease all share a similar ability to cause damage when they invade brain cells.

The finding potentially could explain the mechanism by which Alzheimer's, Parkinson's, Huntington's, and other neurodegenerative diseases spread within the brain and disrupt normal brain functions.

The finding also suggests that an effective treatment for one neurodegenerative disease might work for other neurodegenerative diseases as well. The study by senior author Edward Campbell, PhD, first author William Flavin, PhD, and colleagues is published in the journal Acta Neuropathologica.

"A possible therapy would involve boosting a brain cell's ability to degrade a clump of proteins and damaged vesicles," Campbell said. "If we could do this in one disease, it's a good bet the therapy would be effective in the other two diseases."

Neurodegenerative diseases are caused by the death of neurons and other cells in the brain, with different diseases affecting different regions of the brain. Alzheimer's destroys memory, while Parkinson's and Huntington's affect movement. All three diseases are progressive, debilitating and incurable.

Previous research has suggested that in all three diseases, proteins that are folded abnormally form clumps inside brain cells. These clumps spread from cell to cell, eventually leading to cell deaths. Different proteins are implicated in each disease: tau in Alzheimer's, alpha-synuclein in Parkinson's and huntingtin in Huntington's disease.

The Loyola study focused on how these misfolded protein clumps invade a healthy brain cell. The authors observed that once proteins get inside the cell, they enter vesicles (small compartments that are encased in membranes). The proteins damage or rupture the vesicle membranes, allowing the proteins to then invade the cytoplasm and cause additional dysfunction. (The cytoplasm is the part of the cell that's outside the nucleus).

The Loyola study also showed how a cell responds when protein clumps invade vesicles: The cell gathers the ruptured vesicles and protein clumps together so the vesicles and proteins can be destroyed. However, the proteins are resistant to degradation. "The cell's attempt to degrade the proteins is somewhat like a stomach trying to digest a clump of nails," Campbell said.

Flavin said the finding that protein clumps associated with the three diseases cause the same type of vesicle damage was unexpected. Loyola researchers initially focused on alpha-synuclein proteins associated with Parkinson's disease. So they asked collaborator Ronald Melki, PhD, to send them samples of different types of alpha-synuclein. (To do the experiment in a blinded, unbiased manner, the Loyola researchers did not know which types of alpha-synuclein were which.) Melki, a protein researcher at the Paris-Saclay Institute of Neuroscience, is known for his ability to generate distinct types of alpha-synuclein. Without telling the Loyola researchers, Melki sent other types of proteins as well. This led to the surprise finding that tau and huntingtin proteins also can damage vesicles.

Campbell stressed the study's findings need to be followed up and confirmed in future studies.

The Loyola study is titled, "Endocytic vesicle rupture is a conserved mechanism of cellular invasion by amyloid proteins." It was supported by grants from the Michael J. Fox Foundation, Parkinson's Disease Foundation, Illinois chapter of the ARCS Foundation, Arthur J. Schmitt Foundation and other sources.

Campbell is an associate professor in the Department of Microbiology and Immunology at Loyola University Chicago Stritch School of Medicine. Flavin is a Loyola University Chicago MD/PhD student. Other co-authors are Zachary Green, Stratos Skarpathiotis, and Michael Chaney of Loyola University Chicago; Luc Bousset and Ronald Melki of the Paris-Saclay Institute of Neuroscience; and Yaping Chu and Jeffrey Kordower of Rush University Medical Center.

http://bit.ly/2rLm4UZ

Eating chocolate may decrease risk of irregular heartbeat

Consuming moderate amounts of chocolate associated with significantly lower risk of being diagnosed with atrial fibrillation

Boston, MA - Consuming moderate amounts of chocolate was associated with significantly lower risk of being diagnosed with atrial fibrillation (AF)--a common and dangerous type of irregular heartbeat--in a large study of men and women in Denmark led by researchers at Harvard T.H. Chan School of Public Health and in Denmark.

The study will be published online May 23, 2017 in Heart.

"Our study adds to the accumulating evidence on the health benefits of moderate chocolate intake and highlights the importance of behavioral factors for potentially lowering the risk of arrhythmias," said Elizabeth Mostofsky, instructor in the Department of Epidemiology at Harvard Chan School, a postdoctoral fellow at Beth Israel Deaconess Medical Center, and lead author of the study.

Previous studies have suggested that cocoa and cocoa-containing foods--in particular, dark chocolate, which has a higher cocoa content than milk chocolate--confer cardiovascular benefits, perhaps because of their high content of flavanols, which may promote healthy blood vessel function. But there has been only limited research on the association between consuming chocolate and the occurrence of AF--which affects millions of people around the world and is linked with higher risk of stroke, heart failure, cognitive decline, dementia, and death.

The study included 55,502 men and women participating in the Danish Diet, Cancer, and Heath Study. Researchers considered study participants' body mass index, blood pressure, and cholesterol, which were measured at the time participants were recruited, between December 1993 and May 1997. They also looked at participants' health conditions, including high blood pressure, diabetes, or cardiovascular disease, and data on their diet and lifestyle, from questionnaires.

Diagnoses of AF were identified from the Danish National Patient Register. There were 3,346 cases of AF among the study participants over a 13.5-year follow-up period.

Compared with those who ate a one-ounce serving of chocolate less than once per month, men and women who ate one to three servings per month had a 10% lower rate of AF; those who ate one serving per week had a 17% lower rate; and those who ate two to six servings per week had a 20% lower rate. The benefit leveled off slightly with greater amounts of chocolate consumption, with those eating one or more servings per day having a 16% lower AF rate.

Results were similar for men and women.

"Despite the fact that most of the chocolate consumed by the study participants likely had relatively low concentrations of potentially protective ingredients, we still observed a significant association between eating chocolate and a lower risk of AF--suggesting that even small amounts of cocoa consumption can have a positive health impact," Mostofsky said.

"Eating excessive amounts of chocolate is not recommended because many chocolate products are high in calories from sugar and fat and could lead to weight gain and other metabolic problems. But moderate intake of chocolate with high cocoa content may be a healthy choice."

Senior author of the study was Kim Overdad of Aalborg University Hospital in Denmark. Murray Mittleman, professor of epidemiology at Harvard Chan School, was a co-author.

Funding for the study came from grants from the National Heart, Lung, and Blood Institute (HL-115623), the European Research Council (ERC), EU 7th Research Framework Program (281760), a KL2/Catalyst Medical Research Investigator Training award (an appointed KL2 award) from Harvard Catalyst | The Harvard Clinical and Translational Science Center (National Center for Research Resources and the National Center for Advancing Translational Sciences, National Institutes of Health Award KL2 TR001100) and the Danish Cancer Society and the Danish Council for Strategic Research (Aalborg AF-Study Group).

"Chocolate Intake and Risk of Clinically Apparent Atrial Fibrillation: the Danish Diet, Cancer, and Health Study," Elizabeth Mostofsky, Martin Berg Johansen, Anne Tjønneland, Harpreet S. Chahal, Murray A. Mittleman, Kim Overvad, Heart, online May 23, 2017, doi: 10.1136/heartjnl-2016-310357

http://bit.ly/2qph3S6

How Alcohol & Gut Fungus Team Up to Damage Your Liver

Heavy drinking can lead to liver disease, but a new study suggests that it's not just the alcohol that damages the liver — fungi that commonly live in the human gut appear to contribute to the disease as well.

By Rachael Rettner, Senior Writer | May 23, 2017 05:32pm ET

The study, which involved experiments in both mice and a small number of people, found that consuming alcohol is linked with changes in the types of fungi living in the gut, and that the fungi that tend to be more common in people who drink also worsen the effects of alcohol on the liver. The study is the first to link fungi and liver disease, the researchers said.

What's more, the findings suggest that antifungal drugs may be a possible treatment for alcohol-related liver disease, the researchers said. Alcohol-related liver disease is a category that includes a range of diseases, from the less severe "fatty liver" disease to end-stage liver disease, also called cirrhosis.

The findings suggest that "we might be able to slow the progression of alcoholic liver disease by manipulating the balance of fungal species living in a patient's intestine," study co-author Dr. Bernd Schnabl, an associate professor of gastroenterology at the University of California, San Diego School of Medicine, said in a statement.

Previous studies had found a link between excessive drinking and imbalances of bacteria in the gut, but until now, few studies had looked at the role of gut fungi in the development of alcohol-related diseases.

In the new study, the researchers gave alcohol to mice daily for eight weeks, and found that this chronic alcohol exposure resulted in an overgrowth of certain types of fungi in the animals' intestines.

But if the researchers treated the mice with the antifungal drug amphotericin B, this decreased levels of fungi while also reducing the

severity of alcoholic liver disease in the animals. Mice that received the antifungal drug had lower levels of liver damage and fat accumulation in the liver, compared with mice that did not receive the drug, the researchers said.

The researchers' experiments showed that fungi contribute to alcoholic liver disease in the following way: The fungi release a sugar called beta-glucan and this sugar moves out of the intestine and into surrounding organs, including the liver. When it gets to the liver, beta-glucan can trigger an inflammatory response that kills liver cells and promotes alcoholic liver disease, the researchers said. Thus, heavy drinking boosts the level of fungi in the gut, and this in turn leads to an increase in levels of beta-glucan, which promote more inflammation in the liver.

The researchers also examined fungi in the stool of eight healthy people and in 20 people who had abused alcohol and were in various stages of liver disease. They found that the alcohol-dependent people had a dramatic overgrowth of a type of fungus called *Candida* in their guts.

Next, the researchers analyzed blood samples from a separate group of about 30 patients with alcoholic liver disease, and they measured levels of antibodies that recognize fungus. They found that the people with higher levels of these antibodies — which indicate greater exposure to intestinal fungus — were more likely to die from liver disease over a five-year period.

The researchers cautioned that their studies focused on only a small number of people, and so larger studies are needed to confirm the findings. In addition, future studies should look at whether a single fungus contributes more than others to the progression of liver disease. The researchers are now interested in testing amphotericin B in patients with alcohol-related liver disease to see if the drug helps with the condition. The study was published May 22 in the Journal of Clinical Investigation.

http://bit.ly/2qrJwCU

LSTM and partners develop molecule that may lead to first synthetic one-dose antimalarial

Researchers at LSTM, working in partnership with the University of Liverpool and other colleagues, have developed a molecule which has the potential to become the first fully synthetic, one-dose treatment for malaria.

In a paper published today in the journal Nature Communications, the multinational team describe the molecule, known as E209, as meeting the key requirements of the Medicines for Malaria Venture drug candidate profiles. The molecule is effective against parasites expressing the key genetic marker for artemisinin resistance in in vitro studies

The control and elimination of malaria requires effective treatment strategies. For several years, this has been in the form of artemisinin-based combination strategies (ACTs), which has seen artemisinin based drugs combined with a drug partner with a longer half-life.

The semi-synthetic ACTs have had a significant impact on malaria treatment however, the search for a fully synthetic alternative has been on for over a decade. The growing problem of resistance to current ACTs can lead to complete treatment failure. This has led the group to look at alternatives to retain the effectiveness against parasites with the known genetic markers of resistance while at the same time being fast acting.

LSTM's Deputy Director, Professor Steve Ward, is a senior author on the paper. He said: "Extensive molecular investigations have demonstrated that mutations in the K13 gene are makers for artemisinin susceptibility and are linked to drug resistance in some malaria parasites. These mutations allow the parasite to survive exposure to the drug during the early stages of infection in the red blood cell. E209 is a breakthrough molecule, it is fully synthetic, retains the killing efficiency of the artemisinins, works against K13

mutant parasites and is slowly eliminated raising the hope that it could be used as a single dose cure."

The other lead author Professor Paul O'Neill of the University of Liverpool, said: "E209 is a second-generation peroxide based drug, designed at Liverpool, with significant improvements over the gold standard antimalarial treatment artesunate. E209 contains a unique core with two endoperoxide units; through medicinal chemistry optimization, the stability, potency and pharmacokinetics of this class has now been optimized. The development of E209 has been made possible by our close partnership with the Medicines for Malaria Venture (Geneva) with MMV's Expert Scientific Advisory Committee, providing invaluable input to the project. "

The extensive data set obtained for E209 was obtained through a global collaborative network of scientists around the world allowing this drug discovery project to be rapidly advanced.

http://bit.ly/2qpvQwl

Atlas of the human planet 2017 -- how exposed are we to natural hazards?

One out of 3 people in the world is exposed to earthquakes, a number which almost doubled in the past 40 years; around 1 billion in 155 countries are exposed to floods according to the Atlas

One out of three people in the world is exposed to earthquakes, a number which almost doubled in the past 40 years. Around 1 billion in 155 countries are exposed to floods and 414 million live near one of the 220 most dangerous volcanoes. The 2017 edition of the Atlas of the Human Planet by the European Commission's Joint Research Centre, looks at the exposure of people and built-up areas to the six major natural hazards, and its evolution over the last 40 years. The atlas will be presented during the 2017 Global Platform for Disaster Risk Reduction meeting in Cancun, Mexico.

More and more people and property are exposed to natural hazards

The atlas covers six major natural hazards: earthquakes, volcanos, tsunamis, tropical cyclone winds, tropical cyclone storm surge and floods. Global exposure to these hazards has doubled between 1975 and 2015, mostly due to urbanisation, population growth and socioeconomic development. Some of the hazards pose a threat to a particularly large number of people in different regions of the world.

Earthquakes pose a threat to up to one third of the population

Off all hazards, the largest number of people are exposed to earthquakes. The number of people living in seismic areas increased by 93% in 40 years (from 1.4 billion in 1975 to 2.7 billion in 2015). In 2015, more than 400 million people lived near one of the 220 most dangerous volcanoes, exposed to the consequences of possible eruptions. Tsunamis affect coastal areas in many regions, with dangerous areas more concentrated in Asia. The highest amount of built-up surface exposed to tsunamis is in Japan by far, followed by China and the United States of America. Its population is four times more exposed than that of China, the second most affected country.

European map of natural hazards exposure

More than 170 million people in Europe are potentially exposed to earthquakes, almost a quarter of the total population. In Italy, Romania, or Greece the share of exposed over total population reaches over 80%.

Flooding is the most common of the hazards studied. Germany has the highest number of people exposed to floods, about 8 million (10% of the national population), followed by France with 5.7 million (9%).

Eleven million Europeans live within 100 km from an active volcano, which eruptions could affect not only housing and settlements, but also everyday activities, including transportation. The potentially exposed built-up surface increased by 86% from 1975.

Most potential flood victims live in Asia

Exposure to floods, the most frequent natural disaster, is highest in Asia (76.9% of the global exposed population) and in Africa (12.2%). The world population potentially exposed to flood is around 1 billion

in 155 countries in 2015. 11% of the area built-up on Earth is potentially exposed to this hazard, too.

Tropical cyclones can shatter lives and homes in almost 90 countries

Tropical cyclone winds pose a threat to 1.6 billion people in 89 countries, up from 1 billion in 1975. In 2015, 640 million people were exposed to extremely strong cyclone winds, with the largest built-up surface exposed to strong cyclone winds found in China and Japan. Furthermore, 50 million Chinese are exposed to storm surge as consequence of tropical cyclones, up by almost 20 million in the last 40 years.

Why do we need to calculate exposure to the natural hazards?

Global analysis of exposure and its development over the last 40 years helps us better understand what affects disaster risk over time and risk drivers. It is also useful in identifying effective policy actions for more resilient communities.

The exposure data and the findings of the Atlas support the implementation of the post-2015 international frameworks: the UN Framework Convention on Climate Change, the Sendai Framework for Disaster Risk Reduction 2015-2030, the Sustainable Development Goals (SDGs), and the New Urban Agenda (Habitat III). The Global Human Settlement Layer (GHSL, see below) baseline data provides insights into developments over the last 40 years and into the impact that policies have on them. Researchers and policy makers can also use the data to aggregate exposure information at all geographical scales, from the city level to the region, continent and global.

How to estimate the exposure?

The Atlas of the Human Planet 2017 builds on its first edition published in 2016, in which JRC scientists combined earth observation with spatial modelling techniques to create the Global Human Settlement Layer (GHSL). The GHSL is the first global, fine scale, multi-temporal and open data on the physical characteristics and the dynamics of human settlements, covering 40 years of satellite observations data. The GHSL dataset has been now combined with the best available global hazard maps to measure the potential exposure to natural hazards over time.

At the UN Global Platform for Disaster Risk Reduction, the JRC will present also the report 'Science for Disaster Risk Management 2017: knowing more and losing less', a flagship product of the European Commission's Disaster Risk Management Knowledge Centre (DRMKC), compiling the state-of-the-art in disaster risk management.

http://nyti.ms/2qsqBi5

How Whales Became the Biggest Animals on the Planet

Whales are big. Really big. Enormously big. Tremendously big.

By NICHOLAS ST. FLEUR MAY 24, 2017

Fin whales can be 140,000 pounds. Bowhead whales tip the scales at 200,000 pounds. And the big mama of them all, the blue whale, can reach a whopping 380,000 pounds — making it the largest animal to have ever lived.

But for as long as whales have awed us with their great size, people have wondered how they became so colossal.

In a study published Tuesday in the journal Proceedings of the Royal Society B, a team of researchers investigated gigantism in baleen whales, the filter-feeding leviathans that include blue whales, bowhead whales and fin whales. The marine mammals became jumbo-size relatively recently, they found, only within the past 4.5 million years. The cause? A climatic change that allowed the behemoths to binge-eat.

Whales have an interesting evolutionary history. They began as land-dwelling, hoofed mammals some 50 million years ago. Over several millions of years they developed fins and became marine creatures. Between about 20 million and 30 million years ago, some of these ancient whales developed the ability to filter-feed, which meant they could swallow swarms of tiny prey in a single gargantuan gulp. But even with this feeding ability, whales remained only moderately large for millions of years.

"But then all of a sudden — 'boom' — we see them get very big, like blue whales," said Nick Pyenson, the curator of fossil marine mammals at the Smithsonian Institution's National Museum of Natural History and an author of the paper. "It's like going from whales the size of minivans to longer than two school buses."

Dr. Pyenson and his colleagues measured more than 140 museum specimens of fossilized whales, and then plugged that data into a statistical model. It showed that several distinct lineages of baleen whales became giants around the same time, independently of one another. Starting around 4.5 million years ago, giant blue whales were popping up in oceans across the world alongside giant bowhead whales and giant fin whales.

The researchers suspected that an environmental change happened during that time that essentially caused the baleen whales to bulk up. After some investigation, they found that this time period coincided with the early beginnings of when ice sheets increasingly covered the Northern Hemisphere.

Runoff from the glaciers would have washed nutrients like iron into coastal waters and intense seasonal upwelling cycles would have caused cold water from deep below to rise, bringing organic material toward the surface. Together these ecological effects brought large amounts of nutrients into the water at specific times and places, which had a cascading effect on the ocean's food web.

Throngs of zooplankton and krill would gather to feast on the nutrients. They would form dense patches that could stretch many miles long and wide and be more than 65 feet thick. The oceans became the whales' giant all-you-can-eat buffets.

"Even though they had the anatomical machinery to filter-feed for a long, long time," said Jeremy Goldbogen, a comparative physiologist from Stanford University and author of the paper, "it wasn't until the ocean provided these patchy resources that it made bulk filter-feeding so efficient."

The baleen whales could now gulp down much larger amounts of prey, which allowed them to get bigger. But that was only part of the equation.

"Plentiful food everywhere isn't going to get you giant whales," said Graham Slater, an evolutionary biologist at the University of Chicago and the study's lead author. "They have to be separated by big distances."

Because the ecological cycles that fuel the explosions of krill and zooplankton occur seasonally, Dr. Slater said the whales must migrate thousands of miles from food patch to food patch. Bigger whale ancestors that had bigger fuel tanks had a better chance of surviving the long seasonal migrations to feed, while smaller baleen whales became extinct.

If the food patches were not far apart, Dr. Slater said, the whales would have grown to a certain body size that was comfortable for that environment, but they would not be the giants we see today.

"A blue whale is able to move so much further using so much less energy than a small-bodied whale," Dr. Slater said. "It became really advantageous if you're going to move long distances if you're big."

Ari S. Friedlaender, a behavioral ecologist at Oregon State University who was not involved in the study, said the research improved our understanding of how baleen whales became giants.

"What this does is it allows us to be able to say that there are crucial processes in the ocean that allowed these animals to get this big," he said.

Richard Norris, a paleobiologist at the Scripps Institution of Oceanography, called the study a "nice piece of work," and said that it confirmed scientists' current understanding of changes to the oceans over time. "When we think about what the planet has been like in its long history, a whale of 10 million years ago was a very different type of critter than we have now," Dr. Norris said. "So in a sense we live in a special time where we get to enjoy the majesty of really big animals out there in the ocean."

http://bit.ly/2saDM0y

Cannabis derivative cannabidiol reduces seizures in severe epilepsy disorder

After years of anecdotal claims about its benefits, the cannabis derivative cannabidiol reduced seizure frequency by 39%

VIDEO: Dr. Orrin Devinsky and a family enrolled in the cannabidiol for drug-resistant seizures trial are interviewed about the study. NYU Langone Medical Center

After years of anecdotal claims about its benefits, the cannabis derivative cannabidiol reduced seizure frequency by 39 percent for patients with Dravet syndrome - a rare, severe form of epilepsy - in the first large-scale randomized clinical trial for the compound. The findings were published online May 24 in the New England Journal of Medicine.

"Cannabidiol should not be viewed as a panacea for epilepsy, but for patients with especially severe forms who have not responded to numerous medications, these results provide hope that we may soon have another treatment option," says lead investigator Orrin Devinsky, MD, professor of neurology, neurosurgery, and psychiatry and director of the Comprehensive Epilepsy Center at NYU Langone Medical Center. "We still need more research, but this new trial provides more evidence than we have ever had of cannabidiol's effectiveness as a medication for treatment-resistant epilepsy."

Cannabidiol, or CBD, is a compound in the cannabis plant that does not contain psychoactive properties that induce a high. The study included a liquid pharmaceutical formulation of CBD, called Epidiolex, which is manufactured by GW Pharmaceuticals and has not been approved by the U.S. Food and Drug Administration. GW Pharmaceuticals funded the clinical trial.

For the study, 120 children and adolescents with Dravet Syndrome between the ages of 2 and 18 years were randomized across 23 sites in the United States and Europe to receive either CBD 20 mg/kg or placebo added to their existing treatment over a 14-week period. Seizure frequency was tracked for one month prior to the study for baseline readings, and during the course of the study.

Specifically, seizure frequency dropped in the CBD-treated group by 39 percent from a median of nearly 12 convulsive seizures per month before the study to about six; three patients' seizures stopped entirely. In the placebo group, there was a 13 percent reduction in seizures from about 15 monthly seizures to fourteen. The difference in the degree of seizure reduction between the CBD group and the placebo group was both statistically significant and clinically consistent.

Side effects - experienced by 93.4 percent of patients in the CBD group and 74.6 percent of those treated with placebo - were generally reported as mild or moderate in severity. The most common side effects in the CBD group were vomiting, fatigue and fever. Eight participants from the CBD group withdrew from the trial due to side effects compared to one participant in the placebo group.

The new study confirms results from a December 2015 open-label expanded access program led by Dr. Devinsky that reported reductions in seizure frequency. In that program, both the researchers and patient's families knew they were receiving CBD, which may have introduced a bias into the results.

This new, randomized, controlled clinical study eliminated those concerns as participants and their physicians did not know if they were on CBD or placebo, say the study authors.

Future research will look at whether safety and tolerability might be improved and whether efficacy of CBD can be maintained at lower doses. Longer term studies of CBD for Dravet Syndrome as well as for other forms of treatment-resistant epilepsy are also underway.

In addition to Dr. Devinsky, the co-authors in this study were: J. Helen Cross, PhD, FRCPCH, Linda Laux, MD, Eric Marsh, MD, Ian Miller, MD, Rima Nabbout, MD, Ingrid E Scheffer, MD, PhD , Elizabeth Thiele, MD, and Stephen Wright, MD on behalf of The Cannabidiol in Dravet Syndrome Study Group. Judith Bluvstein, MD, and Daniel Friedman, MD, also served as co-authors at the NYU Langone site involved in the study.

http://bit.ly/2rLrxuU

TSRI scientists find simple copper complex shuts down botulinum neurotoxin poisoning

New therapy can stop the neurotoxin even in its more severe, advanced stages of action

LA JOLLA, CA - Botulinum neurotoxin is probably best known to Americans as BOTOX, a cosmetic medicine, rather than as a cause of potentially dangerous foodborne illnesses. Lesser known is that Clostridium botulinum, the bacterium that causes the neurointoxication, produces one of the most potent toxins on earth and is classified as a potential bioterrorism threat.

While no cure exists--and botulism treatment options are limited--a serendipitous discovery by scientists at The Scripps Research Institute (TSRI) may provide a new therapy that can stop the neurotoxin even in its more severe, advanced stages of action. The finding, based on rodent studies, was published recently in the Journal of the American Chemical Society.

Lead scientist Kim Janda, the Ely R. Callaway, Jr. Professor of Chemistry at TSRI, said he decided to explore botulism neurotoxin due to its debilitating and life-threatening effects, as well as its danger as a potential bioterrorism agent. "It's on the same level as Anthrax, Plague, Ebola and other Category A priority pathogens," Janda said, referring to the Centers for Disease Control and Prevention's (CDC) list of biological agents of highest concern. "Yet there is nothing even in phase I clinical trials."

Botulism is a rare but serious disorder that attacks the body's ability to signal to muscles. Symptoms include blurry vision, slurred speech, muscle weakness and difficulty swallowing. It can lead to paralysis throughout the body, and even death by affecting the patient's ability to breathe. According to the CDC, botulism is primarily transmitted through food or wounds infected by the botulism bacteria, which lives in the environment. In extremely small doses, the botulism toxin is injected for medical purposes, such as to relieve spasticity, and as a cosmetic wrinkle treatment.

To discover potential inhibitors of the toxin, Janda and his research team screened triazole compounds against the botulinum neurotoxin light chain, a proteolytic enzyme that disrupts neuronal signaling to muscles. The triazoles were synthesized using click chemistry--a method developed by TSRI Professor and Nobel laureate K. Barry Sharpless in the mid-1990s. Paul Bremer, a graduate student working in Janda's laboratory and the study's first author, said they hit upon a triazole compound provided by Sharpless's laboratory that appeared to forcefully inhibit the toxin light chain in an enzymatic assay.

Further testing revealed a surprise. "We had found what we thought were active click compounds, but really they were only active because of the copper," Bremer said. Copper is used as a catalyst to accomplish click chemistry and trace amounts would not be anticipated to show activity in a bioassay, he explained. "Upon further experiments, it came as a complete surprise that copper was quite potently inhibiting the enzyme."

The scientists had accidentally landed upon a potential new therapy for type A of the neurotoxin, the most common and deadly cause of human botulism, using copper chloride, an inexpensive, readily available metal salt as the active ingredient.

Next, the researchers designed molecules called ligands to act as delivery vehicles for copper into neuronal cells, an essential step in translating the therapeutic action of copper to biological systems. The TSRI team then sent their ligand-copper complexes to their study collaborators at the University of Wisconsin-Madison, who administered it to mice. The compound extended the animals' lives, even when they were given lethal doses of the toxin.

The researchers said further animal testing is needed to determine optimal dosage, dosing frequency and other factors. Janda said clinical trials to prove efficacy cannot be done in humans due to botulinum neurotoxicity dangers. However, the safety of the copper complex can

be validated through several other clinical trials already underway for different uses, he added.

If found to be safe, Bremer said the copper therapeutic could provide a more effective therapy than existing approaches to botulism. Currently, botulism sufferers receive an anti-toxin medicine that can inactivate the toxin circulating in their system, thereby preventing further poisoning. However, the anti-toxin cannot reverse preexisting paralysis because the toxin acts inside cells. Consequently, disease recovery can be slow, and paralysis may take weeks or months to wear off. "The anti-toxin is antibody-based, which means it only works outside the cells," said Janda. "This new therapy can readily enter cells where it can attack the etiological agent, a protease, which is responsible for paralysis seen from the neurotoxin."

The researchers also noted that the study further demonstrates the need to explore metals for therapeutic uses. Metals are not commonly used in drug design because of concerns about toxicity and specific targeting as compared to organic compounds. However, several metal-based therapies already exist. For instance, gold is used in therapies for certain cancers and rheumatoid arthritis, while other metal-based treatments are currently in clinical trials.

"These are kind of underappreciated medicinal agents," said Bremer. "Our work shows the need to explore their potential further."

The study, "Metal Ions Effectively Ablate the Action of Botulinum Neurotoxin A," was supported by the National Institutes of Health (grant R01A1119564.) In addition to Janda and Bremer, authors of the study include Lisa M. Eubanks of TSRI; Sabine Pellett, William H. Tepp and Eric A. Johnson of the University of Wisconsin-Madison; and James P. Carolan and Karen N. Allen of Boston University.

http://bit.ly/2rcm2op

From 'Magic' Mushrooms to Meth: The ER Rates for Drug Users

Alcohol and marijuana may be the most commonly used recreational drugs in the world, but "magic" mushrooms appear to be the safest, a new survey finds.

By Sara G. Miller, Staff Writer | May 24, 2017 05:30pm ET

Of the more than 12,000 people surveyed worldwide who said they used magic mushrooms in 2016, just 0.2 percent said that they needed emergency medical treatment, according to the survey. At the opposite end, the drug that resulted in the most emergency medical treatments was methamphetamine: Nearly 5 percent of the 1,500 people who reported using it said they wound up needing treatment, the Global Drug Survey found.

Credit: Haakon Nygård/Shutterstock

The results of the survey don't mean that the drugs it includes are harmless. There are risks associated with all of the substances in the survey. For example, long-term use of magic mushrooms may cause flashbacks and memory problems, according to the National Institutes of Health. After methamphetamine, the drug with the second-highest rate of users needing emergency medical treatment was synthetic cannabinoids, the researchers found: Of the 1,300 users in the survey, 3.2 percent reported needing emergency medical treatment after using this drug.

The Global Drug Survey is a London-based research group that's focused on making drug use safer. The results of the 2017 survey were published today (May 24) and included responses from more than 115,000 people from 50 countries.

By looking at the rates of people seeking emergency medical treatment after using a drug, the researchers said that they can get a sense of the risk of acute harms associated with use of the various substances.

The researchers noted that the results of the survey are not applicable to the general population — the survey is aimed at people who do use drugs.

Alcohol was by far the most commonly used substance, with nearly 100 percent of the respondents reporting that they had ever drank alcohol, and 94 percent reporting that they had used it in the past year. Marijuana was the runner-up, with 78 percent reporting having ever used the drug, and 60 percent reporting use in the past year.

The rates of people needing emergency medical treatment after drinking alcohol last year was 1.3 percent, and for marijuana use, 0.6 percent, according to the survey.

The researchers also looked at the rates of emergency medical treatment for other types of drug use. For example, 1.2 percent of the 25,000 MDMA users (the active ingredient in the drug ecstasy) reported seeking emergency medical treatment, and 1 percent of the 22,000 cocaine users reported the same. These rates are higher than those reported by these groups in 2015, the researchers said.

And while the researchers found that magic mushrooms had the lowest reported rates of emergency medical treatments, the rates for the use of other psychedelic drugs were not nearly as low. For example, 1 percent of the 13,000 LSD users reported needing emergency medical treatment in 2016 due to the drug — a rate that's 5 times higher than the one reported by magic mushroom users.

One reason for this difference, the researchers said, is that the amount of LSD in one "dose" can vary significantly, depending on how much of the drug the drug maker adds. In addition, the effects of LSD last much longer than those of psilocybin, the active ingredient in magic mushrooms.

http://bit.ly/2saAdaX

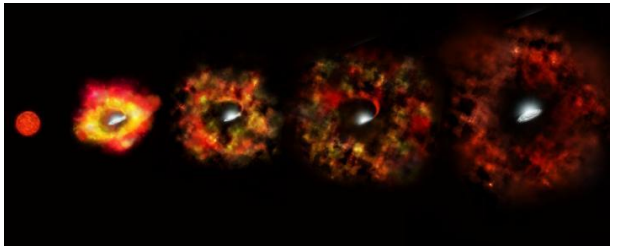
The big star that couldn't become a supernova

One star's 'massive fail' could help solve a mystery

COLUMBUS, Ohio -- For the first time in history, astronomers have been able to watch as a dying star was reborn as a black hole.

It went out with a whimper instead of a bang.

The star, which was 25 times as massive as our sun, should have exploded in a very bright supernova. Instead, it fizzled out -- and then left behind a black hole.



In the failed supernova of a red supergiant, the envelope of the star is ejected and expands, producing a cold, red transient source surrounding the newly formed black hole, as illustrated by the expanding shell (left to right). Some residual material may fall onto the black hole, as illustrated by the stream and the disk, potentially powering some optical and infrared emissions years after the collapse. **NASA, ESA, P. Jeffries (STScI)**

"Massive fails" like this one in a nearby galaxy could explain why astronomers rarely see supernovae from the most massive stars, said Christopher Kochanek, professor of astronomy at The Ohio State University and the Ohio Eminent Scholar in Observational Cosmology.

As many as 30 percent of such stars, it seems, may quietly collapse into black holes -- no supernova required.

"The typical view is that a star can form a black hole only after it goes supernova," Kochanek explained. "If a star can fall short of a supernova and still make a black hole, that would help to explain why we don't see supernovae from the most massive stars."

He leads a team of astronomers who have been using the Large Binocular Telescope (LBT) to look for failed supernovae in other galaxies. They published their latest results in the *Monthly Notices of the Royal Astronomical Society*.

Among the galaxies they've been watching is NGC 6946, a galaxy 22 million light-years away that is nicknamed the "Fireworks Galaxy" because supernovae frequently happen there--indeed, SN 2017eaw, discovered on May 14th, is shining near maximum brightness now. Starting in 2009, one particular star in the Fireworks Galaxy, named N6946-BH1, began to brighten weakly. By 2015, it appeared to have winked out of existence.

The astronomers aimed the Hubble Space Telescope at the star's location to see if it was still there but merely dimmed. They also used the Spitzer Space Telescope to search for any infrared radiation emanating from the spot. That would have been a sign that the star was still present, but perhaps just hidden behind a dust cloud.

All the tests came up negative. The star was no longer there. By a careful process of elimination, the researchers eventually concluded that the star must have become a black hole. It's too early in the project to know for sure how often stars experience massive fails, but Scott Adams, a former Ohio State student who recently earned his Ph.D. doing this work, was able to make a preliminary estimate.

"N6946-BH1 is the only likely failed supernova that we found in the first seven years of our survey. During this period, six normal supernovae have occurred within the galaxies we've been monitoring, suggesting that 10 to 30 percent of massive stars die as failed supernovae," he said. "This is just the fraction that would explain the very problem that motivated us to start the survey."

To study co-author Krzystof Stanek, the really interesting part of the discovery is the implications it holds for the origins of very massive black holes -- the kind that the LIGO experiment detected via gravitational waves. (LIGO is the Laser Interferometer Gravitational-Wave Observatory.)

It doesn't necessarily make sense, said Stanek, professor of astronomy at Ohio State, that a massive star could undergo a supernova -- a process which entails blowing off much of its outer layers -- and still have enough mass left over to form a massive black hole on the scale of those that LIGO detected. "I suspect it's much easier to make a very massive black hole if there is no supernova," he concluded.

Adams is now an astrophysicist at Caltech. Other co-authors were Ohio State doctoral student Jill Gerke and University of Oklahoma astronomer Xinyu Dai. Their research was supported by the National Science Foundation.

The Large Binocular Telescope is an international collaboration among institutions in the United Sates, Italy and Germany. The LBT Corporation partners are: the University of Arizona on behalf of the Arizona University System; the Instituto nazionale di Astrofisica, Italy; the LBT Beteiligungsesellschaft, Germany, representing the Max Planck Society, the Astrophysical Institute of Potsdam and Heidelberg University; Ohio State University; and the Research Corporation, on behalf of the University of Notre Dame, University of Minnesota and University of Virginia.

http://bit.ly/2ruyotb

Russia's disinformation efforts hit 39 countries: researchers

Russia's campaign of cyberespionage and disinformation has targeted hundreds of individuals and organizations from at least 39 countries along with the United Nations and NATO, researchers said Thursday.

A report by the Citizen Lab at the University of Toronto revealed the existence of "a major disinformation and cyber espionage campaign with hundreds of targets in government, industry, military and civil society," lead researcher Ronald Deibert said.

The findings suggest that the cyber attacks on the 2016 presidential campaign of Hillary Clinton—which US intelligence officials have attributed to Russia—were just the tip of the iceberg.

Citizen Lab researchers said the espionage has targeted not only government, military and industry targets, but also journalists, academics, opposition figures, and activists,

Notable targets, according to the report, have included a former Russian prime minister, former high-ranking US officials, members of cabinets from Europe and Eurasia, ambassadors, high ranking military officers and chief executives of energy companies.

In a blog post, Deibert said the Russian-directed campaign follows a pattern of "phishing" attacks to obtain credentials of targets, and carefully "tainted" leaks that mix real and false information to create confusion around the true facts.

"Russia has a long history of experience with what is known as 'dezinformatsiya,' going back even to Soviet times," Deibert said.

"Tainted leaks, such as those analyzed in our report, present complex challenges to the public. Fake information scattered amongst genuine materials—'falsehoods in a forest of facts'... is very difficult to

distinguish and counter, especially when it is presented as a salacious 'leak' integrated with what otherwise would be private information."

Deibert said the researchers had no "smoking gun" that links the campaign to a particular government agency but added that "our report nonetheless provides clear evidence of overlap with what has been publicly reported by numerous industry and government reports about Russian cyber espionage."

Citizen Lab said one of the targets was US journalist David Satter, who has written extensively on corruption in Russia.

Satter's stolen e-mails were "selectively modified," and then "leaked" to give the false impression that he was part of a CIA-backed plot to discredit Russian President Vladimir Putin, the report said.

Similar leak campaigns targeted officials from Afghanistan, Armenia, Austria, Cambodia, Egypt, Georgia, Kazakhstan, Kyrgyzstan, Latvia, Peru, Russia, Slovakia, Slovenia, Sudan, Thailand, Turkey, Ukraine, Uzbekistan and Vietnam, according to the report.

UN officials and military personnel from more than a dozen countries were also targets, Citizen Lab said.

"Our hope is that in studying closely and publishing the details of such tainted leak operations, our report will help us better understand how to recognize and mitigate them," Deibert said.

http://bit.ly/2rclrTQ

Scientists jump hurdle in HIV vaccine design

Scientists at The Scripps Research Institute (TSRI) have made another important advance in HIV vaccine design.

LA JOLLA, CA - The development was possible thanks to previous studies at TSRI showing the structures of a protein on HIV's surface, called the envelope glycoprotein. The scientists used these structures to design a mimic of the viral protein from a different HIV subtype, subtype C, which is responsible for the majority of infections worldwide. The new immunogen is now part of a growing library of TSRI-designed immunogens that could one day be combined in a vaccine to combat many strains of HIV.

"All of this research is going toward finding combinations of immunogens to aid in protecting people against HIV infection," said TSRI Professor Ian Wilson, Hanson Professor of Structural Biology and chair of the Department of Integrative Structural and Computational Biology at TSRI.

The research, published recently in the journal Immunity, was led by Wilson and TSRI Professor of Immunology Richard Wyatt, who also serves as Director of Viral Immunology for the International AIDS Vaccine Initiative (IAVI) Neutralizing Antibody Center at TSRI.

The new study was published alongside a second study in Immunity, led by scientists at the Karolinska Institute in Stockholm, which showed that the vaccine candidate developed in the TSRI-led study can elicit neutralizing antibodies in non-human primates.

"Together, the two studies reiterate how structure-based immunogen design can advance vaccine development," said Wyatt.

Solving the Clade C Structure

HIV mutates rapidly, so there are countless strains of HIV circulating around the world. Of these strains, scientists tend to focus on the most common threats, called clades A, B and C.

Like a flu vaccine, an effective HIV vaccine needs to protect against multiple strains, so researchers are designing a set of immunogens that can be given sequentially or as a cocktail to people so their immune systems can prepare for whatever strain they come up against.

In 2013, TSRI scientists, led by Wilson and TSRI Associate Professor Andrew Ward, determined the structure of a clade A envelope glycoprotein, which recognizes host cells and contains the machinery that HIV uses to fuse with cells. Because this is the only antibody target on the surface of HIV, an effective HIV vaccine will have to trigger the body to produce antibodies to neutralize the virus by blocking these activities.

Building on the previous original research, the scientists in the new study set out to solve the structure of the clade C glycoprotein and enable the immune system to fight clade C viruses.

"Clade C is the most common subtype of HIV in sub-Saharan Africa and India," explained study co-first author Javier Guenaga, an IAVI collaborator working at TSRI. "Clade C HIV strains are responsible for the majority of infections worldwide."

The scientists faced a big challenge: the clade C envelope glycoprotein is notoriously unstable, and the molecules are prone to falling apart.

Guenaga needed the molecules to stay together as a trimer so his co-author Fernando Garces could get a clear image of the clade C glycoprotein's trimeric structure. To solve this problem, Guenaga re-engineered the glycoprotein and strengthened the interactions between the molecules. "We reinforced the structure to get the soluble molecule to assemble as it is on the viral surface," Guenaga said.

The project took patience, but it paid off. "Despite all the engineering employed to produce a stable clade C protein, these crystals (of clade C protein) were grown in very challenging conditions at 4 degrees Celsius and it took the diffraction of multiple crystals to generate a complete dataset, as they showed high sensitivity to radiation damage," said Garces. "Altogether, this highlights the tremendous effort made by the team in order to make available the molecular architecture of this very important immunogen."

With these efforts, the glycoprotein could then stay together in solution the same way it remains together on the virus itself. The researchers then captured a high-resolution image of the glycoprotein using a technique called x-ray crystallography.

The researchers finally had a map of the clade C glycoprotein.

Vaccine Candidate Shows Promise

In a companion study, the scientists worked with a team at the Karolinska Institute to test an immunogen based on Guenaga's findings. The immunogen was engineered to appear on the surface of a large molecule called a liposome--creating a sort of viral mimic, like a mugshot of the virus.

This vaccine candidate indeed prompted the immune system to produce antibodies that neutralized the corresponding clade C HIV strain when tested in non-human primates.

"That was great to see," said Guenaga. "This study showed that the immunogens we made are not artificial molecules--these are actually relevant for protecting against HIV in the real world."

In addition to Wyatt, Wilson and Guenaga, the study, "Glycine substitution at helix-to-coil transitions facilitates the structural determination of a stabilized subtype C HIV envelope glycoprotein," included co-first author Fernando Garces, Natalia de Val, Viktoriya Dubrovskaya and Brett Higgins of TSRI; Robyn L. Stanfield of TSRI and IAVI; Barbara Carrette of IAVI; and Andrew Ward of TSRI, IAVI and the Center for HIV/AIDS Vaccine Immunology & Immunogen Discovery (CHAVI-ID) at TSRI.

This work was supported by the IAVI Neutralizing Antibody Center and Collaboration for AIDS Vaccine Discovery (CAVD; grants OPP1084519 and OPP1115782), CHAVI-ID (grant UM1 AI00663) and the National Institutes of Health (grants P01 HIVRAD AI104722, R56 AI084817 and U54 GM094586).

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Zika Detected in India for First Time

The Zika virus has surfaced for the first time in India, with three cases.

NEW DELHI — India has reported its first three cases of the Zika virus, including two pregnant women who delivered healthy babies.

Health Ministry officials said Sunday that the three patients in western Gujarat state had recovered. "There is no need to panic," Dr. Soumya Swaminathan, a top Health Ministry official, told reporters.

The World Health Organization said in a statement Friday that the three cases that India reported to the WHO on May 15 were detected through routine blood surveillance in a hospital in Ahmadabad, Gujarat's capital. Two cases were detected in February and November last year, while a third case was detected in January this year.

Swaminathan, who heads the Indian Council of Medical Research, said the three patients had not traveled overseas and had acquired the infection locally.

Zika is transmitted by the daytime-active Aedes aegypti and Aedes albopictus mosquitoes. The medical journal Lancet has said 2.6 billion

people living in parts of Asia and Africa could be at risk of Zika infection, based on analysis of travel, climate and mosquito patterns in those regions. The vast majority of people infected by the Zika virus never get sick, and symptoms are mild for those who do, so surveillance systems may have missed cases.

Although Zika was first identified in 1947, the virus wasn't considered a major health threat until a major outbreak in Brazil in 2015 revealed that it can lead to severe birth defects when pregnant women are infected.

The WHO says that although Zika causes only mild symptoms in most people, it sometimes causes complications including microcephaly and Guillain-Barre syndrome.

Babies born to Zika-infected mothers have been found to have microcephaly, or a birth defect where the head is abnormally small and brains might not have developed properly. Guillain-Barre syndrome is a disorder in which the body's immune system attacks part of the peripheral nervous system.

The WHO said the three were the first cases of Zika virus infections from India and provided evidence on the presence of the virus in the country. "These findings suggest low level transmission of Zika virus and new cases may occur in the future," it said.

The WHO said there was significant risk of the further spread of the virus and recommended that governments push ahead with efforts to control mosquitoes. However, the agency did not recommend any curbs on travel to India. Last year, the WHO declared the spread of Zika a global public health emergency.

http://bit.ly/2scRWP5

Shaking the Dinosaur Family Tree

A major reshuffling of dinosaur relationships may be afoot

By Brian Switek on May 24, 2017

On November 24, 1887, naturalist Harry Govier Seeley stood before London's Royal Society to make one of his most important contributions to paleontology. His paper was "On the Classification of the Fossil Animals commonly named Dinosauria" – the terrible lizards being exhumed in greater number and variety than anyone had anticipated.

The likes of *Stegosaurus*, *Allosaurus*, and *Apatosaurus* needed a new system to organize their ranks, Seeley argued. Other experts – such as Edward Drinker Cope and Othniel Charles Marsh from America, as well as Thomas Henry Huxley from England – had proposed their own classifications before, Seeley pointed out at the top of his lecture, but each system was flawed and there was no consensus among experts on which names would be used. So, to sort through the growing taxonomic tangle, Seeley proposed that the major groups of dinosaurs be separated from each other on the basis of their hips.

It was a simple and ingenious solution. The dinosaurs known at the time had the tripartite arrangements of their hip bones in one of two configurations. There were dinosaurs like *Diplodocus* and *Ceratosaurus* with a "lizard-hipped", or saurischian, hip shapes immediately recognizable from a forward-pointing pubis bone. Other dinosaurs, such as *Camptosaurus*, had the pubis pointing backward to join another bone called the ischium in what Seeley called the ornithischian, or "bird-hipped" shape.

Additional traits underscored the division. The saurischian dinosaurs included only theropods and sauropods, further united by pneumatic – or hollow – bones. The ornithischians, by contrast, included dinosaurs like *Stegosaurus* and *Camptosaurus*. And for 130 years, Seeley's arrangement held fast.

There have been challenges and shake-ups over time – for example, when some paleontologists thought that the strange and varied ornithischians were more distantly related to other dinosaurs and deserved a separate grouping outside that famous name – and, admittedly, it's a little confusing that "bird-hipped" dinosaurs don't have anything to do with the ancestry of birds. Still, succeeding generations of paleontologists came to the consensus that Dinosauria is made up of the saurischian and ornithischian branches. The

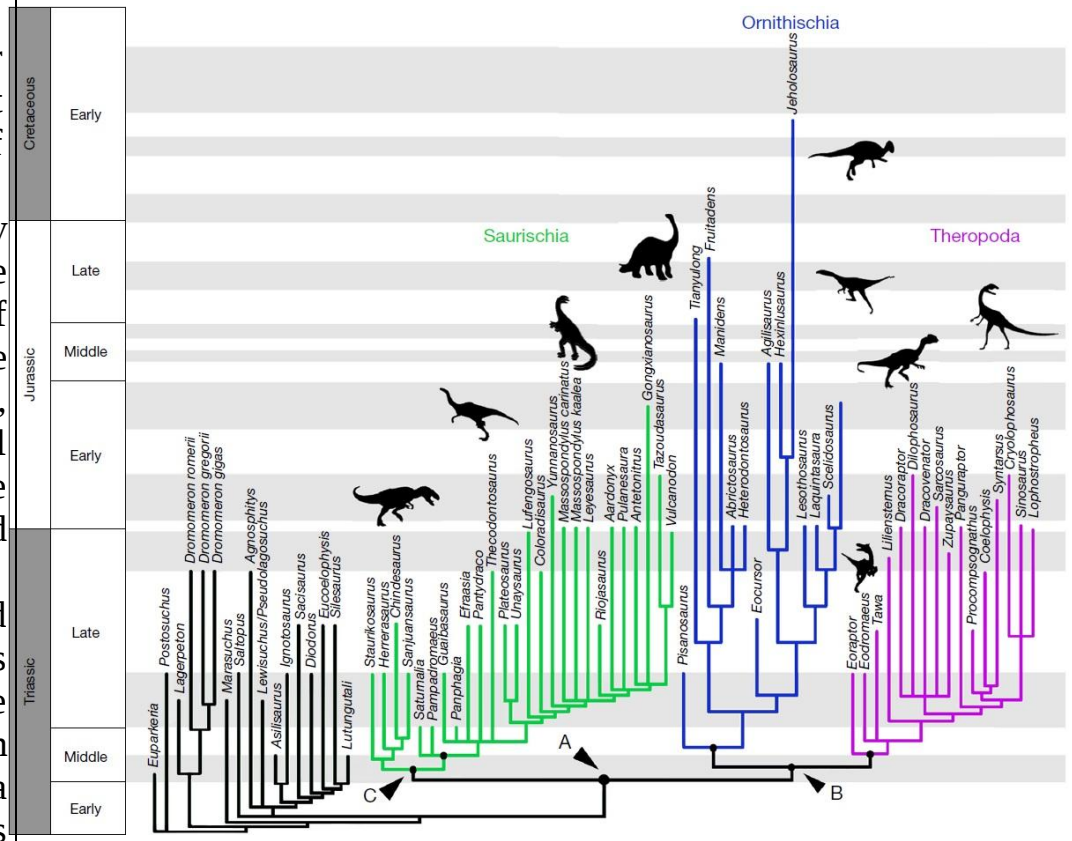
theropods and sauropods make up the saurischian side of the family tree, sharing a closer common ancestor with each other than the ornithischian dinosaurs that make up the other half of the famous family.

Now Seeley's classic arrangement is in question. Earlier this year paleontologists Matthew Baron, David Norman, and Paul Barrett unveiled a new dinosaur phylogeny that offers very different view of who's related to whom.

Baron and colleagues largely focused on protodinosaurs – technically called dinosauromorphs – and early dinosaurs from the Triassic to the early part of the Jurassic. This was the opening chapter of the Age of Reptiles, back when dinosaurs were starting to diversify but we're really ruling the Earth yet. Recent discoveries in South America, Africa, and elsewhere have started to fill in details about this critical time like never before, and, Baron and coauthors argue, the characteristics of these archaic forms suggest some unexpected relationships.

After analyzing 457 skeletal characteristics in 74 taxa, Baron and coauthors concluded that theropods and sauropods are not each other's closest relatives, after all. The new family tree more closely links the earliest ancestors of *Tyrannosaurus* (a theropod) and *Triceratops* (an ornithischian), with the long-necked sauropod dinosaurs out on a separate branch allied to an enigmatic group of early carnivorous dinosaurs called herrerasaurids. In this reshuffled nest of dinosaurian branches, then, theropods and ornithschians would belong to a group called the Ornithoscelida while sauropods and the herrerasaurids would be the new representatives of the Saurischia.

Formal responses to the paper have already started to trickle out. Thomas Holtz pointed out that a tweaked naming scheme might result in less confusing. For example, the existing name sauropodomorpha could be used to label all animals more closely related to *Diplodocus* than the theropods. Then again, the term Pachypodosauria could be used for these dinosaurs. "Such a scheme would accommodate the two competing hypotheses: a conventional Saurischia–Ornithischia split versus the new Pachypodosauria–Ornithoscelida division," Holtz wrote.



The new hypothesis of dinosaur relationships. [Baron et al 2017]

All of this taxonomic wrangling is about more than names. The new tree has major implications for what paleontologists think the earliest dinosaurs were like, not to mention how each of the major subdivisions evolved. If herrerasaurids only look like theropods, but are actually distant relatives, that means hypercarnivorous dinosaurs evolved at least twice near the root of the family tree. Likewise, the new arrangement might explain why some of the earliest-known ornithischian dinosaurs – such as *Heterodontosaurus* – have sharp, roughly theropod-like teeth and seem more omnivorous than their later descendants.

But is the new classification going to stick? Any phylogenetic tree is a hypothesis, subject to testing and change with additional analysis and discovery. Other experts may disagree about the species selected for analysis or how certain skeletal characteristics are coded in the input data. Likewise, the early record of ornithischian dinosaurs is so incredibly sparse that the discovery of any new skeleton could significantly change the results. Not to mention that the new analysis brings up the question of why theropods and sauropods share air sacs that lightened their skeletons and yet ornithischians – more closely allied to theropods in the new analysis – either never evolved or lost this trait.

There's little to do right now except wait. Perhaps the new arrangement will gain traction, pushed along by additional evidence. Or maybe Seeley's classification will be underscored as most representative of dinosaur relationships, after all. There's even the possibility that some other, as-yet-unformulated classification will come out of this. But no matter how this discussion shakes out, the new study highlights how much we're learning about the earliest dinosaurs and their forerunners.

The earliest days of the Triassic used to be known only from slivers and scraps. Now paleontologists are uncovering the story of how dinosaurs, and other forms of life, rapidly originated and diversified once the worst mass extinction of all time cleared the slate for the Age of Reptiles. Paleontologists may disagree over how these finds change dinosaur classification, but the growing wealth of fossil material that spurs these debates can only be a good thing.

This post was supported by my generous backers on Patreon. For details on how you can get an early view of new blog posts and exclusive natural history essays, click here.

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http://bit.ly/2rwKLVE

Genomics tracks migration from lost empires to modern cities

New genomic tools are enabling researchers to overturn long-held beliefs about the origins of populations

Copenhagen, Denmark - New genomic tools are enabling researchers to overturn long-held beliefs about the origins of populations, a researcher will tell the annual conference of the European Society of Human Genetics today (Monday). Dr Eran Elhaik, Assistant Professor of Animal and Plant Sciences at the University of Sheffield, Sheffield, UK, will say that new technologies are enabling scientists to track the origins and migrations of populations with increasing accuracy.

Until recently, assumptions about origins were based on where people were buried. "However, this does not take into account the migrations which we now know took place thousands of years ago," says Dr Elhaik, who carried out the research with colleagues including Dr Umberto Esposito.

Using a recently-developed technology, the ancient Geographic Population Structure (aGPS) tool, the researchers were able to find the geographical origins of ancient DNA, with the only limitation being the availability of DNA data. This in turn enabled them to combine hundreds of snap shots from the past into a reconstruction of modern history from 12,000 BC to the modern era. "This is by far the most comprehensive reconstruction of our genetic history. Our work reveals the colonisation of Europe, step by step, and answers many questions concerning the origins and migrations of Europeans," says Dr Elhaik.

Applied to a dataset of over 300 ancient Eurasians and Near-Easterners during the Ice Age to Late Iron Age period, aGPS localised around 50% of the samples at up to 200km from their burial site, about 32% at between 200 and 1000km, and the remainder at between 1000 and 3,175km. "The migration patterns revealed by our work were remarkably complex and dynamic, and the difficulties in interpreting them correctly are significant.

"The challenge for us now is to understand why these migrations took place. What caused a particular group of people to make a journey of over 3000km at a time when travel was complicated and dangerous? When we combine our results with archaeological and climate data, we can begin to see why," says Dr Elhaik. "For example, we can identify areas where the land became exhausted from over-farming, and thus caused the movement of populations. We can also pinpoint the formation of city states and 'biodiversity centres', corresponding to ancient empires that drew immigrants from other countries."

The results allow the researchers to confirm the theory of the massive migration of populations from the steppes of the Caucasus (the Yamnaya) to Central Europe during the Late Neolithic period (3500 to 2300 BC). "We discovered that Central Europeans were always on the move, continuously mixing with other populations and forming ancient cities in Germany, Denmark and Hungary, for example close to modern-day Hamburg and Berlin, and Budapest. In contrast, Near Eastern peoples tended to stay close to home," says Dr Elhaik.

"Genetic data can answer many questions that archaeology alone cannot. For example, is a specific decoration indicative of an alien culture, or simply an import? These new insights are fascinating, not just in a historical context, but because they provide additional proof of the unlikelihood of a 'day zero' of ethnic homogeneity, except perhaps in a very few isolated places. Even if it had existed, there must be practically no-one alive on earth who could trace all their ancestors to one ethnically homogenous population".

There are endless challenges in this research. "Imagine working with a very short DNA sequences with more holes than bases - not only can we not align this with other ancient sequences, but we also do not know where it is from. And this is before we get to the question of "when?" which is, again, linked to "where?" because different regions entered developmental periods, like the Iron Age, at different times.

"However, our findings to date have already brought about a far greater understanding of the identity of Old World residents, and our goal is now to reconstruct the full "Human Atlas" showing ancient migration patterns worldwide," he will conclude.

Chair of the ESHG conference, Professor Joris Veltman, Director of the Institute of Genetic Medicine at Newcastle University, Newcastle, United Kingdom, said: "This fascinating work illustrates the power of modern genetic approaches to study human history and migration. The scientists demonstrate that information in ancient DNA samples, even of low quality, can be used to provide a very precise geographical localisation of the origin of a person."

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