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EXPLORING LIFE, INSPIRING INNOVATION

CLIMATE CHANGE

WHICH SPECIES ARE MOST VULNERABLE?

ANCIENT PROTEINS RESURRECTED

THE EVOLUTION OF LANGUAGE

MUTATION RATES QUANTIFIED

PLUS

HOW TO STUDY ENDANGERED SPECIES


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60
40
20
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dsDNA
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ssDNA
Protein A280
UV-Vis
Colorimetrics
Fluoro dsDNA
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JULY/AUGUST 2018

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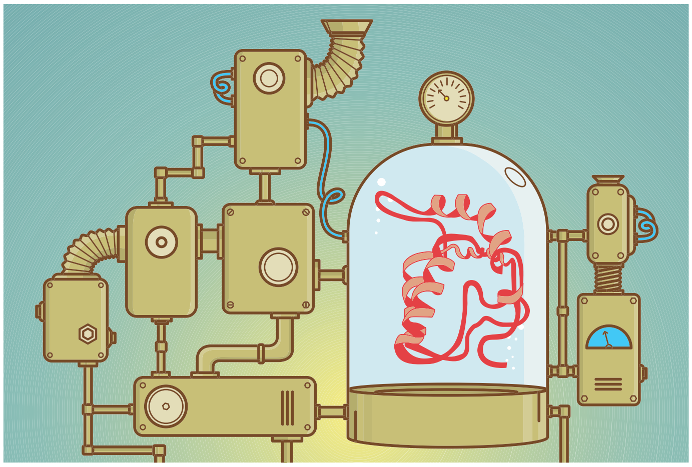

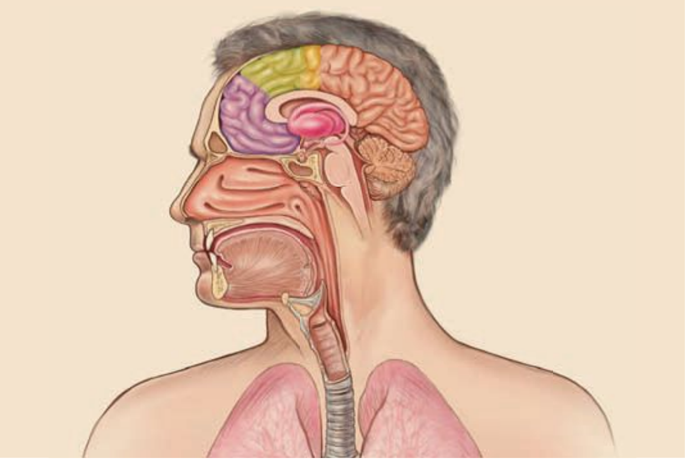

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JULY/AUGUST 2018

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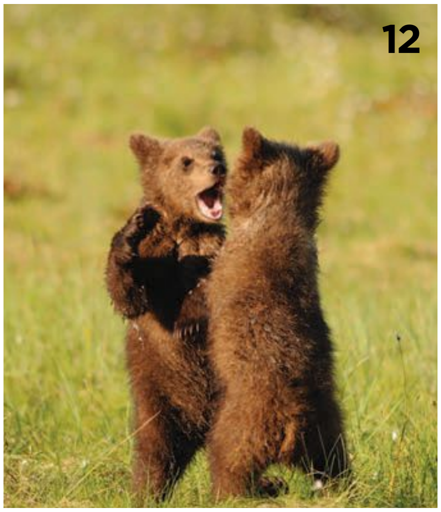

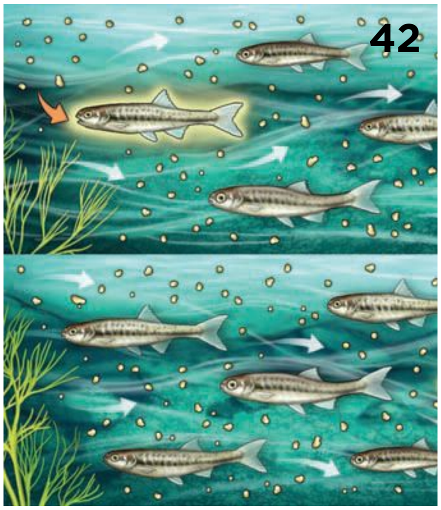

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CORRECTIONS:

The May article "Answers in the Exome" mistakenly referred to "Washington University in Seattle." The sentence should instead have referred to "the University of Washington in Seattle."

The beginning of "The Ancient Ones" (June 2018) has been changed from its original version to reflect the fact that methane does not smell.

In "Cosmic Salad" (June 2018), it was incorrectly stated that Phil Sadler was deceased. He is, in fact, alive. *The Scientist* regrets these errors.

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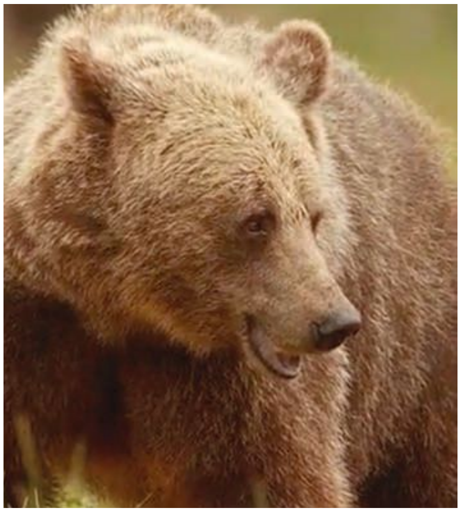

THIS MONTH AT THE-SCIENTIST.COM:

VIDEO
Oh, Captain
Meet Cindy Van Dover, a deepsea explorer and the first female to pilot Alvin, the submersible that has ferried researchers into some of the ocean's deepest depths.

VIDEO
Mama Bear
Brown bears in Sweden are keeping their cubs with them longer than usual, likely the result of hunting laws in the Scandinavian country.

VIDEO
Snaking Over
See how the tiny island of Guam became overrun with brown treesnakes, and learn what biologists are doing to try to eradicate the invasive species.

AS ALWAYS, FIND BREAKING NEWS EVERY DAY, AND LEAVE YOUR COMMENTS ON INDIVIDUAL STORIES ON OUR WEBSITE.

Coming in August at the-scientist.com

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- The promise and peril of using CRISPR in humans
- The issue of research reproducibility hits ecology
- Growing brains in non-human animals
- Plastic waste in the laboratory

AND MUCH MORE

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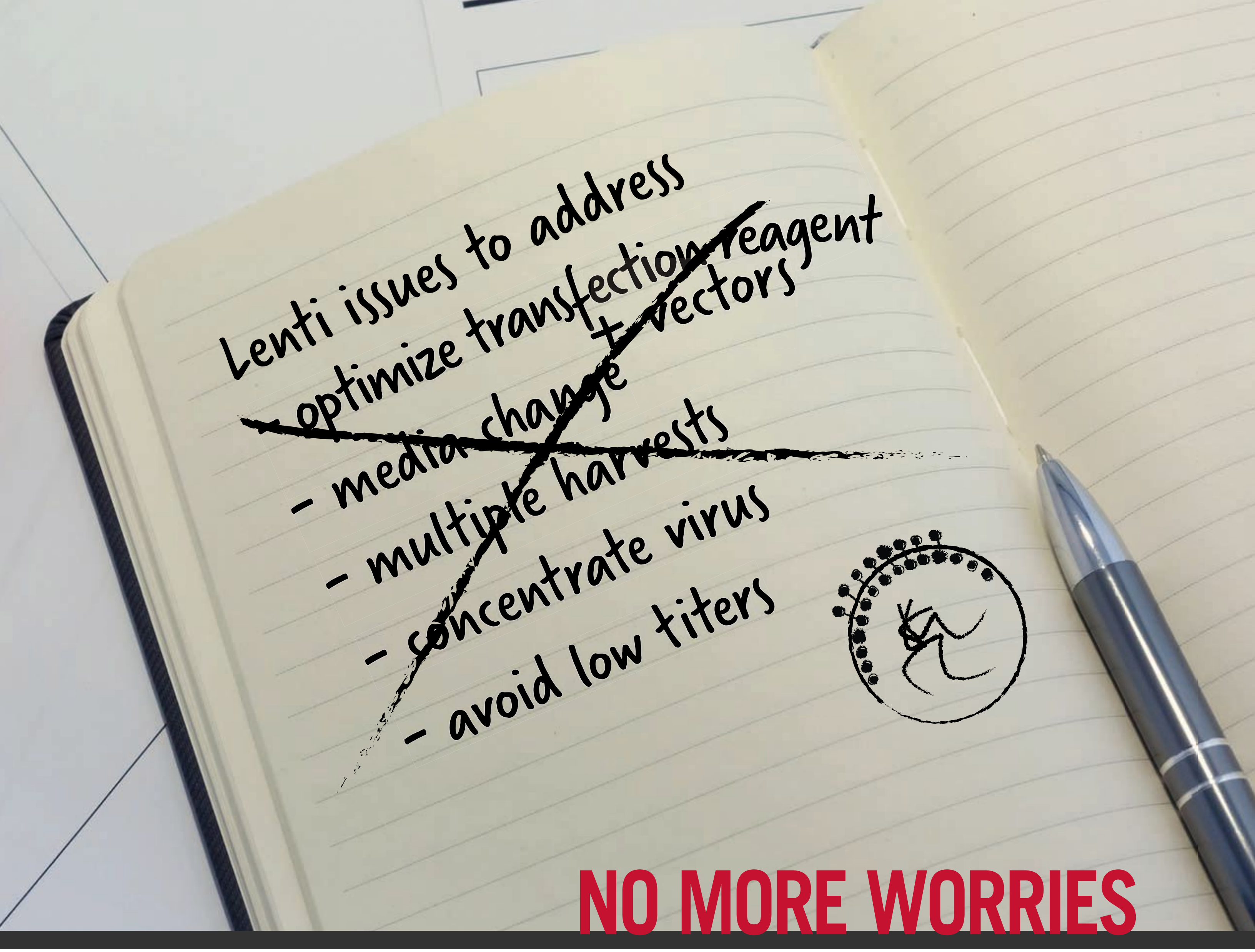

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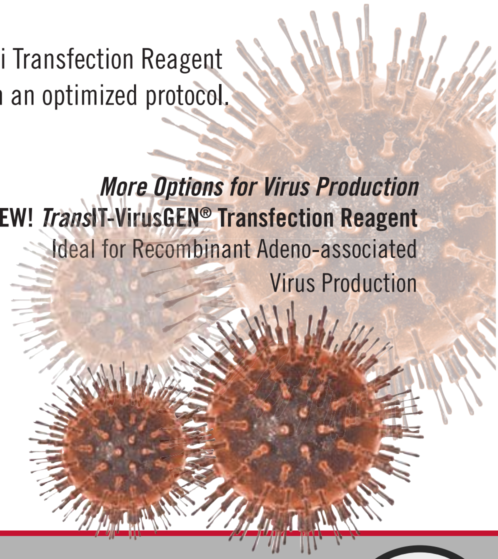

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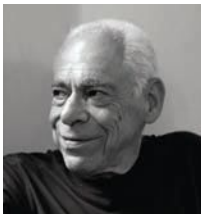

In 1968, **Phillip Lieberman** was taking a bath when he heard a radio report on WGBH, Boston's NPR affiliate, that dramatically changed his life. "Bill Cavness was reading a book by Loren Eisley about why apes can't talk, and I wondered why," he says. At the time, Lieberman was working on his PhD thesis at MIT, investigating how breathing patterns change during human speech. The thesis later became one of the first books published by the MIT Press. "I got this phone call saying, would I mind if they published my thesis," Lieberman recalls, laughing. "I said, no, obviously I don't mind." The cognitive scientist would go on to publish half a dozen more books on human speech. He had initially started studying speech while he was researching secure communications for the US Air Force during the Vietnam War. The 1968 NPR piece piqued his interest in how the vocal tract evolved, and Lieberman began reading books on comparative anatomy. In 1974, he joined the faculty at Brown University, where he continued studying speech and was awarded a Guggenheim Fellowship in 1987. He retired from teaching at Brown in 2012, but he remains as a professor emeritus. Lieberman is also an accomplished photographer whose work has been displayed at the Rhode Island School of Design and the Haffenreffer Museum of Anthropology at Brown. You can read his article "Talking About Language" on page 34.

When he was five years old, historian **Jason Colby** stepped onto a commercial fishing boat in Puget Sound for the first time. He soon fell in love with the Salish Sea, a network of waterways along the coasts of British Columbia and Washington State. In that area, "orcas are the sacred animal of a very secular region," he says. "You see the image everywhere in the Pacific Northwest." The local ubiquity of orca images got him interested in how our relationship to the whales has changed over the last century. During that time, humans' perception of orcas shifted from "a dangerous vermin species up until the mid-1960s to being one of the most celebrated, iconic, and beloved species on Earth," Colby says. While he worked on commercial fishing vessels in Alaska and on fish farms in Puget Sound in his teens and early 20s, he became interested in "the increasingly iconic place that charismatic megafauna had to our shifting environmental politics." In 1997, Colby graduated from Whitman College in Walla Walla, Washington, with a BA in US and international history, and soon began collecting oral histories of pioneering environmental scientists. Colby went on to complete a master's and PhD in international history and foreign relations at Cornell University. But he never stopped studying humanity's complicated relationship with orcas. In April, he published *Orca: How We Came to Know and Love the Ocean's Greatest Predator*. Read his article "Enlightening Captivity" on page 55.

Thirty years ago, **Laurie O'Keefe** started working in what was at the time an obscure field: medical illustration. She says she had always "wavered" between science and art. A biological illustration class she took in her last semester as an undergrad majoring in zoology at Colorado State University focused her interests: "I thought, this is it." After a graduate degree in anatomy with a focus on medical illustration, she started to look for work. Reluctant to leave Colorado, O'Keefe took a research associate position at a hospital in Denver. Conducting research during the day and illustrating at night to build up clientele, she "was pretty much not sleeping." Three years in, she landed three deals for illustrating biology textbooks, something she went on to do for 10 years. More than 100 books later, O'Keefe switched over to doing all manner of illustrations "to stay afloat" in a changing publishing landscape. She even turned down a spot in veterinary school, deciding to devote her career to drawing, rather than caring for, animals. As for her work with *The Scientist*, "I think whenever there's a rat or mouse, that's when I get called up," she says. This time around, her work is devoid of rodents, but her stunning illustrations of the physiology of language production can be viewed on pages 37 and 38.

PHILLIP LIEBERMAN: PHOTO BY GIORGIA MULLER

FROM THE EDITOR

What’s a Consumer to Do?

In a world beset by climate change, marine pollution, and dwindling natural resources, a member of the mushrooming human population pauses to consider his role.

BY BOB GRANT

“Building a house is littering.” This is the thought my seven-year-old son recently shared as we tended our vegetable garden in the late-spring sun. His reasoning went like this: if throwing a gum wrapper out of the window is considered a minor assault on the environment, constructing a relatively massive edifice in a natural setting is littering on an epic scale. This peek into his evolving conception of humanity’s role in the environment came as I found myself struggling with similar quandaries and trying to reduce my footprint in a world that seems overburdened by human activity.

At *The Scientist*, we’ve covered the science behind many pressing environmental issues over the years: from the effects of climate change and pharmaceutical pollution to the decimation of biodiversity and the crisis of plastic contamination in marine and terrestrial ecosystems. It’s this last topic that has really had me thinking lately.

As relayed in an early-June speech by UN Secretary-General António Guterres, more than 8 million tons of plastic ends up in the ocean every year, and “microplastics in the seas now outnumber stars in our galaxy.” Eerie images of wildlife mingling with household plastic goods, mountains of plastic garbage piled up on the outskirts of major metropolises, and discarded water bottles choking the world’s waterways have splashed across the pages of *National Geographic* and other publications.

As a hapless fisherman and an erstwhile environmental scientist, I’ve always thought myself a reasonably good steward of nature. I recycle everything I can. I capture and use rainwater. And my family eats vegetables from the garden that inspired my son’s introspection. But lately, I find it hard to so much as drag a cotton swab through my ear canal and flick it toward the wastebasket without my mind conjuring the image of a seahorse in the South Pacific clinging to my Q-tip.

Yet life requires consumption. Even at the subcellular level, when biological entities stop extracting energy from their surroundings and cease to deposit waste, death is soon to follow.

So how can a privileged but reasonably conscientious organism lessen the negative effects of his existence? For me, the answer lies first in lessening the consumption itself. Eschewing unnecessary conveniences such as plastic bags, plastic cutlery, and disposable water bottles is a start. But maybe thinking more deeply about what I can do without is warranted in this day and age. After all, humanity made do with more-permanent solutions to the inevitable buildup of earwax for millennia (tiny metal scoops and pinkie finger nails come to mind).

ANDRZEJ KRAUZE

But aside from the sort of ecological inventorying we could all do, I return to my abiding trust in the brilliance of the scientific community to help save the planet from its most rabid consumers. Vegetable-based, compostable alternatives to petroleum-based disposable plastic plates and cups were once science fiction but are commonplace today. Researchers are working hard on the front lines of pollution problems, developing innovative ways to break down durable synthetics and remediate areas tainted by the refuse of billions of *Homo sapiens*. And as editor Catherine Offord explores on page 20, scientists are refining methods to predict which species might fare worst under the onslaught of anthropogenic climate change, in the hopes of directing societies’ conservation efforts where they’re needed most.

As I litter my way through life, with my house, car, kids, and recyclable pickle jars in tow, I remain cautiously optimistic on two counts: that journalism from *The Scientist* and numerous other outlets will convince more of the global citizenry, industrialists, politicians, and innovators of the importance of environmental protection; and that scientists will continue to record, predict, and mitigate the often disastrous effects our species is having on the planet and its inhabitants. ■

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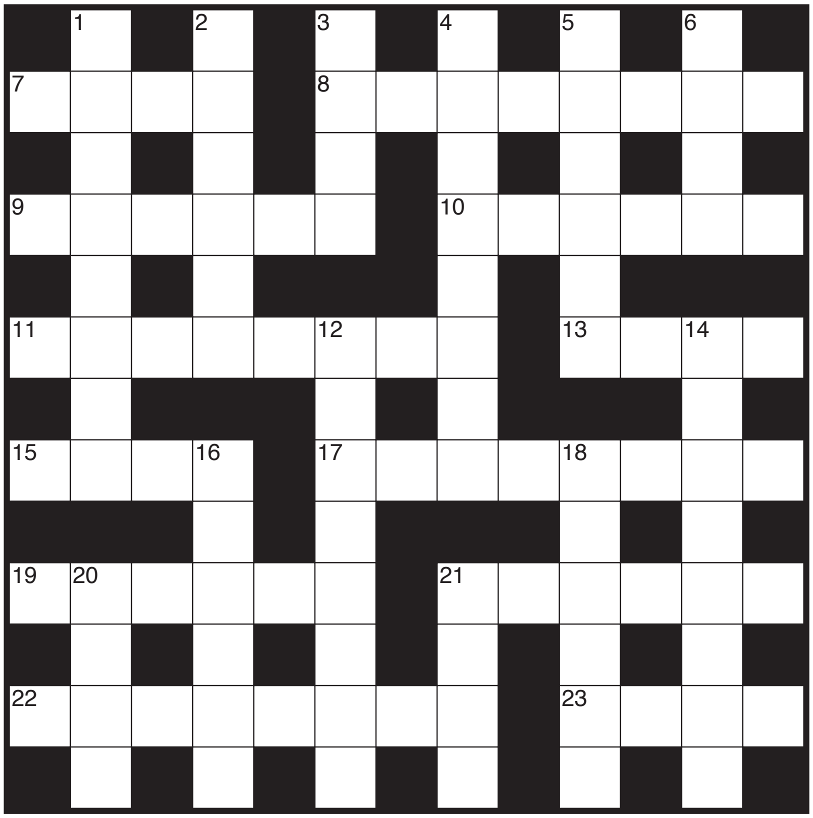
Speaking of Science



Note: The answer grid will include every letter of the alphabet.

BY EMILY COX AND HENRY RATHVON

> By and large we are eating up the natural world for our own purposes. Well that's self-destruction actually. If you damage the natural world in the end you damage yourself and the human race will regret it.

—**Sir David Attenborough**, conservationist and documentarian, discussing the problem of plastic pollution in an interview with *Sky News* (June 8)

> There should be no room for opportunistic and cynical efforts to gain small partial results in the short run while shifting equally significant costs and damages to future generations. Civilization requires energy, but energy must not be used to destroy civilization!

—**Pope Francis** speaking at the Vatican to an audience of executives from major international oil and mining companies (June 9)

ACROSS

7. Phycologist's specimen
8. What Carl Linnaeus is called the "father" of
9. Highest point on the celestial sphere
10. Potential site of mammoth fossils (2 wds.)
11. Like Mendeleev's table
13. Bird giving New Zealanders their nickname
15. Branch of a feather's main shaft
17. Flowers in the genus *Narcissus*
19. Nobelist with a namesake constant
21. Loosestrife hue
22. Body aiding coagulation
23. What balloonfish may do in self-defense

DOWN

1. Succulent plant used in lotions (2 wds.)
2. Island home to the Papenoo River and the Fautaua Waterfall
3. Pruritus
4. Hormone associated with empathy
5. Inuit garment made of caribou skin
6. Prefix on science
12. Storied case of dissociative identity disorder (2 wds.)
14. Ecotourism draw
16. Tuna kin whose name means "pretty" in Spanish
18. What red blackberries are
20. Flower whose family includes onions and garlic
21. Spongy plant tissue

Answer key on page 5

"Someday, son, this will all be yours—and underwater."

ALEX GREGORY/THE NEW YORKER COLLECTION/THE CARTOON BANK

Notebook

JULY/AUGUST 2018

FAMILY TIME: Compared to previous generations of Sweden's brown bear population, today's mother bears are keeping their cubs with them for longer.

SIEGFRIED KLAUS

Care Bears

Deep in the forests of south-central Sweden, brown bears (*Ursus arctos*) emerge from hibernation ravenous. Mama bears and their cubs will consume massive amounts of berries, bees, voles, and maybe other meat to plump up before heading into hibernation again in the fall. This has been the bears' annual routine for millennia.

But a group of researchers in Scandinavia that has been tracking brown bears there for three decades has started to notice something just a bit different in female bears' behavior in recent years. "More and more females are keeping their cubs longer," says Joanie Van de Walle, a graduate student at the University of Sherbrooke in Quebec, Canada, who is studying the ecology of Scandinavian brown bears. While for the most part, mother bears in the region have tended to care for cubs for only about a year and a half, many of the bears in Sweden are now rearing cubs for more than two years.

That's surprising, because for as long as a mother bear has cubs, she isn't fertile and therefore won't mate. The longer she keeps her baby bears around, the fewer offspring she can have in her lifetime, notes Frank van Manen, who studies grizzly bears, a subspecies of brown bear (*Ursus arctos horribilis*), for the US Geological Survey in Yellowstone National Park.

So why are Sweden's brown bear mothers adopting such a seemingly disadvantageous reproductive strategy? That's a question Jon Swenson, an ecologist at the Norwegian University of Life Sciences who has helped to track the Scandinavian bear population, wanted to answer. He and his colleagues have been following female bears from birth to death for 30 years. The team now has data spanning five generations, which it's using to study the social organization of the roughly 3,000 bears in the region, along with the animals' mate choices and life histories.

Based on their three decades' worth of data—the largest and longest-running dataset collected to date for a large carnivore—Swenson, Van de Walle, and colleagues saw that between 1987, when the monitoring project started, and 1995, there was little to no evidence of mother bears staying with their cubs longer than 1.5 years. From 1995 to 2005, the 2.5-year timeframe to raise cubs remained rare, describing only about 7 percent of weaned litters. But between 2005 and 2015, it jumped to around 36 percent.

Now, Swenson and his colleagues think they have found the cause: hunters. In Sweden, legislation that prohibits hunters from killing bears with cubs dates back to at least 1973. Van de Walle, Swenson, and their colleagues found that, for the past 30 years, hunters have been removing mother bears that wean after shorter periods of time from the population, meaning mother bears that keep their cubs longer have a survival advantage over those that don't (*Nat Commun*, 9:1100, 2018). As a result, the authors suggest, the hunting regulation promotes slower life histories among Scandinavian brown bears.

It's hardly the first example of harvesting practices acting as an artificial selective pressure on animal populations. Fishing, for instance, has targeted the largest individuals of certain species, with the result that fish lose reproductive opportunities as they grow larger, selecting for individuals that reach sexual maturity sooner and leading to an overall reduction in the size of individuals within a population. And in animal species with economically valuable or prized trophy features such as horns, antlers, and tusks, those with larger outgrowths are often hunted out of the population, leaving individuals with smaller adornments to mate.

For Scandinavian bears, extra time with mom might carry advantages for the cubs, too. It "might actually make these cubs better prepared for life," Miha Krofel, a carnivore ecologist at the University of Ljubljana in Slovenia who was not involved in the new study, tells *The Scientist* by email. "There is a lot for bears to learn before gaining independence." They need to know where to find food, which habitats to use in which season, how to interact with other bears, and how to avoid people. Cubs that live longer with their mothers could even be less prone to conflicts with humans.

There is a lot for bears to learn before gaining independence.

—Miha Krofel, University of Ljubljana

Van Manen says the reported change in cub rearing and its association with hunting is interesting, but he cautions against "interpreting this observation as a cause and effect, because there may be alternative hypotheses that would be worth exploring." It's puzzling, for instance, that in the Scandinavian brown bear population the 1.5-year weaning tactic was dominant throughout the study period. "The norm for brown bear populations worldwide is that cubs stay with their mothers for 2.5 years or more," he says. "So another way of thinking about the results of this study is why the 1.5-year tactic was relatively common in the Scandinavian brown bear population to begin with." Van Manen suggests the shift in parenting strategy back toward the species norm might have been the result of decreasing densities of aggressive adult male bears, which can attack and kill cubs, presumably to gain access to adult female mates.

Still, the team's observation that hunting changes female bears' strategies for raising cubs has support from researchers studying bear populations elsewhere. Since the 1930s, Slovenia has protected its bear populations and, in 1986, made it illegal to kill a mother with her cubs. There, Krofel says, he and his colleagues are seeing slightly different effects: females first give birth up to a year earlier than females in other brown bear populations around the world. "Understanding these effects is crucial for managers to be able to formulate hunting regulations, which will decrease unwanted side effects of hunting, as well as to help the public decide whether bear hunting is acceptable in [a] given situation or not," Krofel says.

Such decision-making was recently in play for the Yellowstone grizzly bear population. The bears had been on the endangered species list and protected from hunting until last year. Now, the population has reached at least 700 individuals, and the Wyoming Fish and Game Commission unanimously voted to allow the hunting of about two dozen bears east of Yellowstone National Park this year. Some researchers argue that killing females could threaten the sta-

CUB BENEFITS: Scandinavian brown bears' changing parenting strategies may carry advantages for baby bears, too.

SIEGFRIED KLAUS

bility of the grizzly population, but van Manen argues otherwise. The hunt will be extremely well regulated, he says, and "hunting pressure will be very low compared to the Scandinavian study."

For now, Van de Walle notes that the Scandinavian study has raised many more questions than it is has answered. One particular mystery she would like to solve is how the change in parenting strategy is being transferred between generations—whether female bears know instinctively to wean their cubs later, or if they learn to do it from their mothers, she says. "We need a longer study period to verify that."

—Ashley Yeager

Charming Snakes

What really turns a brown tree snake on? That's the question Rocky Parker, a chemical ecologist at James Madison University in Virginia, has been trying to answer these past few years, and it hasn't been easy. To communicate with members of the opposite sex, "the snakes don't just use a single chemical cue or a couple [of] cues," Parker says. "They are using this bouquet of odors."

But there's good reason to narrow in on the chemicals that matter: luring brown tree snakes (*Boiga irregularis*) into traps using sex pheromones is one tactic that Parker believes could help stem an infestation that has plagued the island of Guam for decades. While baiting traps with synthetic pheromones has proven to be an effective method to capture and kill insects, the approach has seen limited success with vertebrates such as rodents, and it has never been shown to successfully control reptile populations.

The brown tree snake has been an unwelcome visitor to Guam since the end of World War II, when the pest hitched a ride on military cargo ships steaming from Australia to the Pacific island. Feasting on rats and tropical birds helped the snake population balloon to as high as 4 million by the 1980s—with several native bird and other vertebrate species going extinct as a result. Guam's brown tree snake population, now with far fewer prey to eat, has hit carrying capacity at 1 million to 2 million snakes, but efforts to control the nocturnal reptile continue.

US federal agencies employ several tactics to keep the serpents at bay. Traps baited with mice keep snakes out of power stations. Snake-sniffing dogs catch the creatures at the seaport. And for the last few years, researchers at the US Department of Agriculture's Animal and Plant Health Inspection Service (APHIS) have been dropping dead mice laced with acetaminophen—poisonous to the snakes—from helicopters into the jungle. A new automated system is set for its first landscape-scale test this summer at Andersen Air Force Base.

"At this point, it's looking pretty clear that nothing is going to be the magic bullet, so what's going to be required is a suite of tools, each of which has strengths that make it useful for particular applications associated with the overall snake problem," says Shane Siers, a supervisory research wildlife biologist with APHIS, which spearheads much of the snake research and control efforts. "[Pheromone research] has been identified as something that has potential that hasn't been fully exhausted yet."

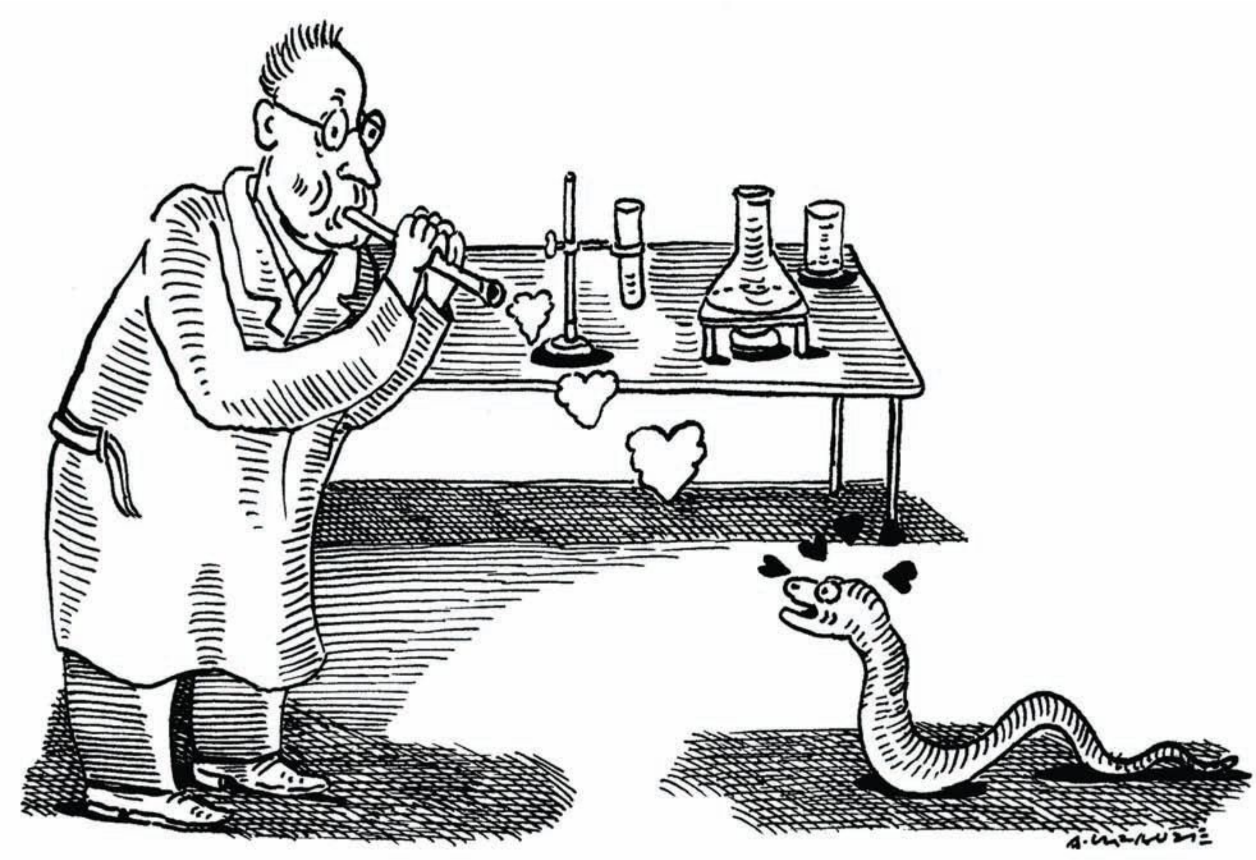
> **Obviously they smelled enough like a female to elicit courtships from males.**
>
> —Rocky Parker, James Madison University

When Parker started work on pheromone-based snake control in 2014 at the National Wildlife Research Center in Fort Collins, Colorado, he had a lead or two to go on. Studies in the late 1990s by his mentor, Robert Mason, a reproductive biologist at Oregon State University, had hinted at a role for a group of chemical compounds called methyl ketones in brown tree snakes' mating behavior. And in 2012, Parker demonstrated that it was possible to make males of a related serpent, the red-sided garter snake (*Thamnophis sirtalis parietalis*), olfactorily resemble females by inserting an implant that released the steroid estradiol under the skin, causing the snakes to produce female sex pheromones (*J Exp Biol*, 215:723–30, 2012).

Armed with this experience, Parker recently tried to find out whether methyl ketones alone would be sufficient to lure Guam's male brown tree snakes into traps. In 2015, he surgically implanted male brown tree snakes with estradiol and found that the serpents produced methyl ketones that looked exactly like those that females produce. What's more, these males provoked overt sexual behaviors, such as tongue-flicking and chin-rubbing, from untreated males. On average, untreated males flicked their tongues 72.75 times per minute in response to a female, and 73.58 times per minute toward an estradiol-implanted male (*J Chem Ecol*, 44:189–97, 2018). "So, obviously they smelled enough like a female to elicit courtships from males," Parker says.

Next, Parker shipped the pheromone extracts he collected in Colorado to a US Geological Survey lab at the Guam National Wildlife Refuge for tests on captured wild males. He placed either methyl ketone isolates or whole skin lipid extracts on filter paper in a dimly lit pop-up tent that acted as a testing arena. Then, he observed the responses of the wild males to the samples—no easy feat given the animals' nocturnal habits. "I had to test the animals with pheromone isolates in the middle of the night with a headlamp on," Parker says. "It was brutal." These experiments, however, revealed a further twist to the story: the wild males showed only weak responses to methyl ketones, compared to the whole lipid extracts.

The results aren't fatal for the viability of a pheromone control strategy, says Parker. "We could just take extracts from females without having to isolate the methyl ketones" to use as a potential bait. That's doable, if lipids are harvested from some of the thousands of snakes caught every year, Parker says. But that approach may not be practical if the effort were to be scaled up. The whole extract would also be harder and prohibitively expensive to biosynthesize. Skin lipids contain hun-



ANDRZEJ KRAUZE

dreds of compounds, and researchers suspect that sex pheromones make up only a small percentage.

Mason, who was not involved in the research, believes Parker is on the right track with the methyl ketones. “He’s getting evidence that something is going on,” he says. “The methyl ketones are definitely a promising avenue, no question about it.” But there may also be other compounds driving snake behavior, he adds.

Rick Shine, an evolutionary biologist at the University of Sydney who is investigating the use of pheromones to control cane toad populations in Australia and was not involved in the study, also recognizes the complexity of the snakes’ chemical communication. Snakes are “vastly more sophisticated creatures than we might expect from an animal with the brain the size of a pea,” he says. Of Parker’s work, he adds, “clearly, we’re not there yet, but this is very sensible research.”

APHIS’s Siers says funding for future projects is there. But Parker says he hasn’t decided exactly what those projects will entail. “I’m very hesitant because of the bioassay [on Guam] not being as strong as I had hoped,” Parker says. Still, he’s hoping to conduct more work in the field. “The real way to test it,” he says, “is to actually put the stuff out in the environment where the snakes are and to see what happens.”

—Steve Graff

Good Fat

Researchers Sam Urlacher and Josh Snodgrass had a problem. The pair had been working together since 2011 to better understand how immune activity hinders children’s growth under a range of preindustrial and urban living conditions. Urlacher, then a graduate student at Harvard University, and Snodgrass, a biological anthropologist at the University of Oregon, needed a reliable way to measure children’s immune responses to infection by pathogens and parasites.

But commercially available kits to test for biomarkers of immune system activity required vials of serum or plasma—a no-go when working with their planned study cohort, children living in indigenous communities deep in the Amazon. It would have been impossible to store the biofluids properly until they could be analyzed, and neither the scientists nor the children and their parents would have wanted to carry out multiple blood draws over weeks or months. So Urlacher, Snodgrass, and colleagues had to devise their own assays to measure the immune molecules in spots of dried blood from finger sticks. It took a year just to develop the test that detects the antibody immunoglobulin G, Snodgrass says.

For the researchers, however, creating the new assays was worth the effort. While it’s known that infections tend to slow children’s growth, the molecular mechanism behind the effect is not well understood. Urlacher and Snodgrass reasoned that launching an immune response is energetically expensive, and that rooting out pathogens and parasites might require easing back on growth, another costly physiological process. The assays would help the team dig deeper into how that trade-off worked, particularly in the types of environments humans have inhabited for most of our species’ history.

With the assays optimized, Urlacher headed to Ecuador to gather data on a group of indigenous forager-horticulturalists called the Shuar. The groundwork for the trip had been laid over nearly a decade of careful relationship building by researchers including Snodgrass, his colleague Lawrence Sugiyama, and later Urlacher himself. "It's a huge amount of work to get something like this going," Snodgrass says. The researchers maintain good relationships partly by making sure the research activities benefit the Shuar: they bring local healthcare workers into participating communities to provide information on diet and combating parasites, for example, and when they take finger-prick blood samples, researchers tell study participants immediately if they find potential disease indicators such as low hemoglobin readings.

For his own study, Urlacher spent about a year and a half in Ecuador, often traveling by foot or canoe, and staying in four different communities he'd gotten to know on previous trips. The sites ranged from remote villages to a town of about 10,000 people. At each study site, Urlacher started by spending a few weeks just talking with people, he says, and seeing whether they'd be willing to let their kids participate. If so, he would collect blood spots from children aged 4–11 years, measure their skin folds (to assess body fat levels), and determine the length of their lower legs with an exceptionally precise instrument known as a knemometer, then repeat the process a week later. The blood spots would later be analyzed for concentrations of C-reactive protein (a marker for inflammation), Epstein–Barr virus antibody, and immunoglobulins G and E. For some of the children, he followed up with the same measurements at 3 months and 20 months.

Catherine Panter-Brick, a medical anthropologist at Yale University who has conducted a similar study, says it's notable that the team was able to confidently measure growth during such a short time period. "The precision involved in that is really very extreme," she says. "When I did it in the 1990s in Nepal, we were able to look at growth in terms of each month, and we were looking at

GROWING UP AMAZONIAN: The Shuar are forager-horticulturists living in Ecuador and Peru. Researchers have been visiting Shuar settlements (top) to study the development of Shuar children (bottom) and thus learn more about the relationship between growth and immune function in pre-industrial societies.

PNAS; SAM URLACHER

centimeters. They were able to look at each week, and they were able to look at millimeters. I think that's a huge advance."

As expected, the team found that higher immune activity in the Shuar children was generally associated with slower growth. But the precise measurements of both growth rates and immune biomarkers also helped Urlacher and colleagues unearth another layer to the trade-off: it turned out that in some children, there was a detectable growth cost not just to acute, symptomatic infections, but also to immune activity that could be detected via biomarkers but caused no outward signs of distress. However, this effect was only seen in children with relatively low levels of body fat. These children grew at about half their normal rate when they had mildly elevated immune activity. In children with higher levels of body fat, there was no such relationship (*PNAS*, 115:E3914–21, 2018).

"At one level it's maybe not surprising, because you've got these fat resources that you're able to draw from in times of energetic stress," says Snodgrass. "But I think what is surprising is [that] even really modest levels of body fat are actually making a difference in terms of how the body's making these physiological choices," allowing it to simultaneously expend energy on growth and immune activity rather than sacrifice one for the other.

The interplay of immunity, growth, and body fat is important because growth stunting "has terrible, terrible consequences for not just your body size, but implications for brain growth and development, brain function," says Barry Bogin, a biological anthropologist at Loughborough University in the U.K. who was not involved in the study. Even lean people have a relatively high percentage of body fat compared with other primates, he says, because humans tend to spend a substantial amount of time acquiring and preparing food, and have the physiological capacity to store the extra energy. Ideally, our capacity to build up fat provides a buffer that allows us to simultaneously sustain our big brains and fight off infection and parasites.

For Urlacher, now a postdoc at Hunter College in New York, one key takeaway of the study is that "humans are acutely sensitive to these immune challenges." Our taxing energy demands could help explain why humans have a prolonged period of development between weaning and puberty that's not found in other species, he notes.

> What is surprising is [that] even really modest levels of body fat are actually making a difference.
>
> —Josh Snodgrass, University of Oregon

Beyond their relevance to human evolution, the data are being put to work to help the Shuar—a community experiencing a rapidly changing environment, with increased economic development upping the rates of chronic diseases even as parasites remain a problem. The research team communicates with the indigenous government about which communities are most in need of improved sanitation systems or other measures to prevent immune-related growth stunting, Snodgrass says. "We're trying to help understand what's going on . . . within the context of this changing society, and making people aware of what's going on."

—Shawna Williams

Raising Brows

In 1921, a Swiss miner named Tom Zwiglaar made an extraordinary find. While working in a lead and zinc mine in what is now Zambia, he stumbled across a remarkably preserved skull. The specimen, now known as Kabwe 1 or the Broken Hill Skull, was sent to paleontologist Arthur Smith Woodward at London's Natural History Museum. He determined the skull belonged to an extinct hominin species he dubbed *Homo rhodesiensis*. Contemporary scientists generally consider the skull, still kept at the Natural History Museum, to be from *H. heidelbergensis* and have dated it to between 300,000 and 125,000 years old.

For Ricardo Godinho, an evolutionary anthropologist at the University of Algarve in Portugal, Kabwe 1 holds particular appeal. "Not only is it one of the best-preserved hominin crania, it also has one of the largest brow ridges in the fossil record," he says. "One of the things that is remarkably different in our species is the lack of a pronounced brow ridge" compared to those of extinct hominins such as *H. heidelbergensis* and Neanderthals. Godinho recently set out to explain that phenomenon as part of work for his PhD at the University of York in the U.K. "We wanted to find out . . . why other species have big brow ridges and we don't," he says.

Researchers have been debating hypotheses explaining the evolution of different brow-ridge sizes almost as far back as the discovery of that first *H. heidelbergensis* skull. "We've had these ideas about why early hominids had such a large brow ridge for a long time," says Melissa Tallman, a paleoanthropologist at Grand Valley State University in Michigan who was not part of Godinho's project. These have ranged from suggestions that the ridge was an elaborate signaling appendage to the argument that it acted as a sun visor. In the 1970s, anthropologist Grover Krantz wore a fake brow ridge every day for six months to try to discover its utility, says Chris Stringer, a physical anthropologist at London's Natural History Museum. From the startled looks Krantz received from passersby, he concluded the brow ridge may have functioned to intimidate foes, says Stringer.

Currently, there are two leading brow-ridge hypotheses in the paleontological community. One, the spatial hypothesis, suggests that the brow ridge shrank as the brain case grew: unlike, say, chimpanzees' eyes, which are set in front of their brain case and protected by a pronounced brow ridge, humans' eyes shelter under the broad forehead that accommodates the frontal lobes. The second, the mechanical hypothesis, argues that big brow ridges protected ancient hominins' faces by distributing stress from their strong biting and chewing muscles—less necessary in modern humans because we prepare our food.

Godinho and his colleagues tested each of these hypotheses with a computed tomography (CT) scan of Kabwe 1 provided by the Natural History Museum. The researchers created 3-D computer models with the CT scan: one of the original skull and two with reduced brow-ridge sizes. The approach is becoming widely popular in paleontology. "This kind of in-depth modeling . . . is the future of our field," says Tallman.

To make the two reduced-brow models, Godinho's team virtually shaved off the brow ridge, and tested whether doing so invaded the eye sockets. Not only was this not the case, but "we concluded that there is more bone than is actually needed for the brow ridge according only to the spatial hypothesis," he says. They next tested the mechanical hypothesis by modeling how the three different brow-ridge sizes affected the skull's biting ability at different levels of strain. "We [didn't] find marked differences between the three different crania," says Godinho. "That tells us that there are slight differences," but these are not significant enough to support the mechanical hypothesis (*Nat Ecol Evol*, 2:956–61, 2018).

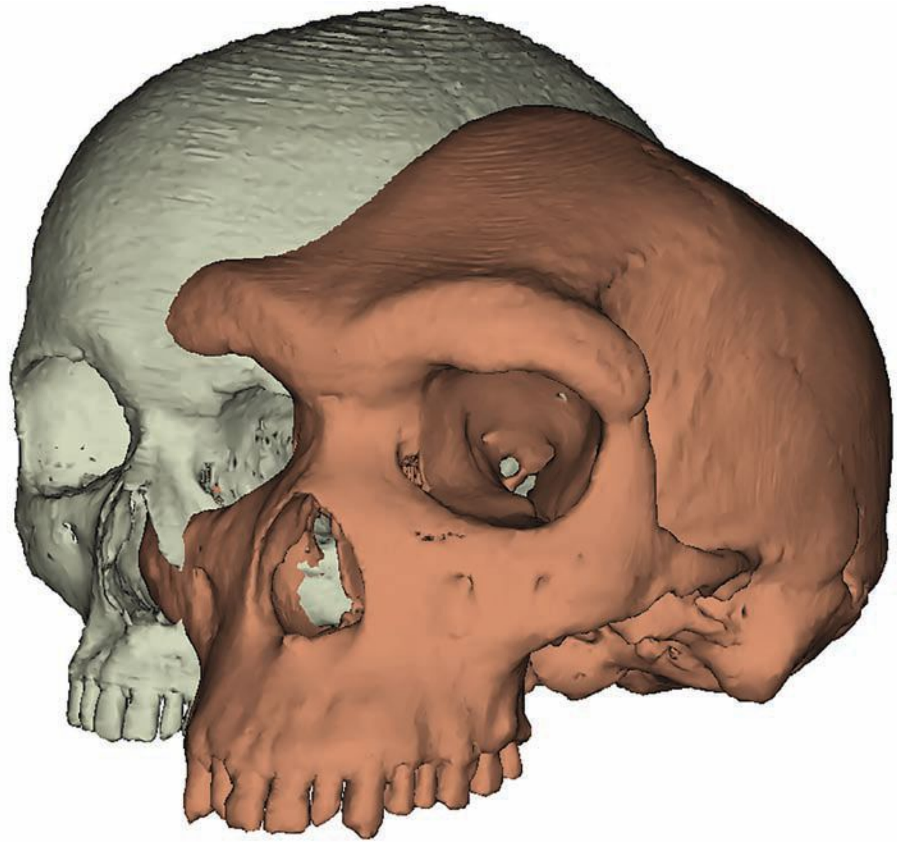
With the main competing hypotheses more or less ruled out, the team turned to nonhuman primates for additional clues. Old World monkeys such as *Mandrillus leucophaeus* and *M. sphinx* have prominent facial swellings that aren't related to spatial or mechanical processes. They use these features for social displays and signaling. Perhaps early hominins' brow ridges had a similar function—as might modern humans' foreheads, along with our expressive eyebrows, Godinho says. "You see that throughout the hominid fossil record, the face is becoming smaller," he says. "As it's becoming smaller, it's also retracting under the braincase. When that happens . . . the forehead becomes more vertical and less sloped backwards. That means that inevitably the muscle that moves the eyebrows has a different orientation." As a result, modern humans' eyebrows are more visible and able to convey subtle, nonverbal messages, he explains.

In their paper, Godinho and his colleagues propose that our communicative foreheads may have arisen as human brains grew bigger across evolutionary history, or as part of some other unrelated and still-unknown adaptive process. One hypothesis is that human populations, by self-selecting for more-social and cooperative individuals, indirectly influenced the evolution of physical features involved in communication, such as eyebrows. Whatever the driver, it "allowed the eyebrows to become more prominent and more relevant in nonverbal communication," he says.

That idea "is very interesting, but I think we have to be cautious," says Ashley Hammond, a paleoanthropologist at the American Museum of Natural History who was not involved in the work. "It's sort of inherently untestable." Modern humans may not necessarily have evolved from a hominin that had a pronounced brow ridge, she adds. Tallman agrees, saying that while the study "pretty convincingly" shows there isn't support for the spatial or mechanical hypotheses, in terms of why the brow has gotten smaller, "I don't think their data actually addresses that [social] question."

Godinho, who completed his PhD last year, stresses that his team isn't suggesting that nonverbal communication via the eyebrows triggered the change in brow-ridge shape. "We suggest that [the change] is a byproduct that has become an advantage," he says, "and which, to a certain degree . . . may have become more relevant as modern humans arose."

—Jim Daley



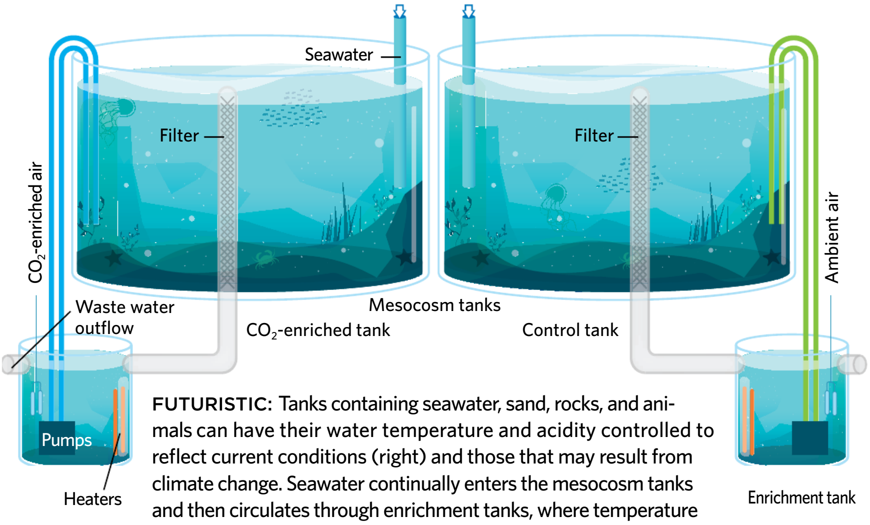
HOW NOW GONE BROW?: Researchers used computer models of an ancient hominin skull (right) to study the evolution of the brow ridge, a feature that is far less prominent in modern human skull structure (left).

PAUL O'HIGGINS, UNIVERSITY OF YORK

Sea Sections

Researchers devise more-naturalistic means of forecasting the effects of climate change on complex marine ecosystems.

BY RUTH WILLIAMS



FUTURISTIC: Tanks containing seawater, sand, rocks, and animals can have their water temperature and acidity controlled to reflect current conditions (right) and those that may result from climate change. Seawater continually enters the mesocosm tanks and then circulates through enrichment tanks, where temperature and acidity are controlled, and returns to the mesocosms.

Increasing levels of atmospheric carbon dioxide are thought to be acidifying and warming Earth's oceans, causing significant changes to marine and terrestrial ecosystems around the world. But many forecasts of future changes to ecosystems have been based on simplified laboratory experiments that include few or even just a single species.

"Looking at individual organisms gives you a very isolated if not distorted picture, so to really understand how communities are responding to global change, you need to go to community-level experimentation," says biological oceanographer Ulf Riebesell of GEOMAR Helmholtz Centre for Ocean Research in Kiel, Germany.

Riebesell and marine ecologist Ivan Nagelkerken of the University of Adelaide in Australia are among the researchers now employing mesocosm experiments—a method that straddles the divide between field- and laboratory-based approaches to allow the study of naturalistic environments under controlled conditions.

While mesocosms themselves are not a novel concept, says Nagelkerken, "they have hardly ever been used in climate change research."

Riebesell's mesocosms consist of 2-meter-diameter, columnar polyurethane bags descending into and containing seawater but cut off from the surrounding ocean. Recently, he and colleagues have found that ocean acidification (via introduction of dissolved carbon dioxide) promoted herring larvae survival—possibly because phytoplankton biomass, a food source, increased. The finding runs counter to those of laboratory studies (*Nat Ecol Evol*, 2:836–40, 2018).

Nagelkerken's mesocosms are 2-meter-diameter tanks, each containing 1,800 liters of seawater pumped in from the ocean, as well as rocks, sediment, and dozens of species of small fishes, large and small invertebrates, algae, and plankton. While Riebesell's mesocosms represent the open-ocean environment, Nagelkerken's recreate near-shore habitats. In studies published earlier this year, he and colleagues found that while ocean acidification alone has a positive effect on herbivores and carnivores, seawater warming, with or without acidification, caused the proliferation of cyanobacteria—which outcompete edible algae but aren't a food source for most marine animals—and the subsequent collapse of the food web (*Nat Clim Chang*, 8:229–33; *PLOS Biol*, 16:e2003446).

"Such mesocosm experiments are important for testing higher-level ecological effects that might not otherwise be detected with simpler experimental designs," says coral reef ecologist Philip Munday of James Cook University in Australia who was not involved in the studies. ■

AT A GLANCE

APPROACH	SET UP	COST PER EXPERIMENT	REPLICATES	RELEVANCE TO REAL WORLD
Single species	Small, bare aquaria holding anywhere from 10 to 100 liters of seawater, depending on the species	Hundreds to thousands of dollars	Small size and low costs allow for many conditions to be tested simultaneously, with multiple replications	Unknown
Mesocosm	Large enclosures with hundreds to thousands of liters containing elements of real-world ecosystems	Tens of thousands to hundreds of thousands of dollars	Replications are limited to a few per experimental condition because of cost and size	Expected to be strong, as naturalistic ecosystems are recreated with a large variety of interacting species

THE SCIENTIST STAFF

WHO DIES?

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Identifying the most likely victims of climate change is crucial to designing effective conservation strategies. But it's a task riddled with challenges.

BY CATHERINE OFFORD

In late 2014, conservationist Ian Gynther lost hope. After days spent crawling into rock crevices, scouring through camera-trap footage, and carefully laying bait around Bramble Cay—a tiny island at the northern end of Australia's Great Barrier Reef—there was little room for doubt. The Bramble Cay melomys (*Melomys rubicola*), a furry little rodent endemic to the island, had gone extinct. "My colleagues and I were devastated," Gynther, a senior conservation officer at Queensland's Department of Environment and Heritage Protection, later told *The Guardian*. "As each day of our comprehensive survey passed without revealing any trace of the animal, we became more and more depressed."

The disappearance of the Bramble Cay melomys became a grim milestone in the history of conservation biology. Its extinction report, published in 2016, determined the cause of death to be anthropogenic climate change, the first such attribution for a mammalian species.[1] The rodents' home had been battered by increasingly extreme weather, storm surges, and rising sea levels, Gynther and his colleagues wrote in the report, pointing "to human-induced climate change being the root cause."

The melomys will not be the last species to meet this fate. As global temperatures rise, more and more of the Earth's millions of species are experiencing environmental change at a rate that may well be unprecedented in our planet's history.

A recent meta-analysis of research on more than 2,000 species suggested that nearly 50 percent of threatened, nonflying terrestrial mammals and 23 percent of threatened birds had already been negatively affected by climate change in at least part of their ranges.[2] And with climate change accelerating many deleterious global dynamics, such as ice melt and ocean acidification, the damage is likely to continue.

Faced with this sobering reality, conservation biologists are increasingly shifting their focus from documenting the effects of climate change on the world's wildlife to trying to forecast the risk that individual taxa or ecosystems will be lost—and do so early enough to intervene. Due to varying exposure and differences in biology, not all organisms are equally likely to suffer. So, to best allocate limited resources, "what we really want to be able to do is pinpoint those species that are most at risk," says the University of Connecticut's Mark Urban, an ecologist who works in Arctic Alaska. "We need to identify the winners and the losers. And then try to help the losers."

Over the last decade, more and more researchers have been working to measure this risk for taxa across the tree of life. The tools that provide the foundations for these so-called climate change vulnerability assessments (CCVAs) range from models of future habitat availability to analyses based on the physiological effects of projected temperature increases, and can be conducted for one or multiple species at a time. The results, which can be expressed as the estimated extinction risk of a species or its categorization into broad classes such as "highly vulnerable," are cited by conservation planning organizations such as the International Union for Conservation of Nature (IUCN) and the Intergovernmental Panel on Climate Change (IPCC).

But conservation biologists are still working to improve the methodology behind these assessments. Bruce Stein, chief scientist at the National Wildlife Federation, notes that researchers are increasingly addressing questions such as, "What does climate vulnerability mean?" and, "What are some of the different techniques for assessing it?" Yet, as in any discipline that deals with prediction, researchers working on CCVAs are grappling with a suite of challenges. Data on many species are limited, and the need to juggle multiple sources of uncertainty—including those inherent to the climate forecasts these models employ and the biological assumptions they rely on—have raised questions about how best to approach vulnerability assessments, and how researchers should make use of their results.[3]

"We're making some headway in thinking more about becoming forecasters rather than just descriptors," says Urban. "But I think we still, as a discipline, have a long way to go."

What could go wrong?

In the Namib Desert of southwestern Africa, quiver trees (*Aloidendron dichotomum*) stand out against the vast, rocky backdrop. These towering succulents grow more than 8 meters tall and live for around 200 years on average. In addition to being culturally significant—they've been used for centuries by local San people to make bow quivers, and their image appears on Namibia's 50-cent coin—the trees provide critical habitat and food for many insects and birds. But by the turn of the millennium, the quiver tree populations of Namibia and South Africa were in serious trouble: large swaths were dead or dying.

Wendy Foden, then a master's student at the University of Cape Town, was one of the researchers who stepped in to investigate. "We went to [almost] every population across its entire range, which is about 2,000 kilometers long," says Foden, now a researcher at South Africa's Stellenbosch University and a climate change specialist for the IUCN. "We looked at how many were alive, how many were dead, how many babies."

Up to 90

Percentage of Pacific corals expected to suffer degradation or bleaching by 2050, even under conservative climate forecasts

Source: Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, 2018

LUKE LEUNG, UNIVERSITY OF QUEENSLAND

More than 50 sites and some 6,000 quiver trees later, the team concluded that the species was being battered in populations at the northern edge of its range as temperatures crept upwards and the desert became drier.[4] Although populations in cooler southern regions were faring better, projected temperature increases suggested that they would soon experience similar conditions. Short of migrating 25 miles south within 15 years—a tall order for a plant species with a juvenile phase of around half a century—the quiver trees were soon going to be well outside their comfort zone.

These sorts of geographical shifts in species' tolerable environmental ranges, or climate envelopes, have become one of the most often-cited consequences of global warming, and a major starting point for biologists to calculate climate-related extinction risk. "The typical approach is to take global climate change models, downscale, and look at how the magnitude and rate of climate change is going to potentially shrink or constrain a species' climate envelope," says Lindsey Thurman, an ecologist at the United States Geological Survey (USGS). An early, influential example, published by the University of Leeds's Chris Thomas (now at the University of York) and colleagues in 2004, applied a version of this approach to endemic species of plants and animals occupying around 20 percent of the world's landmass. By 2050, the team calculated, between 15 percent and 37 percent of species could be "committed to extinction," with especially high losses for species in scrubland and temperate forest.[5]

But these sorts of correlative, distribution-based models have come under fire from ecologists in recent years. For a start, they often equate a species' current range to the range in which it experiences its preferred environmental conditions—an assumption that overlooks other distribution-influencing factors such as food availability. What's more, such models generally fail to capture biological consequences of climate change that are not reflected in distribution, says Urban. Indeed, an analysis he conducted in 2015 found that, compared to other approaches, distribution-based models paint a more optimistic picture of extinction risk.[6] "One of the big issues with these types of models is that they're probably missing many of the key mechanisms that really determine how species respond to climate change," he says.

To address these issues, some researchers use an organism's biological traits to predict its responses under different climate scenarios. This approach often takes the form of thinking, "What can go wrong?" says Foden. "That's the right question to start with." Such trait-based models incorporate data on characteristics that can make a species particularly sensitive to the effects of climate change, such as dependence on certain temperatures for survival, or slow population growth rates. (See "Estimating Vulnerability" on page 25.) More-mechanistic models attempt to incorporate relationships between environmental conditions and a species' developmental or reproductive biology.

Vulnerability assessments built on such foundations are constantly evolving, as biologists turn up ever more answers to the question, "What can go wrong?" For instance, species don't live in a vacuum, notes Urban, so "species interactions are a key point." Thanks to these interactions, species may experience indirect effects of climate change that range from the relatively obvious—if one organism faces climate-driven extinction, its predators may also be at risk—to the more nuanced. Last fall, for example, researchers reported that clownfish living in anemones that were bleached as a consequence of ocean warming showed higher signs of stress and reduced fecundity compared with fish living in unbleached anemones.[7] So-called cascading effects open up a dimension of species' vulnerability that modelers have yet to fully explore.

However, not all of the effort to understand responses to climate change concerns various routes to harm. A growing branch of species vulnerability research takes a more positive view, by investigating how species compensate for their changing environments. Although the phenomenon has long

NATALIE WALLER

R.I.P., RAT: The Bramble Cay melomys (*Melomys rubicola;* far left) was a rodent endemic to the Great Barrier Reef. In 2016, following a survey of the roughly four-hectare island with which it shares its name (left), researchers declared the species extinct as a result of climate change.

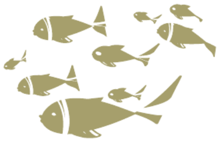
been fundamental to biological theory, researchers are only just beginning to come to grips with it in a climate-change context.

The escape hatch

In 2014, a medium-size butterfly inhabiting the west coast of North America received a surge of media attention mainly because it was still alive. By the mid-1990s, the Quino checkerspot (*Euphydryas editha quino*) had been pegged as a climate-change victim in waiting. With its range eroded from the south by rising temperatures and from the north by urbanization, the butterfly—along with local populations of its host plant, the dwarf plantain (*Plantago erecta*)—was running out of space. "It seemed to me that it was really heading for extinction," says Camille Parmesan, a biologist at the University of Plymouth in the U.K. "This species had such a high number of populations completely gone that I thought were irretrievable, I didn't give it much hope."

But as Parmesan worked on plans to raise captive insects in the lab for future reintroductions, the checkerspot did something unexpected. "It went up the mountain," Parmesan says. In 2015, she and her colleagues reported that the butterfly had relocated east to elevations unheard of for its subspecies, and had switched to a different host plant in the process.[8] "Those populations at the high elevations are really healthy," Parmesan says. "It felt so good to see them really dance, bumping into each other, having a great time."

45 miles



Average shift in the leading edge of marine species' range per decade in response to climate change

Source: *Nat Clim Change*, 3:919–25, 2013

The case of the Quino checkerspot and other species like it offer a reminder of a fundamental biological response to environmental stress: adaptation (a term that, in CCVAs, refers both to evolutionary changes in a population's genetic makeup and to individual plasticity, or acclimatization). "We're often seemingly surprised by how adaptable species end up being," says Stein. "It's this notion that nature can find a way—which is sometimes true and sometimes isn't."

The potential for organisms to escape doom via adaptation is termed "adaptive capacity" by the National Wildlife Federation and several other organizations. Well-recognized adaptation-favoring traits include superior dispersal ability, phenotypic plasticity, and high genetic diversity. "Even with a lot of uncertainty, you know that high levels of genetic variation are certainly going to make those populations more robust in the future, even if you don't know what the drivers are going to be," says Ary Hoffmann, an evolutionary biologist at the University of Melbourne in Australia.

New factors contributing to adaptive capacity are being reported all the time: a study published earlier this year, for example, suggested that warm-blooded vertebrates hold an advantage over their cold-blooded counterparts by being able to tolerate a wider range of climatic conditions and consequently to adapt more quickly.[9] Some researchers are beginning to pin down species' adaptive capacity to variation in specific regions of the genome, too. Scientists in California recently reported that in North American populations of the yellow warbler (*Setophaga petechia*), successful adaptation to climatic changes was associated with genes involved in exploratory and migratory behavior.[10] A study published earlier this summer identified more than 200 regions in the epigenome of the spiny chromis damselfish (*Acanthochromis polyacanthus*) that were tied to increased tolerance of rising ocean temperatures.[11]

Adaptive capacity remains a relatively rare feature of vulnerability assessments, however; a recent USGS review found that, of 124 assessments carried out by the US Department of the Interior as tools for conservation planning, the concept appeared in just a third.[12] There's growing momentum to change that. Ignoring adaptation can lead to overly pessimistic predictions that could result in allocating resources where they're less needed, notes USGS's Thurman. "We feel very strongly that a better understanding of adaptive capacity can improve the cost-effectiveness of conservation plans." The IUCN's current guidelines on vulnerability assessments promote the inclusion of adaptive capacity alongside measures of an organism's sensitivity and exposure to climate change, and Stein and colleagues have published multiple explainers about how to measure adaptive capacity appropriately.

To help get the message across, some researchers are demonstrating the effect of taking adaptive capacity into account for vulnerability assessments of specific taxa. In October, Benjamin Ofori of the University of Ghana, along with Linda Beaumont and collaborators at Australia's Macquarie University, ranked 17 Australian lizard species on vulnerability and found that, based on sensitivity and exposure, seven would be classified as "highly vulnerable" to a warmer and drier climate. However, when they incorporated terms to describe each species' adaptive capacity, that number dropped to two.[13] "You have some species that were previously classified as highly vulnerable being reclassified as moderate," Ofori says. "You even have some species jumping [rank]"—potentially reshaping conservation priorities.

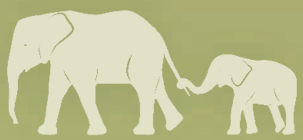
A better understanding of adaptive capacity will not only improve CCVAs, but could also inform new approaches to conservation, says Hoffmann. His group has promoted strategies to increase genetic diversity—and thus, theoretically, adaptive capacity—in the mountain pygmy possum, an endangered mar-

ESTIMATING VULNERABILITY

Researchers use various methods to estimate a species' vulnerability to climate change. One popular class of assessments takes a trait-based approach, calculating organisms' vulnerability on the basis of their exposure to climate change, their sensitivity to that change, and their potential to adapt to new conditions, termed their adaptive capacity.

SENSITIVITY

A measure of how likely a species is to experience negative effects of climate change. Failing to account for traits that confer higher sensitivity can result in overoptimistic estimates of species' vulnerability.



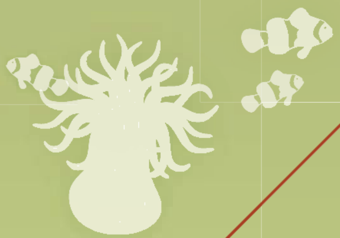
A low reproductive rate can reduce a species' capacity to recover following adverse events.

Narrow tolerance ranges for abiotic conditions such as temperature heighten a species' sensitivity.

Small population sizes magnify the effect of die-offs.

Specialization on a particular habitat or food source increases a species' sensitivity.

A higher number of **species interactions** can multiply the harmful consequences of climate change via indirect effects.

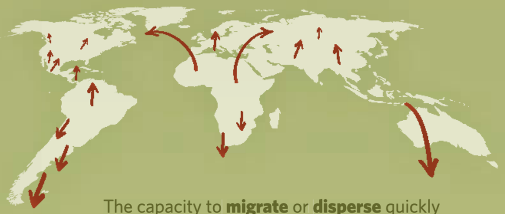


ADAPTIVE CAPACITY

The potential for species and populations to temporarily escape the negative effects of climate change via natural selection or individual plasticity.

Epigenetic variation can help a species acclimate to a rapidly changing environment.

High levels of **genetic diversity** set the stage for faster evolution in a population under environmental stress.



The capacity to **migrate** or **disperse** quickly can help organisms avoid the harmful effects of climate change.

Phenotypic plasticity allows individuals to tolerate a wider range of conditions or to shift the timing of life-history stages such as reproduction.

EXPOSURE

The magnitude and type of environmental changes that a population is likely to experience under future climate scenarios. Estimates of exposure are strongly affected by the choice of climate forecast model, and add a considerable source of uncertainty into climate change vulnerability assessments.

Coastal organisms will experience **rising sea levels.**

Temperature fluctuations and **extreme weather events** will become more frequent around the globe.

An increasing frequency of **fires** will decrease habitat stability.

Increasing **aridity** will lead to more frequent droughts.

Organisms living in the polar regions will be exposed to accelerating and more expansive **ice melt.**

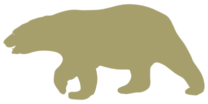
CREDIT LINE

supial inhabiting the rapidly warming alpine zone in southeastern Australia. According to a report from the team, introducing males from one relatively large population to a smaller one appears to have helped double the size of the latter in just three years.[14]

But while adaptation can help rescue species from immediate harm, it can only go so far. "With climate change, you can't stabilize it—certainly not locally, and even globally," explains Parmesan. Climate change creates "a moving target," and an organism that adapts under stress might only have reduced its vulnerability for a while.

Unfortunately, that appears to be true for the Quino checkerspot. Despite its recent escape from extinction, Parmesan says, the butterfly has reached a new dead end: the tops of the mountains. While the high-elevation habitat provides a cool home for now, Parmesan and her colleagues predict that even this region will become uninhabitable in coming decades. "That's when the depression sets in," she says. Moving the insects to more-favorable habitat—a strategy known as assisted migration—is problematic under current environmental regulations. "It's wonderful that these wild critters can surprise us and have more adaptability than we think they have," says Parmesan. "But at the same time, it's just a little bit of buffering. It gives us a few more years to figure something else out."

2008



The year that climate change was first used to justify protecting an animal species, the polar bear, under the Endangered Species Act

Source: US Department of the Interior

Getting it right

As the methodology behind climate change vulnerability assessments evolves, some conservation biologists are concerned that different efforts are out of sync with one another. Reviews of the literature have shown substantial variation in the way models are applied. The Sapienza University of Rome's Michela Pacifici, with Foden, Hoffmann, and others, reported that birds and mammals were by far the most often assessed taxa in CCVAs carried out between 1997 and 2014—even though they constitute a fraction of a percent of the world's biodiversity—and only a handful of studies assessed vulnerability on a global scale.[15] While North American and Australian studies frequently made use of trait-based approaches, Europe overwhelmingly favored those based on distribution.

Such differences can often be traced to the information available on particular taxa or regions, says Thurman. "For many species, we pretty much have no data," she says. "Even understanding basic natural history can be challenging." There's often a difficult choice to be made, therefore, about how much complexity to include. On one end of the spectrum are approaches that require little in the way of biological data such as environmental tolerances and life history traits, but potentially miss important pathways. On the other are more-detailed models that require researchers to make assumptions to fill in the gaps, adding considerable uncertainty to already taxing calculations.

Opinions vary as to how much the choice of approach matters. Last year, the University of York's Thomas and colleagues published an "assessment of assessments" for 12 recent methodologies.[16] The aim, he tells *The Scientist*, was to find out whether different approaches—ranging from distribution-based models to trait-focused assessments—would reach roughly the same conclusions. Using historical data on population distributions and abundances of Great Britain's birds and butterflies, as well as simulated data, the team pitted the models against each other to predict the present from the past. The results, Thomas says, were disappointing. Just two of the models—both of which relied more heavily on distribution than on biological traits—achieved better-than-random accuracy. And "the methods simply disagreed with one another on how they classified species. By definition, that means at least some of them have got to be wrong."

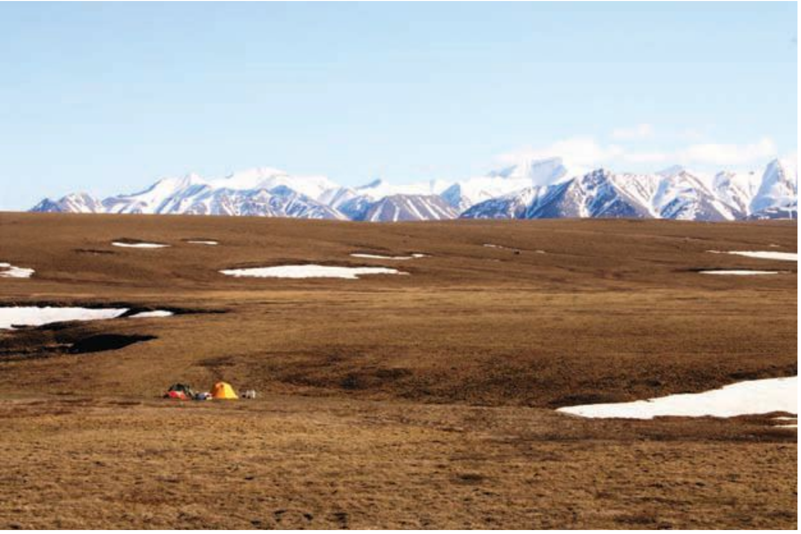
MARK URBAN

CHANGING THE WORLD: In 2015, unusually high temperatures in Arctic Alaska triggered the arrival of spring one month earlier than normal at ecologist Mark Urban's research site (right). Though temperatures followed a more normal schedule the following year (far right), researchers observed the physical effects of the previous summer's heat, such as the collapse of land on the far left side of the second year's image. Both photos were taken in the first week of June.

Thomas says he hopes that one effect of comparative studies such as his will be to motivate more data collection. "We can't just say the data doesn't exist. We have to think, how are we going to put in place the monitoring of things so that a few decades in the future, people aren't wringing their hands still saying, 'We haven't got the data.'" In the meantime, he adds, while models may lack accuracy in predicting exactly when species will go extinct, they can identify taxa likely to be vulnerable at some point.

At the same time, the predictions generated by vulnerability assessments are just one step on a road to the much larger goal of finding practical solutions to conserve at-risk taxa, says Stein. As such, CCVAs shouldn't be seen as "the end product," he says. "That's the beginning. Assessing climate vulnerability allows you then to begin applying that to better conserve these things in light of climatic changes." He and others have advocated for biology-based management strategies that build on CCVAs by helping species realize their adaptive capacity, for example, through assisted migration or breeding programs.

Another crucial consideration is that extinction risk is a product not just of climate change, but of multiple interacting stressors including habitat fragmentation and species invasions. And conservation priorities are based on more than just a species' risk of dying out. Societally influenced considerations such as a species' economic value, cultural significance, or perceived charisma affect how conservation dollars are spent; scientists may also consider a species' importance to the entire ecosystem before making recommendations to decision makers. And some conservationists want to drop the species-focused view altogether in favor of a more holistic, biodiversity-centered approach, Parmesan says. "If we focus on individual species, we're going to be very upset, because there will be a lot of extinctions."



MARK URBAN

1,000

Number of times faster extinctions are happening now compared with the rate before the origin of *Homo sapiens*

Source: *Science*, 344:1246752, 2014

With the clock ticking for many species around the world, it's imperative that biologists, policy makers, and the public decide what really matters, says Stein. To make effective use of concepts such as climate change vulnerability, "we have to be clear about what our values are," he says. "To think we're going to be able to keep things as they are today, or go back to some version it was in the past, just is no longer realistic." ■

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Protein Time Machine

Scientists resurrect proteins from the past to answer today's evolutionary questions and inspire tomorrow's bioengineered molecules.

BY AMBER DANCE

Once upon a time, between 2 million and 4 million years ago, the fruit fly lineage split. One sister species, known today as *Drosophila simulans*, kept up the parent's habit of hanging around and consuming ripe fruit. The other, the *D. melanogaster* beloved by modern geneticists, took a different path. It evolved a more active alcohol dehydrogenase (ADH) enzyme, making it better suited to slurp the high-ethanol content of perfectly rotten fruit.

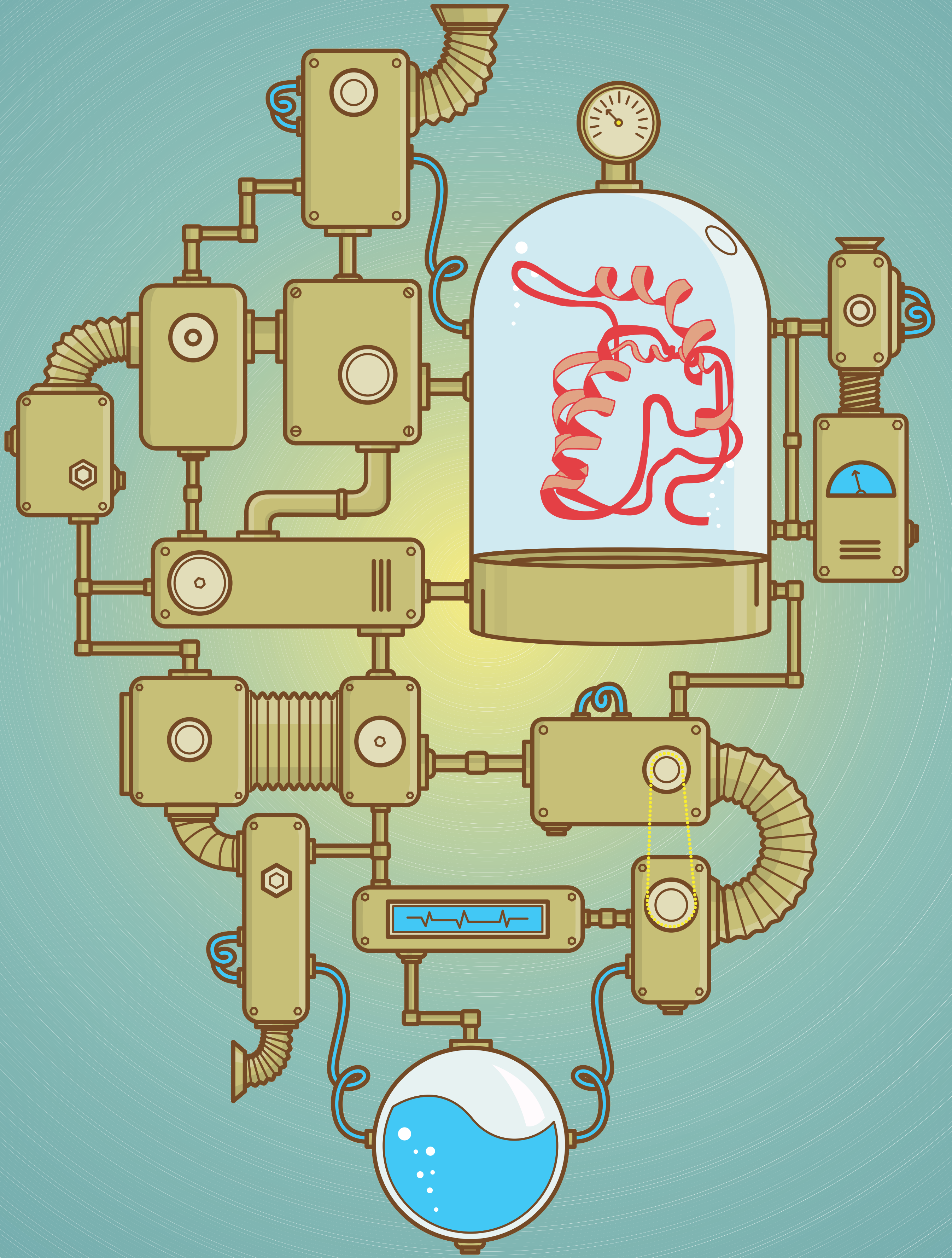
It's a nice story, one that evolutionary biologists touted for decades as an illustrative example of molecular adaptation. Too bad it's wrong.

Last year, researchers at the University of Chicago refuted that just-so scenario by resurrecting the ancient ADH enzyme from the last common ancestor of *D. simulans* and *D. melanogaster*. They replaced a modern *D. melanogaster*'s ADH with the prehistoric version of the protein, from before flies colonized rotten fruit, and it made no difference to *D. melanogaster*'s ability to enjoy a 5-proof or even more alcoholic molasses-cornmeal mash.[1]

The scientists conducting that experiment used a computational technique called ancestral sequence reconstruction (ASR) to determine the amino acids that made up the ancient protein, thus allowing them to revive it. Researchers have been adopting the method over the past decade. "Using ancestral reconstruction, we can test those historical hypotheses directly," says Mo Siddiq, a graduate student who led the *Drosophila* project in the laboratory of Joe Thornton. The team was the first to resurrect an ancient protein in a living animal. (With ADH ruled out, Siddiq now suspects that "a suite of changes" brought *D. melanogaster* to its boozy diet.)

At its heart, ASR addresses "the 'why' of proteins," says Michael Harms, an evolutionary biologist at the University of Oregon. Why did proteins evolve the way they did? Was it through chance, or did some other factors push them in a particular direction? Some biologists also think resurrected proteins offer clues about the past—what the world was like when certain proteins first appeared on the evolutionary landscape, perhaps even when life first evolved some 3.8 billion years ago.

Other researchers are looking to ancient proteins for ideas about the future, taking inspiration from the ancient molecules' forms and functions as they engineer enzymes with new, targeted purposes for industrial, agricultural, or medical use. Ancestral



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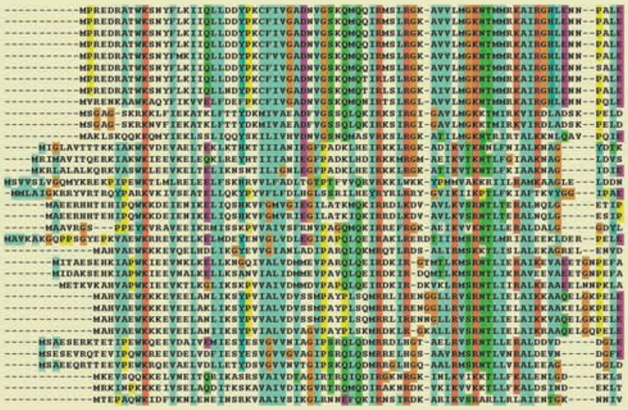
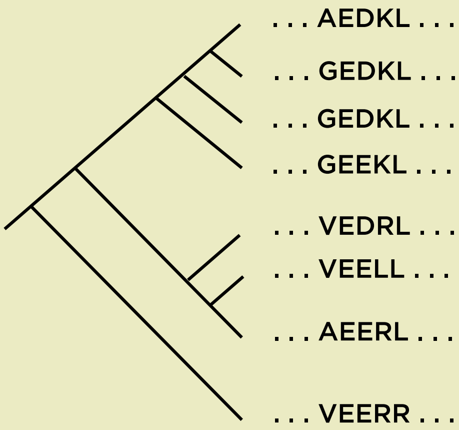
HOW TO RESURRECT A PROTEIN

Ancestral sequence reconstruction relies on phylogeny and statistics to infer the most likely amino acid sequence for an ancient protein.



SEQUENCE ALIGNMENT: Scientists collect sequences from databanks of the modern versions of the protein of interest from different organisms.



TREE BUILDING: Computer algorithms construct a phylogenetic tree for the proteins. (*Curr Opin Struct Biol*, 38:37–43, 2016).

sequences often yield proteins that are highly stable and flexible in function. "They can make a very good starting point for bioengineering," says José Sánchez-Ruiz, a physical chemist studying biomolecules at the University of Granada in Spain.

Hit rewind

University of Arizona evolutionary and synthetic biologist Betül Kacar is interested in basic questions about life's origins. So she's doing a version of what the late Stephen Jay Gould, a prominent evolutionary biologist and science communicator, referred to in his book *Wonderful Life* as "replaying life's tape."

Gould wondered: If you could rewind evolution to a given point, and let it proceed for a second time, would life evolve in a different manner, or arrive at the same endpoint? In other words, is the direction of evolution determined by chance, or is there a most likely sequence of events? It's a question that intrigues not only evolutionary biologists gazing into the past, but also astrobiologists wondering how the process might unfold on other planets.

With funding from NASA, Kacar set out to replay the tape for one particular protein, EF-Tu. Found in all organisms, it delivers tRNAs with their amino acid cargoes to the ribosome. Several ancestral EF-Tu constructs had been developed in the laboratory of Kacar's collaborator and former postdoc advisor, Eric Gaucher of the NASA Astrobiology Institute team at Georgia Institute of Technology in Atlanta. To go back in time to the ancient sequences, Gaucher, then with NASA's team at the University of Florida, had started with amino acid sequences of EF-Tu from 50 modern bacteria. From there, he used computer algorithms to construct a phylogenetic tree for those proteins, and checked that it matched well with other phylogenies for the organisms involved. The ASR algorithms then used the family tree to infer the most likely amino acid sequences at the nodes of the tree, ranging from 3.5 billion to 500 million years ago.[2,3]

Kacar rewound 700 million years, reconstructing an EF-Tu likely to have been encoded by a proteobacterium. Then, like Siddiq, she set about creating a modern bacterium that used the extinct form of the enzyme. After a couple of years' worth of cloning attempts, and thanks to "a good healthy level of obsession," Kacar says, she managed to create an *E. coli* strain that did so. This forced the bacteria to work with an EF-Tu that only poorly interfaced with all the modern partner proteins it needed to bind. They weren't the fittest bacteria, taking about 45 minutes to double their numbers, compared with 20 minutes for thoroughly modern *E. coli*, but they were viable.

> Using ancestral reconstruction, we can test those historical hypotheses directly.
>
> -Mo Siddiq, University of Chicago

Kacar divided those bacteria into six culture flasks, and grew them for about 2,000 generations. Over time, their fitness increased and they attained doubling rates of about 25 minutes. In results published last year, Kacar reported that five cultures played the same tune: they achieved this fitness level by boosting expression of the old gene for EF-Tu, which they did with the help of a mutated promoter.[4] This contrasts with the modern EF-Tu, which—thanks to 700 million years of evolution—differs by 21 amino acids. This allows it to interface properly with the rest of the proteins in modern *E. coli*, thus achieving quick cell division rates. Although the resurrected EF-Tu was far from optimal for modern *E. coli*, providing enough suboptimal EF-Tu seemed to give the protein-making machinery what it needed to grow at a reasonable rate. The researchers confirmed that artificially overexpressing the ancient gene for EF-Tu also improved bacterial fitness.

Bacteria in the sixth flask accumulated several mutations throughout their genomes, and Kacar suspects some of those altered the gene network that controls the EF-Tu gene's transcription, to increase it and improve fitness. So perhaps evolution often takes the most likely route—at least with this one protein.

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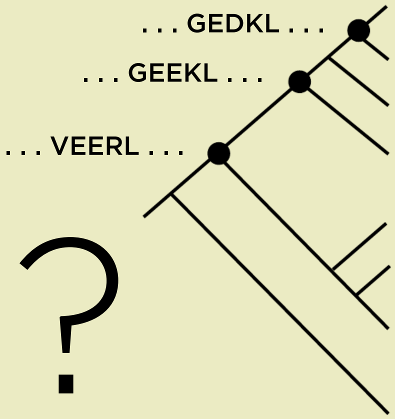
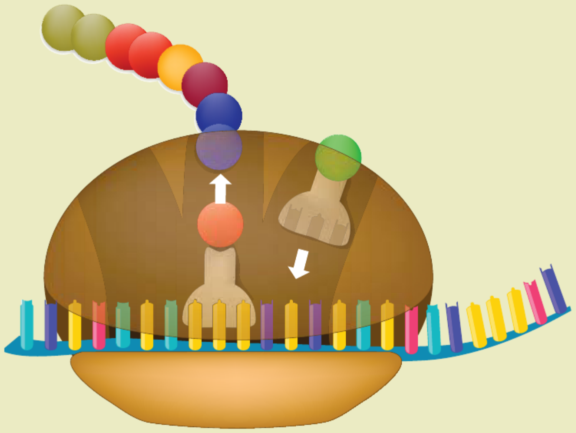


ANCESTRAL RECONSTRUCTION: The programs can then infer the sequences that likely existed at nodes of the tree, before the modern species evolved.



LABORATORY TESTS: Finally, the scientists order synthetic DNA and generate those proteins in the lab to use for experiments.

Most researchers have only studied ASR-derived proteins in vitro; analyzing the ancient proteins in the context of a modern organism is a relatively new application. But the in vivo approach is quickly gaining steam. In addition to Kacar's and Siddiq's experiments, for example, Sánchez-Ruiz and colleagues recently resurrected an ancient gene for thioredoxin and inserted it into modern *E. coli*. Thioredoxin is a redox protein that donates electrons to diverse enzymes, but it also serves as a key factor that allows bacteriophages to propagate in host microbes. When the researchers replaced the modern thioredoxin with versions from 2 million to 4 million years ago, the *E. coli* were unable to support viral propagation.[5] It's not that the old enzyme was better or worse—it's simply that it's not compatible with the modern virus. That mismatch protects the bacteria.

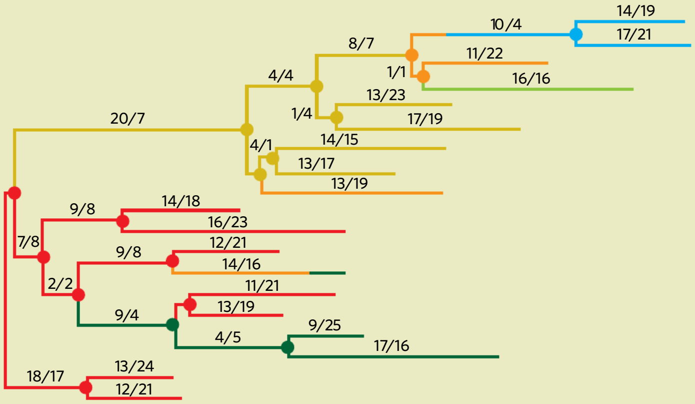
Thus, in just a couple of decades, rewinding evolution using ASR proteins has shed light not only on how the macromolecules changed through the eons, but also how they function in vivo.

Hot or not?

Some scientists also believe ASR offers insights into the habitat preferences of ancient life forms. Sánchez-Ruiz's ancient thioredoxin, as well as Gaucher's ancestral EF-Tu, fit into a common trend among ASR proteins from more than 2 billion years ago: they seem to have liked it hot—about 30 °C to 40 °C hotter than proteins from the last 1 billion to 2 billion years, if the difference between modern and ancient melting points is any indication. The trend has led researchers to speculate that early life lived, and perhaps originated, in hot springs, or

ENSURING ACCURACY

One way to ensure that an ASR protein behaves like the true ancestor is to resurrect and test not only the best amino acid sequence generated by the algorithms, but a few proteins with the second-best guesses, or third-best guesses, and so on. If those alternative ancestors act like the best-guess version, then researchers figure the conclusions are probably robust. Recently, evolutionary synthetic biologist Eric Gaucher of Georgia State University tested ASR accuracy in a different way. He generated an entirely artificial phylogenetic tree, starting with red fluorescent protein and randomly mutating it to evolve 19 diversely colored fluorescent proteins. Then he used ASR to predict the ancestor of those 19 descendants, and compared the results to the true ancestors. The results were reassuring. Overall, the five different ASR algorithms he tried identified the ancestral sequence with about 97 percent accuracy (*Nat Commun*, 5:12847, 2016).



EVOLVING PROTEINS: The experimental evolution began with a red fluorescent protein gene (left). The 19 resulting proteins were sequenced, and the data were used to infer the sequences of the node proteins. (Colors represent protein fluorescence. The number of nonsynonymous and synonymous substitutions are shown along each branch.)

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in the sweltering oceans geochemists believe existed early in Earth's timeline, up until around 3.2 billion years ago or so. Or, it may be that life evolved at a variety of temperatures, but only the most thermostable early organisms survived asteroid bombardment that could have boiled the oceans during the first 700 million-plus years of the planet's history.

Dan Tawfik, an evolutionary biochemist at the Weizmann Institute of Science in Israel, says he was initially quite enthusiastic about the idea that heat-stable ASR proteins indicate a hot origin for life. But doubts crept in. He spoke with Weizmann geochemist Itay Halevy and discovered that the hot-ocean hypothesis isn't universally accepted. Halevy says that the sun was 25 percent dimmer 3.5 billion years ago, and the geological record indicates glaciation during Earth's early history, which was unlikely to happen if the ocean's average temperature was 70 °C or higher. And in his recent analyses of resurrected liver proteins from the common ancestor of mammals, Tawfik found additional reasons to doubt the idea.

Tawfik and colleagues reconstructed a mammalian serum paraoxonase (PON)—a protein that hydrolyzes molecules called lactones and organophosphates, detoxifying them—dating to 65 million to 100 million years ago.[7] Its melting temperature was 13 °C higher than that of a modern PON.[8] Yet the Earth's temperature back then resembled today's. And since mammals can regulate their own temperatures, it would be unnecessary to match their enzyme's ideal temperatures to the environment. So why would Tawfik's PON, plucked from the relatively recent past, exhibit such high thermostability?

One possible explanation could be that the ancient proteins required extra stability for other reasons. For example, Tawfik speculates that perhaps protein translation wasn't all that accurate in the past. If the proteins had hyperstable amino acid sequences, he posits, they'd be better suited to cope with a high rate of translational errors. In that case, thermostability would have evolved as a side effect.

Or, the thermostability may be an artifact of the reconstruction process. After all, ASR is based on a computer program's best guess at an ancestral protein. Some researchers suspect that the ASR sequences, which are inferred based on the family tree of a given protein, are little different from the consensus sequences that are obtained by averaging extant strings of amino acids, without taking evolution into account. And those consensus sequences also tend to be thermostable, says Harms, though he's not sure why that happens. "It's an approximate method," says Harms. "I don't think we've run all the controls that we would need, as a field, to conclude that this isn't an artifact."

Others are more confident of ASR-based conclusions. Consensus and ancestral sequences often do resemble each other, but that doesn't make the ASR-based deductions wrong, says Sánchez-Ruiz. And consensus doesn't always mean stability. For example, Sánchez-Ruiz used modern bacterial sequences to generate ASR beta-lactamases, enzymes that degrade antibiotics, and they were quite thermostable. But when he generated a trio of consensus variants, only one was particularly stable.[10] "Consensus proteins sometimes show enhanced stability, likely because they capture some of the ancestral stability," Sánchez-Ruiz says.

Proteins of the future

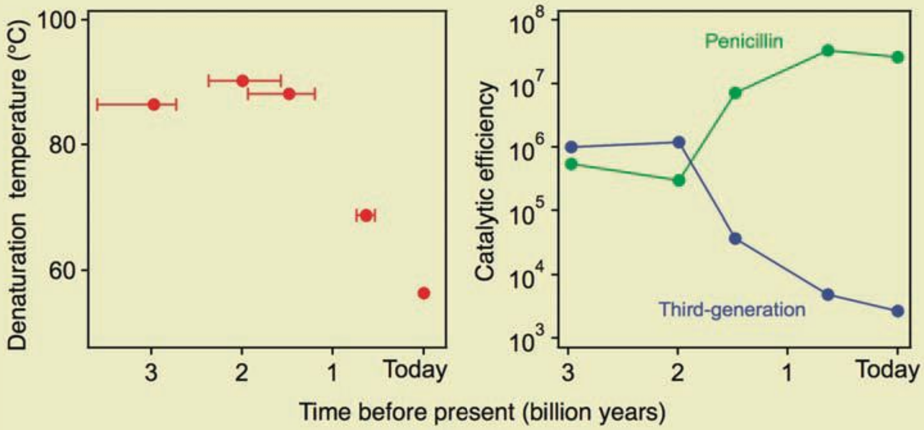
No matter how or why ASR proteins are so thermostable, the trait is good news for bioengineers aiming to create new, application-ready proteins, says Tawfik. "Who cares why it works?" he says. "If we want to engineer an enzyme, we hardly ever start with an *E. coli* or human enzyme, we typically infer the ancestor and use this as a starting point."

Plus, ASR proteins are often promiscuous, binding to or acting on a greater array of partner molecules than their modern counterparts. Sánchez-Ruiz observed this when he analyzed the ancient beta-lactamases. While a modern beta-lactamase specializes in disarming penicillin, the enzymes from 2 billion or 3 billion years ago degrade a broader spectrum of antibiotics.[11] "The modern protein is the outcome of 4 billion years of evolution, and it is highly specialized," he says.

Harms and other researchers have argued that the evidence for a consistent trend, from protein generalists to specialists, has

THE PERFECT STARTING POINT

Bioengineers love resurrected proteins because they often combine two desirable features: thermostability and promiscuity. For example, researchers at the University of Granada in Spain reconstructed several versions of an antibiotic-resistance protein called beta-lactamase, going back as far as 3 million years. As the protein evolved, its melting point dropped from more than 80 °C to less than 60 °C. It also became more specific for penicillin, losing its ability to neutralize other drugs (*J Am Chem Soc*, 135:2899–902, 2013).



J AM CHEM SOC, 135:2899-902, 2013

yet to be established.[9] "I think that ancestral proteins were just as optimal as modern proteins for their environment," Harms says.

But once again, whether ASRs accurately reflect proteins' histories or not, the fact that they're often generalists is a boon for bioengineers. "For a new function to evolve, it has to be there to start with, as something latent," explains Tawfik. ASR proteins may serve as jacks-of-all-trades, giving protein engineers a better starting point.

> ASRs can make a very good starting point for bioengineering.
>
> —José Sánchez-Ruiz, University of Granada

To test that idea, Sánchez-Ruiz, Gaucher, and collaborators are planning a high-throughput experiment. Starting with an ancient enzyme, they hope to nudge its evolution toward desired functions. One test case they're aiming at is the Diels-Alder reaction, a chemical process for building molecular rings. No enzyme that can accomplish this task has ever evolved in nature, though bioengineers have managed to design synthetic proteins that can. If the collaborators can evolve a Diels-Alder enzyme from an ancient precursor in the lab, it will be a good indicator that they can do so for other types of reactions.

One application for such reconstructed enzymes might be in agriculture. After using the ancient version of thioredoxin to engineer disease-resistant *E. coli*, Sánchez-Ruiz's group suggested that a similar approach in plants could protect crops from pathogens.[5] "I hope someone with expertise in plant bioengineering gives it a shot," he says.

Becoming human

ASR can also offer hints for bioengineers with medical applications in mind. That's what happened with Gaucher's investigations of uricase, a useful enzyme that was deactivated at some point in human evolution. While most animals depend on uricase to break down uric acid, apes possess only a dysfunctional pseudogene, which evolved from a functional precursor. Without uricase, uric acid can build up and crystallize in joints, where it causes pain and swelling known as gout. "Something happened when apes evolved," says Gaucher.

To figure out how our uricase lost its mojo, Gaucher resurrected uricases from several points in the past. The prehistoric enzymes showed a stepwise progression from high activity to low. By the last common ancestor of all apes, which likely lived 20 million years ago, uricase's activity was undetectable.[12] At the same time, a uric acid transporter called URAT1 also evolved to increase the blood concentration of uric acid.

What pushed the ancestors of apes to maintain high uric acid, despite the attendant risks? Gaucher and his collaborators suspect it relates to our taste for fruit. High levels of uric acid promote the conversion of fruit sugars into fat. Around the time uric acid metabolism was changing, the climate cooled, causing fewer flowering trees to produce fruit. That meant frugivore primates needed to gorge on fruit whenever they found it, saving energy for a fruitless day. Dropping uricase would have allowed them to store more energy,[14] and might have supported the development of bigger brains, Gaucher suggests. "This is undoubtedly one of the drivers that allowed apes to evolve."

Now, the growing understanding of uricase's antecedents—and the reconstructed versions of them—could offer a potential treatment for gout sufferers. There's already a version of uricase on the market, a recombinant-bacteria-made chimeric protein assembled from pig and baboon sequences. However, when Gaucher and colleagues tested their ASR uricase in rats, its half-life in blood was nearly 100 times longer than the hybrid version.[12]

Gaucher and collaborators have also used ASR to improve the stability and activity of Factor VIII, a coagulant used to treat hemophilia, and they believe the method could apply to any protein-based therapeutic.[15] Gaucher founded a company, General Genomics, to develop uricase and other ancient proteins into medications, and for industrial or agricultural use. "It is quite cool that we are able to push the boundaries of biology a little bit, and engineer systems with ancestral genes," says Kacar. "Now the question is, 'How far can you push this?'" ■

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Talking About Language

Evolutionary changes in both the vocal tract and the brain were necessary for humans' remarkable gift of gab.

BY PHILIP LIEBERMAN

In the 1960s, researchers at Yale University's Haskins Laboratories attempted to produce a machine that would read printed text aloud to blind people. Alvin Liberman and his colleagues figured the solution was to isolate the "phonemes," the ostensible beads-on-a-string equivalent to movable type that linguists thought existed in the acoustic speech signal. Linguists had assumed (and some still do) that phonemes were roughly equivalent to the letters of the alphabet and that they could be recombined to form different words. However, when the Haskins group snipped segments from tape recordings of words or sentences spoken by radio announcers or trained phoneticians, and tried to link them together to form new words, the researchers found that the results were incomprehensible.[1]

That's because, as most speech scientists agree, there is no such thing as pure phonemes (though some linguists still cling to the idea). Discrete phonemes do not exist as such in the speech signal, and instead are always blended together in words. Even "stop consonants," such as [b], [p], [t], and [g], don't exist as isolated entities; it is impossible to utter a stop consonant without also producing a vowel before or after it. As such, the consonant [t] in the spoken word *tea*, for example, sounds quite different from that in the word *to*. To produce the vowel sound in *to*, the speakers' lips are protruded and narrowed, while they are retracted and open for the vowel sound in *tea*, yielding different acoustic representations of the initial consonant. Moreover, when the Haskins researchers counted the number of putative phonemes that would be transmitted each second during normal conversations, the rate exceeded that which can be interpreted by the human auditory system—the synthesized phrases would have become an incomprehensible buzz.

Half a century after this phoneme-splicing talking machine failed at Haskins, computer systems that recognize and synthesize human speech are commonplace. All of these programs, such as the digital assistant Siri on iPhones, work at the word level. What linguists now know about how the brain functions to recover words from streams of speech now supports this word-level approach to speech reproduction. How humans process speech has also been molded by the physiology of speech production. Research on the neural bases

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of other aspects of motor control, such as learned hand-arm movements, suggests that phonemes reflect instruction sets for commands in the motor cortex that ultimately control the muscles that move our tongues, lips, jaws, and larynxes as we talk. But that remains a hypothesis. What is clear about language, however, is that humans are unique among extant species in the animal kingdom. From the anatomy of our vocal tracts to the complexity of our brains to the multifarious cultures that depend on the sharing of detailed information, humans have evolved the ability to communicate like no other species on Earth.

Speech acoustics and physiology

Pipe organs provide a useful analogy for the function of the human vocal tract. These instruments date back to the medieval period in Europe and consist of a bellows, which provides the necessary acoustic energy, and a collection of pipes of various lengths. Each key on the organ controls a valve that directs turbulent airflow into a particular pipe, which acts as an acoustic filter, allowing maximum energy to pass through it at a set of frequencies determined by its length and whether it is open at one or both ends. A longer pipe will result in a set of potential acoustic energy peaks—its so-called "formant frequencies"—at relatively low frequencies, while a shorter pipe will produce a higher set of formant frequencies. In the human body, the lungs serve as the bellows, providing the source of acoustic energy for speech production. The supralaryngeal vocal tract (SVT), the airway above the larynx, acts as the pipes, determining the formant frequencies that are produced.

As Charles Darwin pointed out in 1859, the lungs of mammals and other terrestrial species are repurposed swim bladders, air-filled organs that allow bony fish to regulate their buoyancy. Lungs have retained the elastic property of swim bladders. During normal respiration, the diaphragm as well as the abdominal muscles and the intercostal muscles that run between the ribs work together to expand the lungs. The elastic recoil of the lungs then provides the force that expels air during expiration, with alveolar (lung) air pressure starting at a high level and falling linearly as the lungs deflate. During speech, however, the diaphragm is immobilized and alveolar air pressure is maintained at an almost uniform level until the end of expiration, as a speaker adjusts her intercostal and abdominal muscles to "hold back" against the force generated by the elastic recoil of the lungs.

> **Discrete phonemes do not exist as such in the speech signal, and instead are always blended together in words.**

This pressure, in combination with the tension of the muscles that make up the vocal cords of the larynx, determines the rate at which the vocal cords open and close—what's known as the fundamental frequency of phonation (F0), perceived as the pitch of a speaker's voice. In most languages, the F0 tends to remain fairly level, with momentary controlled peaks that signal emphasis, and then decline sharply at a sentence's end, except in the case of certain questions, which often end with a rising or level F0. F0 contours and variations also convey emotional information.

In tonal languages, F0 contours differentiate words. For example, in Mandarin Chinese the word *ma* has four different meanings that are conveyed by different local F0 contours. In all of the world's languages, however, the primary acoustic factors that specify a vowel or a consonant are its formant frequencies, determined by the positions of the tongue, the lips, and the larynx, which can move up or down to a limited degree. The SVT in essence acts as a malleable organ pipe, letting maximum energy through it at a set of frequencies determined by its shape and length. Temporal cues, such as the length of a vowel, also play a role in differentiating both vowels and consonants. For example, the duration of the vowel of the word *see* is longer than the duration of the vowel of the word *sit*, which has almost the same formant frequencies.

Perceiving the formant frequencies of speech and assigning them to the words that a person intends to communicate is complicated. For one thing, people differ in vocal tract length, which affects the formant frequencies of their speech. In 1952, in one of the first experiments aimed at machine recognition of speech, Gordon Peterson and Harold Barney at Bell Telephone Laboratories found that the average formant frequencies of the vowel [i]—such as in the word *heed*—were 270, 2,290, and 3,010 Hz for 76 adult males. In other words, local energy peaks in the acoustic signal occur at these formant frequencies and convey the vowel.[2] The average formant frequencies of the vowel [u]—as in the word *who*—were 300, 870, and 2,240 Hz for the same group of men. Adult women produced formant frequencies that were higher for the same vowels because their SVTs were shorter than the men's. Adolescents' formant frequencies were higher still. Nonetheless, human listeners are typically able to identify these spoken vowel sounds thanks to a cognitive process known as perceptual normalization, by which we unconsciously estimate the length of a speaker's SVT and correct for the corresponding shift in formant frequencies.

Research has shown that listeners can deduce SVT length after hearing a short stretch of speech or even just a common phrase or word. University of Alberta linguist Terrance Nearey's comprehensive 1978 study showed that the vowel [i] was an optimal signal for accounting for SVT length, and [u] only slightly less so.[3] This explained one of the results of a 1952 Peterson and Barney project aimed at developing a voice-activated telephone dialing system that would have to work for men, women, and people who spoke different dialects of English. The duo presented a panel of listeners with words having the form h-vowel-d [hVd], such as *had* and *heed*, produced by 10 different speakers in quasi-random order, and asked the participants to identify each word. Out of 10,000 trials, listeners misidentified [i] only two times and [u] just six times, but misidentified words having other vowels hundreds of times. Similarly, in a 1994 experiment in which listeners had to estimate people's height (which roughly correlates with vocal tract length) by listening to them produce an isolated vowel, the vowel [i] worked best.[4]

In short, people unconsciously take account of the fact that formant frequency patterns, which play a major role in specifying words, depend on the length of a speaker's vocal tract. And both the fossil record and the ontogenetic development of children suggest that the anatomy of our heads, necks, and tongues have been molded by evolution to produce the sounds that clearly communicate the intended information.

The evolution of the human vocal tract

In *On the Origin of Species*, Darwin noted "the strange fact that every particle of food and drink which we swallow has to pass over the orifice of the trachea, with some risk of falling into the lungs." Because of this odd anatomy, which differs from that of all other mammals, choking on food remains the fourth leading cause of accidental death in the United States. This species-specific problem is a consequence of the mutations that crafted the human face, pharynx, and tongue so as to make it easier to speak and to correctly interpret the acoustic speech signals that we hear.

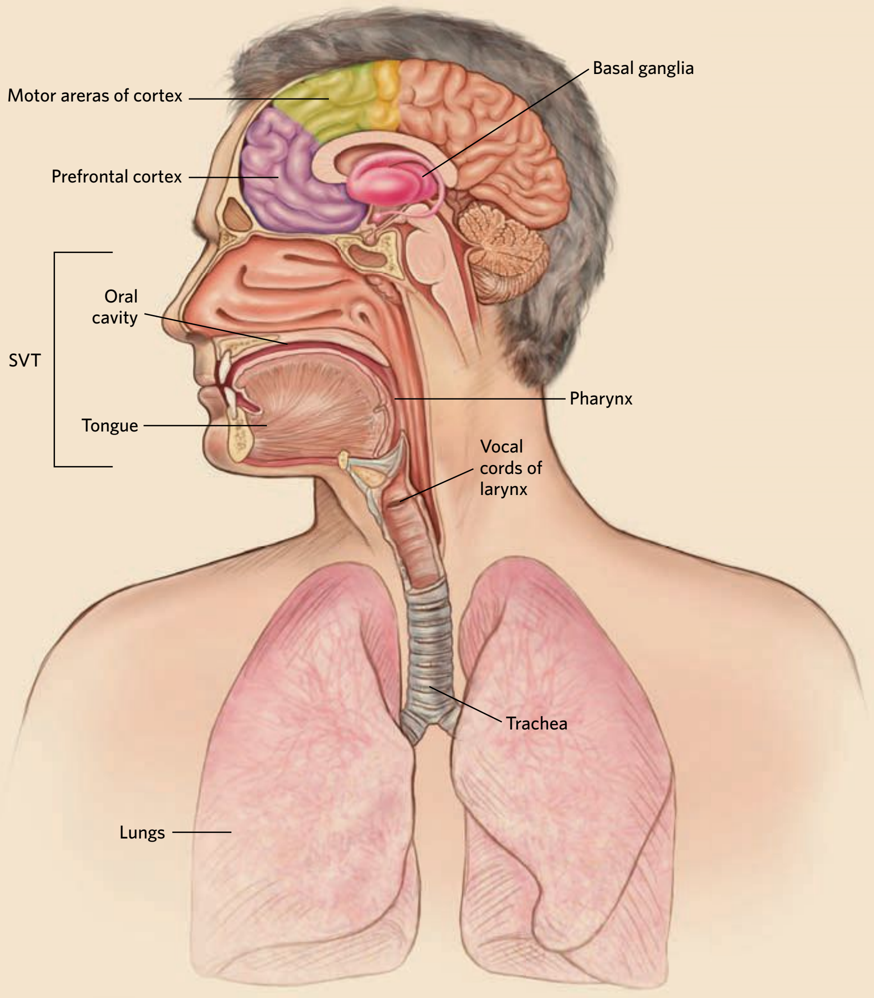
At birth, the human tongue is flat in the mouth, as is the case for other mammals. The larynx, which rests atop the trachea, is anchored to the root of the tongue. As infants suckle, they raise the larynx to form a sealed passage from the nose to the lungs, allowing them to breathe while liquid flows around the larynx. Most mammalian species retain this morphology throughout life, which explains why cats or dogs can lap up water while breathing. In humans, however, a developmental process that spans the first 8 to 10 years of life forms the adult version of the SVT. First, the skull is reshaped, shortening the relative length of the oral cavity. The tongue begins to descend down into the pharynx, while the neck increases in length and becomes rounded in the back. Following these changes, half the tongue is posi-

ACOUSTICS AND PHYSIOLOGY OF HUMAN SPEECH

Humans have a unique anatomy that supports our ability to produce complex language. The elastic recoil of the lungs provides the necessary acoustic energy, while the diaphragm, intercostal muscles, and abdominal muscles manipulate how that air is released through the larynx, a complex structure that houses the vocal cords, and the supralaryngeal vocal tract (SVT), which includes the oral cavity and the pharynx, the cavity behind the mouth and above the larynx.

When air from the lungs rushes against and through the muscles, cartilages, and other tissue of the vocal cords, they rapidly open and close to produce what's known as the fundamental frequency of phonation (F0), or the pitch of a speaker's voice. The principal sounds that form words—known as formant frequencies—are produced by changes to the positions of the lips, tongue, and larynx.

In addition to the anatomy of the SVT, humans have evolved increased synaptic connectivity and malleability in certain neural circuits in the brain important for producing and understanding speech. Specifically, circuits linking cortical regions and the subcortical basal ganglia appear critical to support human language.



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tioned horizontally in the oral cavity (and thus called the SVTh), while the other half (SVTv) is positioned vertically in the pharynx. The two halves meet at an approximate right angle at the back of the throat. The tongue's extrinsic muscles, anchored in various bones of the head, can move the tongue to create an abrupt 10-fold change in the SVT's cross-sectional area. (See illustration below.)

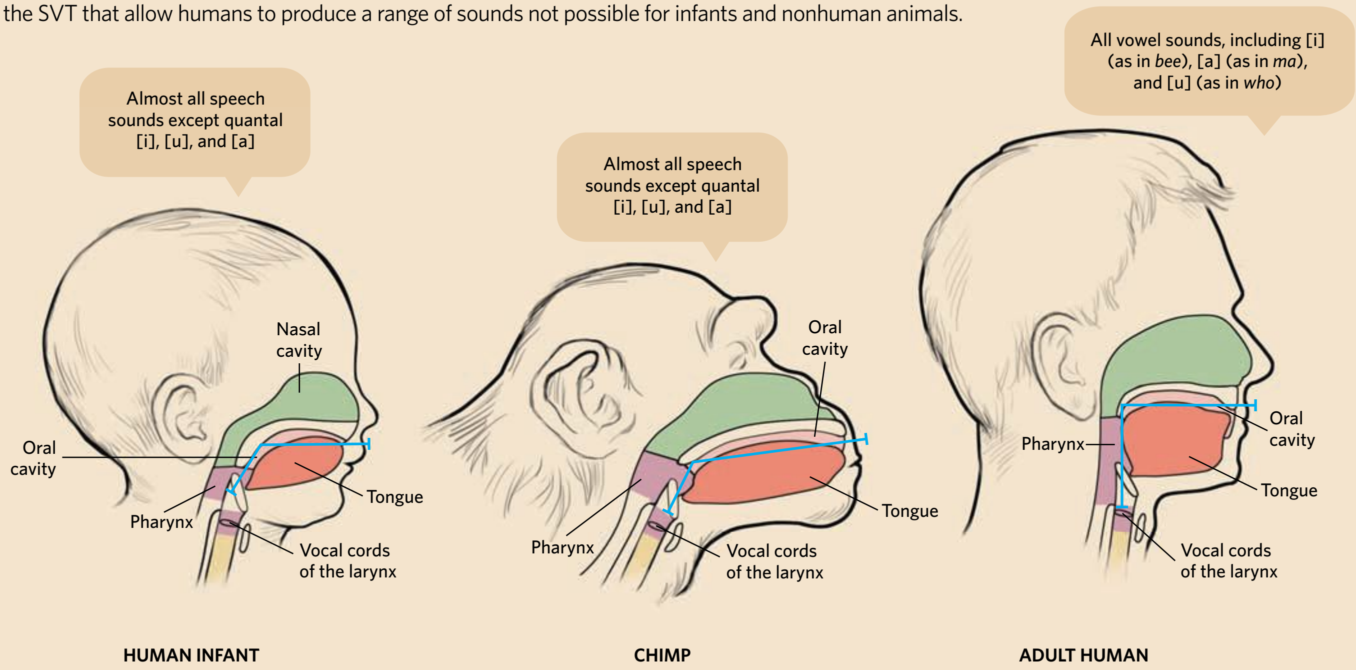
As it turns out, the configuration of the adult human tongue's oral and pharyngeal proportions and shape allow mature human vocal tracts to produce the vowels [i], [u], and [a] (as in the word *ma*). These quantal vowels produce frequency peaks analogous to saturated colors, are more distinct than other vowels, and are resistant to small errors in tongue placement.[5] Thus, while not required for language, these vowel sounds buffer speech against misinterpretation. This may explain why all human languages use these vowels.

This anatomy also begins to answer long-standing questions in language research: How did human speech come to be, and why don't other animals talk? In 1969, my colleagues and I used a computer modeling technique to calculate the formant frequency patterns of the vowels that a rhesus macaque's SVT could produce, based on an estimated range of tongue shapes and positions. We found that even when the monkeys' tongues were positioned as far as possible toward the SVT configurations used by adult human speakers to yield the vowels [i], [u], and [a], the animals could not produce the appropriate formant frequencies. Three years later, using X-ray videos showing the movement of the vocal tract during newborn baby cries, we refined and replicated this study and found that, although chimpanzees and human newborns (which start life with a monkey-like SVT) produce a range of vowels, they could not produce [u]s or [i]s.[6] This finding has since been replicated in independent studies, including in 2017 by the University of Vienna's Tecumseh Fitch and colleagues. Those scientists used current computer techniques that readily model every vocal tract shape that a macaque could produce, and the research team confirmed that monkey vocal tracts were incapable of producing these vowels.[7,8] Fitch's team went on to argue that monkey vocal tracts are "speech-ready," which indeed they are, as research has long since established that these vowel sounds are not prerequisites to language.

Recent genomic studies have discovered epigenetic modifications that appear to account for the evolution of the species-specific human vocal tract. It is now apparent that a massive epigenetic restructuring of the genes that determine the anatomy of the head, neck, tongue, larynx, and mouth enhanced our ability to talk after anatomically modern humans split from Neanderthals and Denisovans more than 450,000 years ago. A few years ago, David Gokhman, then at Hebrew University of Jerusalem,

THE CHATTIEST APE

Infants' tongues are flat and positioned almost entirely in the mouths. As a result, the larynx, which is anchored to the root of the tongue, can form a sealed airway, allowing babies to breathe while suckling. Other mammals have a similar configuration. As humans age, however, their anatomy changes. During the first 8 to 10 years of life, the relative length of the oral cavity shortens and the tongue extends down into the throat. This gives the adult human supralaryngeal vocal tract (SVT) two parts of nearly equal lengths that meet at a right angle: the horizontal portion of the oral cavity and the vertical portion associated with the pharynx. At the intersection of these two segments occur abrupt changes in the cross-sectional area of the SVT that allow humans to produce a range of sounds not possible for infants and nonhuman animals.



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and colleagues reconstructed the methylated genomic regions of a 40,000-year-old Neanderthal fossil, an older Denisovan fossil, four ancient humans who lived 7,000 to 40,000 years ago, and six chimpanzees, comparing these with a methylation map of human bone cells assembled from more than 55 present-day humans. This comparison enabled the team to identify differentially methylated regions (DMRs) between the human and Neanderthal-Denisovan groups, and between humans and chimps.[9,10] The researchers found that the genes that were most affected were those that controlled development of the larynx and pharynx, suggesting that epigenetic regulatory changes allowed the human vocal tract to morph into a shape that is optimal for speech.

> **Current research suggests a deep evolutionary origin for human language and speech.**

The brain adapts

Of course, the fact that monkeys don't talk like humans isn't purely due to the physical limitations of their vocal tracts. They also lack the neural networks necessary for producing and processing speech.

One key contributor to the evolution of human speech is the FOXP2 transcription factor. Humans, Neanderthals, and Denisovans share a mutation in the gene for FOXP2 that nonhuman primates lack. Early evidence of FOXP2's role in human speech and language comes from studies of the KE family, a large extended family living in London in the second half of the 20th century. Some members had only one copy of *FOXP2* and had extreme difficulty talking; their speech was unintelligible, and problems extended to orofacial motor control. They also had difficulties forming and understanding English sentences.

The importance of FOXP2 has been further confirmed by knock-in mouse studies. When the human version of the gene for the FOXP2 transcription factor is inserted into mouse embryos, the animals exhibited enhanced synaptic connectivity and malleability in cortical–basal ganglia neural circuits that regulate motor control, including speech.[11] The evolution of these circuits appears to have a deep evolutionary history going back to the Permian age, 300 million years ago. Avian versions of the FOXP1 and FOXP2 transcription factors act on the basal ganglia circuits involved when songbirds learn and execute songs.[12]

Exactly how the brain dictates the movement of the vocal tract to produce speech remains murky. Many studies have shown that "matrisomes" of neurons in the motor cortex are instruction sets for the motor commands that orchestrate a learned act.[13] Assemblies of neurons in the motor cortex are formed when a task is learned, and these assemblies guide coordinated muscle activity. To sip a cup of coffee or type at a keyboard, for example, hand, arm, wrist, and other movements are coded in matrisomes. Similar matrisomes likely govern the muscles that move the tongue, lips, jaw, and larynx and control lung pressure during speech, but researchers are just starting to explore this idea. In short, brains and anatomy were both involved in the evolution of human speech and language.

In 1971, Yale's Edmund Crelin and I published our computer modeling study of a reconstructed Neanderthal vocal tract.[14] We concluded that Neanderthals had vocal tracts that were similar to those of newborn human infants and monkeys and hence could not produce the quantal vowels [a], [i], and [u]. However, the available archaeological evidence suggested that their brains were quite advanced, and that, unlike monkeys, they could talk, albeit with reduced intelligibility. We concluded that Neanderthals possessed both speech and language. In short, current research suggests a deep evolutionary origin for human language and speech, with our ancestors possessing capabilities close to our own as long as 300,000 years ago.[14]

Speech is an essential part of human culture, and thus of human evolution. In the first edition of *On the Origin of Species*, Darwin stressed the interplay of natural selection and ecosystems: human culture acts as an agent to create new ecosystems, which, in turn, directs the course of natural selection. Language is the mechanism by which the aggregated knowledge of human cultures is transmitted, and until very recent times, speech was the sole medium of language. Humans have retained a strange vocal tract that enhances the robustness of speech. We could say that we are because we can talk. ■

Philip Lieberman is the George Hazard Crooker University Professor Emeritus at Brown University.

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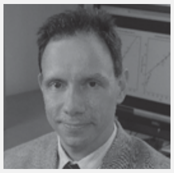

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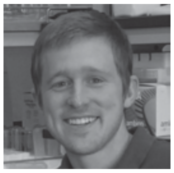

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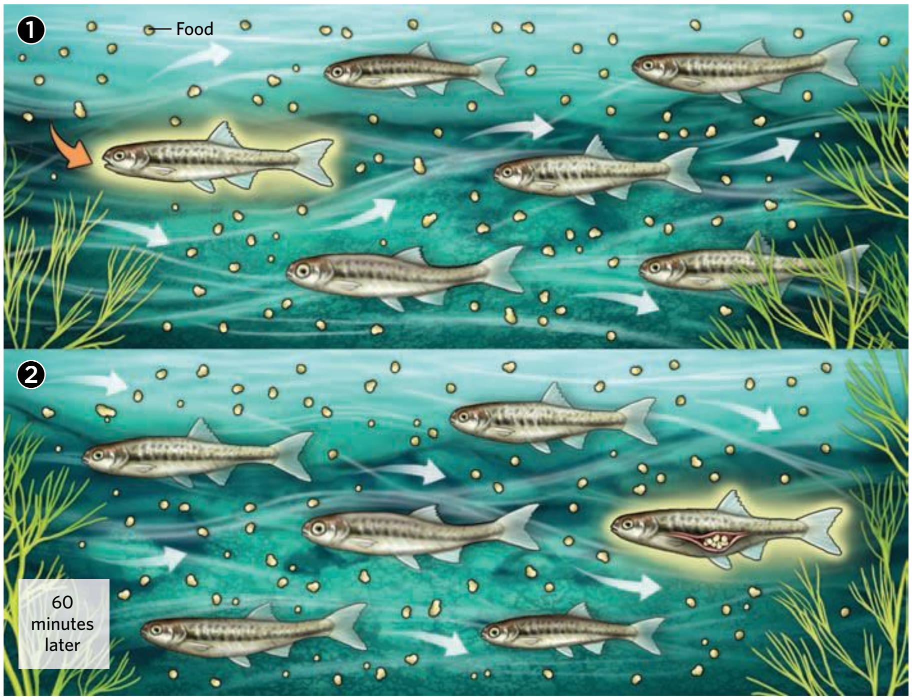
ECOLOGY & ENVIRONMENT

Full Fish

THE PAPER

S. McLean et al., "Metabolic costs of feeding predictively alter the spatial distribution of individuals in fish schools," *Curr Biol*, 28:1144–49, 2018.



SWITCHEROO: Hungry minnows tend to swim at the front of the school and eat until they are full (top). Once the front swimmers have had their fill, they shift to the back of the school where they can expend less energy swimming and more energy digesting their food (bottom).

Lots of animals live and move in groups—elephants in herds, wolves in packs, birds in flocks, and fish in schools. "It's nearly ubiquitous in animals," says Shaun Killen, an ecophysiologist at the University of Glasgow in the U.K. Research has shown that where an individual is spatially located in the group can affect the benefits it gets from hanging out in a crowd, and behavioral traits, such as boldness, and nutritional states, such as hunger, can influence how individuals jockey for position. But, Killen says, researchers haven't yet fully explored the role of physiological processes such as digestion in driving animals' collective behavior.

Killen and his colleagues recently studied schools of Eurasian minnows (*Phoxinus phoxinus*) swimming in a tank against a current. Pieces of chow were constantly whizzing past the fish, and the team recorded how many each minnow ate and the fishes' positions before and after eating. After calculating the metabolic costs of digesting each fish's meal and comparing it to the fish's position, the team observed a trend: fish that had just gulped down a big meal moved to the back of the school, even when they'd swum at the front at most other times. "Eating a big meal reduces the fish's ability to swim," Killen says. "It's a relatable experience. If you're going to run a marathon, you wouldn't eat a pizza right before."

It makes sense that feeding would influence individuals' positions in a group, says Damien Farine, who was not involved in the fish experiments but studies collective behavior in birds from his post at the Max Planck Institute for Ornithology and the University of Konstanz in Germany. If a fish is hungry, it's competing with others in the school to eat, and being at the front gives it access to more food. But once the fish is full, it doesn't necessarily need to be at the front. In addition, "being at the back of the group is less energetically costly for a range of reasons," Farine notes. "An individual at the back doesn't have to contribute to navigating, and by relaxing the brain load it saves more energy."

This observation aligns with other recent studies showing that individuals don't position themselves in a group according to some preference or their observations about where other members are located, as researchers once thought. Animals can form emergent patterns without any individual having to organize this or even know it is happening, Farine says.

Killen says he's been thinking about the pros and cons of being at the back of the pack, such as protection from predators and a boost from schoolmates' slipstream. Changes in position, especially during the basic trade-off between feeding and movement, appear to influence group leadership, information transfer, and group decision making, he says. But the consequences of the trade-offs for group dynamics and survival are not yet understood.

—Ashley Yeager

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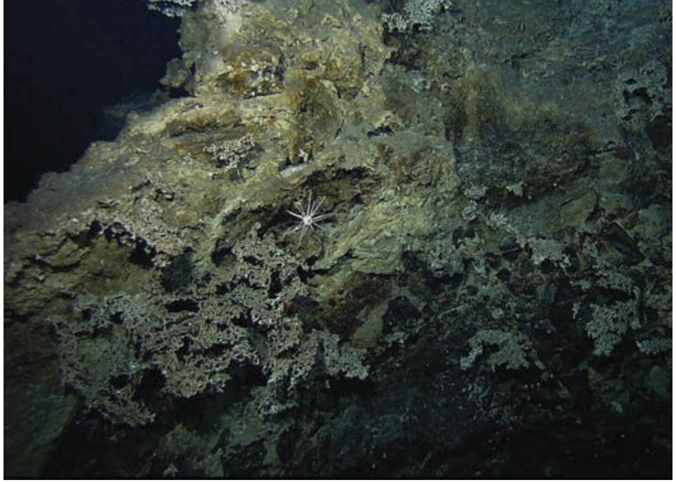


CARBON TRAP: Organic molecules can circulate in the deep ocean for millennia before they're gobbled up by microbes in the crust.

ECOLOGY

Sinking Carbon

THE PAPER

S.R. Shah Walter et al., "Microbial decomposition of marine dissolved organic matter in cool oceanic crust," *Nat Geosci*, 11:334–39, 2018.

SEQUESTERED CARBON

There's as much carbon circulating in the deep ocean in a form called marine dissolved organic carbon (DOC) as there is CO_2 in the atmosphere, says Sunita Shah Walter, a marine chemist at the University of Delaware. "It's one of the largest active organic carbon reservoirs that we have," she says. But not much is known about how this carbon is sequestered in the deep ocean.

UNDER THE SEA

Shah Walter and a team of geochemists and evolutionary biologists set out to determine what's happening to marine DOC in a tectonically active area of the Atlantic Ocean called North Pond, which sits on the Mid-Atlantic Ridge about halfway between Cuba and Western Sahara. They drilled through sediment to the crust and sampled organic molecules and microbes from circulating seawater there, then used radiocarbon dating to determine how long the organisms and organic molecules had been there.

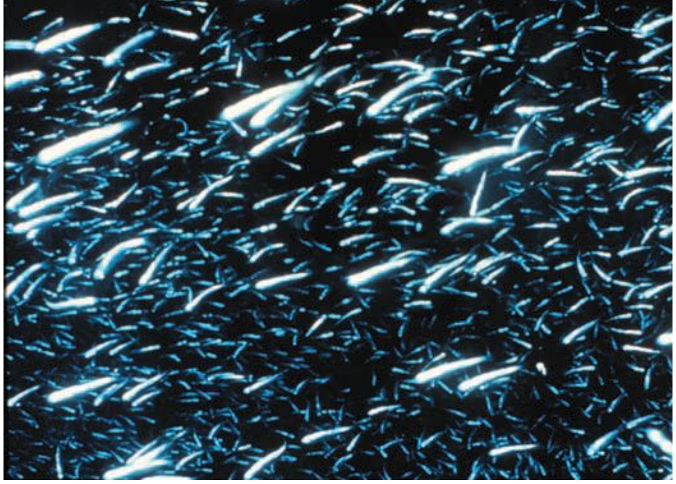
HUNGRY, HUNGRY MICROBES

The organic carbon in the crust was ancient—4,000–6,000 years old. DOC circulates through the ocean on currents and becomes trapped in ocean water in faults along the seafloor's cooling crust. In the crust, the molecules somehow become an attractive food source to deep-sea microbes that would shun them in the open ocean. "I was surprised by how adaptable and flexible these bacteria are," says Shah Walter.

BURIAL AT SEA

"At the moment, we're driving the [atmospheric] CO_2 up, but a lot of it will be taken up by the ocean," says Dan Repeta, a marine geochemist at Woods Hole Oceanographic Institution. The age of the DOC in Shah Walter's samples "suggests that it stays in seawater for quite a long time," he says, meaning that the oceans could have the potential to hold onto carbon for millennia.

—Jim Daley



FUTURE FISH STICKS: How would mid- and deep-sea fish populations respond to commercial trawling?

EVOLUTION

Lantern in the Dark

THE PAPER

J.S.S. Denton, "Diversification patterns of lanternfishes reveal multiple rate shifts in a critical mesopelagic clade targeted for human exploitation," *Curr Biol*, 28:933–40, 2018.

FISHING FOR ANSWERS

Commercial fishing has depleted oceanic stocks at shallow depths, and while companies could turn to catching fish from deeper in the sea, researchers haven't begun to understand how fish populations in these zones would respond to commercial fishing pressure. John Denton, an evolutionary biologist at the American Museum of Natural History in New York City, decided to look for answers to this question in these fishes' evolutionary past.

TRAWLING FOR ORIGINS

Denton investigated the evolutionary roots of a clade known as lanternfish (family Myctophidae), which are plentiful at zones more than 200 meters below the surface. He first needed an evolutionary tree that was temporally precise and included data on a relatively large number of species. "There weren't any trees that satisfied both conditions," says Denton. So he built one using molecular phylogeny techniques, which analyze DNA sequences to determine evolutionary relationships between species.

TREE OF KNOWLEDGE

By using the tree to plot diversification rates through time, Denton found that since their emergence more than 80 million years ago, lanternfish species have diversified at a continuously increasing rate that has undergone three major rate shifts. Those shifts apparently coincided with known changes in ocean CO_2, temperature, and salinity, suggesting that as a clade, lanternfish respond well to environmental threats—which could include fishing.

GO FISH?

"The [lanternfish] group makes up a huge portion of the fish biomass in the open ocean," says Rene Martin, a graduate student in ichthyology and evolutionary biology at the University of Kansas, so the fish are a cornerstone of ocean health. Denton says researchers will need to learn more about modern lanternfishes' biology before making predictions about how they'll respond to commercial fishing.

—Jim Daley

BOTH IMAGES: NOAA

PROFILE

Deep Diver

A pioneering explorer of hydrothermal vents on the ocean floor, Cindy Van Dover now focuses on conserving these unique ecosystems.

BY ANNA AZVOLINSKY

In April 1982, the first-ever biology expedition to the East Pacific Rise set sail from San Diego. It was an exploration of one of the Pacific Ocean's tectonic plate boundaries, where, more than 2,500 meters below the ocean surface, seawater gushes down through the plates, deep into the Earth's crust, and comes out through hydrothermal vents—underwater hot springs that release sulfides and other chemicals from deep within the crust.

The three-ship fleet headed to a spot in the Gulf of California. On one of the ships was *Alvin*, a deep-sea submersible built like a space shuttle to withstand the enormous pressures of ocean depths. Also onboard was a young and eager Cindy Van Dover, who, as a lab technician with no graduate training, was "the lowest person on the totem pole," the Duke University Marine Laboratory professor now recalls.

> I remember how strongly I felt that I did not want to leave the ship. I wanted to stay on that boat forever.

She was too junior for a seat on *Alvin*, which she watched splash into the water every morning and rise from the ocean every afternoon during that month-long excursion. So Van Dover busied herself with getting hold of any sample she could from the submersible. Whenever *Alvin* emerged from its daily dive, the scientists would dash for *Alvin*'s rich haul of animals from the hydrothermal vents—clams, mussels, and giant tubeworms (*Riftia pachyptila*). Van Dover noticed that they ignored the dead and dying squat lobsters—small, flat-bodied crustaceans with long claws and an almost curly tail—wedged among the submarine's outer crevices. Having received permission to collect them, she preserved and cataloged her specimens on the boat, waiting to analyze them back on land.

Once in the lab, Van Dover painstakingly dissected the squat lobsters, which belong to superfamilies Galatheoidea and Chirostyloidea, poring over their gut contents to decipher their eating habits and examining how their eggs and larvae develop. She discovered a new species of commensal fungus living inside their stomachs and circulatory systems of a type that had never been found so deep in the ocean before, and also identified a new lobster species, which she and a colleague named *Munidopsis lentigo*.

That first excursion cemented Van Dover's commitment to a career at sea. "I remember how strongly I felt that I did not want to leave the ship. I wanted to stay on that boat forever," she says. "I couldn't understand people who were ready to rush home, which is why I kept going out to sea as often as I could."

Van Dover has since logged hundreds of ocean expeditions and nearly 100 dives in submersibles to the ocean floor. She even piloted *Alvin*—the only woman to have done so. For the last 36 years, she has explored the unique ecosystems around hydrothermal vents all over the world, making 48 of her deep-sea dives at the helm of *Alvin*. Her fascination with the sea began at an early age, and few who knew her growing up a few miles from the New Jersey shore would be surprised that Van Dover parlayed her sense of adventure, inquisitiveness, and love for the ocean into a career as a professional explorer.

A RISING TIDE

Born in 1954, Van Dover grew up in Eatontown, New Jersey. She spent every summer day at the beach. "That's where I discovered those strange, crazy invertebrates, horseshoe and hermit crabs. They fascinated me because they looked so different from me and my dog," says Van Dover.

Her introduction to ocean science came during a ninth-grade marine biology laboratory course that made daily trips to the beach to collect and analyze animals and plants. "It was a very special experience," she says. Also in high school, she worked in a Rutgers University shellfish research lab, where she collected clams, contaminated them with bacteria, and then placed them into a clean water environment to see how long it would take for the bivalves to flush out the contaminants, a process called depuration.

Despite a guidance counselor telling her she was "not college material and should think about getting married and staying home," as Van Dover remembers, she was accepted into the first coed class at Rutgers in 1972. While there, she spent a semester at the Marine Biological Laboratory in Woods Hole, Massachusetts, working on clam and oyster biology. "Oh, it was just Mecca," Van Dover recalls. "I felt like I had landed where I belonged."

DIVING DEEPER

After graduating from Rutgers, Van Dover set her sights on only one graduate program, the MIT and Woods Hole Oceanographic Institution (WHOI) Joint Program in biological oceanography, but was rejected. Deeply disappointed, but still determined, she sought experience elsewhere.

Over the next four years, Van Dover worked as a technician in various labs, including the Duke University Marine Laboratory and the Smithsonian Marine Station in Florida, then followed a boyfriend to Cornell University where she "hung out and read marine

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CINDY VAN DOVER

Professor, Division of Marine Science and Conservation, Duke University Marine Laboratory
Director of the Duke University Marine Laboratory (2006-2016)
Fulbright Research Scholar (2004) and Fulbright Arctic Chair (2017)
National Science Foundation CAREER Award (2000)

Greatest Hits

- Discovered a novel species of squat lobster that dwells within the hydrothermal vents of the East Pacific Rise tectonic plate boundary
- Became the first woman (and the first PhD scientist) to be a certified pilot of *Alvin*, a deep-sea research submersible
- Discovered infrared-sensing "eyes" in an "eyeless" shrimp species
- Organized a large, multidisciplinary expedition to newly discovered deep-sea vents in the Indian Ocean, where the team collected a new kind of snail with scales on its foot
- Served as the first female director of Duke University's Marine Laboratory

ecology papers." Doing so, she came across the 1977 discovery of hydrothermal vents. Geologists had gone down to the sea floor—where there is zero sunlight and enormous atmospheric pressure—near the Galapagos Islands anticipating utter barrenness. There was not even a biologist on the expedition because no one was expecting to find life there. They were in for a surprise: they found crabs, clams, anemones, and seven-foot-long tubeworms not documented anywhere else on Earth. The discovery set marine biologists scrambling to witness this bustling ecosystem and to understand how these animals survived, let alone thrived, at such depth. Van Dover was instantly mesmerized with this abyssal "Garden of Eden," as the researchers dubbed it. "It showed me how extreme life on Earth could be."

Leveraging her experience analyzing crab larvae and eggs, Van Dover asked Austin Williams, one of the first biologists to describe the animals collected at the vents, to send her some eggs of the hydrothermal vent crab (*Brachyura thermydron*) so she could tell him how the larvae fed.

Williams took her up on the offer, and Van Dover found some lab space at Cornell to do her analyses. The embryos, Van Dover discovered, had mouthparts that indicated they were planktotrophic, feeding on plankton, rather than lecithotrophic, eating maternal egg yolk deposits. She suggested that the larvae likely don't migrate to surface waters to feed, but instead meet their caloric needs at depth because their low-temperature environment means they have a low dietary requirement. Van Dover published her findings two years later. In the meantime, she went to a hydrothermal vent science meeting in Washington, D.C., where she met all of the celebrity vent scientists. There, Van Dover found out about the 1982 OASIS cruise to the East Pacific Rise and asked the organizing researchers if she could come along. "They said, 'Sure!'" Van Dover says. "It was amazing—just by asking, I could live my dream."

When she returned from sea, Van Dover went on to earn a master's degree with an emphasis on theoretical ecology at the University of California, Los Angeles, in 1985. That same year, she had a unique opportunity to be a passenger on *Alvin*, even though she did not yet have a PhD, which at the time was practically a prerequisite to travel on the submersible. Van Dover joined an expedition to the "Rose Garden" hydrothermal vents just north of the Galapagos archipelago. One night, she saw her name on the next day's dive list and was stunned. "I couldn't sleep. I remember looking over the side of the ship imagining what I would see on the sea floor."

The next day, *Alvin*, carrying Van Dover, landed among hundreds of tubeworms, the quintessential Pacific Ocean vent animals whose long bodies are encased in white tubes with bright red plumes sticking out of the tops. "It's astounding how clear the water was down there. Seeing the vibrancy there completely changes the way you see the world."

BECOMING AN *ALVIN* PILOT

Following the cruise, Van Dover received an offer to work with one of the expedition scientists, Carl Berg, at WHOI. With him, she sorted and analyzed the first plankton samples collected at deep-sea hydrothermal vents.

While at Woods Hole, Van Dover met Fred Grassle, a professor who told her to apply again to the MIT-WHOI joint graduate program. This time she was accepted, officially beginning her PhD in 1986 and finishing in 1989, an almost unheard-of time frame.

> **Globally, these vents only occupy an area the size of Manhattan. They are really rare and extraordinary habitats that we need to preserve.**

At the time, hydrothermal vents in the Atlantic Ocean, along the Mid-Atlantic Ridge, had just recently been discovered. In the Atlantic, the most abundant animal was not the tubeworm, as in the Pacific, but the 2-inch-long swarming shrimp (*Rimicaris exoculata*). Now a graduate student with Grassle, Van Dover focused on the shrimp and noticed an unusual paired organ connected to the animal's brain that turned out to be a novel type of eye.

"It was a terrifically exciting finding! What were the shrimp looking at?" says Van Dover. She knew that water spewing from these Atlantic vents—called "black smoker chimneys" for the dark iron sulfide particles they release—reaches nearly 350 °C. The eye organ, Van Dover posited, might detect the near-infrared light emitted from the vents as a result of the high heat. "We think they use their eyes as remote heat sensors, so they can avoid getting cooked in the chimney stack," she explains.

Toward the end of graduate school, Van Dover was working closely with a team of *Alvin* engineers at Woods Hole, helping them draft the first written *Alvin* maintenance manual. Then she took the next step: training as an *Alvin* pilot. After nine months of intensive studying, she passed three grueling, multiday exams, followed by a solo dive without another pilot on board the submersible. She was officially certified in 1990 and, as was tradition, threw a big party at Kansas City BBQ in San Diego Harbor (where parts of *Top Gun* were filmed).

Following her time as an *Alvin* team crew member, Van Dover returned to academia in 1992. She first joined the faculty at the University of Alaska and then at the College of William and Mary in Virginia, and continued to dive to and study deep-sea vents.

Van Dover researched intertidal mussel communities in Virginia while at William and Mary, and collaborated with other researchers to analyze the geology and ecology of hydrothermal vents around the world. But her most substantive efforts in the 1990s, she says, involved authoring two books: *The Octopus's Garden*, published in 1996, and a textbook, *The Ecology of Deep-Sea Hydrothermal Vents*, which came out in 2000. "*The Octopus's Garden* is a memoir and a way I shared with the general public how wondrous the deep sea is," says Van Dover.

In 2000, while at William and Mary, Van Dover organized a large, multidisciplinary expedition to the hardly explored deep-sea vents in the Indian Ocean to document their fauna. There, the team discovered a new kind of snail the size of a ping-pong ball with scales on its foot. "There is no snail in the history of the planet that has scales on its feet, so that was exciting."

COLLABORATING WITH INDUSTRY

Recently, Van Dover has become a pragmatic conservationist. In 2004, following a meeting at the Jamaica-based intergovernmental International Seabed Authority, Van Dover was approached by Nautilus Minerals, a Canadian mining company considering digging for copper and gold in the deep sea, with questions about the resilience of deep-sea vent communities. Between 2005 and 2014, the company gave her modest funding and some time on Nautilus ships for her students to collect samples. Van Dover's research helped shape Nautilus's environmental management of vent habitats. As part of this work, she characterized the intricate food webs at hydrothermal vents, including at the Manus Basin, an inactive vent near Papua New Guinea where Nautilus obtained the first-ever permit for a deep-sea mine.

Van Dover doesn't have a "don't mine the sea floor" mindset as long as there is enforcement of solid environmental regulations. But make no mistake: she is adamant about protecting active hydrothermal vents. "Globally, these vents only occupy an area the size of Manhattan. They are really rare and extraordinary habitats that we need to preserve," she says.

In 2006, Van Dover moved to Duke University, becoming the first woman to head its Marine Laboratory, which she did for 10 years. "It was a different kind of challenge, of planning and implementing, that I really enjoyed," she says.

These days, still at Duke, she is spending all of her time on seafloor management and conservation, working with the International Seabed Authority and other stakeholders to consider proper regulations and monitoring of this dark, underexplored part of the world.

Seeing and studying these remote corners of the globe has changed Van Dover forever. "Experiencing the strangeness of the vent ecosystems freed me from thinking in a prescribed way," she says. "I was able to look for the unusual." ■

Nick Pyenson: Whale Chaser

Curator of Fossil Marine Mammals, National Museum of Natural History, Age: 38

BY JIM DALEY

Nick Pyenson first fell in love with natural history museums as a child, growing up in Montreal when his parents would take him to McGill University's Redpath Museum and Harvard's Museum of Comparative Zoology to learn about the diversity of Earth's animals, plants, and ecosystems. Seeing the skeletons of large animals, especially those of whales, got him thinking about the stories marine mammals had to tell. In 1998, Pyenson went to Emory University and while he was there started studying whale brains. During a college trip, he and his friends "found a dead dolphin on a beach," he recalls, "and I thought it was totally fascinating." The dolphin led Pyenson to question how well the fossil record represents past life. "Understanding pathways of decay and destruction," he says, "is . . . a big part of what paleobiologists do."

In 2003, Pyenson, now a paleobiologist and curator of fossil marine mammals at the Smithsonian's National Museum of Natural History in Washington, D.C., headed to the University of California, Berkeley, where he started his graduate work studying the evolution of whales. Stanford zoologist Jeremy Goldbogen, then a master's student at the Scripps Institution of Oceanography, remembers a conversation the two had about how large whales feed. "Nick . . . brings a lot of knowledge about how living whales work to understand what life was like in the [ancient] oceans," Goldbogen says.

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Pyenson decided to investigate how ancestors of toothed whales, such as dolphins and sperm whales, came to use echolocation. With his Berkeley advisor, David Lindberg, Pyenson published a study in 2007 suggesting that whales developed the trait to hunt cephalopods at night in the shallowest level of the ocean, and later adapted it for diving down to hunt them at greater ocean depths.[1] Pyenson also met Susan Kidwell, a paleobiologist at the University of Chicago, at the time. She'd been comparing distributions of live and dead mollusks to determine how well the fossil record represents animals that lived in the past. "Nick . . . very cleverly thought to try to do the same kind of comparison focused on whales and other marine mammals," she says. But recently deceased whales are harder to find than dead mollusks. So Pyenson reviewed literature and agency records on whale strandings and found that they closely reflect the patterns of richness and relative abundance of modern-day whales along coastlines, suggesting that the fossil record similarly reflects the diversity and relative abundance of whales in the past.[2]

That same year, Pyenson started working with Goldbogen on feeding in baleen whales. These behemoths, such as blue whales and fin whales, use a feeding pouch with specialized blubber that's very stretchy—and lined with muscle and nerves—to take giant gulps of seawater and krill, filter out the water, and swallow the rest, says Goldbogen. Embedded in the pouch is a unique mechanosensory organ that coordinates the movement of different muscles involved in filter feeding, Goldbogen and Pyenson reported in 2012.[3]

In June, Pyenson published *Spying on Whales: The Past, Present, and Future of Earth's Most Awesome Creatures*, which describes how whales evolved from relatively small land-based creatures to the largest organisms that ever lived on Earth. Science, Pyenson says, is all about "telling stories, telling true narratives about the world." It takes creativity, he says, along with a bit of detective work. ■

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A Measure of Change

Mutation rate is a crucial statistic for evolutionary biologists, and there are many ways to estimate it.

BY AMBER DANCE

Mutation: it's the raw material for evolution. That makes knowing the rate at which it occurs crucial to the study of evolutionary biology.

Mutation rate figures into all kinds of calculations. For example, the "molecular clocks" that evolutionary biologists use to estimate when one species first diverged into two are based on species' mutation rates. Scientists also use the rates to track how quickly viruses, such as influenza, evolve. And cancer biologists are interested in using mutation rates to estimate how quickly tumor cell genomes might change over time.

"It is a parameter that you have to input into every mutation-evolution model there is," says Yuan Zhu, a postdoc at the Genome Institute of Singapore.

Scientists used to infer mutations from phenotypic changes, such as the development of drug resistance. Now, thanks to increasingly cost-effective and rapid DNA sequencing, more-sophisticated ways of getting a handle on whole-genome mutation rates have emerged. Among these techniques are methods that researchers can apply to just about any species. Though scientists have primarily analyzed microbes and viruses thus far, they've also tackled lab models such as *Drosophila* and *Arabidopsis*, and even humans. These techniques are revealing how the mutation rate varies across the genome of a single species, and they're pinpointing regions that are especially prone to alteration. They're also uncovering the error rates of different enzymes, such as polymerases and repair enzymes, in the DNA replication process.

Here, *The Scientist* profiles four different ways of studying mutation rates in viruses, yeasts, and humans.

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AU NATUREL

Researchers can identify mutations in natural populations of organisms. Rafael Sanjuán, an evolutionary biologist at the Institute for Integrative Systems Biology in Valencia, Spain, does so with viruses. "They mutate a lot, so it's easy to witness evolution in real time," he says.

HIV, in particular, is known for its astronomical mutation rate, an estimated 3 x 10^{-5} errors per base, per infection cycle. However, that rate was determined with virus growing in the lab. Sanjuán instead investigated the HIV mutation rate in the wild—that is, in blood samples donated by 11 people before they underwent HIV treatment. Because the pathogen mutates constantly, a single untreated person contains a population of ever-diversifying viruses.

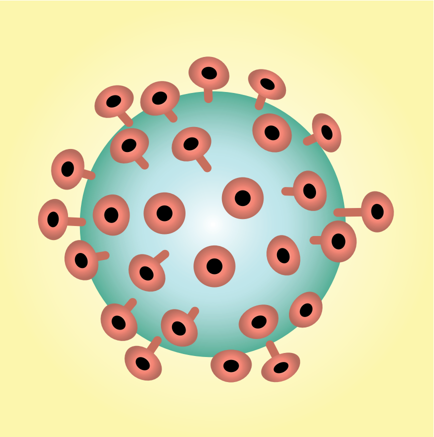
How could one time point give Sanjuán a rate of change? His trick is to look only for lethal mutations. These are found in viral particles that received a faulty copy of the HIV genome. They exist in blood cells, but are unable to infect other cells or replicate any further—they're evolutionary dead ends. That means any lethal mutation had to happen in the generation immediately preceding the dead-end viruses.

Sanjuán and colleagues considered any nonsense mutations, which would insert a premature stop codon, to be probable lethal events. Based on the HIV sequence, the researchers figured this could possibly happen at 732,350 spots in the genome. In their samples, they observed 3,069 likely lethal mutations. Then, it was just a simple fraction: 3,069 actual lethal mutations divided by 732,350 possible lethal mutations gave them a mutation rate of 4.1 x 10^{-3} mutations per base, per cell infection cycle. (*PLOS Biol*, 13:e1002251, 2015)

Presumably, nonlethal mutations would occur at a similar rate. That corresponds to one mutation per 250 bases every time the virus genome is copied, much greater than the in vitro rate—and one of the highest known in biology.

PROS:

- Analyzing "wild" populations, as with viruses in real hosts, gives better information about the real mutation rate, Sanjuán says.
- Sanjuán's lethal-mutation approach, in particular, eliminates the effects of replication or natural selection.
- Natural-population methods, such as the lethal-mutation trick, can work with any sample and any organism, so long as researchers make certain assumptions about sites where mutations are neutral and unaffected by natural selection. Researchers have done similar studies with humans, for example, by picking out unique mutations in a closely related group.



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CONS:

- Scientists working with nonviral wild populations might find that natural selection can affect which mutations persist.
- If the individuals in a sample are distantly related, it can be difficult to tell which mutations are new, notes Zhu.

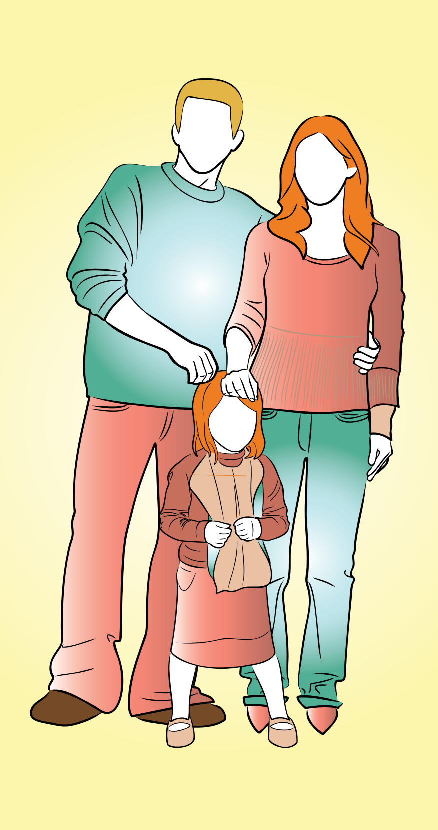
THE POWER OF THREE

New mutations haven't yet had time to fall subject to natural selection. One way to be sure mutations occurred recently is to sequence groups of two parents and their offspring, or trios. Any sequence found only in the offspring must have happened this generation. "It's the most direct observation you can have," says Shamil Sunyaev, a computational geneticist at Brigham and Women's Hospital and Harvard Medical School in Boston.

To understand patterns of mutation across the human genome, Sunyaev and colleagues in the Netherlands examined sequences from 250 Dutch trios. They observed 11,020 new mutations in the children of these families.

The authors generated a map of mutation rates across the human genome. The map revealed that genes were more likely to mutate than noncoding DNA. That's probably because CpG dinucleotides—stretches of the genome where guanines follow cytosines—are more frequent in coding sequences, and are relatively susceptible to error because methylated cytosines have a tendency to undergo deamination, transforming them into thymines. (*Nat Genet*, 47:822-26, 2015).

Though the researchers' goal was not to determine the overall human mutation rate, back-of-the-envelope calculations showed that their data matched nicely with the accepted number, about 1.2 x 10^{-8} mutations per nucleotide, per generation, says Sunyaev. While that mutation rate hardly measures up to that of HIV, "it's a very large number," he notes. That corresponds to about 70 de novo mutations in every baby, about one of which will occur in a protein-coding gene, he says.



PROS:

- You can confirm mutations are novel.
- It works for any sexually reproducing species, if you can collect all members of the trio.

CONS:

- It misses embryonic lethal mutations.
- With large organisms such as humans, Sunyaev notes, there are few ways to experimentally investigate and confirm the mechanisms behind the observed mutations.

IN THE LAB

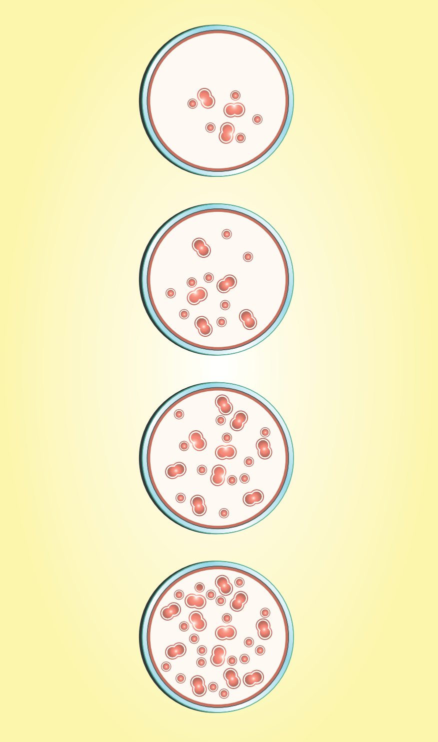
A method that gives scientists more experimental control is a mutation accumulation experiment. Researchers grow organisms in the lab, generation by generation, and track the genetic changes that build up.

Zhu and colleagues used this technique with the yeast *Saccharomyces cerevisiae* when she was a graduate student in the Stanford University laboratory of Dmitri Petrov. Their collaborators at the University of Georgia had grown 145 strains of budding yeast for approximately 2,000 generations each. Every two days, or about 20 generations, they streaked the cultures and used one colony to start the next round. Doing so created a bottleneck and eliminated much of the chance that the fittest yeast would take over the culture. "This is as close to neutral evolution as possible," says Zhu.

At the end of the experiment, the researchers identified almost 1,000 spontaneous mutations, including 867 single-nucleotide swaps and 26 indels. They calculated that the single base pair mutation rate was 1.7×10^{-10} per base, per generation, while the indel rate was 5×10^{-12} per base, per generation. (*PNAS*, 111:E2310-18, 2014).

PROS

- Natural selection is minimal.
- The lab environment gives researchers control.



CONS:

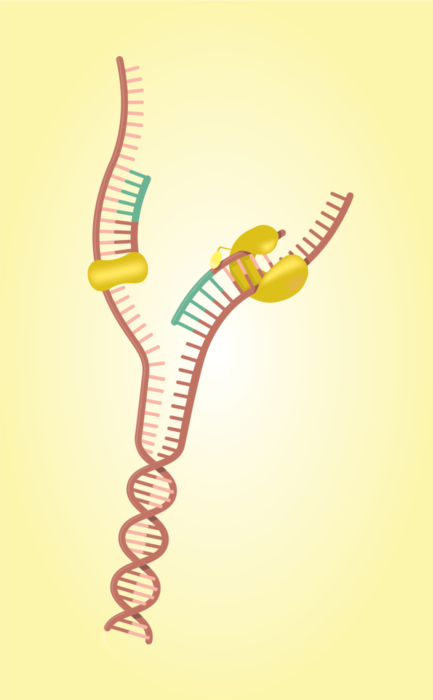
- Mutation accumulation is only feasible for organisms with short generation times, and those that breed well in the lab setting.
- It's always possible that the mutation rate is different in other strains, or in the wild.

ERRORS & REPAIRS

Mutation accumulation experiments can also help scientists understand how mistakes in DNA replication occur, and how cells fix them. That's what bioinformatician Scott Lujan and molecular geneticist Thomas Kunkel, both at the National Institute of Environmental Health Sciences in North Carolina, are interested in. The researchers also analyzed *S. cerevisiae*, over 900 generations, calculating the same mutation rate as Zhu—1.7×10^{-10} per base pair, per generation for wild-type yeast.

To delve into how and why those mutations occur, they also analyzed a variety of strains with defects in the DNA polymerases that synthesize new strands, or in the DNA mismatch repair protein MSH2. By analyzing mutation patterns in these strains, they could discover what kinds of mistakes the polymerases are most likely to make, and what mistakes cells are best able to repair.

Lujan analyzed 40,000 mutations in the eight strains he studied. Among his discoveries, he found that different DNA polymerases work on each strand of a growing DNA molecule. When the two strands separate into a replication fork, replication proceeds differently on each strand because polymerases only work in the 3' to 5' direction. On one side, polymerases can synthesize a single, long strand called the leading strand, moving from 3' to 5'. On the other side of the fork, the polymerases must work 5' to 3'. They do so by synthesizing short chunks of DNA in the 3' to 5' direction, then linking those together. This is called the lagging strand.



Lujan could tell which of three yeast polymerases worked on different sections of DNA because each leaves a unique pattern of errors in its wake. For example, pol delta is prone to create AA mismatches, and these were prevalent along the new DNA synthesized as the lagging strand, indicating pol delta works in that direction.

The mismatch repair system also worked differently on dissimilar mutations. For example, says Kunkel, it was pretty good at fixing a T mistakenly paired with a G, but not so efficient at fixing rarer substitutions, such as a C linked to another C. The cell was better at repairing the more common errors (*Genome Res*, 24:1751-64, 2014). "That's how organisms get very low mutation rates," concludes Kunkel.

PRO:

- Mutations accumulate faster in strains that lack key DNA replication or repair genes.

CON:

- While this works well for microbes, it would be harder to avoid natural selection in animals such as mice. For example, any embryonic lethal mutation would be invisible to the researchers. As Kunkel puts it: "Dead cells tell no tales." ■

THE SCIENTIST STAFF

Needles in Haystacks

From the difficulty of tracking rare populations to the danger of poachers exploiting distribution data, the complications of studying endangered species require creative solutions from researchers.

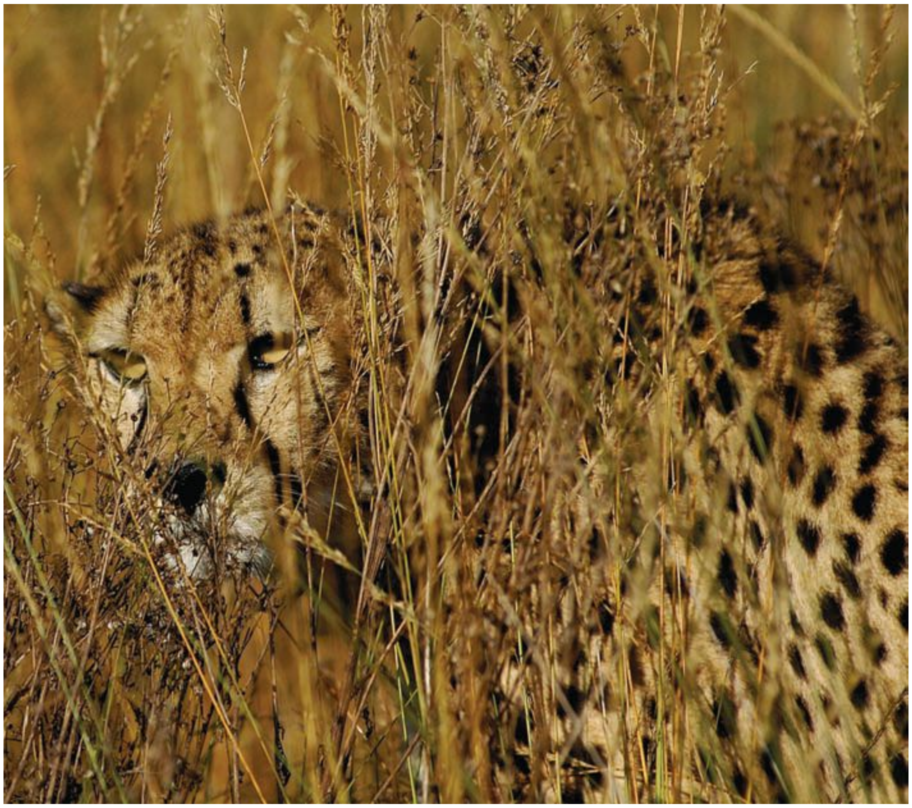
BY JIM DALEY

More than 14,000 species are listed as endangered or critically endangered by the International Union for Conservation of Nature. Some scientists have called for naming the present geologic epoch the Anthropocene, or "human era," after the main source of startlingly rapid rates of species extinction and other environmental perturbations.

Understanding the biology of the species that are most at risk from this disturbance is a critical prerequisite to developing effective strategies to conserve them. But scientists who survey endangered animals have to grapple with a number of special challenges alongside the traditional research pressures of publishing and grant writing.

For a start, there are the problems of finding organisms that are, by definition, relatively rare and may also tend to be elusive, nocturnal, or otherwise difficult to observe. Then, there's the risk of researchers exacerbating the very issues contributing to a species' or population's demise—for example, by increasing human contact or inadvertently raising the species' visibility to poachers.

In the face of these issues, scientists are coming up with unique and creative solutions, from making use of new technologies to advising researchers on how best to present their results.



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Where are you?

The tiger quoll (*Dasyurus maculatus*) is a housecat-size marsupial endemic to Australia. While numbers of the species have been increasing following drastic declines shortly after European colonization, several populations are still considered endangered. Tiger quolls are elusive creatures and provide a challenge to researchers such as Emma Bennett, a wildlife ecologist at Monash University in Melbourne who studies their ecology.

One option to facilitate the search is to use traps. But traps may injure or at the very least stress the animals—an outcome that researchers are obviously keen to avoid. Bennett, instead, is working to develop a far less invasive solution: dogs trained to track down the tiger quolls' scat, which can be analyzed to determine sex, diet, and information about the quolls' distribution. She recently partnered with a search-and-rescue dog trainer to teach volunteer conservation dogs how to locate quoll scat in Great Otway National Park in Victoria. "The dog handlers . . . are just passionate people who are interested in helping the environment," she says.

> Now, you put camera traps out in remote places and that's how you see all this imagery of snow leopards and tigers and all sorts of wonderful animals that you would never see any other way.
>
> —Stuart Pimm, Duke University

Bennett's strategy is just one example of how researchers studying endangered species are coming up with unorthodox solutions to the logistical challenges of tracking or observing organisms that are few and far between. Paul Evangelista, a research ecologist at Colorado State University, came up with his own approach while working in Somaliland, a small breakaway region of Somalia and self-declared state in the Horn of Africa. Somaliland has remote, hazardous regions where directly observing animal populations is very difficult. So Evangelista turned to locals. "I hold a lot of value towards indigenous knowledge, and I was trying to figure out how I could use some of that information to integrate into some of these more computer-based geospatial models," he says.

Evangelista's team surveyed citizens of Somaliland in 2016 and 2017, asking them whether any of 25 species occurred in their local areas. The researchers included a few species in the survey that they already knew were locally extinct as a quality control against false reporting. With the data they collected, the scientists were able to build species distribution models of the animals, including two of high conservation priority, the cheetah (*Acinonyx jubatus*) and the African wild ass (*Equus africanus*).

New technology is playing an increasing role, too, says Duke University conservation ecologist Stuart Pimm. Camera traps, for example, are progressing by leaps and bounds as digital cameras replace film ones. "Now, you put camera traps out in remote places and that's how you see all this imagery of snow leopards and tigers and all sorts of wonderful animals that you would never see any other way," says Pimm. This is filling in gaps in our knowledge of the distribution of these elusive species, he says.

Drones are increasingly being recruited to identify and locate hard-to-find animals as well (see "Fly-by" on pg. 53). "Now you can go out and buy a helicopter kit, put a camera on it . . . and [get] very high-resolution images," Pimm says. In 2016, for example, scientists at Woods Hole Oceanographic Institution and the National Oceanic and Atmospheric Administration (NOAA) used drones to study the health of critically endangered North Atlantic right whales (*Eubalaena glacialis*).

Pimm says that technologies that were either nonexistent or nascent a decade ago have "become quite standard procedures for studying biodiversity and what we humans are doing to it." He notes that technology may be fundamentally changing the nature of biodiversity and conservation research. "We're increasing by many orders of magnitude the rate at which we accumulate data," he says.

> We just have to be very conscious of who sees that data and who has access to it.
>
> —Paul Evangelista, Colorado State University

But even when researchers manage to collect data on their species of interest, challenges remain. The next immediate hurdle involves how to communicate research on endangered species to the larger scientific community—or whether to communicate it at all.

Death by print

When conservation and landscape ecologists David Lindenmayer and Ben Scheele of the Australian National University published location information on pink-tailed worm-lizards (*Aprasia parapulchella*), a species the International Union for Conservation of Nature lists as "vulnerable," their institution soon began getting calls from landowners reporting people trespassing on their property to find the animals. Some of the trespassers, who overturned rocks looking for the reptiles, may have been involved in illegal pet trafficking.

That episode joined a long list of examples of research-savvy poachers targeting rare animals almost as soon as they were described in the literature. Even well-meaning amateur naturalists can unwittingly upset endangered species just by trying to catch a glimpse. "It's quite a specific microhabitat that some of these animals rely on," says Scheele, "and even just searching for animals can be really damaging."

The resulting quandary of whether or not to publish data on endangered species' locations pits science's fundamental need for transparency against the risk of sensitive information falling into the wrong hands. Evangelista says he and his colleagues have sometimes kept sightings of rare organisms "under wraps" because of their concerns about blowing a species' cover. Indeed, when the researchers published their findings from Somaliland this March, they decided not to report details about the distributions of most of the species they studied. "As researchers that are on the ground, it really puts us in a very tough situation," he says. "We're not just doing this to publish papers—we're out here trying to save species, and we just have to be very conscious of who sees that data and who has access to it."

Lindenmayer and Scheele addressed the issue head-on in a paper published last year entitled, simply, "Do Not Publish" (*Science*, 356:800–801). In the paper, the researchers laid out the case for protecting data on critically endangered species, and they proposed an assessment that scientists could use to decide whether they should publish their information in the literature. The assessment includes criteria on a species' status and its risk from poaching. The provocatively titled paper "triggered a debate on how to deal with the data," says Scheele, although he notes that the assessment doesn't apply to most species, as there aren't many that are critically endangered, threatened by poaching, and highly localized. "Only a few species really need the assessment," he says.

The argument grabbed the attention of a number of other conservation biologists. Glenda Wardle, an ecologist at the University of Sydney, was a coauthor on a response that argued for open but responsible publishing. Biodiversity research "requires location information in order [to make] an assessment of the risks and threats," she says. "So if we don't publish—in other words, if we don't allow scientists and managers to know the full extent of the information—we're holding back the actual biodiversity progress that we want to achieve." Wardle argues that conservation biologists have always had good practices for sensitive data, but she adds that the 2017 article, and the response she coauthored, probably helped put the issue back on the conservation biology community's radar.

To help researchers decide how to communicate their research on endangered species, University of Sydney ecologist Ayesha Tulloch and her colleagues recently designed a decision tree for publishing sensitive location data that will allow scientists to weigh the risks due to poaching and amateur visitors against the potential benefits of enhanced conservation work. "Even if you're not in the conservation sphere, you should still be very aware of the conservation implications of your work and the threats to your species," says Tulloch. She says that getting relevant data to non-governmental organizations (NGOs) so they can act on them is a perennial problem in conservation ecology. NGOs can only make good decisions around wildlife management and habitat conservation "if they have the most up-to-date, the most high-quality information on where the species are and what's threatening them."

Making Connections

Getting other parties—such as conservation organizations, local and national governments, and the public at large—involved in studying and protecting endangered species is an ongoing challenge for biodiversity researchers and ecologists. Just acquiring permits from government agencies for observational studies can take years, says Kristin Aquilino, a biologist at the University of California, Davis, Bodega Marine Laboratory. While scientists wait for paperwork to clear, species can become locally extirpated—or worse, go extinct altogether. "It can be hard to act quickly when you have to go through that permitting process," she says. Meanwhile, scant resources make pursuing long-term studies difficult.

For researchers themselves, burnout can set in. Scheele says researchers working with critically endangered species "sometimes have to take a step back." Some of his colleagues have left ecology altogether because seeing habitat destruction occurring before their eyes weighed on them. There may have been several study sites when the research started, but "now they're under a house or a road," he says.

One way researchers are working to improve this situation is by trying to increase public engagement in gathering data on endangered species. Although it is often difficult to get the public to understand the value of animals other than so-called charismatic megafauna—large, beautiful animals such as whales and pandas—a number of initiatives are enlisting technology to get people personally involved in endangered-species assessments.

An increasingly popular app called iNaturalist, for example, encourages researchers and amateur naturalists to upload up to 1 million images a month to a database that maps observations from around the globe. Pimm calls the iPhone "almost the perfect tool" for citizen scientists to explore biodiversity. "I can take my phone and wander out into the woods and take a photograph of a plant or frog or insect . . . and post that observation on the web. Even if I don't know what it is, there will be a crowd of experts out there that will identify it for me."

Aquilino, meanwhile, stresses the importance of collaboration to mitigate the most difficult aspects of working with endangered species. Her lab teams up with agencies such as the California Wildlife Foundation and NOAA to study the effects of ocean acidification due to climate change on white abalone (*Haliotis sorenseni*). "What's so great about having so many partners [is] everyone brings something different to the table," she says. ■

FLY-BY

As unmanned aerial vehicles—commonly called drones—become cheaper, easier to use, and more widely available, conservation biologists are using them more and more to study endangered animals in the field.

Drones have the advantage of being able to fly over terrain that is inaccessible to ground-based researchers, and they may be able to get closer to animals than field workers can without disturbing them. Quadcopters and other hobbyist drones can be equipped with both optical and thermal imaging systems that enable the devices to locate animals that may be otherwise concealed, making survey counts more precise and accurate. Researchers can then analyze those images using computer algorithms, rather than by hand, vastly speeding up data processing and analysis. Some teams are even now turning to drones to track down poachers without putting park rangers' or researchers' lives at risk and to find sick or injured animals.

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But there are also potential adverse effects on wildlife. Flown too close, the devices can disrupt behavior. And a 2015 study reported that American black bears (*Ursus americanus*) exhibit a physiological stress response to the aerial vehicles' presence even when they show no behavioral change, suggesting that drones may be more intrusive than previously thought (*Curr Biol*, 25:2278–83).

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Enlightening Captivity

The capture and housing of orcas changed the scientific consensus on the marine mammals.

BY JASON COLBY

For most of the 20th century, scientists on the Pacific Coast of North America held two basic assumptions about the killer whale (*Orcinus orca*): first, it was a voracious predator inclined to attack anything in the water, including people; second, the species constituted an abundant and cosmopolitan population. Both turned out to be wrong, and it was captivity that revealed the truth.

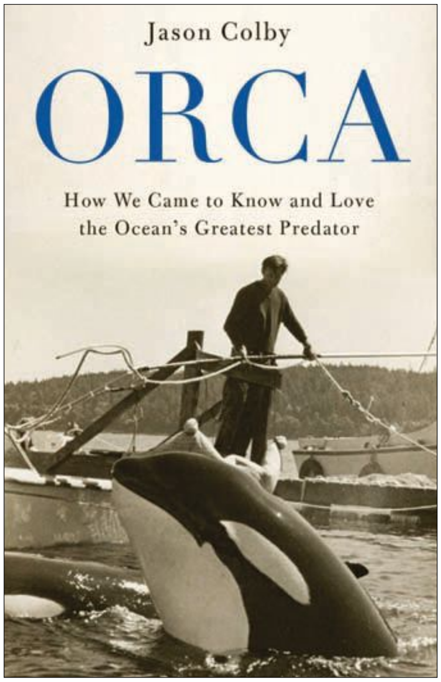
Until the 1960s, research on cetaceans remained extremely limited. Most marine mammalogists worked in connection with commercial industries such as whaling and sealing, and their research involved dissecting target species. This was certainly true of killer whales, which scientists and fishermen regarded as threats to valuable marine resources. In 1961, the Canadian Department of Fisheries mounted a machine gun on Maud Island, between Vancouver Island and the mainland, to cull the "killers" believed to threaten Chinook salmon runs, and between 1960 and 1967 the US government's Marine Mammal Biological Laboratory in Seattle killed and dissected at least 10 orcas to determine whether they were eating northern fur seals.

But in the summer of 1965, entrepreneur Ted Griffin transported an orca he named "Namu" from the waters off British Columbia to his aquarium on the Seattle waterfront, allowing researchers extended access to a living orca for the first time.

In *Orca: How We Came to Know and Love the Ocean's Greatest Predator*, I explore the role of live capture and captivity in the transformation of scientific and popular understandings of killer whales. Within weeks of putting Namu into his enclosure, Griffin himself was swimming and performing with the ocean's apex predator, to the delight of spectators and the surprise of scientists. The interspecies bond made headlines around the world, with *National Geographic* publishing a feature article by Griffin entitled "Making Friends with a Killer Whale." Such depictions raised doubts about the menacing reputation of *O. orca*. "I'm afraid we must toss away some of our earlier preconceptions about these animals," reflected whale scientist A. Remington Kellogg in the piece. "This behavior of Namu is entirely contrary to what anyone could have expected."

In the intervening years, keeping orcas in aquariums has stirred fierce public debate in the Pacific Northwest and beyond, particularly as the species' intelligence and social bonds became evident. But the practice also reshaped scientific understanding of killer whales. In addition to allowing research on the physiology, respiration, and acoustic capacity of the species, captivity raised questions about orcas' diet and ecological role. While Namu and several other orcas caught in the region seemed to prefer salmon, a pod netted off British Columbia in 1970 refused all fish for months.

Existing reference works offered no answers for such behavior, claiming that killer whales roamed the seas and fed on all manner of sea life. The standard marine mammal textbook of the time described *O. orca* as "a single species which travels extensively," and US government policy reflected that assumption. In justifying its decision to permit Sea World to capture killer whales in Puget Sound in 1973, the National Marine Fisheries Service asserted that there was no difference between "a killer whale taken in the Atlantic Ocean [and] one taken in the Pacific" and that "the Puget Sound animals do not form a separate and isolated grouping."



Oxford University Press, June 2018

Yet Canadian scientist Michael Bigg was already painting a different picture. Working partly with captive animals, he developed a system of identifying individual killer whales in the wild using their natural markings. From that point, he would reveal the extraordinary complexity of killer whale social and ecological interactions, which are characterized by matrilineal organization and distinctive food cultures. And he would reveal something more alarming: there were fewer orcas in the shared US-Canadian waters of the Pacific Northwest than anyone imagined. Later labeled the Southern Resident Killer Whales, the endangered population now includes just 76 animals. But the main threat to these iconic orcas is neither bullets nor captivity but rather the decline of Chinook salmon, their preferred prey. ■

Jason Colby is an associate professor of history at the University of Victoria in Canada. Read an excerpt from Orca *at www.the-scientist.com.*

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	14–18	**Immunometabolism, Metaflammation and Metabolic Disorders** (D6) Vancouver, British Columbia | Canada
	14–18	**Small Regulatory RNAs** (D7) Daejeon | South Korea
May	6–9	**Delivering Therapeutics Across Biological Barriers** (E1) Dublin | Ireland
	13–16	**Climate Change-Linked Stress Tolerance in Plants** (M4) Hannover | Germany
June	9–13	**Positive-Strand RNA Viruses** (E2) ♦ Killarney, County Kerry | Ireland
	16–20	**Neural Environment in Disease: Glial Responses and Neuroinflammation** (Z1) *joint with* **Neurodegenerative Diseases: New Insights and Therapeutic Opportunities** (Z2) Keystone, Colorado | USA

Scholarship deadlines precede meetings by four months, abstract deadlines by three months and discounted registration deadlines by two months. View details for each conference at **www.keystonesymposia.org** followed by **/19** and the alpha-numeric **program code** (e.g., **www.keystonesymposia/19A1**). Registered attendees of one meeting in a joint pair may attend sessions of the other at no additional cost, pending space availability, and can take advantage of the joint poster sessions and social breaks. ♦ Global Health Series conference.

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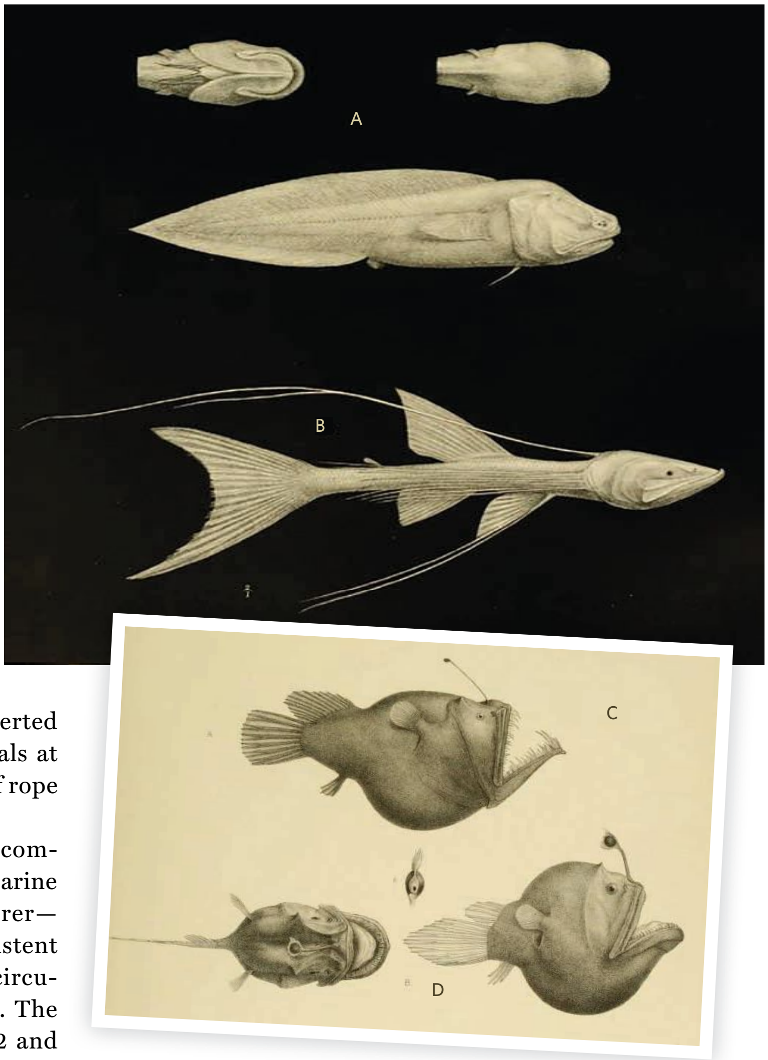
Maiden Voyage, 1872–1876

BY ASHLEY YEAGER



DEEP DIVE: The gelatinous blindfish (*Aphyonus gelatinosus* , A), netted roughly 1.5 miles below the ocean surface; *Bathypterois longicauda*, B, which was found 2.89 miles down; Murray's abyssal anglerfish (*Melanocetus murrayi*, C), named after a biologist on the *Challenger* expedition; and a double angler (*Diceratias bispinosus*, D)

ALBERT GÜNTHER, *REPORT ON THE DEEP-SEA FISHES COLLECTED BY THE H.M.S.* CHALLENGER *DURING THE YEARS 1873-1876* (LONDON: HER MAJESTY'S STATIONERY OFFICE, 1887).

Deep beneath the ocean swells lurk creatures never seen by people—or so some scientists thought in the late 1800s. In *On the Origin of Species*, Charles Darwin suggested the oceans had remained largely unchanged for millions of years and would contain living fossils of the past, providing proof of his idea of evolution. Others envisioned the deep ocean as a vast wasteland, filled only with extremely primitive life forms, or none at all. To settle the debate, the Royal Society of London launched a daring expedition—the voyage of the HMS *Challenger*—to map the ocean floor, to study seawater temperatures and chemistry, and to dredge up deep-sea organisms.

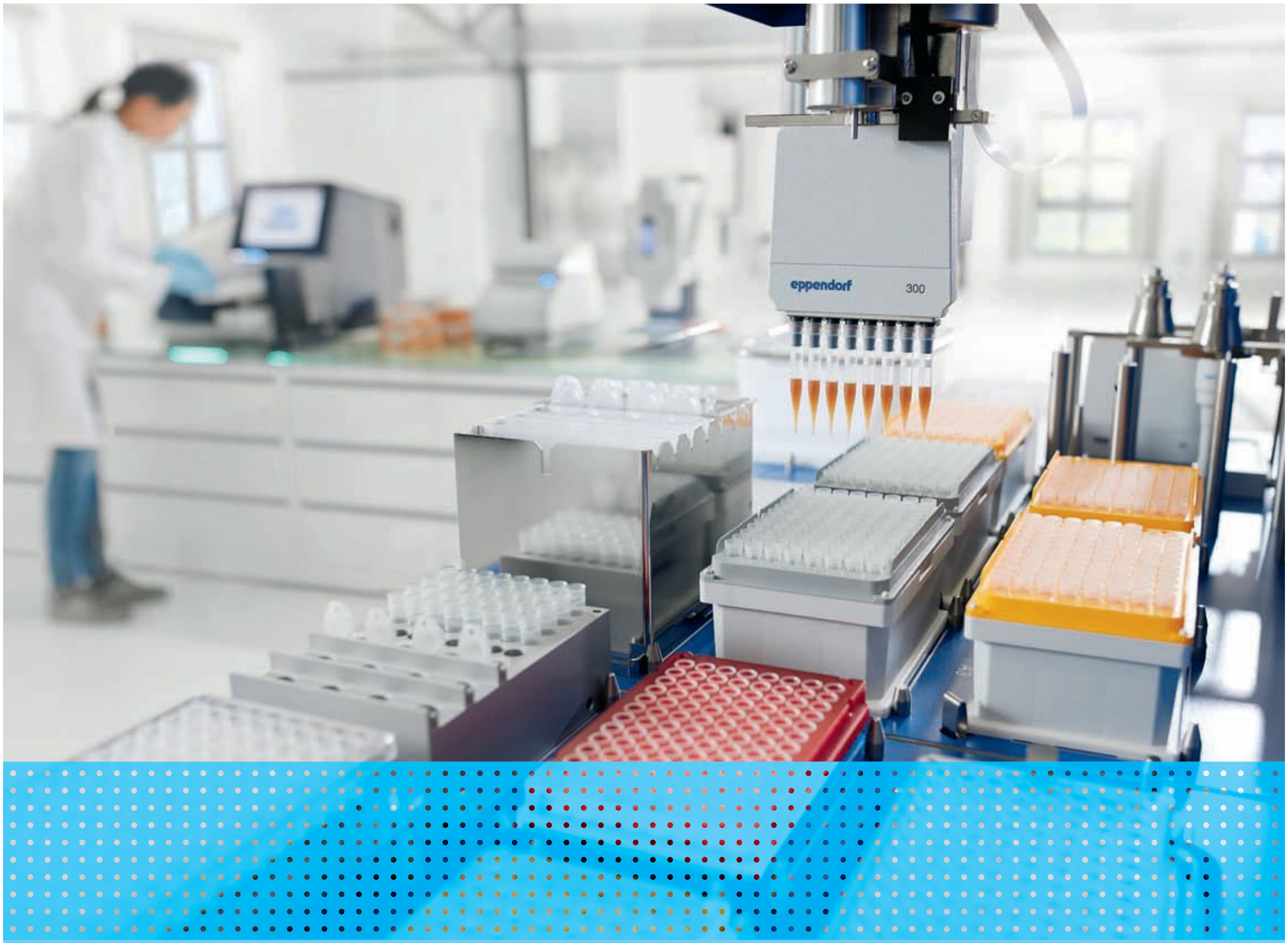
The voyage may have been "nothing less than a last chance to choose between God and Science," writes the biogeochemist Richard Corfield in his 2003 book, *The Silent Landscape: The Scientific Voyage of HMS* Challenger. Work done aboard *Challenger* revolutionized researchers' ideas about Earth's oceans and laid the foundation for the field of oceanography, he tells *The Scientist*.

Challenger was a small warship that had been converted into a floating laboratory, with nets to scoop up animals at varying depths and winches that unspooled long lines of rope to record the depth of the ocean floor.

Captain George Nares, a famous navy surveyor, commanded the 68-meter, wind- and steam-powered ship. Marine zoologist Charles Wyville Thomson, a veteran explorer—whose discovery that ocean temperatures weren't consistent at different depths suggested the existence of ocean circulation—led the *Challenger* expedition's scientific team. The crew left from Portsmouth, England in December 1872 and sailed to the south Atlantic, around Africa's southern tip at the Cape of Good Hope, across the southern Indian Ocean, and into the Antarctic Circle. It then headed eastward to Australia and New Zealand, the Hawaiian Islands, then south around the southern tip of South America, back into the Atlantic, and finally headed for home in May 1876.

Among *Challenger*'s greatest discoveries was what was then the deepest spot detected in the ocean—a section of the Marianas Trench that sits more than 8,200 meters below the western Pacific's surface. (A spot called Challenger Deep now holds the depth title, at 10,994 meters.) Maps of the ocean floor also revealed the first hints of a rise in the middle of the Atlantic Ocean, now named the Mid-Atlantic Ridge. And new species of deep-sea sponges, bizarre anglerfish, and dinoflagellates were discovered. It took researchers roughly two decades to work through all of the data the crew collected, and the analysis occupied 50 volumes.

Many of *Challenger*'s most important findings, however, couldn't be interpreted at the time. Decades later, for example, geologists came to realize that the existence of the Mid-Atlantic Ridge provided evidence for plate tectonics, Corfield notes. And, though the voyage produced evidence to support the theory of evolution, its greater effect was to spark a public fascination with the world's oceans—one that continues today. ■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