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Einstein theory passes black hole test

Paul Rincon

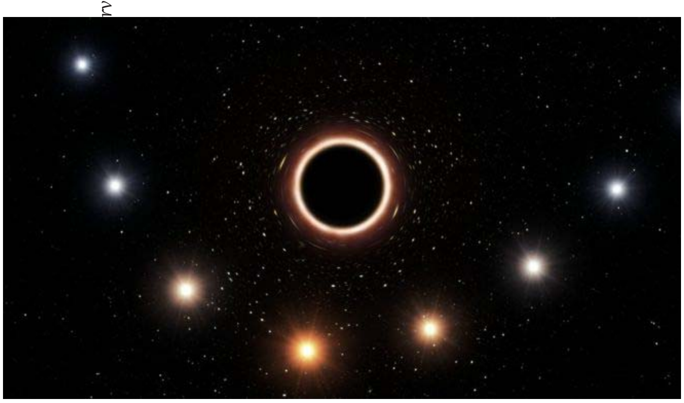
The black hole at the centre of our galaxy has helped astronomers confirm a key prediction of Albert Einstein's ideas.

By observing a cluster of stars near the hole, they were able to confirm a phenomenon known as "gravitational redshift".

It's when the wavelength of light gets stretched out in response to a gravitational field.

The result will help scientists better understand the physics of black holes.

The Very Large Telescope (VLT) in Chile found evidence for Einstein's prediction by observing a star, called S2, that passed through the intense gravitational field of Sagittarius A* - the huge black hole at the heart of the Milky Way.



The effect they observed, gravitational redshift, occurs as particles of light (photons) climb out of a gravitational well like a black hole. As they do, the light's wavelength gets drawn out.

This shifts the wavelength to the red part of the light spectrum - hence "redshift".

It's predicted by Einstein's theory of general relativity, but has never been observed in an intense gravitational field such as that of a black hole.

Frank Eisenhauer, from the Max Planck Institute for Extraterrestrial Physics (MPE) in Garching, Germany, said the measurement opened the door to more studies of the physics of black holes.

In future, he said, "we will see many more effects of general relativity in the galactic centre black hole. We will see the orbits of the stars change, we will see light go in circles, we will even see space-time rotate together with the black hole."

Reinhard Genzel, also from MPE, said: "There is still more work to do to really come as close as you can to the event horizon [the "point of no return" of the black hole] where you might expect strong deviations from Einstein's theory."

Françoise Delplancke, from the European Southern Observatory (Eso), which operates the VLT, said that the laws of physics could only be tested here in the Solar System under particular circumstances.

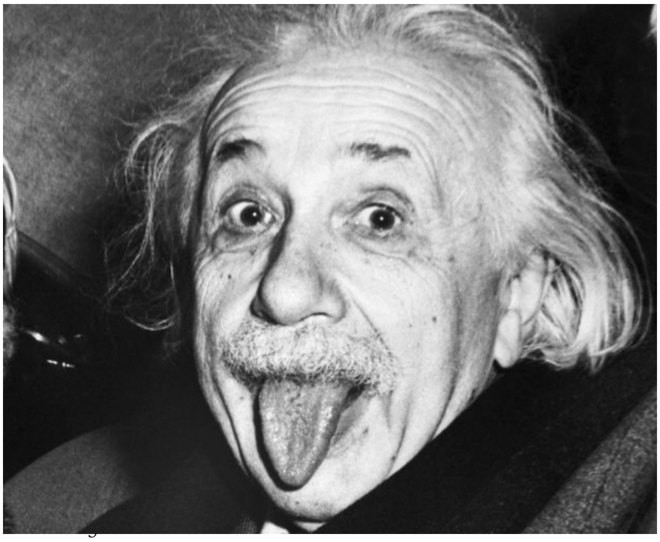
"So it's very important in astronomy to also check that those laws are still valid where the gravitational fields are very much stronger," she explained.

S2 is one member of a star cluster that surrounds Sagittarius A*. These stars reach mind-boggling speeds when they approach the black hole - S2 comes very close to Sagittarius A* every 16 years.

Astronomers followed S2 before and after it passed close to the black hole on 19 May 2018, tracking its progress hour-by-hour.

When S2 passed by the black hole at a distance just 120 times that of the Earth from the Sun, it reached an astonishing orbital velocity of 8,000 km/s. That corresponds to about 2.7% of the speed of light.

The astronomers found that light from the star was indeed stretched to longer wavelengths by the very strong gravitational field of Sagittarius A*.



The results were perfectly in line with the theory of general relativity - and not explained by Sir Isaac Newton's ideas - which exclude such a shift.

"In sport, you would say it was 1-0 for Einstein," said Frank Eisenhauer.

Odele Straub, from the Paris Observatory, in France, said: "What we hope is at some point we will see something in the galactic centre that we can't explain with Einstein's theory - that would be really, really exciting. Because then we could go back to the drawing board and come up with something better."

The astronomers are continuing to observe S2; observations of its trajectory should yield new findings about the extreme conditions around the Milky Way's central black hole.

Gravitational redshift occurs because, in order to escape a gravitational well such as a black hole, particles of light (photons) must expend energy.

However, at the same time, these photons must travel at a constant speed - the speed of light.

Therefore, the photons can't lose energy by slowing down, but must expend it in another way. This lost energy manifests itself as a shift towards the red end of the light spectrum.

The results are published in the journal Astronomy & Astrophysics.

BBC

Changing life as we know it

Gemma Milne

For most people, the words 'artificial' and 'life' only seem to make sense in science fiction movies and dystopian literature.

We all know the story: the lone scientist creates some kind of manufactured being for friendship or military uses; the creation comes to learn about the human race; and ultimately, it takes over the planet, pushing life as we know it into extinction.

With current conversations surrounding genetic editing and artificial intelligence, the words 'artificial life' seem to increasingly be coming together, reflecting the reality in which we currently live.

The concept of 'creating' life is not something society has only explored in science fiction or just in the last few years, however – it is an idea we have wrestled with time and time again throughout recent history.

2018 marks the 40 year anniversary of IVF – or, rather, the 40th birthday of Louise Brown, the first baby born by IVF on 25 July 1978.

Nowadays, IVF is relatively normal – since Louise's inception, there have been over 6 million babies born this way – but before she was born, this method of fertilisation outside the female body was seen as fringe science meddling with life, and had very little backing from both the media and the scientific establishment.

Connie Orbach is leading an upcoming Science Museum exhibition all about IVF and its controversial history.

"As with everything, there's a sliding scale in terms of what's seen as useful and

what's seen as meddling," she says.

IVF at its most simple is just allowing two people who for whatever reason can't have a baby, to have the baby they want to have, in the same way that everyone else is able to do."

But in 1978, the language around the procedure included phrases such as 'test-tube babies', 'designer babies' and even 'Frankenstein science'.

"IVF in the 1960s may have been what genetic editing of embryos is today, but our perceptions do massively change over time.

"Perceptions seem to change when meaningful change is made in people's lives."

However, just because one example of life creation worked out well doesn't necessarily mean all future efforts will follow suit.

Peter Mills, Assistant Director of Nuffield Bioethics, is tasked with investigating the ethical implications for the future of biomedical research.

His team are looking at the implications of artificial life across areas such as human reproduction as well as livestock production - artificial farm animals, as it were.

A key question Peter is asking in his research surrounds the idea of 'normal' – what is at the source of the 'normal' status we assign to things?

For example, we can already tweak embryos to not have a genetic disease – which arguably levels the playing field and gives that embryo more chance of a 'normal' human existence, as opposed to living a 'scientifically enhanced' lifestyle.

But at what point does this 'levelling the playing field' to ensure fewer people have debilitating conditions, turn into introducing extra 'super human' traits?

If we can 'get rid' of diseases through genetic manipulation, then surely we can 'add in' extra resistance to other forms of illness – and when you think about the cost of vaccination, this seems to be a pretty sensible public health strategy.

But what about adding extra muscle mass to someone who will be born with too little, advancing towards adding extra muscle mass to someone who wants to be stronger?

This seems to be less of a public health concern and rather one linked more to personal choice.

Drawing the line can sometimes be seen as truly simple, but can quite easily, at other times, be quite complex.

"One of the things we need to think about is to consider how much more difficult it is for people to make a decision not to go ahead with some kind of edit, based on knowledge gained from, for example, pre-natal screening for Down's Syndrome."

Peter explains, “The norm has changed to limit the number of Down’s Syndrome children, but it’s not a far step from then sterilising people who have the propensity to give birth to children with low IQ.

“There’s nothing wrong with norms changing, but we need to change in an orderly way, and in a way that takes account of those changes, particularly for people in positions of vulnerability – those people who might be collaterally affected without actually being involved in any of these particular choices.”

“An example being, if there are fewer people with Down’s Syndrome, and hence fewer people with genetic disorders, then how do behaviour and resources change for those with other developmental needs which maybe cannot, or have not, been ‘edited’?”

The conversation around artificial life isn’t limited to the advances in biology, however.

Artificial Intelligence is a hot topic in the IT world, and many people are already using technology with AI at its core, without even realising, prompting questions around the ethics of interacting with a human-like digital creation.

Dr Tony Hirst, Senior Lecturer at the Open University and Open Data expert, is interested in the effect that technological systems which humans use every day are having on broader human behaviour.

With some concerns being voiced about how our relationships with voice assistants and chatbots are tending towards being demanding and domineering, many are questioning if that behaviour will translate onto other humans.

“It starts to sound like the same arguments around computer games and violent films,” Tony says.

One set of arguments claim ‘just

because I shout at my female-voiced smart speaker in an abusive way, doesn't mean I will do that to my partner' and hence the behaviour won't transfer, but the other side asks the question 'if you're engaging with something in a very human way, at what point does it transfer?'"

With recent news surrounding Google Duplex – the virtual assistant which adds in 'er's and 'mhmm-hmm's to its speech to mimic that of real humans – many questions have arisen around the merging of malicious intent and machines which can essentially trick humans into thinking they are real people.

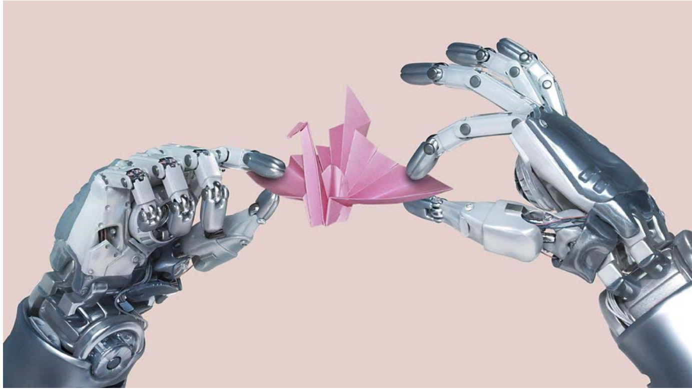
Amazon's Alexa has also made news when it was revealed that its 'Magic Word' feature rewards children who say 'please' and 'thank you', as well as responds to 'Awexa' for kids who haven't yet learnt the letter L, which prompts questions around a machine making real-world decisions off the back of juvenile requests.

Of course the positive elements of both these examples are clear – more useful digital assistants which save you time, and more polite children.

The ethical implications of creating different forms of artificial life are complex – there doesn't seem to be a right or wrong answer – and it's likely the influence and repercussions of these advancements will only be known once they have already made it into society.

Who knows where we'll be in 40 years' time – but if we're to learn anything about the story of IVF, its that sometimes the early views on emerging science can be farfetched and ill thought-out.

But equally, we've never seen computational advancement like we're currently experiencing with AI, so it's right that concern should be aired and discussed.



Connie believes that despite the more controversial advancements still being far away from fruition, we still must debate them now, in order to shape their future development responsibly:

"A lot of what we're talking about is a long way off," she says.

"But equally they may happen at some point, so we need to think about having the right kind of regulation in place, so that whatever we decide to do, it's done within a framework."

"One has to be optimistic," Peter says.

"Generally, people tend to be able to work out their problems – maybe not in the smoothest or least traumatic ways – but generally people do socially respond to each other, and are moral."

As we move forwards into further realms of artificial life, let's hope so.

BBC

What your phone could tell you about your health

Gemma Milne

There's a whole world of untapped data sitting on our mobile devices. Could it be used to make us healthier?

It's no secret most of us feel we spend too much time on our phones.

Scrolling through Facebook, double-tapping down Instagram, retweeting on Twitter – we create so much data on our likes, our lives and our livelihood that advertisers, insurance companies and retailers can read us like a book, by analysing our digital behaviour.

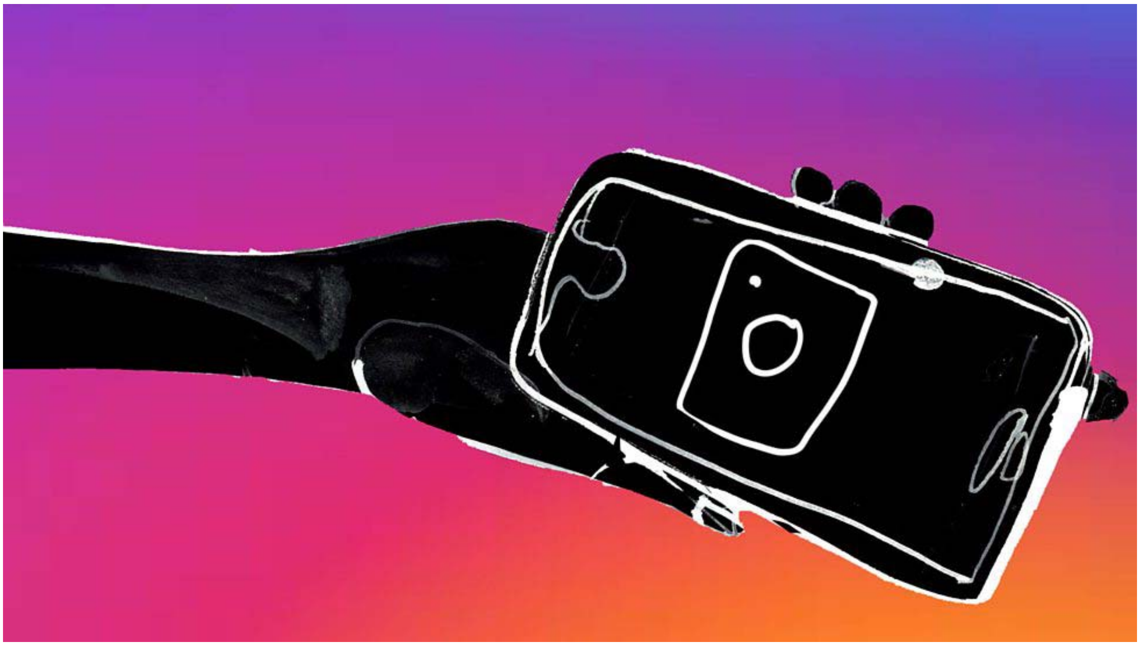
From tracking our emotions and mood through what's called 'sentiment analysis', to simply knowing our physical movements through our GPS records, companies can sell us more relevant goods, and assess what we're really like as individuals.

But what if our time online could be put to better use? What if our phones ceased to only be used for communication, and instead also became our very own medical device?

Paul Dagum is Founder and CEO of Mindstrong Health, a US company working on what's called 'digital phenotyping'.

The idea behind their work, is that the behaviour we exhibit while we use our phones day to day – from the speed at which we type and how fast our responses are, to which apps we use and when – can build a mood profile for each individual and track a person's cognitive function.

They focus on three key areas. Firstly, your voice- tracking sentiment, mood and how coherent you are.



Secondly, human-computer interactions, meaning your swiping and scrolling activity and how often you tap and, finally, the phone's in-built sensors eg tracking your location or how social you are based on messages in versus messages out.

By combining all these different factors, Mindstrong can paint a broad picture of you, and look for signs of negative mental health.

"We can look for changes in cognition, anxiety and depression," Dagum notes, "and we can track day after day, at home, as opposed to in a clinic."

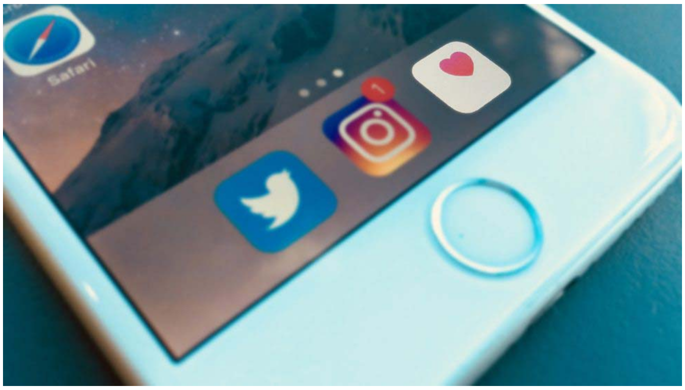
Mindstrong are focusing on building a way for doctors to work with patients with chronic mental health disorders, to spot relapse and allow for earlier intervention with care.

Mothers who might be prone to postpartum depression, and people dispatched from trauma centres – who have a high risk of developing PTSD – are two groups they are looking to target first.

Could technology help diagnose the 'black dog' of depression in smartphone users?

The way we swipe on our phones is one approach to building a digital health profile – another is looking at the actual content we post on social media.

One such example is a recent study looking into photos posted on Instagram, and whether a machine can diagnose depression from the filter chosen, the number of people present in photos and even the frequency of updates.



The study showed promising results, which begs the question of if and when this information should be passed on from the Instagram company computers, to a user's doctor.

Facebook have had a long-standing relationship with the Samaritans, acknowledging that their users will at times post suicidal tendencies and other such worrying posts on their platform.

Together, they have created a way for friends to 'report' an individual's post if they are concerned about their health, so a trained team gets in touch to offer help and support.

Of course, this requires a human to flag a post, but the efficient capability of the service to reach out to those in need suggests that, if we could prove what sort of phrases flags suicidal behaviour, a machine could surely do this unaided.

Dr Taha Yasseri of the Oxford Internet Institute, however, spoke of the limits of using social media alone to conclude how someone is feeling.

"You can't get full passive data with social media – for Twitter, you would need people to be online and tweeting often enough to get full results." There's just as much, if not more, that we don't post online, as we do.

Maxine Mackintosh, a data science doctoral researcher at University College London is working on another such example. She is investigating the link between data generated as a by-product of daily activities, for instance the number of touch points with your doctor over a 20 year period, and dementia.

"Something can be physiologically nonsensical, but also highly predictable,"she explains.

"How often you text, for instance, is not biologically linked to your dopamine levels, but it can be a marker or a representation of change.

It's exactly this concept which drives researchers like Maxine to seek out ways of spotting concerning health issues using the data from our phones.

With such huge amounts of data already being collected by phone companies, social media platforms and internet providers, you would be forgiven for thinking we already have enough information to work out what patterns predict which health issues.

The difficulty comes down to ethics – who has the right to the data, who can properly analyse it, and do we even want these companies to know what's going on in our bodies in the first place?

Recently, Strava released all the location data of their runners online, and it didn't take long for people to work out where secret US Army bases were all over the world, as a result of the open nature of the data.

Fitness app Strava lights up staff at military bases

One example of why we might want to keep our health data private, is that insurance companies and future employers might – deliberately or unconsciously – make judgements on your abilities based on your past health record.

But when you consider how much time and energy we spend with our phones by our side, putting our digital data to better use seems like an inevitable no-brainer.

And when you start to include your fitness tracker data, your existing doctor's health records and any other kind of data you record about your health, you start to see how strong a picture of a person we can create with arguably little effort – as long as we're careful about how we manage that information.

After all, if advertising companies are already using this data to better sell us stuff, we might as well find ways to use our own information to better our wellbeing.

Getty Images

What's the oldest living thing that has had its age verified?

King vulture

Bristlecone Pine tree

Giant tortoise

Bristlecone Pine tree

King vultures aren't the oldest living thing that has been accurately measured. That status belongs to the Bristlecone Pine tree. The oldest known individual tree is currently thought to be 5067 years old! This time-worn specimen lived through the rise and fall of the Roman Empire and predates the ancient Greeks. Discover more about the Bristlecone Pine with CrowdScience: What's the oldest living thing?

Giant tortoise

Yes that's right! The Bristlecone Pine is the oldest living thing that has been accurately measured. The oldest known individual tree is currently thought to be 5067 years old! This time-worn specimen lived through the rise and fall of the Roman Empire and predates the ancient Greeks. Discover more about the Bristlecone Pine with CrowdScience: What's the oldest living thing?

Giant tortoise

Giant tortoises can live for 100 years or more, but they aren't the oldest living thing that has been accurately measured. That status belongs to the Bristlecone Pine tree. The oldest known individual tree is currently thought to be 5067 years old! This time-worn specimen lived through the rise and fall of the Roman Empire and predates the ancient Greeks. Discover more about the Bristlecone Pine with CrowdScience: What's the oldest living thing?

Spiders Can fly Hundreds of Miles Using Electricity

ED YONG

On October 31, 1832, a young naturalist named Charles Darwin walked onto the deck of the HMS Beagle and realized that the ship had been boarded by thousands of intruders. Tiny red spiders, each a millimeter wide, were everywhere. The ship was 60 miles offshore, so the creatures must have floated over from the Argentinian mainland. “All the ropes were coated and fringed with gossamer web,” Darwin wrote.

Spiders have no wings, but they can take to the air nonetheless. They’ll climb to an exposed point, raise their abdomens to the sky, extrude strands of silk, and float away. This behavior is called ballooning. It might carry spiders away from predators and competitors, or toward new lands with abundant resources. But whatever the reason for it, it’s clearly an effective means of travel. Spiders have been found two-and-a-half miles up in the air, and 1,000 miles out to sea.

It is commonly believed that ballooning works because the silk catches on the wind, dragging the spider with it. But that doesn’t entirely make sense, especially since spiders only balloon during light winds. Spiders don’t shoot silk from their abdomens, and it seems unlikely that such gentle breezes could be strong enough to yank the threads out—let alone to carry the largest species aloft, or to generate the high accelerations of arachnid takeoff. Darwin himself found the rapidity of the spiders’ flight to be “quite unaccountable” and its cause to be “inexplicable.”

But Erica Morley and Daniel Robert have an explanation. The duo, who work at the University of Bristol, has shown that spiders can sense the Earth’s electric field, and use it to launch themselves into the air.

Every day, around 40,000 thunderstorms crackle around the world, collectively turning Earth’s atmosphere into a giant electrical circuit. The upper reaches of the atmosphere have a positive charge, and the planet’s surface has a negative one. Even on sunny days with cloudless skies, the air carries a voltage of around 100 volts for every meter above the ground. In foggy or stormy conditions, that gradient might increase to tens of thousands of volts per meter.

Ballooning spiders operate within this planetary electric field. When their silk leaves their bodies, it typically picks up a negative charge. This repels the similar negative charges on the surfaces on which the spiders sit, creating enough force to lift them into the air. And spiders can increase those forces by climbing onto twigs, leaves, or blades of grass. Plants, being earthed, have the same negative charge as the ground that they grow upon, but they protrude into the positively charged air. This creates substantial electric fields between the air around them and the tips of their leaves and branches—and the spiders ballooning from those tips.

This idea—flight by electrostatic repulsion—was first proposed in the early 1800s, around the time of Darwin's voyage. Peter Gorham, a physicist, resurrected the idea in 2013, and showed that it was mathematically plausible. And now, Morley and Robert have tested it with actual spiders.

First, they showed that spiders can detect electric fields. They put the arachnids on vertical strips of cardboard in the center of a plastic box, and then generated electric fields between the floor and ceiling of similar strengths to what the spiders would experience outdoors. These fields ruffled tiny sensory hairs on the spiders' feet, known as trichobothria. "It's like when you rub a balloon and hold it up to your hairs," Morley says.

In response, the spiders performed a set of movements called tiptoeing—they stood on the ends of their legs and stuck their abdomens in the air. "That behavior is only ever seen before ballooning," says Morley. Many of the spiders actually managed to take off, despite being in closed boxes with no airflow within them. And when Morley turned off the electric fields inside the boxes, the ballooning spiders dropped.

It's especially important, says Angela Chuang, from the University of Tennessee, to know that spiders can physically detect electrostatic changes in their surroundings. "[That's] the foundation for lots of interesting research questions," she says. "How do various electric-field strengths affect the physics of takeoff, flight, and landing? Do spiders use information on atmospheric conditions to make decisions about when to break down their webs, or create new ones?"

Air currents might still play some role in ballooning. After all, the same hairs that allow spiders to sense electric fields can also help them to gauge wind speed or direction. And Moonsung Cho from the Technical University of Berlin recently showed that spiders prepare for flight by raising their front legs into the wind, presumably to test how strong it is.

Still, Morley and Robert's study shows that electrostatic forces are, on their own, enough to propel spiders into the air. "This is really top-notch science," says Gorham. "As a physicist, it seemed very clear to me that electric fields played a central role, but I could only speculate on how the biology might support this. Morley and Robert have taken this to a level of certainty that far exceeds any expectations I had."

"I think Charles Darwin would be as thrilled to read it as I was," he adds.

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Parasites Can Mind-Control Animals Without Infecting Them

ED YONG

A tapeworm is essentially a very long, parasitic towel with a grappling hook for a head. It attaches itself to the internal organs of its host with its fiendish head spines, and it absorbs nutrients through its tagliatelle-shaped body. Once fastened, it does very little. It has no mouth or gut, no circulatory or respiratory systems. Its sparse nerves culminate in a cluster that could barely be called a brain. And yet, this very simple creature can manipulate the minds of more complex animals—even without infecting them.

Consider Schistocephalus solidus. Like many tapeworms, this one has a complicated life cycle. It reproduces in the guts of waterbirds, which excrete its eggs in their droppings. After the tapeworm eggs hatch, the larvae infect small crustaceans called copepods. These are eaten by stickleback fish, which are then eaten by waterbirds, completing the cycle.

The tapeworm doesn't passively go along for this convoluted ride. When it enters sticklebacks, it somehow changes their behavior so they swim toward warmer water, where the worm can grow more quickly; at maximum size, it can make up half of a stickleback's weight. The tapeworm also emboldens its hosts. They're more likely to venture outside the safety of a shoal. They're less likely to flee

from predators. And consequently, they're more likely to be eaten by birds.

Nicolle Demandt and Benedikt Saus from the University of Munster developed a simple way of assessing the tapeworm's control over its host. They would put groups of sticklebacks in a tank, lure them to the surface with floating patches of food, and then attack them with an artificial "bird"—a fake beak on a bent stick that could be jabbed into the water with a handle. ("We built it from Lego," says Jörn Peter Scharsack, who led the study. "It's very simple but very efficient.")

After the attacks, groups of uninfected fish would flee to the bottom of the tank, to hide among the plants there. By contrast, infected sticklebacks stuck to the danger zone. "These guys, they don't care," says Scharsack. "If you try to scare them they hardly respond."

Their bold behavior could also influence their peers. Like many animals that live in shoals and flocks, sticklebacks are incredibly sensitive to the actions of their neighbors. Small decisions made by individuals can translate into large collective movements by the group. And if certain individuals are infected by a mind-controlling parasite, to an extent, the group is too.

Demandt and Saus demonstrated this by repeating their experiment with mixed groups of infected and uninfected individuals. They showed that if the infected were in the majority, the uninfected ones followed them, staying in the danger zone instead of fleeing. Such indirect control has never been documented before, and might benefit the parasite. If a larger shoal of devil-may-care fish stays at the water's surface, predators might be more likely to find and attack them, again increasing the chances that they'll swallow an infected individual.

And what of the sticklebacks? Sticking with the group isn't necessarily the wrong decision, given that it provides safety in numbers. But in this case, the tapeworm might be converting safety in numbers into danger for all.

"Over the last half a century, parasitologists have been enamored with the idea that some parasites can alter their host's behavior to serve their own interests," says Julia Buck, an ecologist at the University of California at Santa Barbara. There are wasps that walk cockroaches, worms that turn crickets suicidal, fungi that zombify ants, and more. "This study demonstrates another way that parasites can alter host behavior: without infecting their hosts."

There are lessons here for humans, too. In classic experiments from the 1950s, Solomon Asch showed that volunteers could often be persuaded to give what were clearly wrong answers to simple questions if others around them—actually paid actors—answered wrongly too. In many cases, the volunteers were certain that the actors were wrong, but went along with their decisions nonetheless. A bad idea, just like a parasitic tapeworm, can also influence the minds of those who aren't directly touched by it.

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How jumping genes hijack their way into the next generation of babies

Where do transposons do their transposing?

Kat Eschner

Jumping genes may help drive our evolution—but how?

As we all learned in health class, when a baby animal is created, genetic material from two biological parents combines to create a new being—one with some genes from each parent. What you may not know is that a third genetic element is involved in this process, a hitchhiker whose existence and self-propagation may be essential to life as we know it.

Transposon, or transposable element, is the scientific name for these hitchhikers lurking in our genome. These DNA sequences are able to move around within the genome and replicate themselves, sometimes with negative consequences for their hosts. Transposon-related mutations have been blamed for hemophilia and some kinds of cancer. But research over the past decade has revealed that our relationship with these elements, which make up a large percentage of the human genome, is much more complex than previously thought. The mutations caused by transposons' presence and movements have also shaped evolution over the millennia. Until now, however, nobody had looked at the question of how transposons manage to

incite this change by hitchhiking into the next generation after conception.

For the first time, new research has shown the kinds of cells that transposons target in order to "jump" into the future with embryos who will develop into new beings. Understanding this process will let us understand more about the transposons' function and relationships. To explore this question, Zhao Zhang and his team at the Carnegie Institution for Science relied on the oft-studied fruit fly.

In theory, if transposons were allowed to run unchecked in the body, they'd result in so many genetic errors that we'd simply die. But somewhere along the way, animals developed a defensive strategy: a set of RNA molecules that limit the ability of the transposons to, well, transcribe themselves. Although transposons sometimes manage to slip past these defenses, known as piRNA, the genome is reasonably stable, with the transposons staying put and not transposing all that often.

That makes it difficult to track when they do transpose, specifically into the cells that create the next generation—a question that had never been asked before in any case, says Zhang.

"For our study what we were trying to do is reach single-cell resolution," he says—that is, track how transposons moved through cells on an individual basis rather than find their presence in a piece of tissue that has many different kinds of cells in it. To do this, they turned off a specific kind of piRNA and watched how the jumping genes moved as the egg developed from two germ cells (one from each parent).

Jumping genes, which mobilize around the genome, use nurse cells to manufacture invading products that preferentially integrate into the genome of developing egg cells, called oocytes.

They found that some jumping genes—known as retrotransposons—rely on "nurse cells" that produce genetic supplies like proteins and RNA for the developing egg. They tag along with some of those supplies into the egg, where they transpose themselves into the egg DNA hundreds or even thousands of times.

This research offers new insights into the strange world of transposons and how they have made themselves such a lasting part of our evolution. "It reveals the complex life of transposons," says Cornell University molecular biologist Cedric Feschotte, who was not involved with this study. There's more work to do, of course, but the new research reveals an elegant strategy that these genetic hitchhikers use to keep on heading down the road.

Origin of the species: where did Darwin's finches come from?

Hanneke Meijer

Four of the species of finch observed by Darwin on the Galápagos Islands, showing variation of beak.

Four of the species of finch observed by Darwin on the Galápagos Islands, showing variation of beak. Photograph: Ann Ronan Pictures/Print Collector/Getty Images

When the first of the Galápagos Islands arose from the ocean floor around 3m years ago, they were naked, angry, lava-spewing cones devoid of life. Now, millions of years later, they are alive with some of the world's most iconic animals. Giant tortoises. Sea iguanas. Flightless cormorants. And those finches equipped with Swiss army knife beaks.

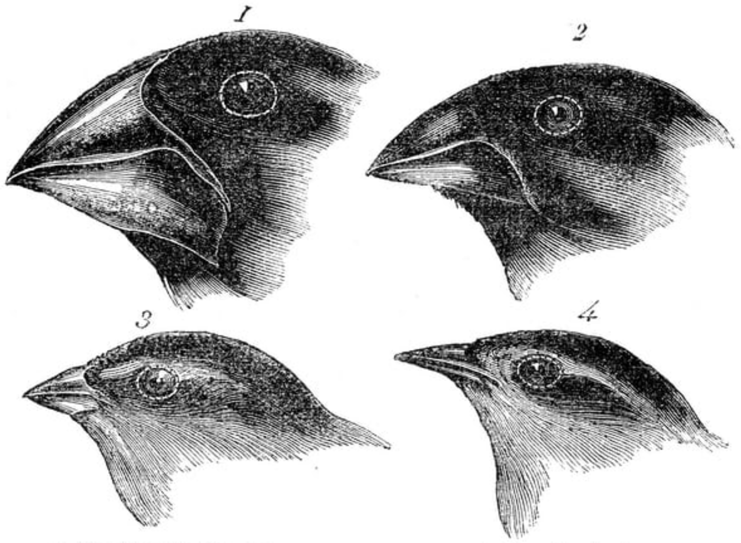
The Galápagos finches are probably one of the most well-known examples of evolution and will forever be tightly linked to Charles Darwin's voyage and his theory of natural selection (although you may be surprised to learn that the Galápagos finches were not as central to Darwin's theory as we like to think). With their diversity of bill sizes and shapes, each species has adapted to a specific type of food; the ground-finch (Geospiza) has a thick beak adapted to feeding on a variety of crunchy seeds and arthropods, whereas the warbler finch (Certhidea olivacea) developed a slender, pointy bill to catch tasty insects hiding between the foliage. The woodpecker finch (Camarhynchus pallidus) even uses twigs or cactus spines to pry arthropods out of treeholes.

The tool-using woodpecker finch probes a branch with a cactus spine on Plaza Island, Galápagos Islands, Ecuador.

The Galápagos finches are seen as a classic example of an adaptive radiation, the rapid evolution of ecologically different species from a common ancestor. Comparisons of anatomical features of the Galápagos finches, as well as modern molecular techniques, show they are indeed more closely related to each other than to any other species. This means they form a monophyletic group, a group of organisms all descended from one ancestral species. Based on the accumulated differences that occurred in their DNA over time (a way of estimating when species split from each other), the ancestral flock likely reached the Galápagos about 2-3m years ago (Grant and Grant, 2008). What did those very first finches look like? And where did they come from?

Although many of the Galápagos Islands themselves are several million years old, the oldest known fossil remains of Galápagos finches come from the Holocene period (the last 10,000 years) (Steadman et al, 1991). These fossils are from two species of ground-finches, Geospiza nebulosi and G magnirostris, that are still living on the islands today. They thus tell us little about what the earliest finches looked like and where they might have come from.

Because of the islands' close proximity to Ecuador, scientists have looked towards mainland South America in their search for the ancestor of the Galápagos finches. The avian palaeontologist David Steadman argued, based on morphological and behavioural similarities (1982), that the blue-back grassquit Volatinia jacarina, a small tropical bird common throughout much of Central and South America, was the most likely direct ancestor of the Galápagos finches. Later studies, such as that of Sato et al. (2001), started using mitochondrial DNA and found that another species of grassquit, Tiaris



1. Geospiza magnirostris.
2. Geospiza fortis.
3. Geospiza parvula.
4. Certhidea olivasca.

obscura, was the most likely ancestral species. This species originated in Central America, but spread into South America as the Isthmus of Panama, the land bridge between North and South America, formed around 3m years ago. From South America, it made its way to the archipelago.

However, others have argued, based on similarities in morphology as well as behaviour, that the Galápagos finches are more closely related to Caribbean species of Tiaris or the Saint Lucia black finch Melanospiza richardsoni (Baptista and Trail, 1988). This possibility of a Caribbean origin of the Galápagos finches was also corroborated by a recent analysis (Funk and Burns, 2018). In this analysis, the majority of species most closely related to the Galápagos finches were found to have their ancestral range in the Caribbean. However, the analysis was not conclusive, and there remains an equal probability of a Caribbean origin or a South American mainland origin to the Darwin's finch radiation.

A Caribbean origin of the Galápagos finches seems counterintuitive, as the nearest mainland from the Galápagos is South America, but dispersal does not always follow a straight line. This is nicely demonstrated by the finch that inhabits nearby Cocos Island, Pinaroloxias inornata. Although this island is closer to the mainland than the Galápagos Islands themselves, genetic research has shown that the Cocos Island finch descended from a Galápagos species, not a mainland one (Grant and Grant, 2008).

Birds are excellent long-distance dispersers, even over open ocean, as demonstrated by the repeated colonisation of the Hawaiian Islands and New Zealand. Moreover, other Galápagos birds, such as mockingbirds and the Galápagos flamingo, exhibit similar Caribbean connections, indicating that a Caribbean origin is plausible. Remarkably enough, this pattern has also been found in other animal groups, such as snakes, moths and sponges (Grehan 2001). Thus the Caribbean remains as a likely source for the origin of Galápagos finches.

Although the lack of fossils means that we don't know much about the appearance of the first finches, we can narrow down their area of origin. The closure of the Panama land bridge altered ocean circulation, and probably brought about changes in wind strength and directions. These changes may have facilitated the colonisation of the Galápagos Islands, especially if that area was the point of departure for a flock of adventurous finches.

Galápagos giant tortoises show that in evolution, slow and steady gets you places

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High-quality genomes reveal new differences between the great apes

Aylwyn Scally

High-quality genome sequences for some of the great apes have been assembled using state-of-the-art sequencing tools. The assemblies provide an unbiased comparison between humans and their closest evolutionary relatives.

Much of evolutionary biology is motivated by the principle that you cannot understand one species without comparing it with another. When nineteenth-century naturalists compared the anatomies of humans and other apes, it became clear that these species shared many features and had evolved from a common ancestor. More recently, developments in DNA sequencing — which enabled assembly of the human genome[1] in 2001, followed by lower-quality 'draft' genomes for other great apes[2–4] — have transformed our understanding of this evolutionary process. Writing in *Science*, Kronenberg *et al.*[5] describe new great-ape genome assemblies, generated using a technology that surpasses previous methods. This work marks a new stage in our ability to study and compare these species.

Genome assembly is often likened to piecing together a jigsaw puzzle — a huge jigsaw for which the box has been lost and we have only a vague idea of what the whole should look like. The analogy holds because sequencing technologies cannot sequence an entire chromosome in one go. Instead, they fragment the genome into many separate pieces, called reads, which have to be matched, overlapped and placed together.

Previous generations of sequencing machines produced reads that were only about a hundred base pairs long, or perhaps a thousand base pairs but at exorbitant cost. Current machines such as Pacific BioScience's single-molecule real-time (PacBio SMRT) sequencer produce reads tens of thousands of base pairs in length. Even with this improvement, hundreds of thousands of reads are needed to span a genome of three billion base pairs such as that of humans, Moreover, in practice, a large excess is used (typically more than 30 genomes' worth) to mitigate errors and resolve overlap ambiguities. A further complication arises from the fact that genomes are filled with stretches of DNA in which the same pattern is repeated many times, either in series or scattered throughout the genome. In apes, such repetitive DNA comprises a substantial fraction of the genome.

Because of these difficulties, the first great-ape genome projects used the human genome as a scaffold to help assemble genomic regions that are structurally similar to those of humans — that is, in which corresponding stretches of DNA lie in the same order and are present in a similar number of copies. This strategy enabled better assembly in such regions. But in regions where genome structure has evolved very differently in humans and other great apes, the great-ape draft assemblies tended to be more fragmented, and the resulting variation in assembly quality effectively constituted a bias towards the human genome. These assemblies provided many evolutionary insights, but there has nonetheless been a deficit in our understanding of the genomic elements that make humans unique.

One reason why structural variation is important, particularly on the short evolutionary timescale that separates humans and other great apes, is that it provides a way for genomes to evolve rapidly. When a whole chunk of DNA is removed or duplicated, its molecular function can be inhibited or enhanced in one step, rather than through successive mutations at individual bases. Indeed, much of the great-ape genome seems to be modular in nature, and is therefore susceptible to the kind of building-block alteration that structural variation allows. It is also thought that gene loss is a key mechanism for evolutionary change6,7. This might seem counterintuitive, but genes often act to constrain, rather than promote, a particular function. Disabling them by removing, duplicating or relocating a chunk of DNA might be the simplest way to confer beneficial effects.

Kronenberg *et al*. used PacBio SMRT to assemble high-quality genomes for a chimpanzee and an orangutan, along with two human genomes for comparison (Fig. 1). The long reads enabled them to do away with the human-genome scaffold used previously, and to increase the typical distance between gaps by about 100-fold compared with previous assemblies. The authors found about 600,000 structural differences between these genomes and that of humans, including more than 17,000 differences specific to humans. Of these, many changes disrupt genes in humans that are not disrupted in other apes. Genes whose activity is suppressed specifically in humans are more likely than other genes to be associated with a human-specific structural variant.

Many genes produce multiple versions, called isoforms, of the protein they encode, each of which can have a different role. Kronenberg and colleagues found evidence that one human-specific structural change — a large deletion in the gene *FADS2* — might have altered the distribution of isoforms the gene produces. These isoforms are involved in the synthesis of fatty acids needed for brain development and immune response8, and are difficult to obtain from a purely herbivorous diet. Correspondingly, *FADS2* has been a target for natural selection associated with dietary changes towards or away from animal fats in recent human evolution8. Chimpanzees eat a small amount of meat, so it is not known what (if any) human-specific traits might have resulted from this deletion, but it does suggest that shifting dietary patterns could have been a feature of human evolution over long timescales.

Structural variation also seems to have had a role in brain evolution. Human brains are much larger than those of other apes, and it is plausible that genes involved in brain growth and development were key to the evolution of this trait. The authors analysed the sequences of genes that are active in radial glial cells, which are progenitors for neurons and other cells in the brain's cortex, and compared protein production by these genes in humans and chimpanzees using cortical organoids — 3D models of brain tissue grown *in vitro*. These analyses revealed that 41% of genes whose activity is suppressed in human radial glial cells are associated with a human-specific structural variant. Again, this is consistent with structural genomic changes causing disruption or loss of gene function during great-ape evolution.

Intriguing as Kronenberg and colleagues' findings are, there is also a broader significance to their work. Several groups and consortia are applying new sequencing technologies to different organisms. Ultimately, researchers want accurate, high-resolution assemblies for all species, and to compare these genomes on an equal footing. This will improve evolutionary analyses and reveal complex mutation processes that have hitherto been obscured. Large genome assembly currently remains hugely expensive, and even state-of-the-art sequencing tools struggle to resolve repetitive sequences on scales above a few hundred thousand base pairs, making assembly of certain genomes challenging. But tools to read whole genomes with negligible errors on inexpensive hardware are not far away, and are almost available for small bacterial genomes9.

It is clear that we are leaving behind the initial period of evolutionary genomics, in which analyses involved comparing a genome of interest to a few 'gold standard' genomes, such as human, mouse or zebrafish. Instead, we are moving towards a more complete and equable genomic view of life.

Courtesy: Nature

How an ancient stone money system works like cryptocurrency

Bruce Bower

Digital currencies, such as Bitcoin, and the blockchain technologies used to record digital transactions on a public ledger may not be so revolutionary.

At least several hundred years ago, islanders on Yap in western Micronesia used principles at the heart of cryptocurrencies to conduct business, says archaeologist Scott Fitzpatrick of the University of Oregon in Eugene.

"Stone money transactions on Yap were the precursor to Bitcoin and blockchain technologies," Fitzpatrick says. At April's annual meeting of the Society for American Archaeology in Washington, D.C., he explained the connection between the carved stone disks, some weighing more than a Honda Accord and standing taller than a man, and today's cyber-tokens floating in digital space.

Based on studies of rock sources and dating of sites on Yap and nearby islands, Fitzpatrick thinks that, before European contact in 1783, inhabitants of Yap sailed about 400 kilometers to other islands in Micronesia to quarry limestone from caves and rock-shelters. Sea voyagers negotiated with local leaders for access to limestone deposits.

Stone carvers went along for the ride and formed stone disks on site. A central hole was cut into each circular chunk of rock so men could run a wooden pole through the opening to hoist the rock.

These weighty pieces of currency, called rai, were transported to Yap on rafts.

Arriving back home, travelers presented newly acquired rai to their fellow community members at a public gathering. Everyone heard which individuals or clan groups took ownership of particular disks. Each rai was assigned a value based on size, evenness of shape, stone quality and risks taken on the journey. After being inspected and verified by a local chief, rai were displayed at communal spots, such as ritual dancing grounds.

Ownership of a disk could be transferred, for instance, as a wedding gift, to secure political allies or in exchange for food from residents of nearby islands after a severe storm. These deals also occurred in front of the whole community. No matter who acquired a rai, it stayed in its original location.

Bitcoin and blockchain work in much the same way, Fitzpatrick says. Bitcoin "miners" solve complex mathematical puzzles to release units of currency. Those units are transported and securely stored across the public blockchain ledger. Full transaction histories for each bitcoin are available to all network participants. Bitcoins can be exchanged for goods or services or given away at any time by participants in the digital system.

A comparison of stone money on Yap to blockchain technology "is legitimate," says anthropological archaeologist Kathryn Sampeck of Illinois State University in Normal. Yap islanders pioneered a public, oral system for securely tracking and exchanging rai. Blockchain does the same by maintaining digital histories and updates about units of cryptocurrency.

Others disagree. Researchers such as anthropologist David Graeber of the London School of Economics and Political Science, who view money as the product of government taxation and debt, don't think Yap disks qualify as currency. For instance, rai can't be divided into smaller parts to make purchases or easily carried from place to place.

Digital currencies don't live up to their name either, the same group argues. Bitcoin and its cousins are unregulated exchange units with wildly fluctuating values. That makes these digital creations unlikely to catch on among consumers and tax collectors, critics predict.

The fate of cryptocurrencies is, for now, cryptic. "Not a whole lot of people buy stuff with Bitcoin and the concept of cryptocurrencies is very abstract," says anthropological archaeologist Joanne Baron of Bard High School Early College in Newark, N.J. Stone money's future on Yap is also up in the air, Fitzpatrick says. Although rarely exchanged for anything these days and often abandoned in the jungle, rai are now being rescued and renovated by islanders interested in their past.

Courtesy : www.sciencenews.org

Here's why wounds heal faster in the mouth than in other skin

TINA HESMAN

QUICK FIX The inside of the mouth heals much faster than external skin does. Scientists have discovered some proteins that contribute to the mouth's speed healing.

Mouth wounds heal faster than injuries to other parts of the skin, and now scientists are learning how the mouth performs its speedy repairs.

Some master regulators of gene activity work overtime in the mouth to heal wounds without scarring, researchers report July 25 in Science Translational Medicine. Those regulators — proteins known as SOX2, PITX1, PITX2 and PAX9 — are active in skin cells called keratinocytes in the mouth, but not in skin cells from the arm. The regulators hold down inflammation that can lead to scarring and turn on molecular programs involved in cell movement and wound closure, say the researchers, from the University of California, San Diego and the National Institutes of Health in Bethesda, Md.

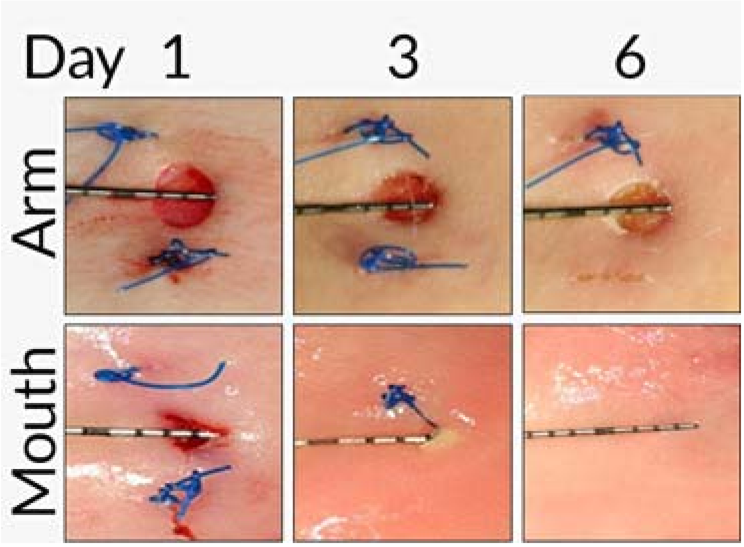
Closed up

Small wounds made in arm skin (top row) took more than six days to heal, but wounds in the mouth (bottom row) closed quickly with no scar. A probe marked in millimeters (black and white bar) shows how big the wounds are. Blue stitches indicate where the wound was made.

Knowing how the mouth performs its speed healing may eventually lead to therapies that fix skin sores without forming scars. Because the regulators are involved in many biological processes, including guiding an organism's development, scientists need to discover which of these processes is important for wound healing, says Luis Garza, a skin researcher and dermatologist at Johns Hopkins School of Medicine. The study may provide some clues.

Researchers made small wounds in both the mouths and the inner upper arms of 30 volunteers. The mouth wounds healed about three times as fast as the wounds made in the arm skin — on average at a rate of about 0.3 millimeters a day in the mouth compared with less than 0.1 millimeter a day on the arm. Reducing amounts of PITX1 and SOX2 in mouth keratinocytes grown in lab dishes altered the activity of genes involved cell movement. Boosting SOX2 levels in the skin of mice shortened healing time — from about nine days to about three.

Perhaps it shouldn't be a surprise that the lining of the mouth and other mucus membranes heal quickly. It may be a product of vertebrates evolving in the ocean, Garza says. "We spent most of our time learning how to repair wounds underwater. So it makes sense that we repair wounds really well on our moist mucosa."



Children of the Atomic Bomb

Who and Why:

Dr. James Yamazaki in His Own Words

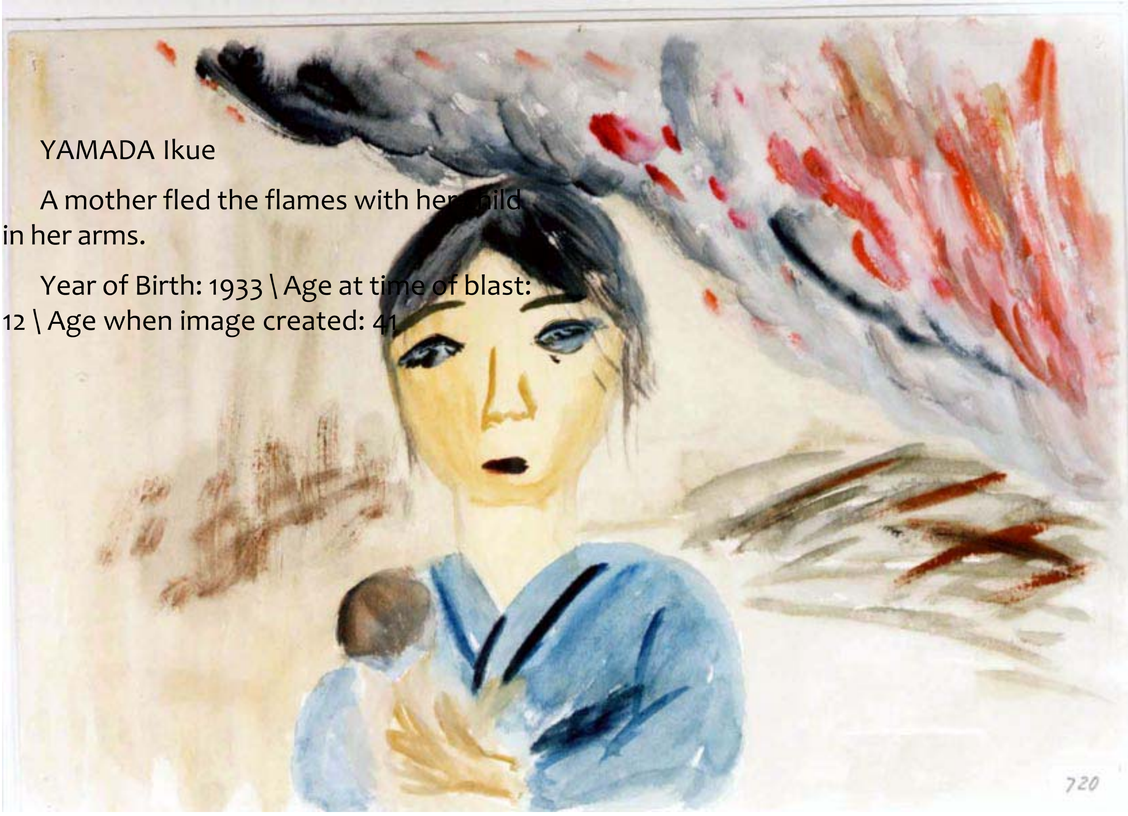
Dr. James N. Yamazaki, at the age of 33 in 1949, was the lead physician of the U.S. Atomic Bomb Medical Team assigned to Nagasaki to survey the effects of the bomb. This bomb was a deliberate act of destruction that destroyed human bodies, brains, and genes for generations.

The human and physical toll, for all mankind, speaks for itself. Yet, in the 21st century, nations continue to jockey for the control and manufacture of even more nuclear weapons. Dr. Yamazaki, today in his 90s, continues to monitor “the children of the atomic bomb” and to write and to speak out on behalf of a humankind facing nuclear destruction.

Hiroshima and Nagasaki: Two Cities, One Destiny

On 8:15 A.M. on August 6, 1945, the nuclear weapon "Little Boy" was dropped on the city of Hiroshima, followed seventy-six hours later on August 9 by the detonation of the "Fat Man" nuclear bomb over Nagasaki.

In a blinding, searing flash of light, one bomber and one bomb instantly blasted the



YAMADA Ikue

A mother fled the flames with her child in her arms.

Year of Birth: 1933 \ Age at time of blast: 12 \ Age when image created: 41

two cities to rubble. The great difference between the devastation of the two cities was a result of the different topography. Hiroshima was on a low flat delta interlaced by seven tributary rivers; Nagasaki was divided by a mountain spur into two distinct valleys.

In Hiroshima, the bomb exploded over the center of the city, destroying everything in a one-mile radius. In Nagasaki, the bomb was detonated in an industrial valley flanked by a mountain spur so that the total destruction took place within a half a mile that shielded the major business and residential districts. Yet the more powerful Nagasaki bomb of 20 kiloton (TNT equivalent) compared to the 15 kiloton Hiroshima bomb caused a far greater radius of damage than in Hiroshima.

The Human Toll

The nature of an atomic explosion explains the magnitude of the human casualties in the immediate and delayed aftermath. A measure of the enormity of the energy released by atomic weapons is that the light of the bomb in brightness is comparable to the sun, and the temperatures and pressure are comparable to those in the sun's interior. The light rays consist of thermal radiation that burns the cities and bodies and nuclear radiation that penetrates the body.

In the immediate aftermath, a quarter to a third of the population was killed by burns, trauma or radiation, or by a combination of these. The principal delayed effects of radiation concern the development of cancer, especially among those exposed in early childhood compared to adults; the brain damage to the fetus born to mothers exposed to the atomic bomb; and the genetic effects to the children born to the survivors.

Living With the Bomb

What is an Atomic or Nuclear Bomb?

A general name given to any weapon in which the explosion results from the energy released by a reaction involving atomic nuclei, either by fission—of uranium or plutonium; or, fusion—of a heavier nucleus with two lighter hydrogen ones. Thus, the A-for atomic bomb, and the H, for hydrogen bomb are both nuclear weapons. In the history of the modern world as we know it, the atomic bomb was only used once to kill human beings: it was dropped on the Japanese people in Hiroshima and Nagasaki in 1945.

Nuclear States, Nuclear Stakes

Behind any discussion of radiation must necessarily loom the specter of full-scale atomic war. That a single thermonuclear weapon can cause severe radiation damage hundreds of miles beyond its area of immediate devastation is all too well known. That enough such weapons exploded in an all-out war might render the entire earth, or large parts of it, uninhabitable, is at least conceivable.

The nuclear stakes are global: life-maintaining and life-diminishing decisions must be made by informed individuals, communities, and nations today.

Children of the Atomic Bomb Survivors

Seventy thousand new-borns were examined in Hiroshima and Nagasaki. In Nagasaki, 500-800 babies were examined in their homes. No evidence of genetic injuries were detected at that time. But today, in 2008, new studies done on survivors and their offspring are revealing conclusive DNA genetic changes and malformations. These studies utilize newer modalities to detect DNA injuries. The children of survivors, now adults, are concerned how genetic damage from the bomb may be transmitted to their children through generations.

Aside from the physical injury and radiation the most significant effect of the atomic bomb was the sheer terror which it struck into the citizens of these bombed cities. Such terror, unprecedented in humankind, was etched forever onto the bodies and minds of the persons who experienced it.

The tragedy of Hiroshima and Nagasaki is not just Japan's, but it is the world's. Therefore, it is the responsibility of all nations to prevent another nuclear disaster for the safety and well-being of all our children.

Today: 159,000 Hiroshimas!

Aside from the the physical injury and radiation the most significant effect of the atomic bomb was the sheer terror which it struck into the peoples of the bombed cities.

Today, the U.S. nuclear stockpile contains 2,400 megatons, the equivalent to 159,000 Hiroshimas! An enormous nuclear caldron simmers that adds fire to current threats of global warming and changes in our water, atmosphere, and the delicate human, animal, and food chain through which we are all interlinked.

http://www.aasc.ucla.edu/cab/index.html

Back wrapper:

KIYOYOSHI Goro

One hour after the explosion: From a hill on the outskirts, we looked out over the city engulfed in flames.

Year of Birth: 1897 \ Age at time of blast: 48 \ Age when image created: 76

Date of image depicted: 1945/8/6

Distance from hypocenter in meters: 1600

Hiroshima Peace Memorial Museum

GE14-02

Explanation in picture: From Futabayama Hill, we looked down on the Second Army Headquarters and Nigitsu Shrine. In front of us the city was rising in flames around Hiroshima Castle and Shukkeien Garden. Lines of people fled from the Hakushima area to the Eastern Drill Ground. Many had fallen in the river and were caught in the current; others lay naked on the ground. This is what the city looked like one hour after the bombing from the hill behind our house.

Borassus

Type species

Borassus flabellifer L.

Lontarus Adans.

Borassus (Palmyra palm) is a genus of five species of fan palms, native to tropical regions of Africa, Asia and New Guinea. These massive palms can grow up to 30 m (98 ft) high and have robust trunks with distinct leaf scars; in some species the trunk develops a distinct swelling just below the crown, though for unknown reasons. The leaves are fan-shaped, 2–3 m long and with spines along the petiole margins (no spines in B. heineanus). The leaf sheath has a distinct cleft at its base, through which the inflorescences appear; old leaf sheaths are retained on the trunk, but fall away with time. All Borassus palms are dioecious, with male and female flowers on separate plants; male flowers are less than 1 cm long and in semi-circular clusters, sandwiched between leathery bracts in pendulous catkins; female flowers are 3–5 cm wide, globe-shaped and solitary, sitting directly on the surface of the inflorescence axis. The fruits are 15–25 cm wide, roughly spherical and each contain 1-3 large seeds. Depending on species, fruit color varies from black to brown, yellow or orange; the fibrous pulp is aromatic and sweet to taste. Each seed is enclosed in a woody endocarp, which protects it when the fruit is consumed by elephants, monkeys and other frugivores. At germination, the young seedling extends downwards into the soil and only a few leaves are visible above ground; this provides some protection against frequent fires in its savanna habitat;

after an indeterminate number of years (the establishment phase), the seedling forms a stem and quickly grows above the savanna vegetation, where it is then less vulnerable to fire.[3]

Species[edit]

Borassus aethiopum - African Palmyra palm, Rônier (and other names) (tropical Africa & Madagascar)

Borassus akeassii - Ake Assi's Palmyra palm (West and Central Africa)

Borassus flabellifer - Asian Palmyra palm/ Lontar palm/Doub palm (southern Asia from India to Indonesia)

Borassus heineanus - New Guinea Palmyra palm (New Guinea)

Borassus madagascariensis - Madagascar Palmyra palm (Madagascar)

Cultivation and uses[edit]

The main entrance of Angkor Wat to the temple proper, seen from the eastern end of the Naga causeway and Asian Palmyra palm

Young African Palmyra palm (Borassus aethiopum)

Palmyra palms are economically useful and widely cultivated, especially in Southeast Asia. The Palmyra palm has long been one of the most important trees of Cambodia and India, where it has over 800 uses. The leaves are used for thatching, mats, baskets, fans, hats, umbrellas, and as writing material.

In Cambodia, the tree is a national floral symbol/emblem that is seen growing around Angkor Wat. Palmyra palms can live for over 100 years.

In ancient India and Indonesia, Palmyra leaves were used as writing paper, with their parallel veins providing a useful rule. In India, mature leaves of suitable size, shape and texture were chosen and preserved by boiling in salt water with turmeric powder. Once dry enough, the leaf surfaces were polished with pumice, cut to the proper size and a hole was cut in one corner. Each leaf has four pages and a stylus is used to write; the style is cursive and interconnected. Completed leaves are then tied up as sheaves.

The black timber is hard, heavy, and durable and highly valued for construction, especially in structures exposed to water, such as wharves, fences and boats.

Ake Assi's Palmyra palm (Borassus akeassii) fruit

Jelly-like seeds of Palmyra palm (Borassus flabellifer) fruit

The tree yields many types of food. The young plants are cooked as a vegetable or roasted and pounded to make meal. The fruits are eaten roasted or raw, as are the young, jelly-like seeds. A sugary sap, called toddy, can be obtained from the young inflorescence, both male and female, and this is fermented to make a beverage called arrack, or concentrated to produce a crude sugar called jaggery/palm sugar. It is called Gula Jawa (Javanese sugar) in Indonesia and is widely used in Javanese cuisine. The roots can be dried to form Odiyal, a hard chewable snack. In addition, the tree sap is taken as a laxative, and medicinal values have been ascribed to other parts of the plant.

In Tamil culture[edit]

The Palmyra tree is the official tree of

Tamil Nadu. In Tamil culture it is called karpaha,"nungu" "celestial tree", and is highly respected because all its parts can be used. The recently germinated seeds form fleshy sprouts below the surface which can be boiled and eaten as a fibrous, nutritious food. The germinated seed's hard shell is also cut open to take out the crunchy kernel which tastes like a water chestnut but sweeter. The ripe fibrous outer layer of the fruits is edible after boiling or roasting. When the fruit is tender, the kernel inside the hard shell is an edible jelly that is refreshing and rich in minerals. When the crown of the tree from which the leaves sprout is cut one can make a cake. In ancient times, dried palm leaves were used to write manuscripts.

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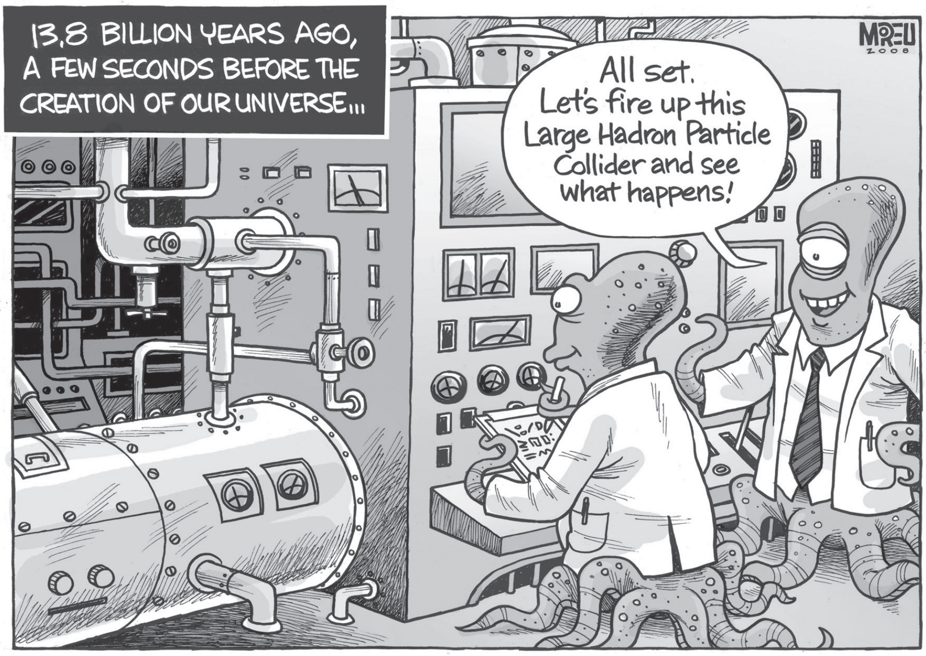

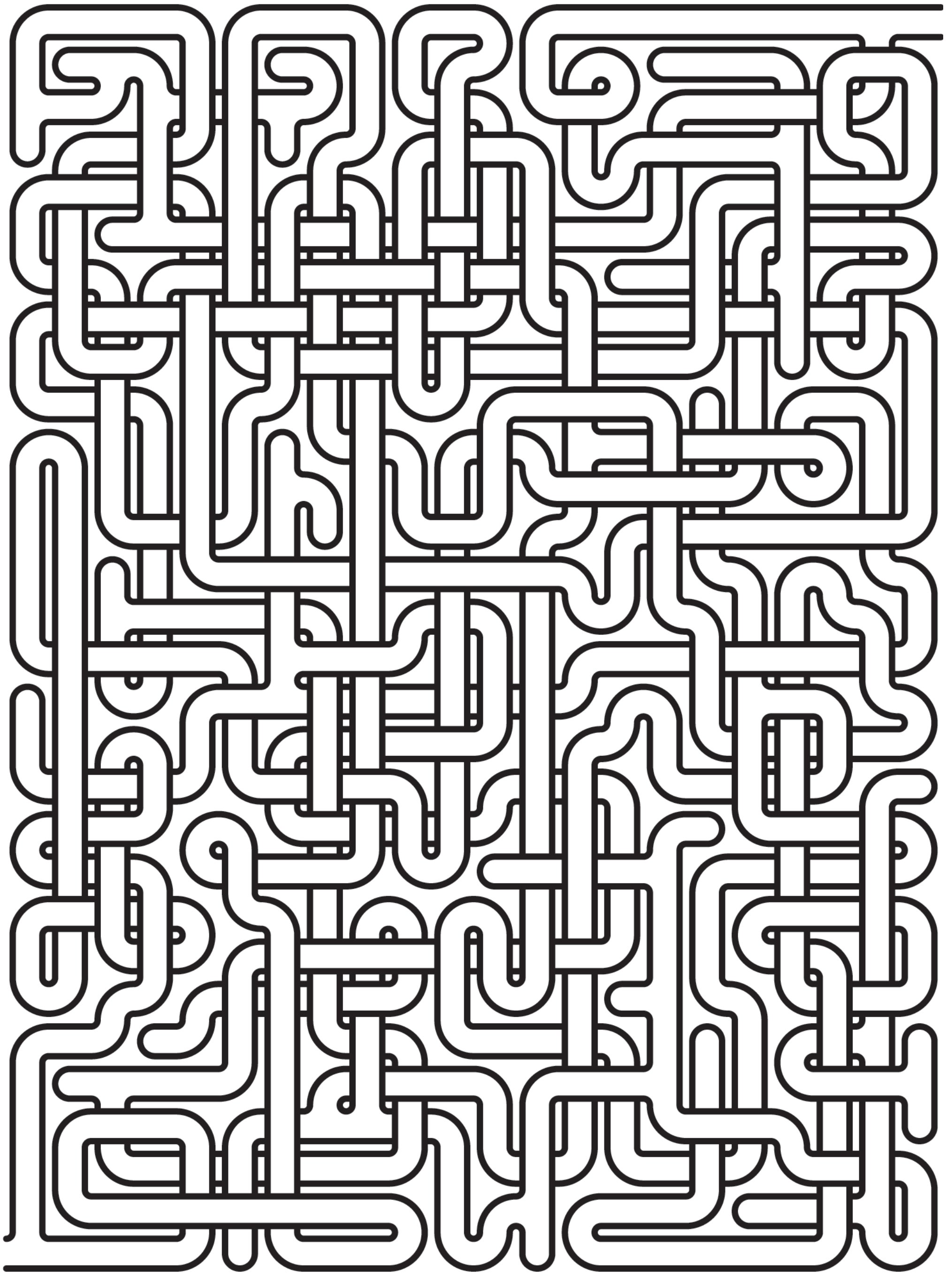

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