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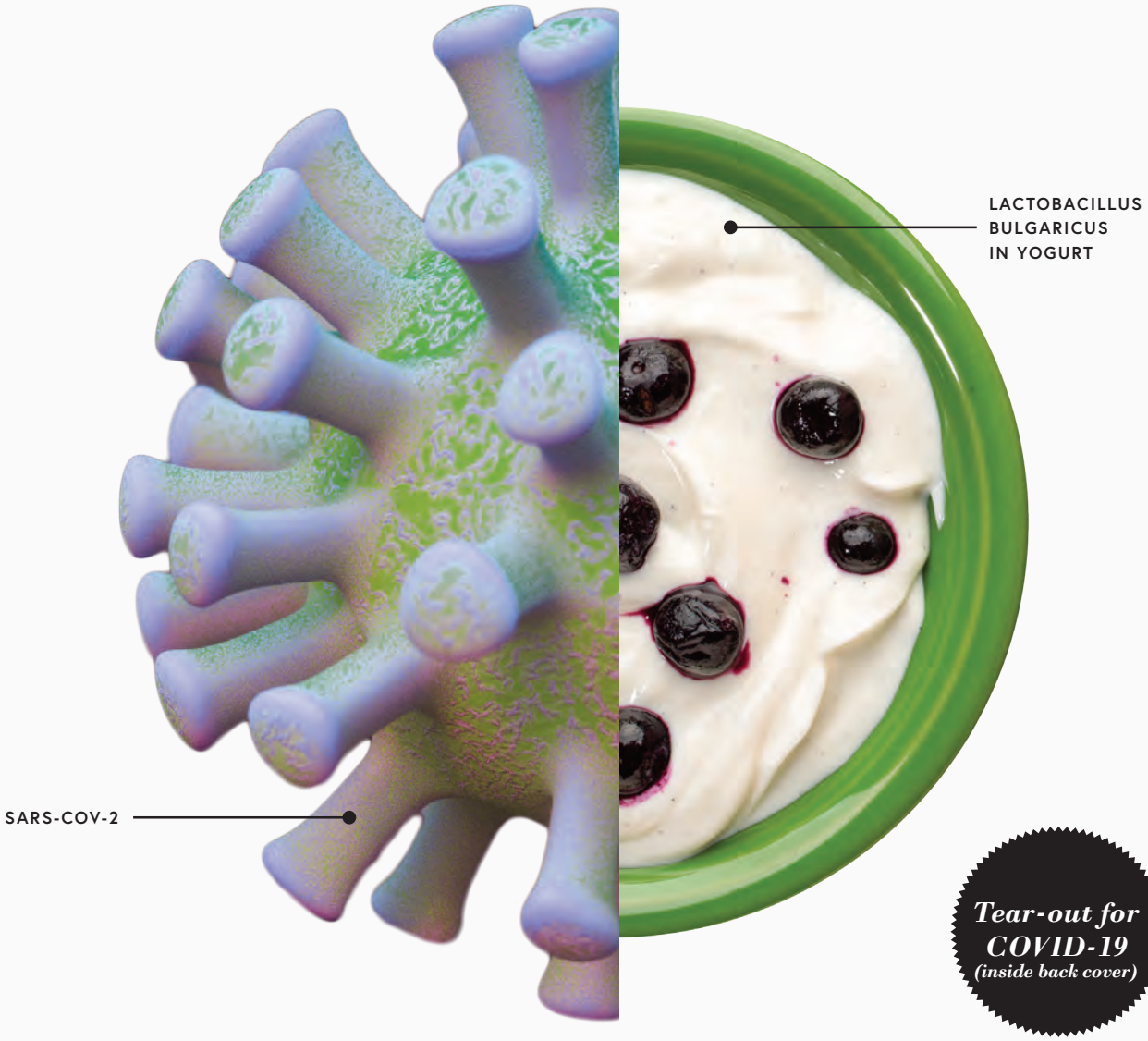

Tear-out for COVID-19 (inside back cover)

HOW MICROBES ARE CAUSING & SOLVING HUMANITY'S BIGGEST PROBLEMS

AMERICAN SOCIETY FOR MICROBIOLOGY

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CONTRIBUTORS

ANGEL CORONA, PH.D. is a science writer in Cambridge, Mass. He earned his Ph.D. in microbiology and immunology at the University of Maryland, Baltimore. You can find him on Twitter at @AFCorona343.

JENNIFER TSANG, PH.D. is the science communications and marketing coordinator at Addgene and a freelance science writer. She has a Ph.D. in microbiology and studied antimicrobial resistance as a postdoctoral fellow. She is the creator of a microbiology blog called The Microbial Menagerie.

JULIE WOLF, PH.D. is the science communications specialist at ASM and the host of ASM's newest podcast, Meet the Microbiologist. In her free time, she teaches at the community biolab Genspace.

KATHERINE HEITZ, MSC. is a program specialist with the Global Public Health Program at ASM.

KATHERINE LONTOK, PH.D. is the scientific and digital editor at ASM. She holds a Ph.D. in molecular biology and biochemistry from the University of California, San Francisco.

STEPHEN ORNES is a science and medical writer and the creator and host of Calculated, a podcast collection of stories about people at the intersection of math, art and culture. Visit him online at stephenornes.com.

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From the editor

STANLEY MALOY, PH.D.
EDITOR IN CHIEF

THE YIN-YANG OF MICROBES

Unlike a common refrain from the 1960's, "If you're not part of the solution, you're part of the problem," microbes both cause and provide solutions to many of our world's biggest problems. This is not surprising to microbiologists, who are aware of the tremendous genetic, metabolic and ecological diversity of microbes that allows them to live virtually anywhere in nature, including in humans, animals, plants and inhospitable environments.

Responding rapidly to microbial challenges and opportunities relies on basic and applied research done long before the needs arise. This research requires a continual influx of trained scientists working in academia, industry and clinical labs, expensive equipment and reagents, and — as noted by Katherine Heitz in this issue of *Microcosm* — appropriate biosafety conditions to protect the researchers, community and environment. Most microbiology research is financed by government funding, requiring awareness and support from the public and policymakers.

The public typically learns about microbes from the media. Despite their broad impact on human lives, from medicine, public health, agriculture, the environment, economic development and many things in between, news about microbes is often focused on exotic or esoteric stories like diseases that affect distant countries or the number of bacteria on shower curtains. Hence, although microbes often make splashy headlines, they are quickly forgotten as the news cycle moves on to other issues.

In contrast, the COVID-19 pandemic has been front-page news for several months now, as the public wants to understand questions like: Where did it come from? Why weren't we prepared? Why does it take so long to develop new anti-viral therapeutics and vaccines? What is the probability that my family will be infected? And, how long will it last?

The article by Stephen Ornes provides useful perspectives on the COVID-19 pandemic, although our understanding of the disease continues to evolve as we learn more on a daily basis. The challenges of implementing effective and appropriate responses to this pandemic emphasize why it is critical for the public and politicians to understand how science works, why evidence-based decisions require thoroughly testing hypotheses and where to find trustworthy expertise.

Once the COVID-19 pandemic has subsided, many people will focus on other things and forget the importance of microbiology in all of our lives. We need to be prepared for the next pandemic, with an understanding that the initial outbreak could happen anywhere in the world and be quickly transmitted around the globe.

Sometimes people have a narrow focus on human disease, seemingly forgetting that microbes influence plants and animals as well, and that human health depends upon agriculture for food. This is nicely emphasized in Julie Wolf's article on bananas.

However, it is critical that people understand that many microbes are beneficial. Microbes can influence CO_2 sequestration, thereby tilting the balance of climate change. Microbes influence health and disease resistance in the rhizosphere, the microbiome of farm animals, and the human microbiome. Microbes produce foods, vitamins and therapeutics. Microbes degrade our waste products and generate energy.

Both thwarting problematic microbes and harnessing microbial solutions requires continuing support for research and education. ASM's communications and advocacy play an invaluable role in engaging the public and policymakers about these issues, but we all need to do our part to inform the public and policymakers about why microbes matter, the importance of evidence-based research and the need for an educated workforce.

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An Appealing Solution:

Applying a Microbial Solution to a Banana Infectious Disease Problem

BY ***JULIE WOLF, PH.D.***

THE BANANA & ITS DISEASE

Among fruit in the United States, bananas are top banana. Americans ate an average of 28.22 pounds of bananas in 2018 — that's 80 bananas for each person — and a survey found that more people had bought bananas than any other fruit within the prior 12 months. Despite their popularity, the inexpensive snack (prices have remained at an average of $0.57 for the past 48 months) is under attack: A fungal disease is threatening to eliminate our favorite fruit.

This isn't the first time bananas have come under microbial siege. In the 1960s, bananas were under attack from banana wilt disease. That same disease is now threatening the Cavendish variety bananas that we love, just as it did the then-popular Gros Michel banana variety. In that case, the fungus won, essentially eliminating the Gros Michel and forcing banana farmers to switch to a new variety. The Cavendish became the major banana variety when neither scientists nor farmers could halt the spread of or cure Gros Michel banana trees sick with the disease; the Cavendish variety has a natural resistance to the banana wilt disease of the Gros Michel variety. Cavendish now comprise up to 40% of global banana production.[1]

Fusarium wilt disease (also called Banana wilt or Panama disease) is caused by the fungal plant pathogen *Fusarium oxysporum f.sp. cubense* (FOC). FOC is further divided into different lineages, called races, which are determined by the variety of banana each group can infect; FOC race 1 ravaged the Gros Michel bananas. Cavendish banana plants are resistant to FOC race 1 and for decades were able to thrive in the same soils in which Gros Michel had previously been grown. However, Cavendish bananas are now being threatened by a relative newcomer: FOC tropical race 4.

FOC tropical race 4 (FOC TR4), a subcategory of FOC race 4, is the most destructive of these groups of fungi by several metrics: It has the widest range of banana variety hosts that it can infect, and it can be found in a wide range of temperatures and climates.[2] Once TR4 emerged in the 1990s, cases quickly sprang up in regions such as southeast Asia, Oceania and the Middle East, demonstrating the ability of the fungus to grow in any conditions that the banana plant can.

Fusarium fungi reside in the soil, where the fungus can access the roots of plants to initiate infection. Like many fungi, it exhibits many cell morphologies, and *Fusarium* chlamydospores are a dormant form of the fungus that

can subsist until the presence of plant root exudates induces germination to a vegetative state. These dormant spores are thought to persist up to 30 years, which can lead to contaminated soils unable to sustain susceptible plant crops for decades.

Within 10 days of planting, a banana tree in infected soil will have its roots colonized with clamydospores and hyphal cells found among the root hairs.[3] The fungus makes its way through the vascular system, eventually infecting the leaves and causing them to yellow and decay. The entire plant will succumb to its infection within months of disease onset. Due to the spread of FOC TR4, the Cavendish is now in the same danger as its Gros Michel predecessor. The disease threatens bananas that are snack foods in the United States but are vital sources of nutrients in the regions where they are grown, which consume 85% of the bananas produced.

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There are many banana varieties in the world, and you might expect the genetic diversity within the banana species to be an advantage that produces fungal resistance. But few bananas have all the characteristics that allow for worldwide distribution: thick skin to prevent bruising, growth in large numbers within tight bunches, ability to grow in varied climates, a flavor and texture that appeal to people all over the world, and the ability to withstand days or weeks of shipping. The Cavendish carries these traits (though it doesn't ship as well as the Gros Michel), and because of its near-singular perfection, farmers grow it in monoculture.

To grow new trees, the farmer takes the bottom of an old tree, the part known as the rhizome, and cuts it into many smaller pieces. The rhizome is the below-ground plant stem that sends out roots and shoots. When separated from the original tree, pieces of the rhizome will grow into new seedlings that can be harvested and planted in orchards. Each Cavendish tree is therefore derived from its parent and carries the same genetic material, creating a near-clonal population.

In 2017, scientists published that they had successfully created a genetically modified Cavendish variety that is resistant to FOC TR4, and that additional genetic-modification tools may help address plant vulnerability to this problem.[4,5] No commercially resistant banana strain is yet available, but FOC TR4 is extremely widespread. Previously thought to be confined to southeast Asia and Australia, the first cases in the Middle East were reported in 2013. The first identified case in Colombia in August 2019 means the disease is now in Latin America, the world's largest banana-producing region, and new countries continue to report infections. Multiple means of fighting infection are the best bet for success. Some scientists think a different approach will address the ability of plants to grow in FOC-infected soils: manipulating the other soil microbes around the fungus.

RHIZOSPHERES & MICROBIOMES

Like animals, plants have a microbiome, and the composition of this microbiome varies in different parts of the plant; the leaf microbiome has different microbial members than the stem microbiome. The rhizosphere microorganisms (microbes directly surrounding the rhizome) are a part of this plant microbiome. The roots release exudates into the soil directly surrounding them, which encourage microbial growth in the immediate proximity of the plant. These fungi and bacteria play important roles in plant health, such as producing phytohormones that regulate plant metabolism and defense systems, and they occupy space that might otherwise be available to a plant pathogen.[6]

The importance of the rhizosphere in plant health goes back to the early days of microbiology, when agricultural botanist Lorenz Hiltner recognized that *Rhizobium* inoculants improved nitrogen acquisition in crop legumes. Hiltner focused his research efforts on the rhizosphere and soil microbiology in the early 1900s and went so far as to hypothesize that "the resistance of plants towards pathogenesis is dependent on the composition of the rhizosphere microflora," though he worked most famously on warding off seed phytopathogens. Nevertheless, the idea was planted.

Soil microbiomes are regularly manipulated to benefit healthy growth, but often this involves providing additional nutrients, such as nitrogen. Brazilian Microbiologist Johanna Döbereiner spent her life studying nitrogen fixation, and when Brazil ramped up soybean production to become the primary soybean producer in South America, it did so using largely microbial nitrogen sourcing, rather than the chemical fertilizers preferred by farmers in the United States. By discovering new nitrogen-

fixing bacteria, Döbereiner's research allowed some sugar cane (Brazil's top export) to obtain 60% of its nitrogen via microbial means.[7] Large-scale soil microbial manipulation for improved plant health is therefore feasible.

CAN THE RHIZOSPHERE BE MANIPULATED TO WARD OFF PLANT PATHOGENS?

Many lab-scale experiments show promise when a variety of natural and genetically engineered plant pathogens are tested for this purpose. Microbes use many mechanisms to kill or inhibit other microbes, especially in nutrient-limited environments like soil, and these mechanisms can be hijacked by people to protect crops. The question is always whether these results can be replicated at the necessary scale.

For example, the oomycete *Phytophthora infestans* is a major pathogen of many plants. The soil bacterium *Streptomyces* is well known for secreting antimicrobial compounds, and some of these act against plant pathogens like *P. infestans*. By isolating and characterizing *Streptomyces* from many sources, strains that are more potent against crop pathogens can be identified and used by farmers as part of a "green manure" — a mix of microbes that provides nutrients, growth stimulation and disease prevention in place of chemical means. This practice has successfully reduced *Phytophthora* root rot on alfalfa, among other diseases.

This worked for the oomycete pathogen, but what about antifungal activity that would be necessary to treat FOC TR4 infection?

BANANA MICROBIOME MANIPULATION

Altering the soil microbiome with a biological agent of control has been a goal of plant pathologists studying plant infectious disease since the 1970s, when the protective role of some microbial species became popularly studied. Biological agents of control act as probiotics to the rhizosphere by promoting plant health through the direct inhibition of plant pathogens. Several microorganisms have moderate success when applied to banana plants in field experiments, including *Pseudomonas, Trichoderma, Bacillus,* and non-pathogenic *Fusarium* species, which when used aim to titrate out the pathogenic *Fusarium* by competing directly for the same nutrients and niches.

Pseudomonas species such as *P. fluorescens Pf1* have been successfully applied as biocontrol agents against *Fusarium* wilt of chickpeas and *Fusarium* wilt of tomatoes, though these diseases are caused by different lineages of *F. oxysporum*.[8] Several studies have suggested that *P. fluorescens Pf1* is one of the strongest inhibitors of FOC TR4, but field studies using a mixture of *Pseudomonas* strains have been most successful in inhibiting experimental disease.

P. fluorescence is a bacterial endophyte, which are part of the internal microbiota of the plant. All plants have signature bacterial and fungal endophytes, which differ based on plant species, environmental conditions and niche within the plant. Though they exist inside the plant, endophytes access internal structures from the roots, which means the first plant/endophyte interactions occur below ground, the same as initial *Fusarium*/plant interactions. The presence of *P. fluorescens Pf1* within banana plants is enough to double the phenolic content within treated plants, as well as induce expression of plant genes like peroxidase and chitinase that act as antifungal defenses;[9] both have been proposed to explain the protective effect of this strain.

More recently, other bacterial species have been tested in tandem with P. fluorescens Pf1 to better decrease Fusarium infection. Field experiments combining *Pf1* with two *Bacillus subtilis* strains decreased disease nearly 80% compared to untreated controls. In their experiments, Kavino and Manoranjitham inoculated the seedlings in a greenhouse to allow establishment of the microbial consortium before moving the plants to the field.[10] Changes in farming practices, in addition to multipronged beneficial microbial applications, may be necessary to treat infected soils.

Several studies suggest that additional practices, such as crop rotation, could influence the soil microbes present to influence *Fusarium* growth in local soil. The successive monoculture of banana plants was associated with an increase of *Fusarium* incidence, which also correlated with a higher fungal richness within the soil.[11] Rotating crops can decrease the soil fungal population: Two-year cycles of pineapples rotated with bananas decreased both FOC TR4 abundance in the soil and disease incidence relative to non-rotated bananas or bananas rotated with maize.[12] Successfully fighting *Fusarium* wilt may require both microbial treatments and changed behaviors.

Many aphorisms that hold true for human infectious diseases also hold true for plant infectious diseases. A pound of prevention remains worth an ounce of cure: Treating the microbiome works best if the beneficial microbes are present before the fungus attacks. But how

can the bacteria be added to the plant rhizosphere? There are as many formulations for plant therapeutic deliveries as there are for animal therapeutic deliveries. Though powder and capsule formulations have specific purposes, liquid applications can inoculate beneficial microbes into the rhizome pieces used for propagation and can also be applied to seedlings after planting.[13] Liquid disseminates beneficial microbes, but it can also spread the fungus, so applications must be carefully considered before use.

Many other microorganisms are also under study for use in fighting FOC TR4 infection. These microbial solutions are often multipurpose: some microbes, such as the fungal endophyte Trichoderma, show promise in fighting both *Fusarium* wilt and Black Sigatoka, another infectious disease of bananas. The ability to fight multiple infectious diseases, plus the ability to promote plant growth through phytohormone production, has created a strong incentive for scientists and banana producers to develop robust and accessible microbial solutions for banana infectious disease problems.

Ecological, economic, and societal hurdles remain to be crossed before *Fusarium* wilt will be reined in, but the scientific and producer communities are galvanized. The Food and Agriculture Organization of the United Nations has convened a Fusarium TR4 Task Force and provides a TR4 Global Network for educational and research resources.[14] Gert Kema, Ph.D., whose lab at Wageningen University in the Netherlands confirmed the Colombian Fusarium isolate, spoke at the 2018 International Congress of Plant Pathology,[15] where he said:

"It is clear that we never should underestimate the threat of Panama disease. By continuously putting it on the agenda, we take our responsibility and realistically call for action. Rather than paper over the cracks and create false hopes, we generate new data and strategies for structural and overall banana improvement."

Hopefully, the global focus on *Fusarium* wilt can provide a solution to save the Cavendish-variety banana before it goes the way of the Gros Michel.

"It is clear that we never should underestimate the threat of Panama disease. By continuously putting it on the agenda, we take our responsibility and realistically call for action."

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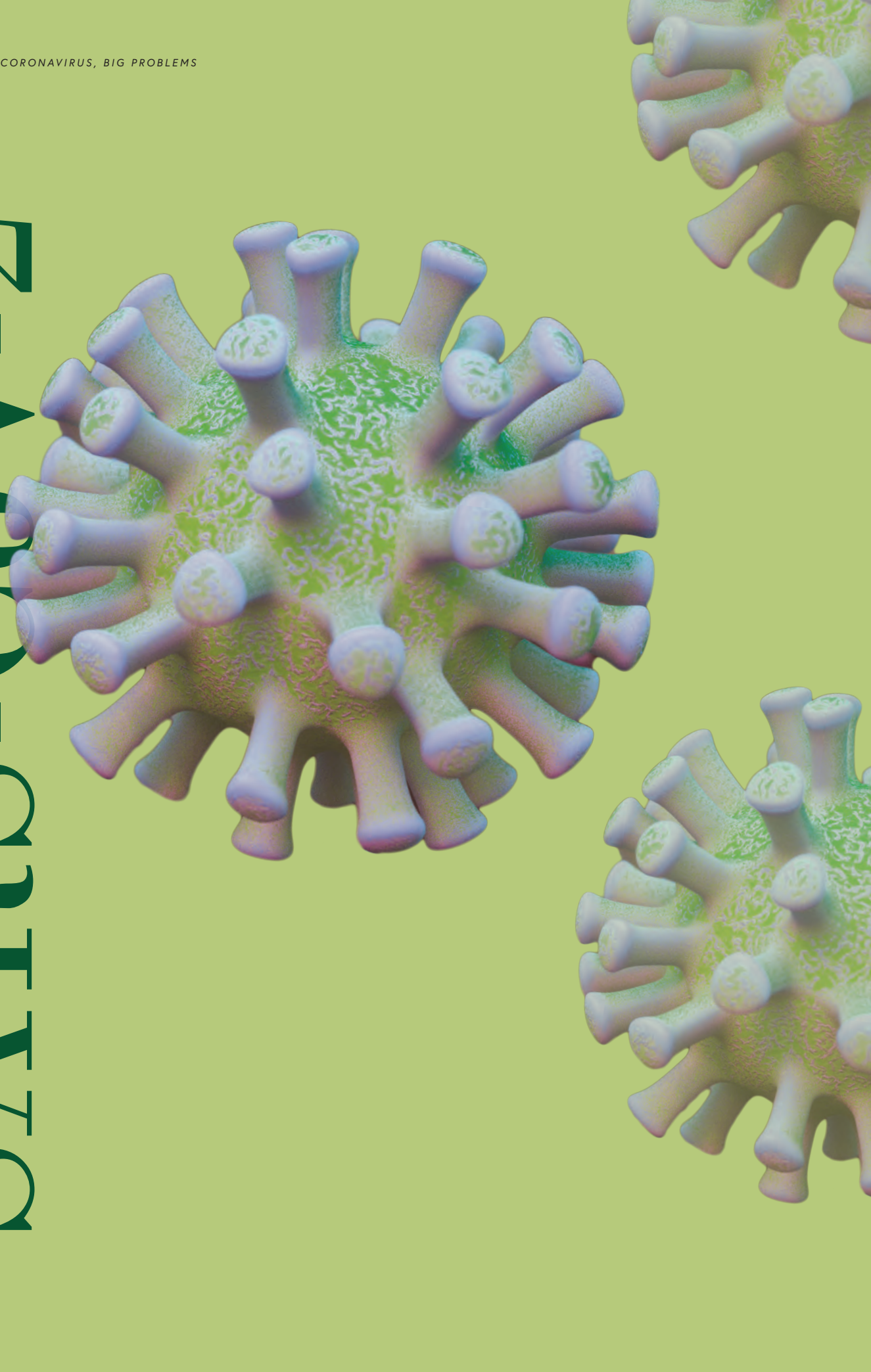
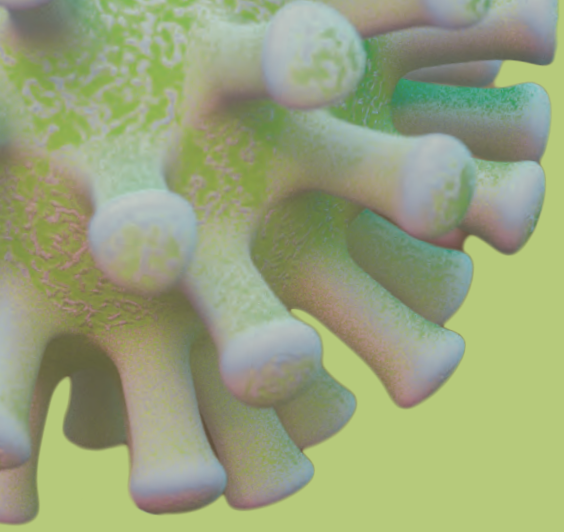
SARS-CoV-2





SARS-CoV-2: Tiny Coronavirus, Big Problems

The rapid spread of the coronavirus behind COVID-19 has turned the outbreak into the international health crisis of our time. Around the world, against a backdrop of unreliable data, government missteps and widespread misinformation, researchers race to understand the virus, target its vulnerabilities for new treatments and ultimately develop vaccines.

BY ***STEPHEN ORNES***

The call came on Sunday morning, Jan. 19, and Chas DeBolt, M.P.H., answered it. She had to: as a senior epidemiologist for the Washington Department of Health, in Seattle, DeBolt was on call over the holiday weekend. She listened as a clinician described a 35-year-old patient who thought he had a fever and definitely had a mild cough. X-rays didn't reveal anything suspicious, but the clinician heard rattling sounds — known as rhonchi — when the patient breathed. His temperature barely registered above normal. He tested negative for an array of probable causes for his condition, including influenza A and B, adenovirus, rhinovirus and four known human coronaviruses.[1]

He'd returned from visiting family in Wuhan, China, 4 days earlier.

In January, DeBolt and her colleagues had received alerts that a new respiratory illness was spreading quickly in the area around Wuhan, and the novel coronavirus behind the infection, which led to pneumonia-like symptoms, had been identified in January (a pneumonia outbreak was recognized in December 2019). If clinicians learned of anyone who'd recently been to the region and met certain vague criteria — a fever, lower respiratory illness — then staffers were instructed to call the U.S. Centers for Disease Control and Prevention (CDC) in Atlanta.

Which is what DeBolt did. "I really wasn't sure the CDC would want to test him because he had a pretty minimal temperature and a clear chest film," she says. But they did. "They were definitely being conservative," she says. DeBolt and a microbiologist from her office drove one county north, where the patient lived, to collect samples. They packaged the samples and drove to the airport, where they met a courier who flew the package to Atlanta. The CDC scanned the patient's sample for viral fragments.

The next day, the CDC confirmed that the patient had been infected with the new coronavirus, which has since been named SARS-CoV-2. Scientists in China had made the genomic sequence of the virus available on Jan. 10.[2] The disease, which causes pneumonia-like symptoms, is named COVID-19 (from CO-rona VI-rus D-isease 2019). DeBolt says she has managed multiple outbreaks over her 15-year career but remains surprised that the CDC caught that first case, based on such slight criteria.

"I still marvel at that," she says. "To me, it's just amazing that they decided to test."

we're learning day by day, sometimes hour by hour, about what's happening

The World Health Organization (WHO) declared a world health emergency in late January.[3] It has ignited efforts to get trustworthy diagnostic kits to the populations who need them. Microbiologists, virologists and epidemiologists around the world are racing to better understand the pathogen, with the goal of developing a safe and effective vaccine. That process, however, will likely take at least 12-18 months because before it can be approved by the FDA, an experimental vaccine has to go through a series of clinical trials that ensure it's safe and effective. Experts warn that a rushed vaccine could exacerbate the problem.

The pandemic is also sparking heated debates about fatality rates and other statistics, and produced torrents of misinformation that similarly spread like a virus. National and international travel, tourism and trade have been disrupted. So has education: As of mid-April the United Nations estimated on that schools had closed in 191 countries around the world, affecting more than 91 percent of schoolchildren.

This is how the pandemic began. How and when it will end remain open questions.

"This is very much an evolving situation," says Robin Patel, M.D., president of the American Society for Microbiology and head of the Infectious Diseases Research Laboratory at the Mayo Clinic in Rochester, Minn. "We're learning day by day, sometimes hour by hour, about what's happening."

GETTING TO KNOW SARS-COV-2

Coronaviruses make up a large and contagious family of pathogens that can infect animals or people. Four are known to cause mild respiratory infections, including the common cold. A fifth, identified in 2002, causes severe acute respiratory syndrome, or SARS, which infected 8,098 people and killed 774 during a 2003 outbreak. The sixth causes Middle East Respiratory Syndrome, or MERS, which was identified in 2012. In an outbreak that same year that spread to 27 countries, about 2,500 people contracted MERS and 858 died as a result, suggesting that the virus kills more than a third of people who become infected (though that rate is debatable, as an unknown number of cases likely went unreported).

The new coronavirus is the 7th known to be able to infect people. On Feb. 11, 2020, the International Committee on the Taxonomy of Viruses — the organization charged

with naming and classifying new viruses — reported that the new coronavirus, a "sister virus" to the one that causes SARS, would be named severe acute respiratory coronavirus 2, or SARS-CoV-2.[4]

The viruses behind MERS, SARS and COVID-19 all originated in animals and jumped to people. At first, researchers believed MERS-COV began in bats, but studies later confirmed dromedary camels as the animal reservoirs. Experts suspect that both SARS-CoV and SARS-CoV-2 originated in bats.

"Where there are bats, there are coronaviruses," says Lin-Fa Wang, Ph.D., director of Duke-NUS Medical School's Programme in Emerging Infectious Diseases in Singapore. There are other viruses, too: Bats can harbor the Ebola virus, Marburg virus, Nipah virus and Hendra virus without showing symptoms. Wang is currently developing technologies that could speed up the sequencing process of new viruses, with the ultimate goal of building a genetic library of bat coronaviruses. Such a resource, he says, could help researchers better surveil pathogens and track outbreaks.

In the case of SARS-CoV-2, researchers suspect that the virus may have jumped from bats to another animal before infecting humans, but an intermediate host — or hosts — hasn't been identified.

TO TRAVEL OR NOT TO TRAVEL?

COVID-19 has had a ripple effect on the world, the end of which is not yet in sight. Its origins are murky, though genetic analyses show that it likely began in bats. Many of the people first diagnosed with the disease had recently visited a seafood market in Wuhan, leading epidemiologists to suspect that the virus had jumped species there. But that's not certain: A study published in *The Lancet* in late January reported that the first patient had symptoms beginning Dec. 1 and didn't have a known link to later cases or the market.[5] That suggests the patient may have contracted the virus in November and raises the possibility that someone carried the virus into the market before it reverberated outward.

The next population to be diagnosed with the disease included people who had been in contact with people at the market, or who had been in the vicinity (such as the first U.S. case, near Seattle). In late February, the CDC reported cases of the disease in people in the U.S. with no obvious route of transmission — suggesting the possibility of community spread.

Even in mid-March, it was likely that the numbers of reported cases lagged behind the actual situation, and that the virus had been moving through large populations for weeks. A series of setbacks delayed the ability of local health departments to test local patients. The first involved getting a reliable test.

"Prior to this emergency, we did not have tests for SARS-CoV-2," says Patel. The CDC's first effort at distributing tests was botched when the agency sent out hundreds of kits that turned out to be faulty. The test looks for three specific genetic sequences, but it wasn't working correctly. "Ultimately what we saw was a problem with the assay, and many of those tests ended up being recalled," said Michael Mina, M.D., Ph.D., from Harvard University, during a Feb. 28 panel discussion hosted by the USC Annenberg Center for Health Journalism. That misstep, he says, did "significant damage" in hampering efforts to estimate the number of new cases.

A second roadblock, says Patel, emerged when the U.S. declared the situation to be a public health emergency, which meant that local laboratories, outside the CDC and public health departments, would not be permitted to use their own tests for SARS-CoV-2. That restriction effectively prevented researchers from being able to test patients at the local level.

"Many members of ASM develop and offer their own lab-developed tests," says Patel. On Feb. 28, ASM sent a letter to the Food and Drug Administration (FDA) to change the requirements, noting that the SARS-CoV-2 regulations were more stringent than for other viral tests. On Feb. 29, the FDA issued a new policy that relaxed the restrictions. "There hasn't been enough access to testing," says Patel, but that will likely change as labs put their own tests into play.

The ripple effect hasn't only moved through populations and public health agencies; it's also significantly dampened travel, tourism and trade. Passengers on cruise ships were quarantined away from home as they waited for test results. The American Physics Society canceled its largest annual meeting in March because of the virus, and at least two dozen other major medical or scientific conferences have been called off out of fear of spreading the outbreak.

The U.S. Travel Association, a nonprofit advocacy group, estimates that as people begin to make decisions based on the risks of the coronavirus and face government restrictions, international inbound travel to the United States will fall by 6% over the next three months, representing the steepest decline since the financial crisis in 2007 and 2008. For perspective, Chinese citizens make up the third-largest group of international travelers who visit the United States, with each spending about $6,500 during their trip.

On a broader scale, economists note that the outbreak has fueled more volatility in financial markets, evidenced by historic drops in the stock market in the first week of March. "The truth is that uncertainty is becoming the new normal," noted Kristalina Georgieva, managing director of the International Monetary Fund, on Feb. 19.

DIAGNOSTICS, TREATMENT & VACCINES OUTLOOK

Emerging studies have begun to identify how the virus attacks cells, especially in the lungs, and how those mechanisms might be exploited for new therapies. In March, for example, researchers reported that the virus attaches to an angiotensin-converting enzyme 2, or ACE2, receptors in the lungs. The FDA hasn't approved any drugs shown to effectively treat coronavirus infections. But there is a frontrunner: an antiviral drug called remdesivir. In a paper published Feb. 13 in the Proceedings of the National Academy of Sciences, NIH researchers reported that the drug successfully prevented rhesus macaques from being infected with the MERS coronavirus, which is closely related to SARS-CoV-2[6].

How it works has remained a mystery, in large part. In a study published Feb. 24 in the *Journal of Biological Chemistry*, Canadian and American researchers — including some from Gilead, the company that makes remdesivir — made some headway. They showed that the virus incorporates the drug molecule, which resembles a chunk of RNA, into an enzyme needed for replication. That process inhibits the virus from making additional copies of itself.

But who would benefit the most from the drug? Patterns are starting to emerge, but they're not clear yet. Epidemiologists and other scientists have struggled to make meaningful estimates of how quickly the virus will spread, and how lethal it will be.

Notably, they're trying to make sense of the case fatality rate. At a press conference on March 3, Tedros Adhanom Ghebreyesus, Director-General of the WHO, noted that "globally, about 3.4 percent of reported COVID-19 cases have resulted in death." That number is based on a basic calculation, dividing the number of deaths by the number of known diagnosed cases. However, other experts caution that the numerator and denominator of that ratio change quickly, and that number may not reflect an accurate picture of the viral danger.

In a study conducted on more than 1,000 patients in China and published in the *New England Journal of Medicine*, researchers reported a case fatality rate of 1.4% in the study population. In the paper, they similarly noted that estimating the rate is subject to high likely error. In particular, patients without debilitating symptoms might not have sought medical attention — and wouldn't have been captured in the study data — which means the real-world rate might be even lower, even below 1%.[7]

"If you look at the weight of the data, the risk group is very, very clear," said immunologist Dr. Anthony Fauci, M.D., Director of the National Institute of Allergy and Infectious Diseases, at a press conference on March 6. Elderly patients — especially those with other underlying medical conditions like heart disease, chronic lung disease, diabetes and obesity — are much more likely to get very sick or die. Case studies show that some younger people have also died from the disease, but the risk is much lower.

At the other end of the spectrum, the rate for children less than 19 years old is nearly negligible, and even the incidence rate is almost undetectable. "I don't totally understand it, the lack of detectable infections in children," Dr. Fauci said. "It's not as though they're not getting infected — they have to be," he added. "Why they're not developing clinical disease is really interesting, and it's something that we really need to study."

FINDING RELIABLE INFORMATION

Keeping abreast of current and correct information during an outbreak can be a challenge, says Patel. NewsGuard, a misinformation watchdog group started by journalists, recently launched a Coronavirus Misinformation Tracking

Center, which collects articles about the outbreak published on fake news sites. That number, since the launch of the tool in late February, has grown to more than 100. During a 90-day period this spring, the group reported some sobering figures: People "engaged with" information from the CDC or WHO a few hundred thousand times. For comparison, people engaged with information from notably unreliable sources more than 52 million times.[8]

To find credible information, the CDC recommends people stick to vetted organizations like the WHO and studies published in peer-reviewed journals. News articles that cite — and link to — published studies can easily be checked for accuracy. Finally, a number of journals and professional organizations, including the ASM, have established online information portals with the latest published findings.

DeBolt, back in Washington, says the case of SARS-CoV-2 is unusual not only because of how quickly it spreads, but also because of the rapid dissemination of information, good and bad.

As of mid-April, more than 658,000 cases have been reported and more than 32,000 people have died. Several studies estimate that the number of infected people doubles about every six days, which means it's following a pattern of exponential growth. If that continues, the number could reach 4 million infected by the middle of May. In the worst-case scenario, COVID-19 cases could overwhelm the U.S. health system.

How will it end? In late February, the WHO reported that the number of cases in China had peaked, and since then the rate of new diagnoses has fallen steadily there — even as the outbreak spreads elsewhere. In a comment published online March 6 in *The Lancet*,[9] epidemiologists from the United Kingdom point to efforts like social isolation, voluntary and required quarantine, and closing institutions where infections have emerged as effective ways to slow the spread of the virus. "Individual behavior will be crucial to control the spread of COVID-19," the authors noted.

However, some experts say the virus has spread too far, too quickly, for its effects to be controlled by containment. Some estimate that the virus could ultimately infect between 20 and 60 percent of the world's population before an effective vaccine has been developed. Even though 80% of cases of COVID-19 are mild, such a large number of infections means millions of people could die.

"How is it different from previous outbreaks? We just don't know yet," says DeBolt. "But we do know that the CDC is learning about the virus, right along with Washington state."

→ *To stay updated on the latest coronavirus research, visit* ***ASM's COVID-19 Research Registry*** *at* ***asm.org/covidregistry****.*

The Registry is a platform that provides timely access to top COVID-19 research vetted by experts. This curated database will ensure that scientists have an efficient way to find the timeliest and most valuable SARS-CoV-2/ COVID-19 research from the latest journal articles and preprints.

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Changing CO_2 Levels Require Microbial Coping Strategies

BY ***JENNIFER TSANG, PH.D.***

Carbon sustains life. It's the basis of all of life's building blocks — the nucleic acids, proteins, carbohydrates and lipids that make up living cells. Carbon is also at the heart of one of the most pressing issues on our planet: climate change. In the form of carbon dioxide and methane, carbon contributes to the warming of our planet, trapping heat in the atmosphere.

Microbes are another player in climate. They transform the state of carbon by sequestering carbon from and releasing carbon into the atmosphere, oceans, and biosphere. Climate change shapes microbes, and microbes shape the climate.

MICROBES AND THE CARBON CYCLE

Most of earth's carbon lies in rocks and kerogens[1] (from which petroleum and natural gas form), with the rest found in ocean waters, living organisms and the atmosphere. Microbes sequester carbon by turning it into biomass, but they also release CO_2 as they grow. This organic matter is converted to fossil fuels over millions of years.

This flow of carbon has been predictable until now (Figure 1). With the burning of fossil fuels, we're releasing carbon into the atmosphere much faster than the rate that carbon can be stored via the carbon cycle.

"We're releasing carbon at an alarmingly fast rate, much faster than the rate that carbon can be stored via the carbon cycle."

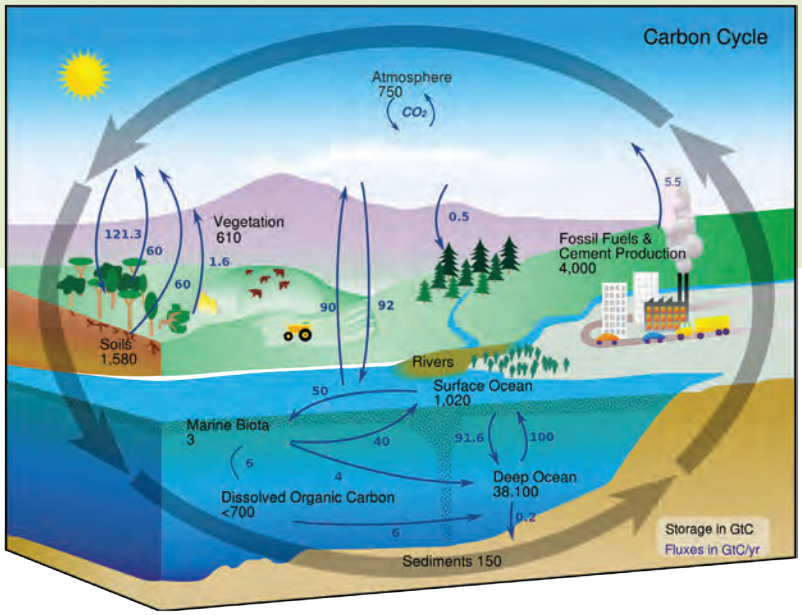

figure 1: Diagram of the carbon cycle.

Credit: Wikimedia Commons

THE CARBON CYCLE OF THE OCEANS

Much of carbon sequestration takes place in the oceans, where about 45% of CO_2 released by humans is sequestered. And microbes, despite their small size, have a lot to do with this.

When carbon dioxide from the atmosphere dissolves into the ocean, photosynthetic bacteria and eukaryotes absorb it and change it into biologically useful forms. Through a process called carbon fixation, a byproduct of photosynthesis, marine microorganisms incorporate carbon into their molecular building blocks, resulting in two important outcomes: (1) the carbon is introduced to the food web; and (2) molecular oxygen is released as a byproduct into the ocean, and eventually into the atmosphere.

oceans currently absorb

45%

of carbon dioxide released by humans

Microscopic organisms called phytoplankton are thought to be responsible for creating 50-85% of the oxygen on earth[2] through photosynthesis. The name "phytoplankton" comes from the Greek words phyton (plant) and plankton (wanderer or drifter), since these photosynthetic, single-celled microorganisms float through the ocean. There are both prokaryotic and eukaryotic phytoplankton, such as diatoms and dinoflagellates.

Microorganisms introduce carbon into the food web by serving as food for more complex organisms. When other organisms consume these microscopic creatures, that carbon is transferred to the larger organisms, which carry the carbon in their bodies or release it into the ocean as waste or through decay after death. Most of the carbon in the food web stays within the top 100 meters of the ocean, where it can eventually return to the atmosphere.

However, a fraction of the carbon in the food web eventually sinks to deeper waters as marine snow: tiny specks of dead animals, algae and waste materials that escape consumption by other organisms. When this happens, the carbon is more likely to be stored in the ocean instead of being released into the atmosphere. The carbon reaches a depth where it's unlikely to be brought back up to the surface for hundreds of years and is considered sequestered.

HOW INCREASING CO_2 LEVELS DECREASES MICROBES' CARBON-SEQUESTRATION ABILITIES

The increased CO_2 in the atmosphere has dire consequences for the oceans' food webs via two main drivers: ocean acidification and rising ocean temperatures. Atmospheric CO_2 increases lead to more CO_2 dissolved in the oceans, decreasing the ocean's pH. Additionally, the heat trapped by atmospheric CO_2 is absorbed by the oceans, thus increasing their average temperature.

These changes have a diverse set of effects on microorganisms, many of which have the same end result: decreased carbon sequestration.

DISSOLVING SHELLS

For phytoplankton that grow shells, ocean acidification is especially bad news. The extra CO_2 drops the pH of the oceans to a point where shells on organisms can become deformed and begin to dissolve. It also becomes harder for them to grow shells in the first place, since the shells are built using carbonate ions, which are less available with ocean acidification (Figure 2).

Fewer phytoplankton in the ocean means the amount of CO_2 that becomes fixed in the oceans decreases, leading to lower rates of long-term carbon sequestration.

CHANGING RELATIONSHIPS BETWEEN MICROORGANISMS

For the *photosynthetic* bacterium *Prochlorococcus*, ocean acidification presents a different problem because higher CO_2 levels affect its interactions with other microorganisms, such as its "helper" bacterium, *Alteromonas*.[3] *Prochlorococcus* is responsible for about 5% of all photosynthesis on earth, so environmental changes that alter *Prochlorococcus* could have additional effects on climate.

Prochlorococcus lacks the catalase enzyme, which breaks down hydrogen peroxide, a product of many biological processes that is toxic to *Prochlorococcus*. *Alteromonas* normally makes plenty of this enzyme to share and breaks down the hydrogen peroxide to benefit both organisms.

With changing levels of dissolved CO_2 in the water, *Alteromonas* takes on a different behavior. When researchers from Columbia University, the University of Alabama at Birmingham and the University of Tennessee tested the *Prochlorococcus*/*Alteromonas* relationship under 800 parts per million CO_2 (the amount of CO_2 expected to be in the atmosphere by 2100), *Alteromonas* became more antagonistic to *Prochlororoccus*.[4] *Alteromonas* produced less catalase and instead began producing proteins that increased the free radicals surrounding it. *Prochlorococcus* couldn't get rid of these toxins, and *Alteromonas* began to consume the dying cells.

This is a bad sign for carbon question. Less *Prochlorococcus* in the ocean means less carbon will make it into the food web, leading to less carbon sequestration.

INCREASED MICROBIAL ACTIVITY MEANS MORE CO_2 RELEASED

Marine microbes are also more active at higher temperatures. As phytoplankton sink through the ocean, zooplankton and bacteria may consume the phytoplankton

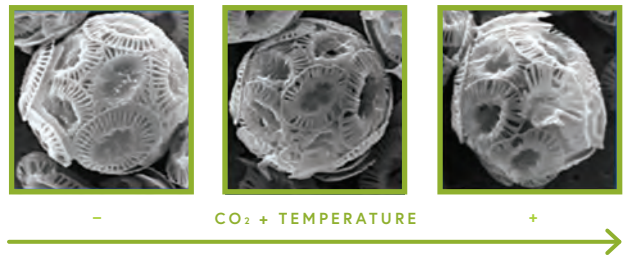

figure 2: Phytoplankton morphology as acidification and warming increases in a cultured experiment.

Credit: UAB

before it can reach the ocean floor. Increased phytoplankton consumption means the phytoplankton's carbon molecules are more likely to be released as CO_2, and potentially back into the atmosphere, rather than reach the deep ocean for long-term sequestration.

In a study from the University of Tasmania, researchers harvested samples of decaying phytoplankton and measured the microbial respiration rate over a 10°C temperature range to estimate the effect of warming temperatures on carbon sequestration.[5] Using a projected warming of 1.9°C by 2100, they calculated that carbon sequestration could decrease by 17%, ± 7%.

USING MICROBES TO INCREASE CARBON SEQUESTRATION

These examples show how microbial cycles can trigger damaging feedback loops: warmer temperatures either reduce microbial populations or reduce their ability to sequester carbon, and propel further increases in temperature. On the flip side, scientists have been seeing whether microbes could increase carbon sequestration by iron fertilization — the intentional introduction of iron into iron-depleted ocean waters to stimulate phytoplankton growth. The intended outcome? To accelerate carbon sequestration from the atmosphere.

Iron is often a limiting nutrient in many areas of the ocean; evidence lies in the large phytoplankton blooms that can result from increasing iron levels. Adding just enough iron to promote marine microbial activity, without overstimulating to create a phytoplankton bloom[6], may help counteract higher CO_2 concentrations.

Iron fertilization is not a new concept. In the 1930s, biologist Joseph Hart speculated that areas of ocean surface that seemed rich in nutrients but could not sustain plankton activity were iron-deficient. Oceanographer John

Martin later hypothesized that increasing phytoplankton photosynthesis could reduce global warming by sequestering CO_2. IronEx I, the first iron-enrichment experiment[7] near the Galapagos Islands in October 1993, found that enriched areas showed increased primary production, biomass and photosynthetic energy conversions relative to untreated waters.

However, iron-fertilization experiments have yet to demonstrate[8] increases in carbon sequestration. Even biological oceanographer Penny Chisholm, who discovered *Prochlorococcus*, has doubts.[9] By increasing carbon flux into the sea, the food webs below may be altered in unintentional ways, as phytoplankton blooms can lead to blooms of other organisms that can re-release the carbon back into the atmosphere. Thus, there is potentially no benefit in terms of long-term carbon sequestration. And it's hard to predict the long-term, global consequences of iron fertilization with small-scale and short-term experiments like IronEx I.

This makes it difficult to find solutions for carbon storage in the oceans. We can't prevent changes in one part of the ocean from affecting another part of the ocean. The conditions in one area of the ocean may be quite different from another area, or the conditions in one area may change from night to day, or day to day. This only highlights the importance of considering these parameters both spatially and temporally. We are only beginning to understand how these tiny microorganisms have impacts on a much larger, global scale.

"We can't prevent changes in one part of the ocean from affecting another part of the ocean."

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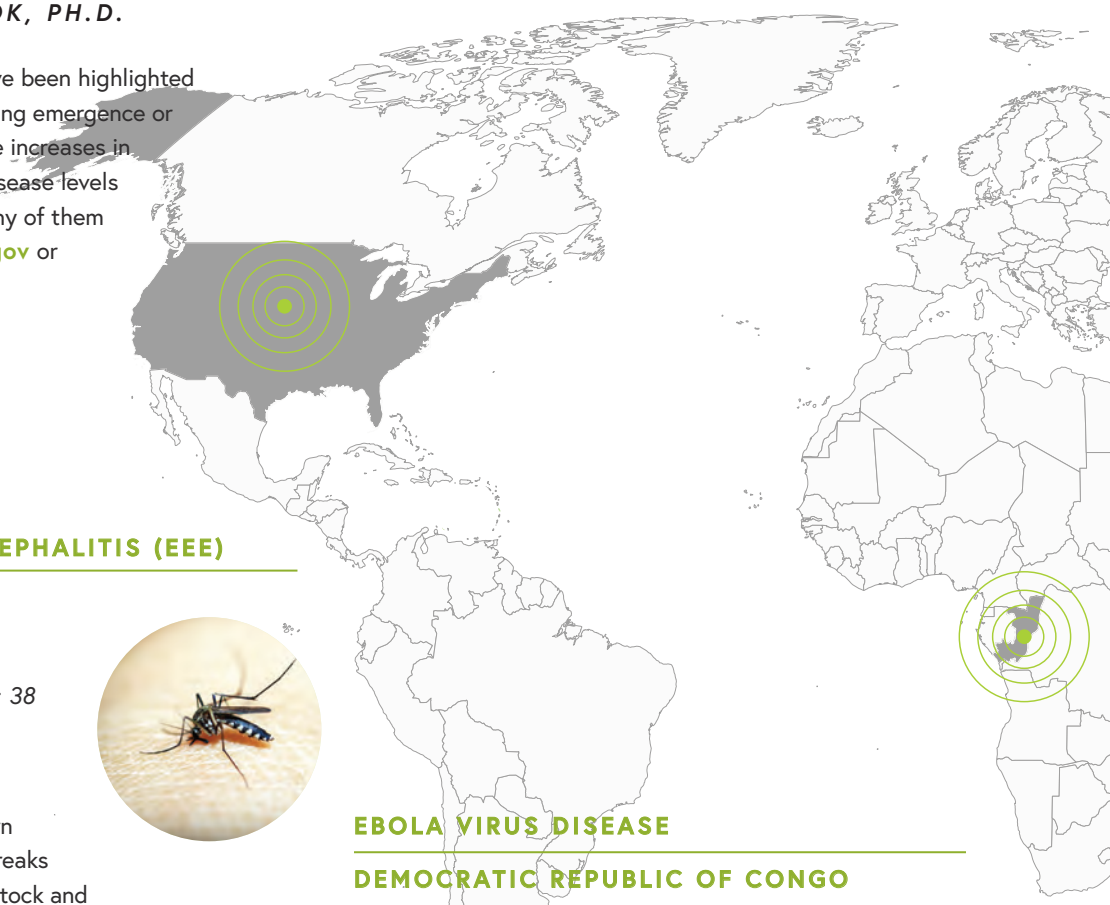
5 Notable Outbreaks in 2019

BY ***KATHERINE LONTOK, PH.D.***

These particular outbreaks have been highlighted because they represent troubling emergence or reemergence of diseases, large increases in case numbers over endemic disease levels or high case fatality rates. Many of them are ongoing. Please visit **cdc.gov** or **who.int** for more information.



EASTERN EQUINE ENCEPHALITIS (EEE)

UNITED STATES

Began in summer 2019
Cases (confirmed to Dec. 17): 38
Deaths: 15
Case Fatality Rate: 39%

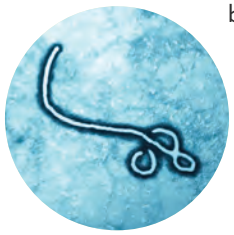
Caused by an arbovirus, Eastern equine encephalitis (EEE) outbreaks have been documented in livestock and people in the United States since the 1830s. The United States typically records 7 EEE cases in humans per year, but 2019 saw a huge jump to 38 confirmed cases with 15 deaths across 10 states. The EEE virus cycles between *Culiseta melanura* mosquitoes (which do not routinely feed on mammals) and wild birds. Rare infections in mammals, including horses, pigs and humans, instead stem from "bridge vectors," mosquito species that feed both on birds and mammals. The uptick of human cases may indicate the emergence of EEE as a seasonal threat in North America akin to the West Nile virus.

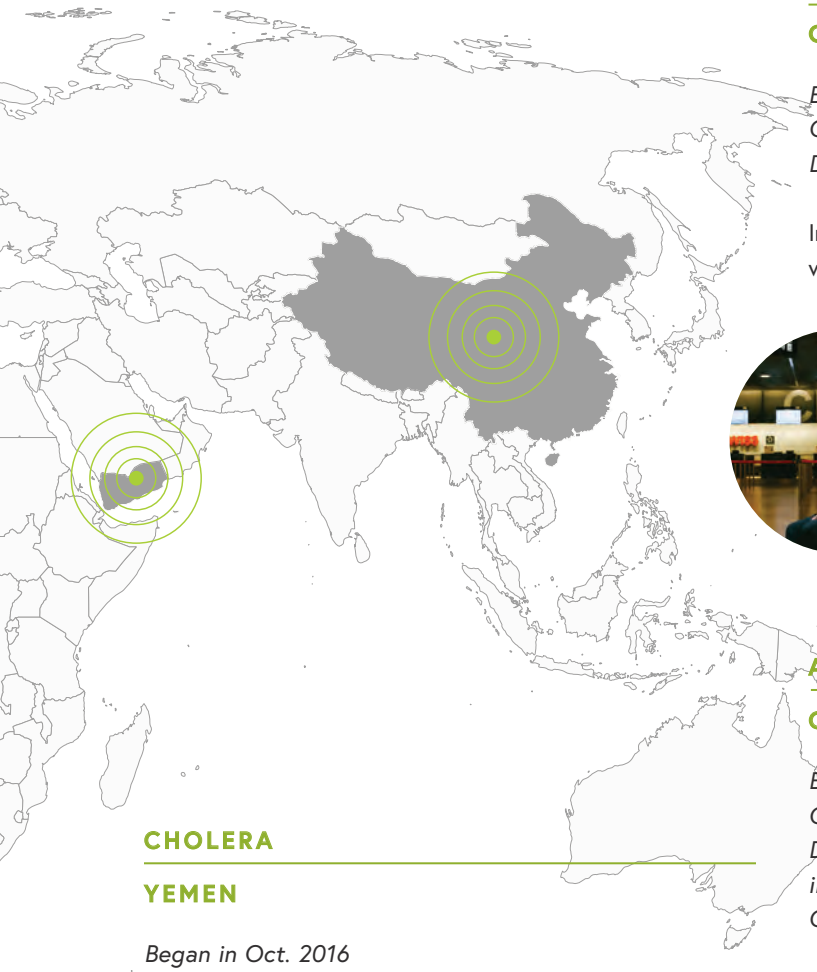
EBOLA VIRUS DISEASE

DEMOCRATIC REPUBLIC OF CONGO

Began in April 2018
Cases (confirmed + probable to Dec. 22, 2019): 3,362
Deaths: 2,266
Case Fatality Rate: 66%

The ongoing Ebola virus outbreak in the Democratic Republic of Congo is the largest since the 2014-2016 West African outbreak, which killed more than 11,000 people. The current outbreak has been difficult to contain because of conflict in the area, disrupting public health efforts. Mass migration of refugees has also stoked fears of spread to neighboring countries. In fact, the Republic of Uganda reported 3 cases imported from DRC in June 2019.





COVID-19

CHINA

Began in Dec. 2019
Cases (confirmed as of April 2020): 658,000
Deaths (confirmed as of April 2020): 32,000

In December 2019, China reported a cluster of patients with pneumonia-like symptoms of unknown cause in Wuhan City. By early January 2020, a new coronavirus capable of person-to-person transmission, SARS-CoV-2, was identified as the culprit. Although the precise spillover event is still being debated, the virus appears to originate in bats. As of May 6, 2020, 215 countries have confirmed more than 3.5 million total cases.

CHOLERA

YEMEN

Began in Oct. 2016
Cases (suspected to Dec. 2019): 2,280,585
Deaths: 3,895
Case Fatality Rate: 0.17%

The only bacterial disease on the list, cholera is caused by *Vibrio cholerae* and spreads in conditions of poor sanitation and limited access to medical care. Yemen's cholera outbreak, which began in October 2016 and is now in its second wave, is directly related to the ongoing civil war. More than 2.2 million suspected cases have been reported, with 3,895 deaths. Blood banks and clinics were closed.

AFRICAN SWINE FEVER IN PIGS (ASF)

CHINA

Began in Aug. 2018
Cases: Unknown
Deaths: Estimated to be millions, control measures include culling affected populations
Case Fatality Rate: N/A

One of the most significant outbreaks in 2019 was the continuing spread of African swine fever among pigs in southeast Asia. ASF had never been reported in the region prior to arriving in China in August 2018. Since then, it has spread to wild and domestic pigs in 10 additional southeast Asian countries. *Ornithodoros* ticks act as a vector for the ASF virus, but the virus is also highly contagious and can be spread through contaminated fomites, like feed. Because there is no vaccine or treatment for infected pigs, millions of domestic pigs have been culled to contain the virus, significantly increasing the price of pork globally.

Behavior is the Key Ingredient in Global Biosafety

BY ***KATHERINE HEITZ, MSC.***
PROGRAM SPECIALIST, ASM'S GLOBAL PUBLIC HEALTH PROGRAM

Ethical integrity and responsible conduct in the life sciences are vital to scientific advancement. Laboratory management systems that prioritize collective accountability and leadership behavior while nurturing effective biorisk management principles play an important role in creating an international culture of safety.[1] In laboratories where equipment and institutional mentoring are limited, staff must focus on what they can control. Out of this global need, ASM has been implementing a unique biosafety curriculum promoting behavioral and technical best practices, based on cooperative and collaborative learning. As the number of individuals requiring training on safe practices in high biocontainment laboratories increases, standardized introductory biosafety training is critical to reducing the potential for human error. While complications and challenges abound regarding regulatory frameworks, global health governance and guidelines for biosafety risk management, creating a culture of responsibility[2] is a critical component to promoting worker and community safety.

WHAT IS BIOSAFETY?

Biosafety addresses the safe handling and containment of potentially infectious microorganisms and hazardous biological materials. The goal of biosafety is to reduce the risk of laboratory-acquired infections to individual workers and their environment, reducing the potential consequences for accidental introduction of a pathogen into the community.[3] Human error is often the main cause of preventable exposures of lab workers to dangerous pathogens. Biosafety relies on both equipment and reagents, as well as the development and application of appropriate biosafety and biosecurity behavioral best practices.

In recent years, there has been a global expansion in laboratory-based diagnostic and research capacities driven by an increased demand for disease detection and control. However, despite the increase in infectious disease surveillance and diagnostics, sustainable capacity in biosafety and biosecurity management remains constrained by many variables, including the lack of national biological safety regulatory guidelines and biosafety curricula, as well as limited laboratory infrastructure and limited dedicated funding, particularly in lower-resource countries. Without resources for PPE, or the ability to reinforce biosafety and biosecurity practices, researchers working with infectious microorganisms, whether for clinical diagnosis or population-based surveillance, remain at risk of infection.

52 WEEKS BUILDS LAB BIOSAFETY CAPACITY

ASM implements a curriculum known as the "52 Weeks program" to address the biggest risk factor for biosafety: human behavior. Scientist participants learn critical behavioral skills for the control and accountability of biological agents, as well as the knowledge and processes to protect themselves and their communities from preventable exposure to infectious disease. Participants include public health leaders from multiple public health-related fields, as engagement of all aspects of the laboratory workforce is essential to improving biosafety and strengthening the biorisk-management practices of their hospitals, universities and laboratories.

The 52 Weeks program hopes to build laboratory capacity by creating a culture of accountability, consciousness and education. This year-long mentorship program combines monthly webinars, virtual office hours and capacity-building assignments to improve biosecurity and biosafety knowledge and behavioral practices at the worker level and containment measures at the institutional level. 52 Weeks culminates in a five-day workshop, facilitated by a Biosecurity and Laboratory Behavioral Safety Specialist. The 2019 workshop was held in Cairo and convened 18 laboratory scientists who serve many of Egypt's public health microbiological laboratories, as a cohort that included clinical microbiologists, epidemiologists and infection-control officers who handle high-consequence pathogens. The workshop focused on skill-building in donning and doffing of PPE, emergency response drills and other relevant areas. It also focused on instilling a culture of responsibility in scientific communities through positive behavioral, procedural and institutional change through the creation of standardized training, codes of conduct and reinforcing shared values of scientific integrity.

BIOSAFETY IS BEHAVIOR

As a behavior-based training approach, 52 Weeks provides an overview of the four primary controls of biosafety, phases of biological risk mitigation and biosecurity strategies. This program also ensures that participants understand laboratory risks and demonstrate behaviors needed to mitigate those risks, and develop customized and innovative solutions for their institutions — thereby increasing professional resilience and sustainable behavioral competencies in biosafety. The primary focus of 52 Weeks is on the psychology of individuals as they engage in decision-making, interpersonal relations, and small group activities. Instructional methods for the use of PPE as part of contamination and protocol adherence, specifically donning and doffing methods, are emphasized to participants throughout the course of the program. At the Cairo workshop, participants practiced best techniques for glove removal in a Glo-Germ exercise. In this simulation exercise, participants were asked to put on disposable lab gloves, Glo-Germ was added to gloves, then students were asked to remove their gloves as they would in the lab. Their hands were examined using ultraviolet lighting in a darkened room to see where and how the Glo-Germ had spread, simulating self-inoculation. Best-use studies and CDC guidelines around doffing methods emphasizes that standardized PPE use is one of a hierarchy of controls aimed at eliminating hazards from infectious disease exposures.

Through repeated skills practice, participants can experience increased confidence in demonstrating safe donning and doffing procedures, becoming experts who then return to their home labs and spread these behavioral competencies to the rest of their lab colleagues. In addition to technical skill development, complimentary behavior-based instruction is taught. Courses titled, "Behavioral Cues, Distinguishing Safety Climate and Safety Culture, and Personality" are core parts of the 52 Weeks curriculum, which supports positive conditioning, thereby shaping our actions through repeated exposure to environmental stimuli.

Never has there been a more prescient time to recognize that global health security is a shared responsibility of the international community. While outbreak protocol, surveillance and reporting are important, it is the behavior of communities that has the ability to drive change toward success or failure. In recognition of this collective responsibility, ASM's Global Public Health Program promotes global health security by strengthening biosafety and biosecurity management practices through delivering behavior-based biosafety curricula for the scientists who are on the front lines of disease detection and control. By combining an integrated culture of responsibility with technical laboratory skills training, ASM strives to sustain a safe and effective generation of laboratory scientists through capacity development and accountability.

EGYPTIAN MICROBIOLOGISTS PRACTICE DONNING AND DOFFING OF PERSONAL PROTECTIVE EQUIPMENT (PPE) AS PART OF THE 52 WEEKS OF BIOSAFETY CURRICULUM.

→ *To become involved in ASM's Global Public Health Programs as a consultant, volunteer or country ambassador, please visit* ***www.asm.org/globalhealth****.*

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Disease Eradication: What does it take to wipe out a disease?

BY ***ANGEL CORONA, PH.D.***

By analyzing the successful eradication campaigns of smallpox and rinderpest, can we apply lessons learned to current disease-eradication campaigns?

Disease eradication is the holy grail for health officials, as eradication of disease and better health ultimately benefit ecosystems on a global level. Initiatives such as One Health, embraced by the Centers for Disease Control and Prevention (CDC), aim to integrate human health, animal health and environmental factors when tackling disease prevention, treatment and eradication. One Health considers the impact that climate change, increased human presence in previously unpopulated locations, increased human/animal interactions, and global human and animal migration have on the spread of disease.

To date, the World Health Organization (WHO) has declared only two diseases officially eradicated: smallpox, caused by the variola virus (VARV), and rinderpest, caused by the rinderpest virus (RPV)[1]. Smallpox was an ancient disease that had caused epidemics throughout human history, resulting in 300-500 million deaths (an estimated 10% of all deaths in the 20th century)[2]. Rinderpest was a deadly bovine disease that caused the deaths of cattle herds throughout Europe and Africa from the 18th to the 20th century, until a dedicated global campaign led to its eradication.[3]

ERADICATION: DEFINITIONS DEFINE SUCCESS

Eradication can be hard to conceptualize. Infectious disease anthropologist Thomas Aiden Cockburn defined disease eradication as "the extinction of the pathogen that causes disease."[4] By this definition, smallpox and rinderpest are not eradicated. Samples of both viruses still exist in the world: the United States and Russia have stocks of VARV securely stored, while samples of RPV remain in many facilities around the globe.[5, 6] Extinction would require the destruction of these stocks, a complex topic involving geopolitics and cultural norms, as well as microbiology.

Another definition of eradication, one that is widely accepted by many organizations including the WHO, is "the permanent reduction to zero of the worldwide incidence of infection caused by a specific agent as a result of deliberate efforts."[7] The last reported case of smallpox occurred in Somalia in 1977, and the last reported case of rinderpest occurred in Kenya in 2001.[8] Since then, health officials have scaled back those eradication campaigns and no new infections have been detected, leading to the declaration of eradication for smallpox in 1980 and rinderpest in 2011.

Attempts to eradicate other diseases have had limited success. Organizations like the WHO and the Chan Zuckerberg Biohub have shifted to use of the term "disease elimination," a less stringently defined and more attainable goal than eradication, in an effort to spur

confidence in global health initiatives. Disease elimination does not require the permanent reduction of disease incidence to zero, but rather the reduction of incidence to zero in a particular geographic area. One example of this difference would be the elimination of cholera from countries like Peru, despite the fact that *Vibrio cholera* has not been eradicated globally.

THE MICROBIOLOGIST'S CHECKLIST FOR DISEASE ERADICATION

To determine whether a disease can be eradicated, consider the science, the political climate and the economics involved. Both smallpox and rinderpest had particular characteristics that facilitated their eradication.

#1 *IS THE DISEASE EASILY DIAGNOSABLE?*

Disease symptoms are one way to quickly diagnose the presence of a disease at the individual or community level. The smallpox eradication campaign benefited from characteristic sores and rashes caused by VARV infection. These distinct leisons allowed health officials to easily, and effectively, diagnose patients and track disease epidemiology in their communities. As another example, poliomyelitis, caused by poliovirus (PV), produces characteristic, rapid-onset paralysis in a subset of patients that has been used as a marker for active community transmission.[9]

In contrast, malaria, a disease that has been targeted for elimination, requires skilled medical professionals who are able to interpret patient blood smears to identify infected individuals. The lack of trained parasitologists in endemic areas proved to be one of the reasons why the 1950s campaign to eradicate malaria failed.[10]

#2 *IS THERE A NON-HUMAN RESERVOIR OR VECTOR?*

Disease-causing pathogens can sometimes infect multiple species, crossing phylogenetic boundaries. In these cases, the pathogen exists in a species that serves as a "reservoir" for future infections of other species. Consider SARS, caused by the SARS coronavirus (SARS-CoV). While the virus was able to infect and cause severe disease in humans, humans were not the original host for this virus.[11] The non-human reservoir for SARS-CoV is suspected to be bats, as viruses that share striking similarity with SARS-CoV have been detected in bats.[12] Although successful containment strategies eliminated transmission of SARS among people, the continued presence of an animal reservoir means that SARS is not yet an eradicated disease.

The recent emergence of SARS-CoV-2, and the subsequent pandemic of Coronavirus-Induced Disease (COVID-19), further highlights the role of non-human reservoirs. While it is generally thought that SARS-CoV-2 also emerged from bats, there have been preliminary reports of pangolins playing a potential role as an intermediate host.[13, 14] Until the true animal reservoir of SARS-CoV-2 is found, the risk of reinfection and reemergence of this coronavirus will persist.

Other pathogens not only have the ability to infect multiple species, but have also adapted to use one host species as a 'vector' for transmission to another host species.[15] Many arthropods are vectors for human diseases and show little to no symptoms from pathogens that cause pathology in people. For example, dengue fever, caused by the dengue flavivirus (DENV), is transmitted to people through mosquito vectors. Even if diseases are eliminated in human populations, their presence in non-human reservoirs or vectors allows for reinfection and further spread.

Because the smallpox variola virus only infects humans, it was a good target for eradication. Human-to-human transmission could be interrupted through targeted vaccination campaigns. Similarly, poliovirus, which only infects humans, was eliminated in 193 countries, and an official declaration of eradication is within sight.[16]

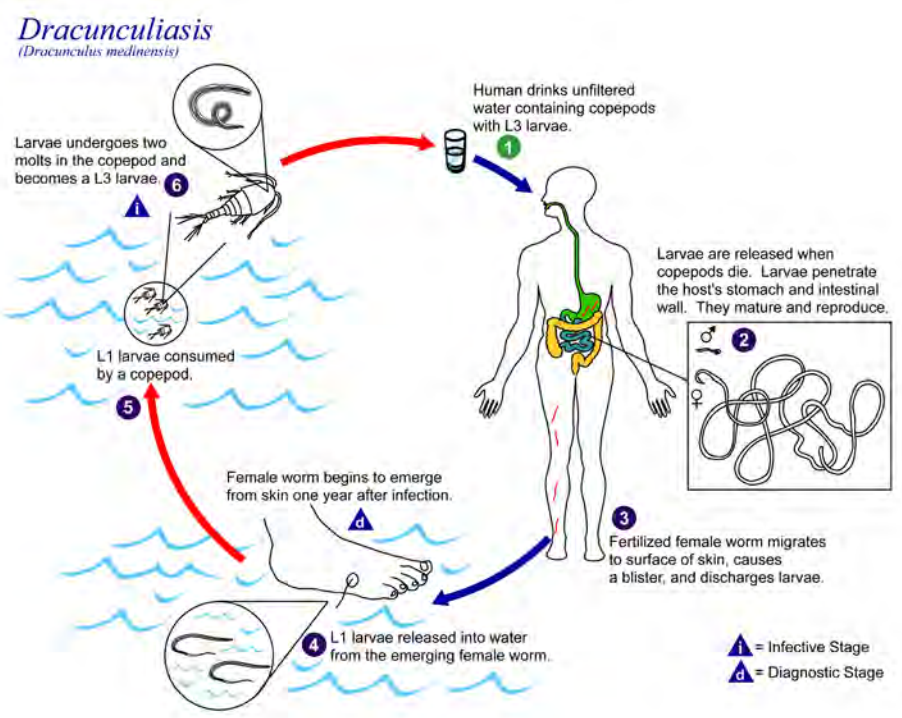
In contrast, yellow fever, caused by yellow fever virus (YFV), is reemerging. In Nigeria, vaccination efforts against YFV halted transmission and caused incidence to drop to zero in 1996.[17] Unfortunately, decreased vaccination rates, along with the existence of an arthropod vector and primate reservoirs, caused an outbreak of yellow fever in September 2017.[18] Nigeria has experienced seasonal yellow fever outbreaks ever since.

Dracunculiasis is likely to be eradicated in the near future. It is caused by ingestion of *Dracunculus medinensis* larvae from contaminated water sources. A year after infection, patients experience excruciatingly painful blisters on their feet and legs. They seek relief by soaking blisters in water sources, triggering the emergence of the adult worm, which releases infectious larvae into rivers and ponds. There are no available therapeutics or vaccines for dracunculiasis.

#3 *IS THE DISEASE GEOGRAPHICALLY RESTRICTED?*

Many of the diseases that have been eradicated (smallpox and rinderpest) or targeted for elimination by WHO (such as polio, malaria, measles and rubella) are present in multiple countries.[19] However, as a disease approaches eradication, disease incidence becomes more geographically restricted. This phenomenon has multiple effects.

Regions that have zero disease incidence see benefits plateau from eradication campaigns, with no change in the societal, political and economic costs. This may cause nations that are no longer affected by the disease to scale back their support, a problem that plagued smallpox eradication. Polio faces a similar obstacle.



The life cycle of *Dracunculus medinensis*

One positive benefit of a more restricted geography is the ability to narrow a campaign's focus on specific regions. Some diseases, such as dracunculiasis (guinea worm disease) or yaws, have never been widespread geographically.[20] Consequently, the WHO and other organizations created targeted campaigns that have pushed these diseases to the brink of eradication.

#4 *IS THERE A VACCINE? ARE THERE OTHER TRANSMISSION-DISRUPTING ALTERNATIVES?*

Vaccines have saved countless lives and prevented an untold amount of suffering. The smallpox and rinderpest eradication strategies relied on vaccines, and the majority of ongoing disease-elimination campaigns include vaccination strategies. But is a vaccine truly necessary to push disease transmission to zero?

How is guinea worm disease close to eradication without a vaccine? This is where creative infectious disease containment strategies come into play.

The CarterCenter, in collaboration with UNICEF, has distributed water-filtration systems and increased efforts to provide potable drinking water to affected communities. Health workers also prevent patients from entering water sources, instead wrapping the adult nematode around a stick and slowly pulling it out. Community education and identification of infected individuals has led to the reduction of disease incidence from 3.5 million in 1986 to 53 cases in 2019.[21] If dracunculiasis is eradicated, the campaign will be the first to do so without a vaccine, suggesting that there are multiple ways to eradicate a disease that do not rely on vaccination.

DISEASE ERADICATION: THE WAY FORWARD

We cannot forget that disease eradication is not solely dependent on scientific context. Successful eradication of smallpox and rinderpest required political, economic and social education efforts. Global coordination and tracking of disease outbreaks requires cooperation on an international level. Without political support, global health campaigns cannot hope to succeed. Without economic support, crucial resources cannot be mobilized effectively.

One of the more concerning recent developments is increased mistrust of science, as evidenced by the rise of anti-vaccination sentiment. Gaining and maintaining public trust in global health initiatives will be the linchpin for eradication campaigns. Smallpox eradication was the prototype for future eradication campaigns and provided valuable lessons. Will disease eradication become the norm, or will smallpox and rinderpest remain outliers? Only time will tell.

"Without political support, global health campaigns cannot hope to succeed. Without economic support, crucial resources cannot be mobilized effectively."

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LEADERSHIP UPDATE

Expanding Availability of SARS-CoV-2 Testing & Access to SARS-CoV-2 Research

BY ***ROBIN PATEL, M.D.***
ASM PRESIDENT

As the COVID-19 pandemic rapidly evolves, we want you to know that ASM has been working hard to create the conditions for expanded availability of SARS-CoV-2 testing, provide free access to SARS-CoV-2 research findings and deliver accurate, timely information to the public.

ASM has been working with the White House Coronavirus Task Force, the Food and Drug Administration and Centers for Disease Control to address the many challenges that come with testing – including reagent and supply shortages, regulatory hurdles under FDA's Emergency Use Authorization (EUA) that hindered the use of diagnostic tests, and increased oversight of serology testing.

One of the key needs of the White House Task Force is to understand the real-time status of the supply/equipment pipelines and variations in regional availability in each of the states. This is part of an overarching effort to maximize opportunities for large-scale testing in all parts of the country. The White House Task Force recognizes that ASM, because of its network of 300 lab directors, is a valuable partner in building the connection with clinical directors and clinical microbiologists.

As leaders in the microbial sciences, it is our responsibility to allow free and rapid access to important research related to SAR-CoV-2. ASM is providing free access to more than 50 research articles published over the last year in its scholarly journals and is expediting review for submitted papers related to coronavirus.

On April 15, ASM launched the COVID-19 Research Registry, a platform that provides timely access to top COVID-19 research vetted by past ASM President Lynn Enquist and a team of experts. This curated database will ensure that scientists have an efficient way to find the timeliest and most valuable SARS-CoV-2/COVID-19 research from the latest journal articles and preprints. You can explore the latest research on the Registry at **asm.org/covidregistry**.

ASM also convened an international summit of coronavirus experts on March 23, during which coronavirus experts summarized the value and potential uses of two types of tests for SARS-CoV-2, nucleic acid amplification tests for viral RNA and antibody detection tests. The recording is available on the ASM website.

Looking ahead to preparedness for future pandemics, ASM has requested that Congress initiate a high-level, comprehensive review of the SARS-CoV-2 response once the immediate public health emergency subsides. By fully understanding both what went well and gaps in our response protocol, we can help thwart, or at least minimize, the effects of the next pandemic.

From examining the method of SARS-CoV-2 infection to studying the blood of recovered COVID-19 patients to develop a treatment, ASM members are on the front lines of ground-breaking research that is helping us understand and combat this novel coronavirus. On ASM's podcasts, our experts have reviewed the latest epi curves, person-to-person transmission and the length of time the virus remains on surfaces. Our members are using next-generation sequencing to study how coronaviruses spread in animal populations, which will help monitor how they may spread in humans.

I encourage you to take advantage of the ASM COVID-19 resource page, available at **asm.org/covid19**, which includes a public outreach toolkit to inform your community on the COVID-19 situation and new developments.

What's Hot
in the microbial sciences

BY ***STANLEY MALOY, PH.D. & JULIE WOLF, PH.D.***

1

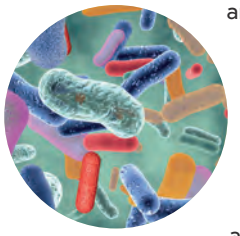
PROMISES AND CHALLENGES IN VIRAL-MEDIATED GENE THERAPIES

There are 29 clinical trials listed on clinicaltrials.gov that are testing gene therapies for sickle cell disease (SCD), and some are beginning to show promising results. Bluebird Bio's LentiGlobin BB305 Drug Product, under Phase I/II trial for safety and efficacy of the lentivirus-based therapy for severe SCD, was highlighted in a recent *New York Times* feature. For treatment, patient stem cells are collected and reprogrammed using a modified human immunodeficiency virus to express a fetal form of globulin before being readministered to the patient. Studies using a different viral vector, a modified adeno-associated virus (AAV), have revealed potential long-term negative effects, including virally carried DNA integration throughout the genome in a dog study. This data was presented at the American Society for Hematology's annual meeting and written up in *Science* magazine. Studies involving gene therapies are expected to increase, and the U.S. Food and Drug Administration has announced the release of a number of important policies to guide the manufacturing and clinical development of these therapies as safely and effectively as possible.

2

AN ARCHAEON BY ANY OTHER NAME

Defining broad categories of organisms helps scientists understand the diversity of life, but categorizing microbes is a huge challenge. A *Nature Ecology and Evolution* analysis of 3,000 gene families in archaea and eukaryotes revealed consistent eukaryotic origination from within the archaea, supporting a two-domain tree of life. This contrasts with the current broadly accepted three-domain tree of life consisting of bacteria, archaea and eukarya. An *mBio* analysis of 3,500 genomes suggested changes to categorizations within bacterial and archaeal domains. The authors proposed categorizing microbial genera using average nucleotide identity, genome-alignment fraction and the distinction between type- and non-type species. This framework is meant to better demarcate breakpoints between genera at the genome level.



3

CRISPR-MEDIATED DIAGNOSIS OF INFECTIOUS DISEASE

Technologies using DNA- or RNA-recognizing molecular machinery to detect and diagnose infectious disease are being adapted for clinical microbiology applications. A *Journal of Clinical Microbiology* study reports accurate identification of mycobacterial species, including non-tuberculosis mycobacteria (NTM), using a Cas12a/guide RNA-based platform to recognize mycobacterial DNA. The Cas12a/gRNA platform correctly identified 72 of 73 clinical *Mycobacterium* isolates, comparable with *rpoB* gene-sequencing results, and could provide a method to accurately differentiate *M. tuberculosis* from NTM. A variation on Cas12a DNA

ARTICLE 1 Kolata G. At 16, She's a Pioneer in the Fight to Cure Sickle Cell Disease. *New York Times*. Jan. 11, 2020. https://www.nytimes.com/2020/01/11/health/sickle-cell-disease-cure.html.

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ARTICLE 2 Williams T.A. *et al.* Phylogenomics Provides Robust Support for a Two-Domain Tree of Life. *Nature Ecology and Evolution*. Dec. 9, 2019. https://www.nature.com/articles/s41559-019-1040-x.

Barco R.A. *et al.* A Genus Definition for Bacteria and Archaea Based on a Standard Genome Relatedness Index. *mBio*. Jan. 14, 2020. https://mbio.asm.org/content/11/1/e02475-19.

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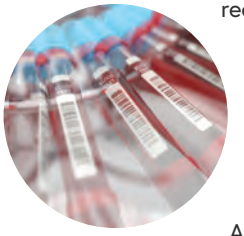

recognition may lead to rapid, low-cost diagnosis of African swine fever virus (ASFV), a viral disease that has led to the culling of over 1 million pigs in China since August 2018. The Cas12a-based on-site and rapid-detection system (CORDS) identifies ASFV DNA at femtomolar sensitivity in 1 hour at 37°C, as reported in *Frontiers in Microbiology*. A third system, reported in *Nature Communications*, uses Cas13 to recognize bacterial RNA. The allosteric probe-initiated catalysis and CRISPR-Cas13a (APC-CAS) system identifies low numbers of *Salmonella enteritidis* cells in mouse serum and distinguishes mice with early- and late-stage infection from uninfected mice, showing potential clinical applications for early pathogen diagnosis. A *Nature Protocols* article provides step-by-step instructions to perform specific high-sensitivity enzymatic reporting unlocking (SHERLOCK), including either fluorescent or colorimetric readouts.

PHAGE STRUCTURE EVADES CRISPR

4

Phage can protect their genetic material by generating a nucleus-like protein structure inside their host bacterial cell. Following the discovery that bacteriophage can generate a proteinaceous structure during viral replication in 2017, published in *Science*, two new studies have confirmed that these structures can protect phage against anti-viral CRISPR responses. A *Nature* paper demonstrated that the *Pseudomonas aeruginosa* phage ΦKZ is resistant to many immunity mechanisms that target DNA during infection, but that the phage DNA is susceptible to nucleases *in vitro*. A similar discovery was reported in *Nature Microbiology*, in which a *Serratia*-infecting phage, PCH45, was found to make a protein nucleus-like shell that protected PCH45 DNA. Both phages remained susceptible to RNA-targeting immunity mechanisms, supporting a widespread mechanism that protects phage genetic material, but not the mRNA that must travel to the bacterial cytoplasm for translation.

VACCINE SUCCESSES AND FAILURES

The U.S. Food and Drug Administration has approved Ervebo, the first vaccine for Ebola virus disease (EVD), for use in people 18 years of age and older. "The FDA's approval of Ervebo is a major advance in helping to protect against the Zaire ebolavirus, as well as advancing U.S. government preparedness efforts," said Peter Marks, M.D., Ph.D., director of the FDA's Center for Biologics Evaluation and Research, in a press release. Ervebo is a vesicular stomatitis virus-based vaccine with the surface glycoprotein of Zaire ebolavirus. Vaccine efficacy was established in trials during the 2014-2016 West African Ebola outbreak; the vaccine will be produced by Merck. In disappointing vaccine news, the HVTN 702 HIV vaccine trial in South Africa has been halted after an independent data and safety monitoring board (DSMB) revealed that the vaccine regimen did not prevent HIV infection. The trial was testing an investigational prime-boost vaccine regimen based on the results from the RV144 clinical trial in Thailand. The South African vaccine had been adapted to the HIV subtype most prevalent in southern Africa. While the vaccine was found to be ineffective, it raised no further health concerns for the trial participants.

5

Shen J. *et al.* Sensitive Detection of a Bacterial Pathogen Using Allosteric Probe-Initiated Catalysis and CRISPR-Cas13a Amplification Reaction. *Nature Communications*. Jan. 14, 2020. https://www.nature.com/articles/s41467-019-14135-9.

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News Release: First FDA-Approved Vaccine for the Prevention of Ebola Virus Disease, Marking a Critical Milestone in Public Health Preparedness and Response. Dec. 19, 2019. https://www.fda.gov/news-events/press-announcements/first-fda-approved-vaccine-prevention-ebola-virus-disease-marking-critical-milestone-public-health.

News Release: Experimental HIV Vaccine Regimen Ineffective in Preventing HIV. Feb. 3, 2020. https://www.niaid.nih.gov/news-events/experimental-hiv-vaccine-regimen-ineffective-preventing-hiv.

6

MICROBES AT THE ROOT OF PLANT HEALTH

Several studies have focused on the relationship between plants, specifically their root structures, and soil microbes. A *Cell* study focused on how plants perceive their microbial surroundings by specifically looking at the location of pattern-recognition receptors (PRRs) that recognize microbe-associated molecular patterns. These PRRs are expressed at low levels on outer cell layers but can be upregulated by neighbor cell damage; after damage events, plant immune responses can stem from even non-immunogenic, beneficial bacteria. Understanding the ways that plants detect and react to their microbial neighbors may help scientists develop ways to manipulate plant local immune responses. An *Applied and Environmental Microbiology* study looked at the colonization levels of plant-beneficial phenazine-producing *Pseudomonas* species. These beneficial plant colonizers produce antimicrobial compounds that are effective against plant pathogens while boosting plant immunity, but the effects are dependent on strain colonization. The authors identified key metabolic and genomic determinants presumably required for the efficient colonization of the model plant *Arabidopsis thaliana* and *Solanum tuberosum* (potato), which may be used in future crop soils to boost plant health. Aboveground interactions can have belowground repercussions, as demonstrated by a second *Applied and Environmental Microbiology* report. Here, scientists showed how bark beetle infestation can affect soil water availability, pH, and microbial community composition and function. Understanding the plant-root interactions as part of a larger ecosystem will be important as scientists develop applications for improving plant health.

7

BETTER DIAGNOSTICS AND DRUGS FOR MRSA

Scientists have announced improvements for detecting and fighting methicillin-resistant *Staphylcoccus aureus* (MRSA) disease. In December, the U.S. Food and Drug Administration (FDA) authorized the marketing of a new bacteriophage-based test to detect MRSA in hours rather than the days that traditional culture techniques require. The cobas vivoDx, which can detect MRSA in as little as five hours, will be sold by Roche and is hoped to improve both diagnostics and infection control to prevent MRSA spread in healthcare settings. Meanwhile, a study in the *Journal of Antimicrobial Chemotherapy* evaluated the ability of the Next Gen Diagnostics (NGD) automated bioinformatics tool to predict the phenotypic resistance of MRSA isolates based on genomic sequence. Analysis of 778 MRSA clinical isolates accurately predicted 99.69% of phenotypes for 11 antibiotics, confirming that NGD provides accurate and rapid prediction of antibiotic susceptibility. Finally, a discovery published in *Nature Chemical Biology* may facilitate the use of β-lactam antibiotic compounds against MRSA. Screening 45,000 compounds revealed a small molecule compound, MAC-545496, that reverses β-lactam resistance in the community-acquired MRSA USA300 strain. MAC-545496 inhibits GraR, a regulator that responds to cell-envelope stress that is an important determinant of antibiotic resistance.

8

CELLS THINK, THEREFORE THEY ARE

Can microbes make decisions? A study published in *Nature Communications* investigated the chemotactic strategies of *Escherichia coli* in a T-maze spiked with chemical gradients. Single-cell observations showed that cells have heterogenous responses to the gradients, despite the genetic identity of the cells tested. The distribution

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Custer G.F. *et al.* Structural and Functional Dynamics of Soil Microbes Following Spruce Beetle Infestation. *Applied and Environmental Microbiology*. Jan. 21, 2020. https://aem.asm.org/content/86/3/e01984-19.

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Omar M. El-Halfawy *et al.* Discovery of an Antivirulence Compound that Reverses β-lactam Resistance in MRSA. *Nature Chemical Biology*. Nov. 25, 2019. https://www.nature.com/articles/s41589-019-0401-8.

News Release: FDA Authorizes Marketing of Diagnostic Test that Uses Novel Technology to Detect MRSA Bacteria. Dec. 5, 2019. https://www.fda.gov/news-events/press-announcements/fda-authorizes-marketing-diagnostic-test-uses-novel-technology-detect-mrsa-bacteria.

of phenotypes among the clonal population may serve as a bet-hedging strategy that provides diversity within the population. Meanwhile, a *Current Biology* report investigated the behaviors of the single-celled ciliate *Stentor roeseli*. *S. roeseli* was found to exhibit a hierarchy of avoidance behavior, including bending, ciliary alteration, contraction and detachment. This was established via repeated exposure to negative stimulus, sometimes minutes apart, and observing a change in *S. roeseli*'s behavioral response, suggesting that decision-making and learning occur in non-neural organisms. These ciliate experiments replicate a contested previous study by Herbert Spencer Jennings performed over 100 years prior.

9

MICROBIOME RESEARCH FOR BEE HEALTH

Research into the bee microbiome aims to increase population fertility and decrease susceptibility to disease. Research published in *mSystems* characterized the *Bombus lantschouensis* (bumble bee) microbiome across developmental stages in order to better understand the gut microbiota function in the reproductive success of bumble bee queens. The researchers used targeted quantification PCR to characterize the bacterial abundances in unmated, mated and ovipositing queens to establish differences in diversity and composition that will be useful in future studies of bumble bee health. Bumble bee queens are the only hive member to hibernate over winter, and thus aren't affected by colony collapse disorder (CCD), a condition that strikes honey bees (*Apis mellifera*). A study published in *Science* aims to manipulate honey bee microbiomes as a means to activate honey bee immunity and protect them from pathogens that may contribute to CCD. The bee symbiotic gut bacterium *Snodgrassella alvi* was engineered to produce double-stranded RNA that interferes with viral and mite genes, both of which cause disease in honey bees. The symbiont-mediated RNAi method provides a tool for both studying bee genomics and potentially protecting bees from pathogens.

VIRAL DISCOVERIES IN UNUSUAL PLACES

Scientists are becoming increasingly adept at discovering microorganisms in unusual ecological niches. In a recent *Journal of Virology* article, scientists reported the discovery of a virus that infects a *Nanoarchaeota*, which are small cells with reduced genomes that are obligate ectobionts (external parasites) of other microbial species. The *nanoarchaeota virus* 1 (NAV1) is the first virus of a new viral family discovered to infect these nanoarchaeota, and was discovered by using metagenomics-sequencing technologies on samples from hot springs found in Yellowstone National Park. A second virus discovery is complicating viral classification: more than 90% of genes within the yanavirus, a new lineage of amoebal virus, have never been described. No related viral genomes were found in 8,535 publicly available metagenomes, suggesting low abundance of the virus. Among the mysterious open-reading frames encoded by the double-stranded DNA genome are six types of tRNAs that do not match commonly used codons. The yanavirus discovery is pending peer review and is currently published on *bioRxiv*. These studies further demonstrate the remarkable genetic diversity of viruses.

10

ARTICLE 8 Salek M.M. *et al.* Bacterial Chemotaxis in a Microfluidic T-Maze Reveals Strong Phenotypic Heterogeneity in Chemotactic Sensitivity. *Nature Communications*. April 23, 2019. https://www.nature.com/articles/s41467-019-09521-2.

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Leonard S.P. *et al.* Engineered Symbionts Activate Honey Bee Immunity and Limit Pathogens. *Science*. Jan. 31, 2020. https://science.sciencemag.org/content/367/6477/573.

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COLLOQUIUM REPORT:
Microbial Genomics of the Global Ocean System

The year 2020 marks the 10th anniversary of the Deepwater Horizon (DWH) disaster. From April through July 2010, an estimated total of 4.9 million barrels of oil and 250,000 metric tonnes of natural gas were discharged into the Gulf of Mexico. Not only were 11 lives lost, the tragedy also left a lasting impact on the Gulf's marine and coastal ecosystems and on the residents who depend on these habitats for their livelihood. After the oil spill, the Gulf of Mexico's microbial communities played a critical role in the cleanup, contributing core hydrocarbon bioremediation services. Despite its importance, marine hydrocarbon microbiology is a young field. Prior to the spill, relatively little was known about marine hydrocarbon degraders.

Beginning in 2010, the development and application of genomics and bioinformatics tools enabled researchers — for the first time — to identify and examine individual microorganisms within their complex communities in unprecedented detail. Today, technical advances and new discoveries have revealed a natural capacity of microbes in the Gulf of Mexico to catalyze bioremediation of petroleum hydrocarbons. This knowledge is critical to guide mitigation and future restoration strategies that build on the microbes' natural bioremediation capabilities without further disturbing sensitive ecosystems.

This report is based on the deliberations of experts who participated in the joint colloquium of the American Academy of Microbiology (ASM's honorific leadership group), the American Geophysical Union (AGU) and the Gulf of Mexico Research Initiative (GoMRI) in April 2019. The report highlights new research tools, methodologies, data resources, collaborations, and models that will advance basic and applied research to provide data-driven solutions to environmental challenges.

→ *This report is available at* ***asm.org/microbe_oceansystem***.

asm microbe 2020

ASM Microbe 2020 Cancelled

After much thoughtful discussion, the American Society for Microbiology Board of Directors has made the difficult decision to cancel ASM Microbe 2020, scheduled for June 18-22, 2020, in Chicago, Ill. We have notified speakers, poster presenters, exhibitors and attendees of the cancellation individually and shared specific details they will need. We regret any inconvenience these changes to our meeting may cause, and thank you for your understanding and continued support as we respond to the COVID-19 pandemic.

The health, safety and well-being of the ASM global community, including the city of Chicago, is our highest priority. Meeting leaders are working with the Program Committee on alternate plans for members of the microbial science community to present and discuss their research, including digital and virtual options. We wish you continued good health during these challenging times and look forward to seeing you in person next year at ASM Microbe 2021 scheduled to take place on June 3-7 in Anaheim, Calif.

→ *In the meantime, please visit* ***asm.org*** *for the most up-to-date information.*

Advocacy During a Pandemic

ASM has been actively advocating for the microbial sciences and for the needs of clinical microbiologists during the rapidly unfolding SARS-COV-2 pandemic. Since the virus first garnered attention from science and public health leaders, ASM has been navigating the challenges and moving parts with Congress and the Administration, and has stayed in close contact with our members on the front lines.

From the moment ASM members sounded the alarm in February about the inability of clinical labs (and some public health labs) to test for COVID-19 at the point of patient care, ASM began to closely engage with both the Food and Drug Administration and with Congress, urging that policies be altered to allow for use of laboratory-developed tests (LDTs) more broadly under the Emergency Use Authorization (EUA) that had been put into place. As challenges continued to develop, including shortages of key testing supplies and reagents, ASM went to work on behalf of its members.

In addition to the clinically focused issues, ASM also advocated with Congress for increased funding for medical research, public health response and preparedness, surveillance, and advanced molecular detection technologies in a series of emergency supplemental funding bills passed by Congress. This additional funding will shore up programs at the Centers for Disease Control and Prevention (CDC), boost public health laboratory capacity, and ensure that the National Institute of Allergy and Infectious Diseases (NIAID) has the resources it needs to conduct urgent work to develop a COVID-19 vaccine and continue clinical trials of antivirals that might serve as therapeutic options for those suffering from the disease.

ASM also recognizes the need for a science-based, comprehensive review of the national COVID-19 response once the immediate crisis subsides. We have been leading efforts in the community to call for a nonpartisan commission or the National Academies to review and make forward-looking recommendations about how our country can head off the next pandemic.

→ *Learn more & sign up for updates at* ***asm.org/advocacy****.*

Arizona/Southern Nevada Branch

branch profile

The Arizona/Southern Nevada Branch of ASM was formed in 2007 when the University of Nevada Las Vegas (UNLV) faculty in Southern Nevada formally asked to join the Arizona Branch. They had been attending the Arizona Branch meetings for some time prior to their formal request to join. Currently, the Branch has a little more than 100 members representing institutions in Arizona and Nevada. The Branch supports three Student Chapters: the Arizona State University Microdevils, the University of Arizona Student Chapter, and the University of Nevada Las Vegas Student Chapter. The mission of the Arizona/Southern Nevada Branch is to "promote microbiology within Arizona and Southern Nevada."

The Branch holds its Annual Branch Meeting every April, rotating venues between Northern Arizona University in Flagstaff, Arizona State University in Tempe, the University of Arizona in Tucson, and one of the institutions in Nevada. The annual meetings encourage the participation of undergraduate students, graduate students and postdocs through poster and short oral presentations. The purpose of these meetings is to present the most recent microbial research within Arizona and Southern Nevada, promote networking opportunities, and encourage early career scientists to present their work. The scope of research presented at the meetings includes medical and environmental topics ranging from studies on bacteriophages and honey bees to Valley Fever (coccidioimycosis), which is endemic in the desert Southwest. The Branch provides travel awards for Branch members to encourage participation for ASM meetings and conferences, such as ASM Microbe.

In 2019, Northern Arizona University hosted the 58th Arizona/Southern Nevada Branch ASM conference, which had a record-breaking 160 attendees from 13 unique academic or research institutions. The conference also had a high level of attendee participation, as indicated by the 87 research projects presented in the form of 35 oral presentations and 52 posters. The early-career-development workshop "A Case for Peer Mentoring" was highly attended among students, and the feedback was strongly positive. Good energy was felt throughout the day of the conference, where networking and the exchange of ideas were the predominant activities. The conference was an incredible success, and the Arizona/Southern Nevada Branch continues to thrive and attract new institutions.

Arizona and Southern Nevada are popular places to retire. Therefore, the Branch is reaching out to retired microbiologists in the area to help mentor younger Branch members. If you are thinking about retiring to Arizona or Nevada, please look up the Branch (http://asm.unlv.edu/index.htm). Your participation in the Arizona/Southern Nevada Branch is welcome, and your expertise is valued!

Microcosm will be highlighting one ASM branch in each issue. If your branch would like to be featured, please send a high-resolution photo and information on your branch's history, members, activities, student chapter and website to **communications@asmusa.org**.

AMBASSADOR PROFILE

KARL ANDERSON, *ASM'S YOUNG AMBASSADOR TO NORTH DAKOTA*

Karl Anderson has been an ASM member since 2012 and ASM's Young Ambassador (YA) to North Dakota since 2018. He is currently a Ph.D. student at North Dakota State University (NSDU) in Fargo, N.D. In 2012, he started teaching and conducting research with the University of Minnesota Crookston. Karl is an NDSU graduate research assistant working with the U.S. Department of Agriculture (USDA) Agricultural Research Service (ARS).

Tell us about your research and current role as an NDSU graduate research assistant.

I work with USDA microbiologists and chemists from several locations, including North Dakota, Nebraska and Idaho. We work on projects related to antimicrobial-resistance fate and transport, particularly examining the airborne transmission of antimicrobial-resistant bacteria, genes and antibiotic residues from concentrated beef operations. I've also learned about antibiotic sampling and detection via liquid chromatography-tandem mass spectrometry.

What has been the greatest impact of your research? How has your work affected the environment and the microbial sciences?

I have been lucky to work with great scientists with outstanding records of accomplishment, and I hope to emulate their passion for advancing the microbial sciences throughout my career. Currently, the USDA projects I'm associated with are ongoing, but my greatest impact on the environment and microbial sciences stems from my undergraduate teaching and research. My research group began mapping Minnesota's freshwater sponge population and examining associated microbial communities. This work will be one of the first analyses of freshwater sponge microbial diversity, laying the foundation for understanding the relationship between the sponge microbiome and species of freshwater sponges. This project has also stirred public interest, as citizen scientists are reporting freshwater sponge locations and inquiring about their relationship with microorganisms.

As an ASM YA, how do you represent ASM in your community and strengthen science globally?

As an ASM YA, I have made new connections in my region, promoted collaborative research opportunities and provided access to microbiology seminars. I have established new lines of communication for students and researchers from Minnesota, Nebraska, Canada, and even Togo, Benin and Cameroon. I'm currently involved in six separate projects with microbiologists in my community and four other countries, some of which I will be presenting at ASM Microbe 2020.

Why did you become an ASM YA, and what has been your most rewarding experience thus far?

The value of collaboration and positive interactions with ASM members piqued my interest to become an ASM YA. I love microbiology and enjoy learning and sharing information with others. As an ASM YA, I encourage those already working in the microbial sciences and the microbiology-interested public. My most rewarding experience as an ASM YA is the comradery I've experienced with international YAs. I'm currently collaborating with Ghislain Ntignonawoe (YA, Togo), Louis Komlan (ASM member, Togo), and Victorien Dougnon (YA, Benin) on mosquito-control projects and establishing RAB-Togo, an educational organization that provides access to educational opportunities for students in resource-limited areas. The organization also works to educate and encourage young Togolese women to pursue careers in STEM. With the help of ASM members in my area, I've worked to send more than 1,000 lbs. of microbiology laboratory equipment to West Africa, including 24 microscopes.

What are your plans and future goals as an ASM YA?

During my final year as an ASM YA, I will continue connecting microbiologists and encouraging collaborative opportunities. Recently, I helped connect the White Earth Tribal & Community College with Tiny Earth, a network of instructors and students focused on studentsourcing antibiotic discoveries from soil. My goal is to foster similar collaborations with other campuses in my region.