A publication of the American Society for Microbiology

Microcosm

Summer 2019

ASM Microbe 2019

Special Issue

AMERICAN SOCIETY FOR MICROBIOLOGY

THANK YOU FROM ASM

YOUR COMMUNITY

Thank you for being a member of the global community committed to advancing microbial sciences through:

Sharing Science • Building Careers • Networking with Peers • Advocating for Science • Improving Global Health • Publishing Peer Reviewed Research

As we approach the membership renewal season, we would like to notify you of the ASM 2020 membership dues. The ASM Board of Directors approved an increase to the 2020 dues for all membership categories, with the exception of Global Outreach members in resource-constrained countries. This will allow ASM to continue offering excellent member benefits and advancing member priorities.

ASM 2020 Membership Dues:

- Premium member: $195
- Clinical lab scientist member: $115
- Contributing member: $90
- Supporting member: $45
- Postdoctoral member: $40
- Student member: $35

If you have not yet signed up for auto-renewal, log into your account, and select “Enroll Now” under “My Membership” link.

Thank you for your membership.
We look forward to another great year together!

AMERICAN SOCIETY FOR MICROBIOLOGY
1752 N St. NW
Washington, DC 20036

Questions? Contact service@asmusa.org

AMERICAN SOCIETY FOR MICROBIOLOGY

agar art®

Start planning your microbial masterpiece today!

Sept.10, 2019	Oct. 22, 2019	Nov. 4-13, 2019	Nov. 20, 2019
Contest opens for submissions	Submission deadline	People’s Choice voting on Facebook	Winners announced

asm.org/agarart

ASM’s 2019 Agar Art Contest is open to all:

PROFESSIONAL
Bioartists and life scientists, including postdocs, graduate and undergraduate students

MAKER
Non-experts who are 13 years old or older

kids
Those 12 years old and younger

Interested in hosting a public Agar Art workshop in your BSL-1 space?
Contact communications@asmusa.org.

Contents

Microcosm Summer 2019

Contributors

Vaughn Cooper, Ph.D.
is the past chair of the ASM Council on Microbial Sciences (COMS) and holds a Ph.D. in zoology/ecology and evolutionary biology from Michigan State University. His research focuses on the evolution, ecology and genome dynamics of experimental and clinical microbial populations.

Katherine Lontok, Ph.D.
is the public outreach manager at ASM where she works to engage non-expert audiences with the microbial sciences. She holds a Ph.D. in molecular biology and biochemistry from the University of California, San Francisco.

Julie Wolf, Ph.D.
is the science communications specialist at ASM, where she uses social media, the web and live events to communicate and help others communicate their science. She is the host of ASM's newest podcast, *Meet the Microbiologist*, and in her free time teaches at the community biolab Genspace.

Correction: In the Spring issue of *Microcosm*, Monika Buczek was incorrectly credited as "Monica Buczek."

Microcosm

Summer 2019

Microcosm, published by the American Society for Microbiology, 1752 N Street, NW, Washington, DC 20036-2904, 202-737-3600, is mailed to all ASM members. It is published three times per year, one volume per year.

For advertising, please email *communications@asmusa.org*.

POSTMASTER: Send address changes to *Microcosm*, 1752 N Street, NW, Washington, DC 20036-2904.

from the editor

As a member of ASM since I was a student, I always look forward to the annual ASM meetings. In 2015, ASM combined the ASM General Meeting and the Interscience Conference of Antimicrobial Agents and Chemotherapy to create ASM Microbe. ASM Microbe was created with the goal of evolving into the most exciting, all-encompassing and groundbreaking forum for the microbial sciences. So far, we've taken this conference experience to Boston, New Orleans, Atlanta and San Francisco.

We receive nearly 5,000 abstracts highlighting cutting-edge science during the submissions process for ASM Microbe. The poster presentations, workshops and sessions at the meeting reflect the best of the best of those scientific abstracts. ASM Microbe brings together more than 8,000 microbiologists, engineers and scientists from all over the world to share their research, connect with each other and celebrate the field of microbial sciences.

For our second 2019 issue of *Microcosm*, we want to share the experiences, capture the moments and highlight some of the science that came out of the ASM Microbe meeting this year. We know not every member can join us every year, and we want to ensure that all of our members get to see the exciting science and professional development at ASM's flagship conference.

We offer track hubs in the ASM Microbe exhibit hall so people can connect with "their people." These hubs, based on the meeting's scientific tracks, offer specialized sessions and deeper dives into distinct disciplines. The ASM Microbe planning committee also curates track-based curriculum experiences for attendees to help them navigate the conference.

If you had a chance to make it to the ASM Microbe 2019 exhibit hall, perhaps you stopped by the ASM booth. This highly interactive area encompassed a live studio theater, where milestone episodes of *This Week in Microbiology, microTalk* and other ASM podcast sessions were recorded. You could play pathogen plinko, participate in user testing for the ASM website, get a personalized, hand-drawn button of your favorite microbe, visit the gift shop for everything from water bottles to baby onesies and, of course, find out everything you need to know about ASM.

I hope you enjoy the interviews, the photo spread and the science highlights in this issue of *Microcosm*. As always, I had a wonderful time at ASM Microbe this year, meeting new people and connecting with old friends. I listened to talks about exciting science, visited posters to learn about the latest research, discovered new opportunities for ASM members at the track hubs, explored new tools at the exhibits and watched ASM leaders discuss the future of microbiology and advance our mission "to promote the microbial sciences."

You can view video footage from ASM Microbe at ASM's YouTube channel *www.youtube.com/c/AmericanSocietyforMicrobiology*. I hope to see you next year in Chicago. Remember that we offer an array of travel awards to help scientists gain exposure to the meeting and ultimately the science. You can view them at *asm.org/travel-awards*.

Stanley Maloy, Ph.D.
Editor-in-Chief

COUNCIL ON MICROBIAL SCIENCES

COMS UPDATE

by Vaughn Cooper, Ph.D.

The Council on Microbial Sciences (COMS), ASM's new, dynamic governance structure that is the creative mind of the society and the "clutch" between the Board of Directors and membership, has instituted several exciting programs over the past year to support members at all career stages.

The Conference Grant Program, which empowers members to host their own events and gatherings, has expanded. After three successful cycles of the program, this year we reviewed 251 applications and awarded 26 grants. This has amounted to about $100,000 worth of conference grants in the 2019-2020 cycle, an increase from the $60,000 in grants in 2018-2019.

The Peggy Cotter Travel Award Program helped 82 early career scientists from ASM branches attend ASM Microbe this year.

COMS is excited to continue working as the "creative mind" of ASM, but to do so effectively we must continuously seek input throughout the society. We're moving toward a more connected model of COMS, and we're excited for improved engagement with members and the Board of Directors. We also plan to solicit input from branch and division members, allowing us to open dialogue and continue fostering an environment where ideas and feedback are freely exchanged.

I am so proud of the impactful work that COMS has contributed to this year, and I look forward to even more progress in the second half of 2019.

Vaughn Cooper, Ph.D., is the past chair of the ASM Council on Microbial Sciences (COMS) and holds a Ph.D. in zoology/ecology and evolutionary biology from Michigan State University. His research focuses on the evolution, ecology and genome dynamics of experimental and clinical microbial populations.

How do I reach out to COMS?

If you have ideas you would like to share with us, please email us at coms@asm.org. We would love to hear your thoughts on how we can serve you better!

APHL Resources for You

APHL tools and guidelines for Antimicrobial Resistance, Tuberculosis, HIV, Hepatitis C, Sexually Transmitted Diseases Testing and more!

www.aphl.org/ASM

- CRE/CRPA Breakpoint Implementation Toolkit
- *Mycobacterium tuberculosis*: Assessing Your Laboratory, 2019 Edition
- Updated Guidelines for Submission of Sputum Specimens for Tuberculosis Testing
- Issues in *Mycobacterium tuberculosis* Complex (MTBC) Drug Susceptibility Testing: Rifampin (RIF)
- New Training Module: Mycobacteriology False-Positive Case Studies
- HIV/HCV Testing Integration Toolkit
- 2019 Update to HIV Suggested Reporting Language
- BioPlex 2200 HIV Ag-Ab Assay: Addressing Its Role and Results in the HIV Testing Algorithm
- Hepatitis C Virus Testing Factsheet
- New Resources for *M. genitalium* and *N. gonorrhoeae* Testing

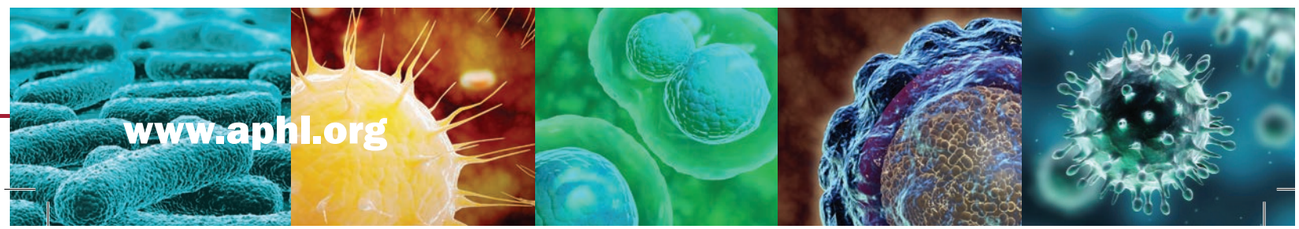
Save the Date!

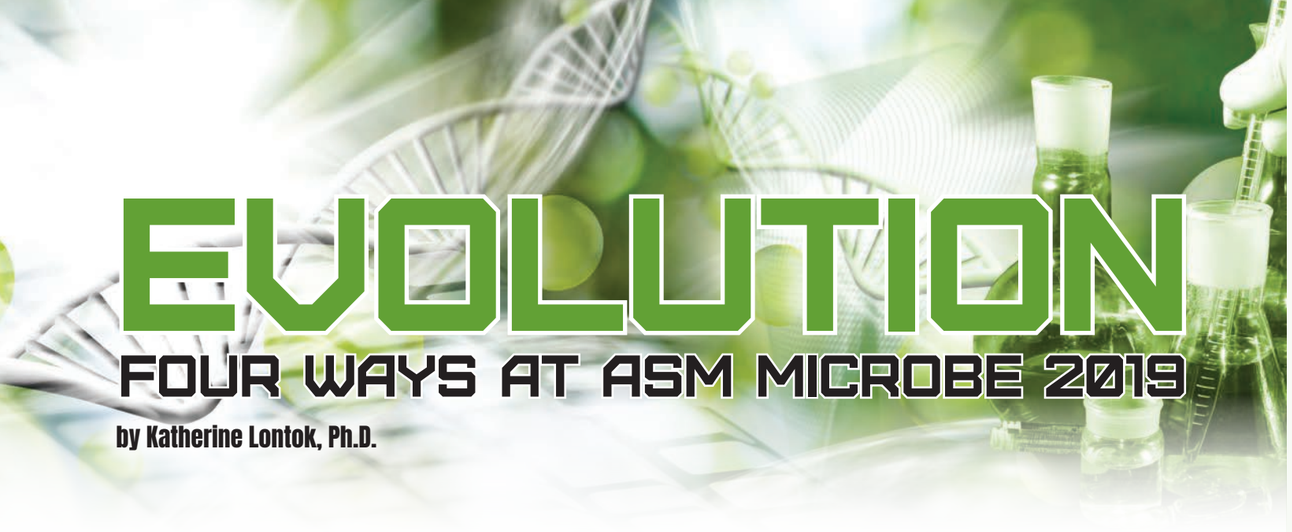
September 19 at 3:00 pm ET

A Webinar with Janet Hindler: Update on Multi-Drug Resistant Organisms and Novel Multi-Drug Resistant Organisms

Registration link is available at www.aphl.org/ASM.

APHL ASSOCIATION OF PUBLIC HEALTH LABORATORIES®





EVOLUTION

FOUR WAYS AT ASM MICROBE 2019

by Katherine Lontok, Ph.D.

As evolutionary biologist Theodosius Dobzhansky proclaimed, "nothing in biology makes sense except in the light of evolution." The four speakers in the "Evolution in the Wild" session at ASM Microbe 2019 highlighted advances in fields from infectious disease to microbial ecology that hinged on the unifying concept of evolution:

- **Anticipating Evolution Combats Multi-Drug Resistant Pseudomonas Infections**
- **How Evolution, Symbiosis and Environmental Conditions Intertwine**
- **Gene Flow Defines and Uncovers Microbial Populations**
- **The Short- and Long-Term Evolution of Our Gut Microbiomes**

ANTICIPATING EVOLUTION COMBATS MULTI-DRUG RESISTANT PSEUDOMONAS INFECTIONS

As antibiotics continue to lose efficacy against bacterial pathogens, researchers and clinicians are turning to bacteriophages as alternate therapies. ASM awardee and Yale University Professor Paul Turner, Ph.D., has always been interested in the evolution of viruses. In recent years, his lab started to investigate the evolutionary pressure that viruses exert on bacterial populations —with remarkable results. Turner's strategy manipulates the evolutionary dynamics between phage and the bacteria they target, and shows great promise for treating multidrug-resistant bacterial infections.

Phage therapy harnesses lytic bacteriophage viruses as natural predators of pathogenic bacteria. The concept emerged in the 1920s, not long after the discovery of bacteriophages themselves. However, it was largely abandoned in the West with the rapid development of antibiotics, and research into phage therapy was relegated to scientifically isolated Soviet countries during the Cold War. Turner highlighted several advantages to the technique in contrast to antibiotics: bacteriophages are specific to particular species of bacteria, they self-amplify and they are highly efficient in killing their bacterial hosts. However, just as bacterial populations exposed to antibiotics shift toward antibiotic resistance over time, they also have the capacity to evolve resistance to phage.

Turner's group used this potential for bacteria to become phage resistant as an advantage. They went hunting specifically for phage that attach to and infect *Pseudomonas aeruginosa* bacteria using cell surface factors involved in antibiotic resistance. In theory, treating drug resistant *P. aeruginosa* with such phage should select for individuals with mutations in this factor, thereby reversing drug resistance. So far, the group has recovered a candidate phage, OMKO1, that interacts with OprM, the outer membrane component of an efflux pump that confers multidrug resistance to *P. aeruginosa*. *In vitro* experiments showed the phage indeed selected for bacteria with mutations in the targeted factor.

Since their isolation, Turner and his colleagues have used OMKO1 and other phages to successfully treat otherwise intractable infections in 13 patients, with no adverse reactions. This impressive track record includes treatment of a patient who developed a biofilm of chronic, drug-resistant *P. aeruginosa* on an aortic graft. A single round of therapy with OMKO1 phage in combination with antibiotics completely resolved the infection. Quantitative modeling by Joshua Weitz's group at Georgia Tech in collaboration with Turner's group suggests that the bacteriophage + antibiotic combination can lower overall bacterial load to the point that a patient's immune system can successfully clear the infection.

A single round of therapy with OMKO1 phage in combination with antibiotics completely resolved the infection.

In another case, a cystic fibrosis patient with chronic, multidrug-resistant *P. aeruginosa* in her lungs was treated with a combination of two phages. Although the infection was not completely cleared, her bacterial load was significantly reduced and the remaining population was resensitized to a variety of antibiotics. Given that bacterial pneumonia is a major complication of cystic fibrosis, the ability to treat chronic *P. aeruginosa* even after it has become resistant to antibiotics is a clear victory for Turner's strategy. The discovery and successful clinical application of these phages demonstrates that leveraging evolution and natural selection can lead to better therapeutics.

HOW EVOLUTION, SYMBIOSIS AND ENVIRONMENTAL CONDITIONS INTERTWINE

Nitrogen-fixing rhizobia bacteria form nodules on the roots of legumes like clover and peanut plants and are essential for providing plants with nitrogen in a usable "fixed" form in exchange for plant carbohydrates. Importantly, this relationship is the primary natural mechanism on land for converting inert atmospheric nitrogen into compounds like ammonia. Indiana University Associate Professor Jennifer Lau, Ph.D., investigates how environmental conditions affect the evolution of the mutualistic relationship between leguminous plants and rhizobia bacteria.

To study mutualism between plants and rhizobia *in situ*, Lau's group took advantage of the W.K. Kellogg Biological Station at Michigan State University which houses several long-term agricultural experiments. Her group collected soil samples from plots fertilized continuously since 1988 and control plots that have never been fertilized. They then inoculated clover plants with these soil samples, providing the plants with access to the rhizobium population from each type of plot.

How does nitrogen fertilization affect the important relationship between rhizobia and plants? Lau hypothesized that more than 20 years of exposure to artificial fertilizer altered the soil's rhizobium population, favoring bacterial strains that would be less cooperative within the legume-rhizobium relationship. Indeed, plants inoculated with soil from the fertilized plots produced fewer, smaller root nodules and had lower overall biomass. Her group confirmed their findings by replicating these inoculation experiments with single, isolated rhizobium strains from the fertilized plots, which again proved to be less cooperative with their plant hosts than the strains isolated from control plots. Her group has since gone on to show that genetic changes on a plasmid involved in symbiosis in rhizobia explain some, but not all, of this evolution of less cooperative strains. Lau's research suggests that the use of artificial fertilizer is changing the capacity of rhizobia to fix atmospheric nitrogen, thereby altering a key component of the terrestrial nitrogen cycle.

Lau's research suggest that the use of artificial fertilizer is…altering a key component of the terrestrial nitrogen cycle.

GENE FLOW DEFINES AND UNCOVERS MICROBIAL POPULATIONS

One of the major challenges in microbial ecology is defining distinct populations of microbes, particularly when the microbes involved all have highly similar genomes. In macroorganisms, populations are typically defined as geographically distinct groups of individuals of the same species where a species is the largest group of individuals where any two individuals (of opposite mating types) can produce fertile offspring. Organisms that reproduce asexually and exchange genetic material through horizontal gene transfer (HGT), like bacteria and archaea, defy this classic definition. Currently, researchers primarily define microbial species and populations by the genome-wide sequence similarity between individuals, using somewhat arbitrary cutoffs. It is unclear how well this approach reflects groups of microbes that form distinct, ecologically relevant units—aka, populations.

Massachusetts Institute of Technology Professor Martin Polz, Ph.D. is using new bioinformatic methods to address the problem of defining microbial populations by measuring the evolutionary relationships between individual microbes. Polz's group seized on the concept underlying the traditional definition of a population: gene flow, or the exchange of genetic information between groups of individuals. Distinct populations of organisms experience limited gene flow with more gene flow within each discrete population than between them.

Polz's group seized on the concept underlying the traditional definition of a population: gene flow.

To measure prokaryotic gene flow, Polz's group developed PopCOGenT, a method that produces a size distribution of segments of identical sequence across any two genomes. More recent HGT events should result in longer segments of sequence uninterrupted by single nucleotide variants, similar to the concept of haplotypes. At a genome-wide level, if more of these long, identical sequence segments are identified that would be expected assuming evolution through purely clonal, asexual reproduction (i.e., with no HGT). Then there is evidence of recent gene flow occurring between the two genomes, placing them within the same microbial population.

Using this pairwise method, Polz was able to tease out distinct gene flow networks among diverse groups of bacteria and archaea. These networks recapitulated previous ecological characterizations of the isolates into distinct microbial populations. Following this validation of the PopCOGenT method, Polz's group applied it to a gut microbiome dataset from healthy individuals and individuals with ulcerative colitis or Crohn's disease. PopCOGenT distinguished two populations of microbes, with one population particularly enriched in Crohn's disease patients. This more sophisticated method of interrogating microbial communities by understanding their genetic histories holds promise for unearthing previously invisible but potentially important population structures.

THE SHORT- AND LONG-TERM EVOLUTION OF OUR GUT MICROBIOMES

Limitations to resolving different strains of a microbial species from metagenomic data mean that the short- and long-term evolution of microbial lineages in the microbiome have been understudied relative to other aspects of this community. To address these limitations, University of California, Los Angeles Assistant Professor Nandita Garud, Ph.D., looked at allele frequencies at synonymous sites in the core genomes of ubiquitous species within the gut microbiome. Based on the individual profile of frequencies from each sample for each prevalent species, she and her research group have demonstrated that some people are colonized by one dominant lineage for a given species, while others are likely colonized by a handful of divergent lineages. Samples in the first category have a straightforward population structure, making them ideal for investigating evolutionary dynamics.

Does a person's microbiome change after it is established and, if so, how? Do the existing lineages continually adapt to the host or do lineages get replaced? To answer these questions in the short term, Garud's group analyzed Human Microbiome Project samples with dominant lineages for a given species at two consecutive timepoints, six months apart. Most sample pairs showed no major changes over six months, indicating no evolutionary change in the lineage over that period of time. A small portion of sample pairs contained a handful of genetic changes at high frequency in the later timepoint, indicating adaptation of the original dominant lineage over six months. An even smaller portion of sample pairs showed thousands of genetic changes at high frequency in the later sample over this time period. The high number of changes for these sample pairs is inconsistent with adaptation of the original lineage, and Garud's group interpreted these instances as strain replacement events. Within the six months between samples, those people were colonized by an entirely new, divergent strain that out-competed their original strain.

Do the existing lineages continually adapt to the host or do lineages get replaced?

These analyses offered a fascinating view of dynamics within the gut microbiome on a relatively short timescale indicating that both strain adaptation and replacement can occur, but they introduced new questions: Are strain replacements common to everyone or are certain individuals prone to replacement events? To answer these questions, Garud's group looked at longer timescales using data from the UK Twin Study. This dataset includes microbiome information from sets of twins who shared their environments for their first decades of life (ensuring colonization by similar microbial strains), but then went on to establish separate households. In contrast to the short six-month timescale, twins who lived apart for more than 20 years had a high proportion of divergent strains. Assuming each twin in a pair started out with the same dominant lineage, this finding suggests that replacement events are common over a lifetime. These analyses are likely just the tip of the iceberg, but provide an intriguing view into how our microbiomes grow and evolve with us.

Katherine Lontok, Ph.D., is the public outreach manager at ASM where she works to engage non-expert audiences with the microbial sciences. She holds a Ph.D. in molecular biology and biochemistry from the University of California, San Francisco.

It Takes a One Health Village:

Fighting AMR Through Research, Guidelines and Implementation

by Julie Wolf, Ph.D.

Addressing the widespread problem of antimicrobial resistance (AMR) requires all scientific hands on deck. Because AMR permeates human, animal and environmental ecosystems, many feel that a comprehensive approach is the best way to contain the further spread of resistance. This has led many scientists, researchers and policymakers to believe that a One Health perspective, in which human health is understood to be intertwined with the health of animals and the environment, is the best approach to fight the spread of AMR between and within these niches.

Thus one of the most integrative sessions at ASM Microbe 2019, "One Health Solutions for Tackling Antimicrobial Resistance," featured experts from academic research, veterinary research and the Centers for Disease Control and Prevention (CDC). These experts presented their experiences in building evidence-based policies to combat AMR.

Research Builds a Foundation of Evidence

Livestock-raising practices have been indicted to be a major source of AMR, but how strong is the evidence linking livestock to AMR? Shannon Manning, associate professor of microbiology and molecular genetics at Michigan State University, studies this link, focusing on enteric infections. She works with hospitals in the surrounding area to identify risk factors for infection with resistant pathogens. Simultaneously, her group surveys cattle to look at the prevalence of cattle carriage of resistance. By using comparative genomics in human and cattle isolates, she hopes to understand the relationship between these isolates. These insights will be especially helpful because Michigan is not a member of FoodNet—a collaboration between the CDC, 10 state health departments, the U.S. Department of Agriculture Food Safety and Inspection Service (USDA-FSIS) and the Food and Drug Administration (FDA)—which tracks common foodborne pathogens.

Risk of human infection with *Campylobacter jejuni*, one of the bacterial pathogens Manning studies, is associated with consumption and handling of meat from *Campylobacter*-colonized chickens and cattle. Manning confirmed this correlation for people living in nearby rural areas but also found that using well water as a drinking water source correlates with increased risk. Contaminated soils and waters are a common source of *Campylobacter*.

Whole-genome sequencing of patient isolates from local hospitals revealed that resistant isolates were frequently identified as sequence types (STs) associated with foreign travel (yet another risk factor for *Campylobacter* infection). The most common fluoroquinolone-resistant STs among those studied matched one that recently emerged in Europe. However, Manning observed that tetracycline-resistant isolates were more likely to be categorized as a bacterial ST previously found in ruminants called ST-982. Patients with tetracycline-resistant *C. jejuni* were also more likely

to report contact with cattle.

To complement these studies, Manning's team investigated *C. jejuni* at nearby farms. A 2017 study characterized the isolates from a set of three cattle herds, one of which prophylactically uses chlortetracycline in their feed. The scientists found a diversity of STs in these herds, but the chlortetracycline-fed herd had a higher prevalence of ST-982, most of which were tetracycline-resistant. They found other tetracycline-resistant isolates as well.

Are the tetracycline isolates from the cattle related to the isolates in people? This was a short-term study, so conclusions regarding how ST-982 came to be found in both cattle and people can't be made yet. It may have passed from cattle to people, from people to cattle, or back-and-forth between the species multiple times. To convict tetracycline-containing feed as the culprit in spreading tetracycline-resistant infections, longitudinal studies are needed to determine transmission patterns of AMR *C. jejuni.* But as Manning points out, these studies represent a critical first step toward implementing surveillance for AMR in multiple populations: "It's hard to address a problem like AMR unless you know what's there."

As Manning points out, these studies represent a critical first step toward implementing surveillance for AMR in multiple populations: "It's hard to address a problem like AMR unless you know what's there."

Gathering Evidence in Additional Niches

While Manning continues to study a link between livestock raising practices and *C. jejuni* transmission, some outbreaks stem from an animal reservoir that lives closer to home: puppies. A puppy-driven 2018 multidrug-resistant outbreak of *Campylobacter* required communications between medical doctors, veterinarians and public health workers to pinpoint the source and challenged the conventional association of *Campylobacter* with cattle. Jeff Bender, DVM, MS, professor in the Division of Environmental Health Sciences at the University of Minnesota and the Director of USAID's multi-disciplinary One Health Workforce Project, used this example to highlight the importance of a One Health approach to identify, treat and eliminate antimicrobial resistance.

The input of informed professionals across the ecosystem—those who work with people, animals, agriculture, plants and water systems—is the collaborative infrastructure necessary to tackle a big problem like antimicrobial resistance. Pets receiving antibiotics, as highlighted in this case, are an area less spotlighted, but this matter is one where both pet owners and veterinarians can contribute to the AMR fight.

Just like infections in their human companions, Bender noted that animal health care workers can fight resistance by preventing and treating infections, improving antibiotic prescription practices through stewardship and developing new drugs and diagnostics to add to the antibiotic arsenal. These practices have been incorporated into the American Veterinary Medical Association's new guidelines on antimicrobial use in pets. Now, many of the same stewardship practices used in people can be applied to pets and help extend the useful lifespan of medically important antimicrobial compounds.

Water: The Prototypical One Health Issue

Manning found an association between well water and risk of *Campylobacter* infection, but in fact 11 of the 18 major antimicrobial resistant threats listed by the CDC can be transmitted by water, allowing outbreaks to quickly grow in geographic scope and case numbers. This makes water the prototypical One Health issue, according to Amy Kirby, Ph.D., MPH, senior service fellow in the Waterborne Disease Prevention Branch of the CDC.

The Environmental Protection Agency (EPA) maintains standards that recreational waters must meet to keep swimmers safe. These standards include maximum contaminant levels of total coliform counts, which are used as an indicator of other potential pathogens. However, a 2017 outbreak of multidrug-resistant *Escherichia coli* O157 at a private lake in California showed that recreational water meeting these standards can still pose a risk. Our drinking water is another potential source for antimicrobial resistance. Although most microbial life is removed through a multistep process, no step includes monitoring for AMR.

Thus far, no consensus exists on how to tackle the huge issue of screening water for AMR. What waters should be screened, and what methods should be used? Kirby argued that screening surface water (e.g., lakes, streams) may be most productive since it is the source for both drinking and irrigation water and receives treated wastewater and untreated runoff. Kirby also explained that microbial culturing must be used in combination with sequencing techniques. Culturing water samples allows quantitative recovery of extremely small populations of drug-resistant isolates, while sequencing adds details about the AMR genotype and any mobile genetic elements of the isolates.

In an Atlanta pilot program, 66% of collected surface water samples had detectable levels of Extended-Spectrum Beta-Lactamase-producing (ESBL) *E. coli,* with increased contamination after rainfall. These isolates had similar STs to uropathogenic *E. coli* and extraintestinal pathogenic *E. coli,* suggesting human pathogenic potential, and 94% were resistant to two or more classes of antibiotics. This pilot study demonstrates that new screening methods may better identify waters contaminated with AMR bacteria. Identifying contaminated waters is important to protect people using these water sources and to prevent the spread of contamination into new ecosystems.

Transforming Research into Action

The outbreak of multidrug-resistant *Campylobacter* infections linked to puppies points to a need for all parties to contribute to AMR National Action Plans to ensure potential sources of AMR outbreaks and opportunities to implement stewardship plans aren't omitted. Currently, 85% of countries have or are developing National Action Plans, most of which address measures for infection prevention and control in people. Only 7% include surveillance for livestock, indicating a clear area of need.

Currently, 85% of countries have or are developing National Action Plans, most of which address measures for infection prevention and control in people. Only 7% include surveillance for livestock, indicating a clear area of need.

Fortunately, international organizations are addressing the multiple scientific communities whose work is vital to tracking and treating AMR. Scott McEwen, professor in the Department of Population Medicine at the University of Guelph, has experience working with several international organizations, in particular the World Health Organization (WHO). He introduced the WHO Guidelines on Use of Medically Important Antimicrobials in Food-Producing Animals, which aims to control AMR through various interventions to reduce unnecessary antimicrobial use in animals.

Quality evidence forms the basis of WHO guidelines, so documenting evidence for guidelines is critical. The WHO makes recommendations only after considering the supporting evidence and taking steps to minimize bias, since the goal of these recommendations is to inform end-users about what to do in specific situations and lead to a change in habits, as well as influence national policies. One example comes after the WHO recommended to stop the use of all medically important antimicrobials for improving growth of food-producing animals. Many countries have adopted this measure, including the United States, which banned the use of antibiotics as growth-enhancement for livestock animals in 2017.

The steps presented by these experts: conducting thorough research to determine AMR sources, building surveillance systems to screen for AMR and using these data to build guidelines that lead to changed behaviors are our chance to maintain the usefulness of antibiotics for treating infectious disease. The contribution of many scientists with varied backgrounds and experiences provides the best hope in our fight against AMR.

This story is based off the following presentations given at ASM Microbe 2019:

Scott McEwen. *Use of Medically Important Antimicrobial in Food-Producing Animals: The Need for World Health Organization (WHO) Guidelines.*

Shannon Manning. *Livestock and AMR: What is Being Done to Reduce the Spread?*

Jeff Bender. *Enablers and Barriers to Antimicrobial Stewardship in Veterinary Practice.*

Amy Kirby. *Tackling Global Water Supplies to Reduce the Spread of AMR.*

Julie Wolf, Ph.D., is the science communications specialist at ASM, where she uses social media, the web and live events to communicate and help others communicate their science. She is the host of ASM's newest podcast, Meet the Microbiologist, *and in her free time teaches at the community biolab Genspace.*

Up Close and Personal with

ASM Microbe 2019 Attendees

Menglan Zhou

Peking Union Medical College, China

Menglan Zhou is a Ph.D. student majoring in clinical microbiology. Her research focuses on the antimicrobial resistance and virulence of clinical important bacteria and fungi, such as *Streptococcus pneumoniae,* carbapenem-resistant *Enterobacteriaceae* and *Kodamaea ohmeri*. She is an ASM Infectious Disease Fellows Program Travel Award recipient and an ASM Microbe first-time attendee.

As a first-time ASM Microbe attendee, how would you describe your experience?

I'm deeply impressed by the vast size and scope of the meeting. It covers all topics from clinical microbiology, infectious disease, pharmacology and more. Sometimes it was very hard to decide which session to attend because there were so many interesting lectures happening at the same time.

What was the most rewarding aspect of attending ASM Microbe?

ASM Microbe provided an opportunity to learn about the forefront of clinical microbiology and infectious diseases. I had the chance to learn from respectable scientists talking about their research. It really inspired me.

What sessions inspired you the most at ASM Microbe and why?

The most unforgettable session for me was "Battle of the Brains." It's a trivia competition concerning clinical microbiology and infectious disease knowledge between groups from different hospitals. This session was very challenging and popular because every time a question was raised, both the participants and audience started brainstorming. If the participants couldn't give an answer, they could ask the audience for help. The whole session was very exciting.

How has attending ASM Microbe influenced your professional development and career goals?

I got to know some of the experts in my field, especially through the Infectious Diseases Fellows Program. They shared growth stories and life experiences that really inspired me. Also, I learned that the ASM Microbe Subcommittee on Postgraduate Program provides a two-year fellowship program that prepares scientists and physicians for leadership careers in medical and public laboratory microbiology or immunology. My goal is to be accepted into this fellowship program.

What are the benefits of receiving a travel award to attend ASM Microbe?

I'm really appreciative that I was selected as a travel award recipient. It was so nice to have my airfare and accommodations covered, so I didn't need to worry about the cost too much. More importantly, by holding the breakfast briefing session every morning, the Infectious Diseases Fellows Program provided an excellent opportunity for all the awardees to get together, listen to professionals speak, communicate with experts and share with each other. I had close contact with some experts in the field and got to know people from all over the world. It was a very precious and unforgettable experience.

Joanna Karczewska-Golec

University of Warsaw, Poland

Joanna Karczewska-Golec, Ph.D. is a science and technology policy advisor whose research focuses on applied and environmental microbiology. She is the ASM Country Ambassador to Poland and is a postdoctoral member of the ASM Membership Committee.

How would you describe your 2019 ASM Microbe experience compared to previous years?

I have attended every ASM General Meeting since 2013 when I was appointed the Young Ambassador of Science. ASM Microbe, which combined the General Meeting with a more clinically-focused meeting, has evolved into a truly global, versatile and multidimensional event. By gathering people from the breadth of disciplines in microbial sciences, ASM Microbe lays the groundwork for developing off-trail, interdisciplinary collaborations. It provides microbiologists with an opportunity to receive feedback on their results from scientists specializing in different research niches.

ASM Microbe is the most inspiring and prestigious microbiology conference, offering the highest level of speakers. Poster sessions consistently gather large and active audiences, which is usually not the case at other meetings.

What was the most rewarding aspect of attending ASM Microbe?

For me, it was the ASM Membership Committee meeting, where we worked on advancing ASM as a scientific society and improving the opportunities ASM provides for its members. I advocated for refining the ASM grants portfolio. I have always promoted the idea of expanding eligibility criteria in some ASM grants to international members. The Career Development Grants for Postdoctoral Women will soon be open to international female microbiologists. It is rewarding to see how advocacy benefits ASM members, mostly early-career scientists, and that ASM is becoming an increasingly inclusive, global, member-centered society.

What sessions inspired you the most at ASM Microbe and why?

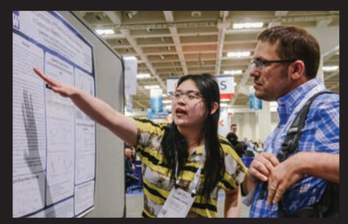
Three events truly inspired me. One was Pat Brown's keynote. Pat is a role model for science policy and diplomacy and demonstrates how each scientist can personally commit to science policy matters.

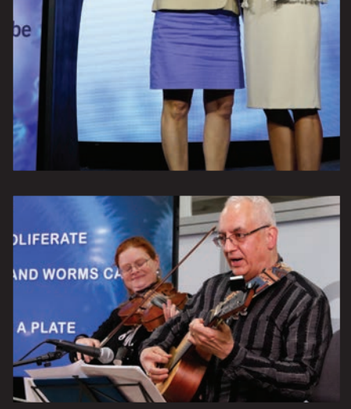
The Resource Recovery session presented successful, real-life applications of bacteria and phages in waste treatment, energy recovery and creating value-added products. The Early Career Grants to Bootstrap Your Research pre-conference workshop focused on research grants in the United States, which are similar to grant proposals in Europe. Speakers offered practical advice with specific examples on how they successfully addressed challenges securing research funding.

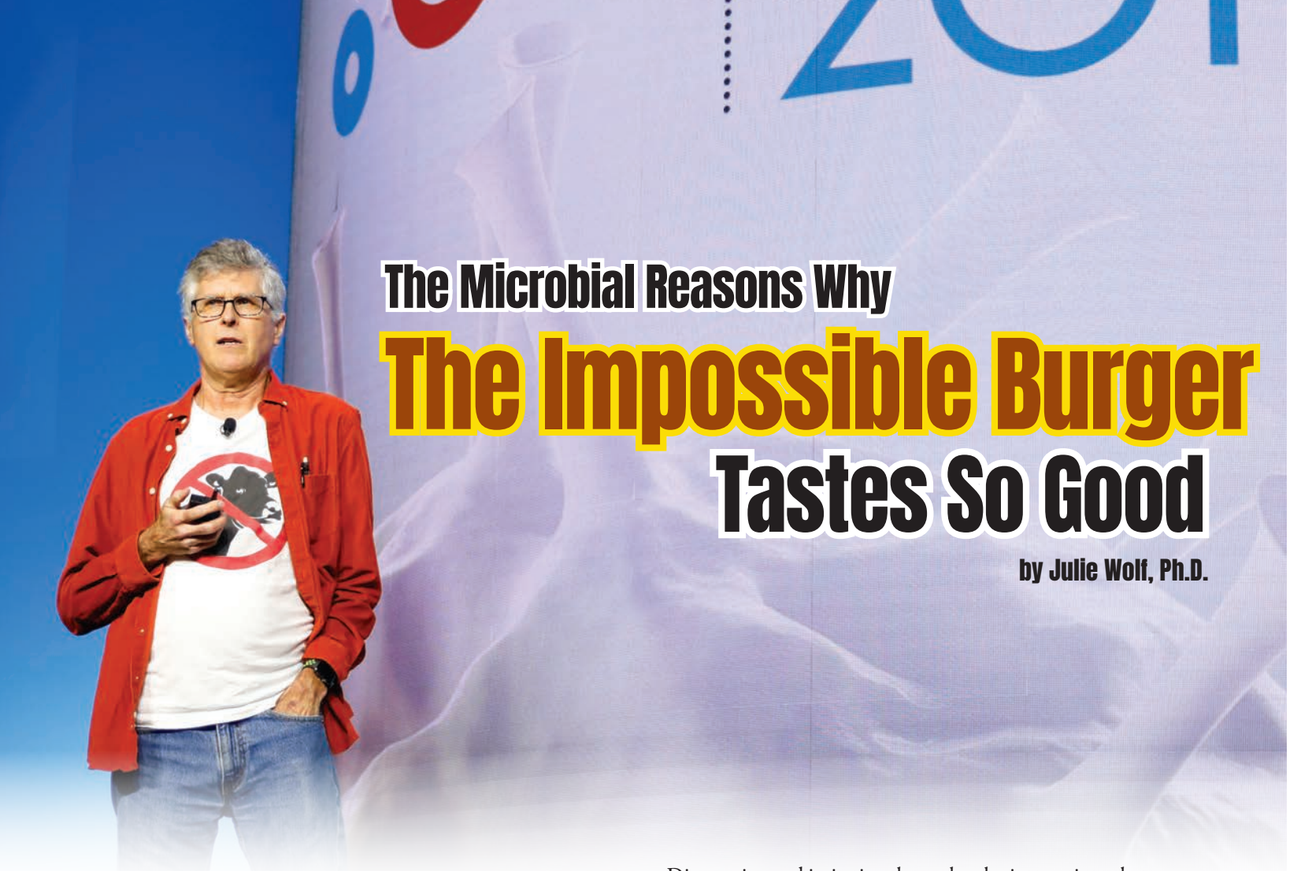
How has attending ASM Microbe influenced your professional development and career goals?

It has confirmed my desire to continue dedicating myself to science policy and diplomacy and real-world research applications of microbiology, from bench to market. This year, I gained a number of inspirations and will share lessons learned with local microbial communities. The pre-conference workshop taught me what kinds of training can be offered to European scientists to develop skills in grant writing. Preparations for leading such a workshop in Poland are already underway.

Highlights from key events at ASM Microbe 2019, including the opening session, poster presentations, evening receptions, fireside chats, ASM studio recordings and the Discovering Microbiology STEM festival.







The Microbial Reasons Why The Impossible Burger Tastes So Good

by Julie Wolf, Ph.D.

Microbes Make the (Plant-Based) Meat

What makes meat delicious? This arguably understudied question is the scientific focus of the research team at Impossible Foods, the company Pat Brown founded and whose mission is to completely replace animals as a food production technology. Brown gave the Keynote Address during ASM Microbe 2019.

Discovering and imitating the molecular interactions that make meat delicious "is the most important scientific question in the world right now," Brown says.

Discovering and imitating the molecular interactions that make meat delicious "is the most important scientific question in the world right now," Brown says. Brown explained the science to ASM.

Part of what makes meat delicious is its high concentration of heme, a family of iron-containing molecules that serve a variety of functions, including oxygen transportation and involvement with electron transport and redox reactions. Every living plant or animal cell contains heme proteins, and animal muscle has a high concentration of hemoglobin. When Brown set out to develop a recipe for a meat replacement, he was pretty sure heme would play an important role.

It turns out that heme is an integral part of why meat tastes good, but not only because of the iron it provides: heme plays a central role as a chemical catalyst during cooking. According to Brown and his research team, many meat-specific aromas rely on heme interactions with cellular proteins and biomolecules as it cooks. "Heme catalyzes very specific types of chemical reactions," says Brown, "that transform abundant, simple nutrients into this explosion of hundreds of diverse volatile odorant molecules. When you experience them, together they add up unmistakably to the smell and taste of meat."

To replicate the delicious taste of meat, Brown and his scientific team needed to find an alternative source of heme.

Rhizobia to the Rescue: A Role for Microbes in Meat

Brown's inspiration for a heme source came from a high school biology teacher, who had taught him that the chemistry of nitrogen fixation is sensitive to oxygen concentrations. This is particularly important for legumes, a group of plants that form symbiotic relationships with nitrogen-fixing bacteria called rhizobia. The rhizobia live in root nodules on the plants, where they convert atmospheric nitrogen into ammonia that can be incorporated into bacterial or plant metabolic pathways. To verify the high concentration of legume heme proteins yourself, slice open the nodules on clover (a legume) and note the bright pink color associated with the presence of heme.

Every legume has its own rhizobial species with which it has an evolved relationship, and Brown turned to one of the largest crop legumes as a potential heme source for Impossible Foods: soybeans. The roots of these crops have long-studied relationships with *Bradyrhizobium* and *Sinorhizobium* species, and soybeans produce a heme protein called leghemoglobin to regulate the oxygen for their nitrogen fixation activities. Given that soybeans constitute 89.6 million acres of crops in the United States, Brown suspected using the roots leftover after harvesting would be a sustainable source of heme for his product.

Soybean roots became a major focus for the Impossible Foods team. For a year and a half, scientists and engineers concocted a number of Rube Goldberg-like contraptions designed to separate the nodules from the root and soil, and tried various methods to purify the leghemoglobin. While this generated enough leghemoglobin to make a proof-of-concept burger, the process was too labor intensive and inefficient to scale up for mass production. They needed a better way to produce heme proteins.

Yeast Make Production More Efficient

The scientific team turned to yeast to explore recombinant protein production. Using a recombinant system freed the team to explore other heme sources, including hemoglobin and myoglobin

from animal sources. Though the goal is to generate a sustainable protein source that replaces the ecologically taxing way people currently raise livestock, Brown had no qualms about sourcing genetic material from animals, if the result is a better-tasting, more environmentally-friendly burger: "The problem we're trying to solve here is the catastrophic effect of covering the planet with cows. If we're producing a heme protein that's encoded normally by the cow genome but we're producing it in a way that isn't an environmental catastrophe, that would be fine. We're fixating on the best heme protein for performance in meat."

The heme production machine became *Pichia pastoris,* a yeast used for large-scale production of a number of recombinant proteins. Developed in the 1980s and 1990s, Pichia has been used as a factory for proteins used in therapeutics and food preparation, and was a good fit for housing the complex metabolic pathways that constitute heme protein production. After testing a wide variety of heme proteins, however, it turned out that the first one was the best fit: It was leghemoglobin that created the best-tasting burger.

It may seem counterintuitive that a plant hemoglobin would have superior performance to one from the animal whose tissues the scientists wanted to mimic. Brown says the reason lies in the purpose of this particular hemoglobin. "For us, (the protein) doesn't need to do everything that it did in the cow. The enzymes, catalysts and small molecules in the system have to be able to reproduce the biochemistry that produces flavor in meat." Those other roles of hemoglobin in a normal cell—function in the electron transport chain, muscle contraction or glycolysis—are dispensable as long as the key properties of meat are reproduced. Though other components of the Impossible Burger recipe have changed over the years, leghemoglobin produced by yeast has remained an essential ingredient.

It may seem counterintuitive that a plant hemoglobin would have superior performance to one from the animal whose tissues the scientists wanted to mimic. Brown says the reason lies in the purpose of this particular hemoglobin.

Why Replace Meat?

"The whole reason the company exists, and the reason we have so many amazingly great scientists working here, is that we are working on the most important and urgent problem in the world right now. Arguably, the most important and urgent problem our species has ever faced is the catastrophic meltdown in biodiversity and the relentless progression of climate change," says Brown. The food system has contributed to both of these problems, he argues.

Brown's background is neither in environmental nor food sciences. But he has a history of tackling problems that lay outside his field of expertise with gusto. As a basic scientist studying HIV, he wanted a better way to test global gene activation. The technology he invented to solve his problem, the microarray, became integral to the gene expression studies of the 1990s and 2000s. While producing microarrays, he learned that not all gene sequences published by scientists were freely available. This inspired him to work on an open-access movement, culminating in the founding of the Public Library of Science (PLOS) nonprofit publishing company. Having created new scientific technologies and publishing models, Brown thought hard about what truly big, global problem he might address in his next career act.

Brown's background is neither in environmental nor food sciences. But he has a history of tackling problems that lay outside his field of expertise with gusto.

Many are familiar with the ecological impacts of raising livestock: it requires a lot of freshwater, it produces pollutants that contaminate soil, water and air, and it eliminates the natural biodiversity that would otherwise fill the land. "The single biggest reason it's so destructive is because it's land-intensive," says Brown. "Something like 45% of the entire area of land on earth is actively in use raising animals for food right now." This includes both land for the livestock pastures as well as land spent growing feed crops. As global meat production nearly doubled between 1980 and 2004, so did the land required for its production.

The solution isn't to use these numbers to criticize people for eating meat, but to make a better tasting burger that meat lovers prefer. "The only way to do it is to create products that consumers prefer that can compete successfully in the marketplace against those products."

A competitive Impossible Burger must be more delicious, nutritionally superior ("which we already are," says Brown), and economical compared to traditional beef burgers. The process to make Impossible Burgers uses one-tenth the water, less than one-twenty-fifth the land and less than one-tenth the fertilizer input, which basically means the fundamental drivers of cost are vastly lower than using animal production. Lower resource use means lower cost at scale. As Brown has learned, heme goes a long way toward re-creating the indescribable umami of beef. But perhaps the lower environmental and financial costs associated with the Impossible Burger will also make it more palatable. As Impossible Burgers become increasingly available at restaurants around the country, Brown hopes the nutritionally superior, lower cost and better-tasting burger choice will make an argument for itself.

As Brown has learned, heme goes a long way toward re-creating the indescribable umami of beef. But perhaps the lower environmental and financial costs associated with the Impossible Burger will also make it more palatable.

Julie Wolf, Ph.D., is the science communications specialist at ASM, where she uses social media, the web and live events to communicate and help others communicate their science. She is the host of ASM's newest podcast, Meet the Microbiologist, *and in her free time teaches at the community biolab Genspace.*

Want to hear more about the microbial contribution to plant-based meat?

Listen to an interview with Pat Brown on ASM's *Meet the Microbiologist* podcast!

Download or stream to listen today:
http://bit.ly/PatBrownMTM

What's Hot in the Microbial Sciences

by Julie Wolf, Ph.D., and Stanley Maloy, Ph.D.

New Immunization Strategies

Scientists are looking at numerous methods to build better immunization strategies. One exciting avenue involves new delivery systems. Research published in *NANOletters* introduces a micromotor pill that embeds itself into the intestinal mucosa, using the chemistry of the intestinal environment to activate uncoating and propulsion from a magnesium-based core. Another delivery system called a self-orienting micromillimeter applicator (SOMA), published in *Science*, autonomously orients itself for drug delivery through gastrointestinal tissue and may also be useful for delivery of vaccine or antimicrobial therapies. A second exciting avenue is manipulating B cells to recognize and fight specific pathogens; two recent papers describe using genome-editing methods to do so. A study in *eLife* engineered patient B cells from three volunteers, replacing the heavy chain variable region with that from an HIV broadly neutralizing antibody, while a study in *Science Immunology* engineered both human and murine B cells to express antibodies targeting a number of viruses. In the latter study, transferred engineered B cells were able to protect mice against respiratory syncytial virus challenge. These strategies provide promise to generate protective immunity against a wide range of microorganisms.

- *Wei X. et al. Biomimetic Micromotor Enables Active Delivery of Antigens for Oral Vaccination.* NANOletters. *February 6 2019. https://pubs.acs.org/doi/pdf/10.1021/acs.nanolett.8b05051*
- *Voss J.E. et al. Reprogramming the Antigen Specificity of B Cells using Genome-Editing Technologies.* eLife. *January 16 2019. https://elifesciences.org/articles/42995*
- *Moffett H.F. et al. B Cells Engineered to Express Pathogen-Specific Antibodies using CRISPR/Cas9 Protect against Infection.* bioRxiv. *May 17 2019. https://immunology.sciencemag.org/content/4/35/eaax0644?utm_campaign=toc_imm_2019-05-24&et_rid=17908298&et_cid=2831520*
- *Abramson A. et al. An Ingestible Self-Orienting System for Oral Delivery of Macromolecules.* Science. *February 8 2019. http://science.sciencemag.org/content/363/6427/61*

The Importance of Testing Diverse Samples

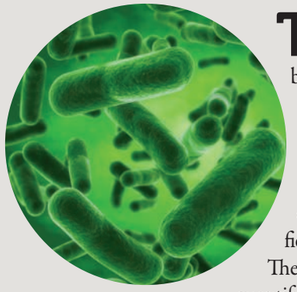
Microbiologists have focused on a single bacterial strain for much of the history of genetic and physiological characterization studies. However, it is now clear that there are often substantial differences between the reference strain and other strains of the same bacterial species found in nature. A comparison of ten *Pseudomonas aeruginosa* PAO1 reference strains, published in the *Journal of Bacteriology*, described variable phenotypic changes, including differences in secreted molecules such as exopolysaccharides, extracellular DNA, quorum sensing molecules and outer membrane vesicles, despite limited genetic differences between strains. The lack of genomic changes suggested these variations may be due to differences in transcriptional, translational or other regulatory processes that occur through microevolution during strain propagation. A second *Journal of Bacteriology* study extended this to wild populations of *Vibrio fischeri*, which must form biofilms to colonize its Hawaiian bobtail squid host. A study of worldwide isolates demonstrated that the signaling pathways regulating biofilm formation have undergone several rounds of genetic shuffling, resulting in heterogeneous regulation within the natural *V. fischeri* populations. These studies emphasize the importance of incorporating diverse strain backgrounds into understanding bacterial molecular mechanisms. These phenotypic differences within bacterial populations can be exacerbated by the method of bacterial inoculation, a consideration recently highlighted in an *Applied and Environmental Microbiology* report.

- *Chandler C.E. et al. Genomic and Phenotypic Diversity Among Ten Laboratory Isolates of* Pseudomonas aeruginosa *PAO1.* Journal of Bacteriology. *January 31 2019. https://jb.asm.org/content/jb/201/5/e00595-18.full.pdf*

- *Natural Strain Variation Reveals Diverse Biofilm Regulation in Squid-Colonizing* Vibrio fischeri. Journal of Bacteriology *April 9 2019. https://jb.asm.org/content/jb/201/9/e00033-19.full.pdf*

- *Kragh K.N. et al. The Inoculation Method Could Impact the Outcome of Microbiological Experiments.* Applied and Environmental Microbiology. *February 14 2018. https://aem.asm.org/content/84/5/e02264-17*

What Are the Chances?
A Role for Stochasticity in Biology



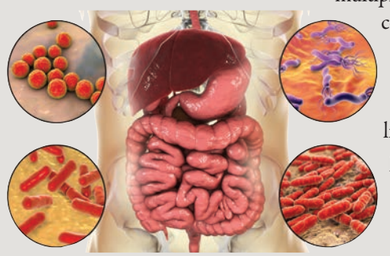
Two new studies support a role for stochasticity in biological processes. A study published in *mBio* investigated the role of stochastic processes, environmental selection and dispersal in microbial composition using an intact field community experiment. The research team found that quantifying stochastic processes was key to understanding microbial diversity, although stochastic effects on taxonomic composition were smaller than expected. A second study published in *Nature Microbiology* measured the effects of a set of *Bacillus subtilis* mutants across 19 different environments, finding that different alleles dominated in parallel replica experiments. A majority of the tested alleles showed opposing fitness effects under different conditions, allowing the research team to conclude that the range of mutants that persisted was a result of a combination of selection, pleiotropy and chance.

- *Albright M.B.N, Chase A.B, and Martiny J.B.H. Experimental Evidence that Stochasticity Contributes to Bacterial Composition in a Decomposer Community.* mBio. *April 16 2019. https://mbio.asm.org/content/10/2/e00568-19*

- *Noda-García L. et al. Chance and Pleiotropy Dominate Genetic Diversity in Complex Bacterial Environments.* Nature Microbiology. *April 1 2019. https://www.nature.com/articles/s41564-019-0*

The Gut Microbiome is a Dynamic Ecosystem

A series of papers published in *Cell Host & Microbe* have explored ecosystem stability of the gut microbiome ecosystem. The first demonstrated that the gut microbiome constantly evolves, even within healthy individuals. The study focused on the *Bacteroides* population, showing that multiple lineages can coexist within one individual and that de novo mutations arising in these lineages can affect phenotypes such as bacterial polysaccharide metabolism and capsule synthesis.



The second study demonstrated that a probiotic *E. coli* strain can also evolve in the mammalian gut, with carbohydrate metabolism being the most frequently affected phenotype. A third study showed that removal of a specifically targeted bacterial species can have major effects on the remaining members within a defined, ten-member bacterial consortium. Researchers in this study used a bacteriophage to eliminate one member of the consortium, observing that the loss of even minor populations changed the proportions of the remaining bacterial species. The importance of a single species in maintaining ecosystem balance was emphasized in an *mSystems* study, which used species omitted from a defined microbial consortium to define metabolic roles within the gut microbiome. These studies will prove vital as gut microbiome manipulations like probiotic and bacteriophage treatment gain popularity for gut health improvement.

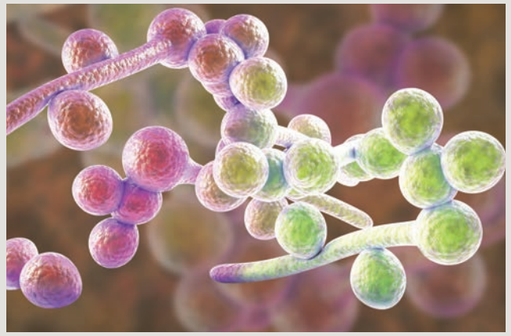
- *Crook N. et al. Adaptive Strategies of the Candidate Probiotic* E. coli *Nissle in the Mammalian Gut.* Cell Host & Microbe. *April 10 2019. https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(19)30101-5*

- *Zhao S. et al. Adaptive Evolution within Gut Microbiomes of Healthy People.* Cell Host & Microbe. *May 8 2019. https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(19)30159-3*

- *Hsu B.B. et al. Dynamic Modulation of the Gut Microbiota and Metabolome by Bacteriophages in a Mouse Model.* Cell Host & Microbe. *June 12 2019. https://www.cell.com/cell-host-microbe/fulltext/S1931-3128(19)30246-X*

- *Gutiérrez N. and Garrido D. Species Deletions from Microbiome Consortia Reveal Key Metabolic Interactions between Gut Microbes.* mSystems. *July 16 2019. https://msystems.asm.org/content/4/4/e00185-19*

Threat of Multidrug-Resistant *Candida* Species Looms Large



Drug resistance is a problem across all microorganisms, including fungi. A session at ASM Microbe 2019 focused on the multidrug-resistant *Candida* species: epidemiology, diagnosis and treatment for these recalcitrant infections. Unlike bacteria, there is no official definition for multidrug-resistant *Candida*, complicating discussions around this growing problem. Newly emerged species like *C. auris* add further complexity by confounding previous diagnostic algorithms with their inconsistent aggregation and CHROMagar phenotypes.

The burden of *C. auris* is likely underestimated, due to the fact that countries such as India and others have high incidence but do not list *C. auris* as a notifiable disease. Infection control is the best way to prevent the spread of resistance; fortunately, preventions for infection control of multidrug-resistant *Candida*, including *C. auris*, are similar to those used for any MDR organism in a hospital. However, *C. auris* is resistant to quaternary compounds so disinfectant choice is critical for effective infection control.

This hot topic is based on ASM Microbe 2019 session 136: *Epidemiology and Management of Multidrug-resistant* Candida *Species*

- *Anuradha Chowdhary.* Candida auris – *Epidemiology, Clinical Features and Management*
- *Maiken Arendrup: Diagnosis and Treatment of Multidrug-resistant* Candida *Species*

Experimental Evolution Provides Biological Insights

Experimental evolution, or learning about microorganisms by creating artificial selective pressures, allows scientists to make unbiased discoveries about microbes and microbial processes. Experimental evolution provides insight into speciation when researchers ask questions about bacteria-virus interactions, demonstrating that lambda phage generalists that use multiple *Escherichia coli* receptors can produce specialized preferences that may result in reproductive isolation. Experimental evolution also provides insights into *de novo* gene birth when researchers ask questions about *Saccharomyces cerevisiae* proto-genes, non-genic open reading frames that can influence an organism's relative fitness. Adaptive proto-genes are enriched in predicted transmembrane domains, suggesting that intergenic sequences may have inherent properties that are exposed upon translation, which counters the old model of gene evolution whereby a new random protein sequence evolves its function protein through selection. Further, experimental evolution provides insight into domestication of wild microbes, with a *Nitrosocaldus yellowstonensis* isolate sequences from a decade of lab propagation revealing 56% of mutations affecting amino acid sequences, including an ammonia transporter. These changes may partially explain the decrease in isolate doubling time from 20 to 14 hours. Experimental evolution even won a Nobel Prize for Frances Arnold, whose work directing evolution of enzymes using natural processes proved more efficient at developing new enzymatic functions than those designed by scientists, and has led to enzymatic applications for previously nonbiological processes, such as silicon-carbon bond formation.

This hot topic is based on ASM Microbe session 001: the Opening Session and session 386: *Molecular Insights from Experimental Evolution,* which included the following presentations:

- *Frances Arnold. Innovation by Evolution: Bringing New Chemistry to Life*
- *Anne-Ruxandra Carvunis.* De novo *Emergence of Adaptive Membrane Proteins from Thymine-Rich Intergenic Sequences*
- *Joshua M. Borin. A Biophysical Trade-Off Governs Adsorption to Host Receptors in Bacteriophage Lambda*
- *Jesse Bloom. Using Experiments in the Lab to Understand Influenza Virus Evolution in Nature*
- *Elizabeth J. Winters. Progressive Adaptation of the Thermophilic Ammonia-Oxidizing Archaeon* Nitrosocaldus yellowstonensis *to Laboratory Culture Conditions*
- *Justin Meyer. Viral Host-Range Evolution and Evolvability Facilitated by Receptor Binding Protein Bistability*

Mucus is a Dynamic Environment for Microbial-Host Interactions

Mucus forms one of the largest ecological niches for human microbiota and studies of this niche have implications for both basic and applied sciences, as highlighted at a session during ASM Microbe 2019. Mucus confers a layer of defense both by forming a physical barrier and by influencing microbial biology, promoting a planktonic (rather than biofilm) state and suppressing virulence-associated pathways in opportunistic pathogens such as *Pseudomonas aeruginosa* and *Candida albicans.* The intestinal mucus layer can be fortified by the metabolic byproducts of commensal bacteria such as *Bifidobacterium dentium,* which promotes glycan maturation and mucin glycosylation, lending potential for use of *B. dentium* as a probiotic. In addition to bacteria, bacteriophages are a common member of the mucus microbiota. Phages can adhere to mucus to provide non-host-derived immunity against bacterial pathogens. Despite these protective features, microbes can still penetrate the mucus layer with various mechanisms, such as the polar distribution of neuraminidase on influenza virus particles that clear mucin-associated sialic acids in its wake. Understanding the microbe-host interactions at mucosal surfaces will help scientists manipulate these interactions to benefit human health by development of probiotic strains or prebiotic nutrients to promote growth of beneficial bacteria.

This hot topic is based on ASM Microbe 2019 session 282: *Stuck on You: Mucin-Microbe Interplay in Health and Disease*

- *Katharina Ribbeck. Mucin-Glycans Attenuate Microbial Virulence*
- *Sarah K. Lucas. Anaerobic Mucin Degradation as a Bacterial Phenotype Associated with Chronic Rhinosinusitis Pathogenesis*
- *Melinda Engevik. Fortifying the Intestinal Mucus Layer Using Commensal Microbes*
- *Eric Irons. Host ST6Gal-1 Expression Alters the Neonatal Gut Microbiome to Suppress Local and Systemic IL-17 Responses*
- *Jeremy Barr. Bacteriophages and Mucosal Immunity*
- *Michael Vahey. Influenza A Virus Surface Proteins are Organized to Help Penetrate Host Mucus*

Challenges in Influenza Diagnostic and Vaccine Strategies: Genetic Shift and Drift Affect Influenza Tools

Changes in the influenza A virus due to genetic shift and drift affect both vaccine efficacy and accurate diagnostic testing. Molecular diagnostics use a World Health Organization-recommended conserved genome region for PCR. The A/H3N2 strain, now circulating for more than 50 years, evolves more rapidly than other strains. Multiple subclasses of H3N2 have emerged, with significant genetic drift occurring among them; this drift affects performance of many diagnostic tests, just as it affects vaccine efficacy and is one of the reasons an annual influenza shot is required. To improve the influenza vaccine, multiple approaches to improve vaccine efficacy are being intensively pursued, including novel platforms for vaccine delivery. Examples of potential vaccine platforms include inactivated, live attenuated and recombinant hemaglutinnin (HA)-based vaccines. Vaccines that generate antibodies for the conserved HA stalk have a much greater breadth for viral strains, conferring protection through IgG Fc domains, and mosaic HA molecules are one avenue being explored to boost immunity to exotic HA molecules. Clinical trials are ongoing to test this mosaic HA strategy, as well as those testing a headless HA that lacks its antigenically variable headgroup.

This hot topic is based on ASM Microbe 2019 session 370: *New Issues in Flu*

- *Kathleen Stellrecht. The Drift in Molecular Testing for Influenza*
- *Lynda Coughlan. Universal Influenza Vaccine*

Eliminating Malaria and TB: What Can We Learn from History?

What are the challenges to eliminating infectious disease? Case studies such as elimination of smallpox and polio clue scientists and public health workers into the requirements to eliminate disease, which included mass vaccination and aggressive, active search for cases followed by ring vaccination of contacts (and their contacts) to completely eradicate smallpox. Global elimination efforts of malaria and tuberculosis may one day have a similar history, but both require more effective vaccines than are currently available. The complexity of tuberculosis combined with the lack of good correlates of infection pose challenges in knowing what strategy will lead to a successful vaccine. The past failure of the MVA85A clinical trial, which demonstrated safety but did not confer protection, highlighted the difficulty in using animals to model human tuberculosis. The good news is that the pipeline of candidate tuberculosis vaccines is full and several have shown promising results, including phase 2 and phase 2b trials for H4:IC31 and M72, respectively. For malaria, irradiated whole organism vaccines are being explored but require extreme accuracy of irradiation to balance protection and immune response; monoclonal antibodies from vaccinated individuals is being explored as well. The hope is that effective vaccines will increase potential of global health campaigns to eliminate these disease scourges.

This hot topic is based on ASM Microbe 2019 session 15: *What New in TB and Malaria Vaccines?*
And session 272: *Global Elimination of Infectious Disease.*

- *Kirsten Lyke. RTS,S and Beyond: New Malaria Candidate Vaccines in the Pipeline*
- *Hazel Dockrell. Roadblocks and Progress in Developing New and Effective TB Vaccines*
- *Jon K. Andrus. Global Elimination of Infectious Diseases: A Historical Perspective*
- *Alberto Severini.Global Elimination of Measles and Rubella*
- *Nicholas Day. Global Elimination of Malaria*
- *Ibrahim Abubakar. Global Elimination of TB*

What's New at ASM

Sharing Microbiology Outside the Lab

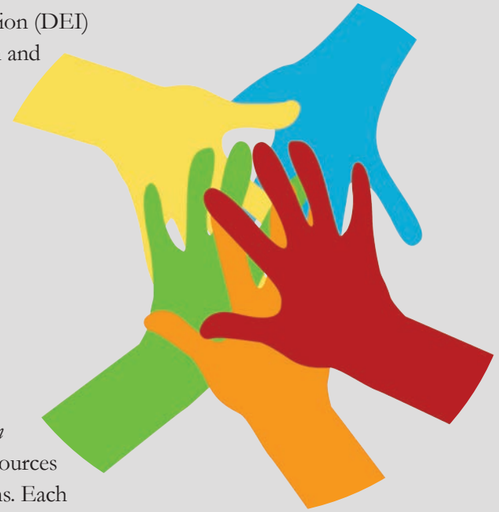
On June 20, ASM took over the atrium of the main San Francisco Public Library, pulling in passersby of all ages to engage with the microbial world. More than 15 ASM Microbe 2019 attendees volunteered for Discover Microbiology: A STEM Festival, representing organizations such as Counter Culture Labs, EvolveSTEM, GIANTmicrobes, Playful Science and Queer Science. Many volunteers brought their own activities and demonstrations from a Spanish comic book about the adventures of two young bacteria to magnetic soil bacteria to sequence assembly puzzles. An estimated 200 people participated in the activities, and a microbial good time was had by all!

Science Communication with a Twist

You haven't really experienced ASM Microbe until you've seen The Up Goer Five Thing: Simple Words for Tiny-Life Studies. Designed to get scientists thinking about their reliance on technical language, this unique symposium challenges presenters to discuss their science using only the 'ten hundred' (1,000) most common words in the English language (a concept adapted from Randall Munroe's "Up Goer Five" xkcd comic). This year, presenters were divided into competing teams: Team People Running Things and Team People Still Learning. Both teams put on an excellent show, and Dr. Sheldon Cambell of Team People Running Things raised the bar even further by singing his presentation. In the end, the audience chose Team People Still Learning as their overall favorite. Kudos to Rebecca Ferrell, Ph.D., a professor at Metropolitan State College of Denver, and Medini Annavajhala, Ph.D., a postdoctoral researcher at Columbia University Medical Center, for earning MVP on their respective teams. Best word or phrase also went to Dr. Annavajhala for the moniker "blood cleaner" to describe the function of the liver. Think you're ready for the challenge? Try it out at *https://splasho.com/upgoer5/*.

ASM's Commitment to Diversity, Equity and Inclusion

This past year, ASM recommitted to expanding Diversity, Equity and Inclusion. The ASM Board of Directors created a Diversity, Equity and Inclusion (DEI) Taskforce to further advance a culture of inclusion, and promote growth and sustainability.



ASM also endorsed the Harassment in Science Act of 2019, a federal bill that authorizes funding for research to better understand the causes and consequences of sexual harassment in science, technology, engineering and mathematics fields, examine policies to reduce harassment, and encourage interagency efforts in these matters.

Recognizing the important role that scientific societies play in ensuring a safe and inclusive environment, ASM's Events Code of Conduct reinforces our commitment to a climate that encourages the free expression and exchange of scientific ideas and promotes equal opportunities and respectful treatment for all participants. ASM is also on the leadership council of the *Societies Consortium on Sexual Harassment in STEMM*. This consortium will provide research- and evidence-based resources to address issues of sexual harassment to other professional organizations. Each of the 53 member groups will contribute to the development of the model policies and procedures aimed to end sexual harassment in STEM fields.

ASM Microbe 2019 Research Makes a Splash in the News

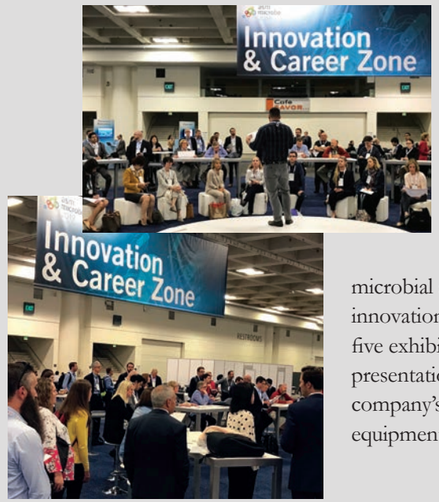
We had another successful year for media coverage at ASM Microbe 2019. During the meeting, 1,600 news stories mentioned ASM Microbe 2019! From press releases on the antibiotic properties of Cannabidiol (CBD), to the transmission of *Candida Auris* in healthcare environments, the ASM Microbe press room featured the most significant and timely research being presented in the microbial sciences. Not only was key research from the meeting covered in top scientific news outlets—*STAT, New Scientist, MedPage Today* and *The Scientist*—but mainstream media outlets also took notice. U.*S. News & World Report, Bustle, Gizmodo* and *Newsweek* covered research with important public health impacts, such as how swimming in the ocean influences the skin microbiome and that phages are found in kitchen sponges.

Career Exploration, Grant Reviewing and Lab Inspection Tips in the Career Zone

Career and professional development is key to a successful and fulfilling career. For the first time at ASM Microbe 2019, space was dedicated in the Exhibit and Poster Hall for career and professional development activities in the Career Zone. Reaching about 320 people over three days, volunteers provided one-on-one feedback on CVs, resumes, grants and manuscripts, both in science and education. Small group discussions were offered on different career paths, local and global opportunities to get involved with ASM, options for graduate school and tips on laboratory management and inspections.

Dr. Monica Trujillo, a participant of the science manuscript reviewing session and professor at Queensborough Community College, was surprised when she walked into the room to find Dr. Peggy Cotter, ASM's past president, reviewing her manuscript. She was very grateful to have an opportunity to connect with someone from a different background. The CV/resume review session buzzed with over 90% of participants finding the feedback useful.

Thank you to everyone who volunteered to make the Career Zone a success! If you would like to volunteer with ASM's career and professional development opportunities, please email us at education@asmusa.org.



Showcasing Cutting-Edge Technology in the Innovation Zone

The Innovation Zone, the newest addition to the ASM Microbe 2019 Exhibit and Poster Hall, showcased companies in the early stages of development and highlighted the latest technologies in the microbial sciences. Attendees interacted with company representatives at each innovation pod and attended presentations in the Tech Talk Theater. Twenty-five exhibitors participated in the "Industry & Science Tech Talks," 15-minute presentations educating attendees on new technology and/or products in their company's pipeline. Nearly 100 attendees were eager to hear about cutting-edge equipment, inspiring science and innovative services in the microbial sciences.

The Alaska Branch

ASM Alaska Branch research scientist Ursel Schütte (left) from University of Alaska Fairbanks, and graduate student Tracie Haan (right) from University of Alaska Fairbanks, using the MinION for DNA sequencing.

Photo by JR Ancheta

The Alaska Branch was established in 1983 and includes members from the University of Alaska faculty, state and federally employed microbiologists and employees of environmental consulting firms. Each year, the branch hosts an annual meeting in the fall that, historically, rotates between Fairbanks and Anchorage. These meetings are well attended by students and early career researchers. Since Alaska is such a large state, the branch provides travel support to facilitate student travel to meetings.

Many Alaska Branch members use long-read sequencing enabled by portable MinION devices and are engaged in outreach activities such as running Genomics Hackathons across the state and sea. The Fall 2018 Branch meeting provided a workshop on how to use the MinION to help spread the use of this technology.

Field work in Fairbanks, Alaska where University of Alaska Fairbanks undergraduates Taylor Seitz, Scout McDougall and Jennie Humphrey collect soil cores.

Photo by DM Drown

Additional projects using long-read sequencing include:

- Sequencing full genomes of emerging RNA viruses in avian and marine mammal species
- Tracking the spread of African Swine Fever Virus and understanding the genomics of virulence
- Microbial functional profiling and genomics of isolates from mud volcanoes with high CO_2 flux
- Tracking recolonization after volcanic eruptions on the Aleutian Islands
- Re-sequencing genomes after artificial laboratory evolution on the International Space Station
- Disentangling Arctic microbial genomes

In addition to discussing the breadth of projects using the latest sequencing technology, the workshop gave an overview of the operation and bioinformatics of the technology. Similar to other Branch activities, the workshop participants included students, early career faculty, senior investigators and mentors. In a state sparsely populated, with large spans of open country, the Alaska Branch is a bridge that brings microbiologists together.

For more information, visit: ***http://www.asmbranches.org/brAK/index.htm***

ASM Alaska Branch microbiologist Eric Henderson and Brooklyn, NY, artist Stephanie Rae Dixon collect samples near the Arctic National Wildlife Refuge on a field trip for the "Microbial Worlds" collaborative arts-humanities-science project.

Photo by Mary Beth Leigh

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.

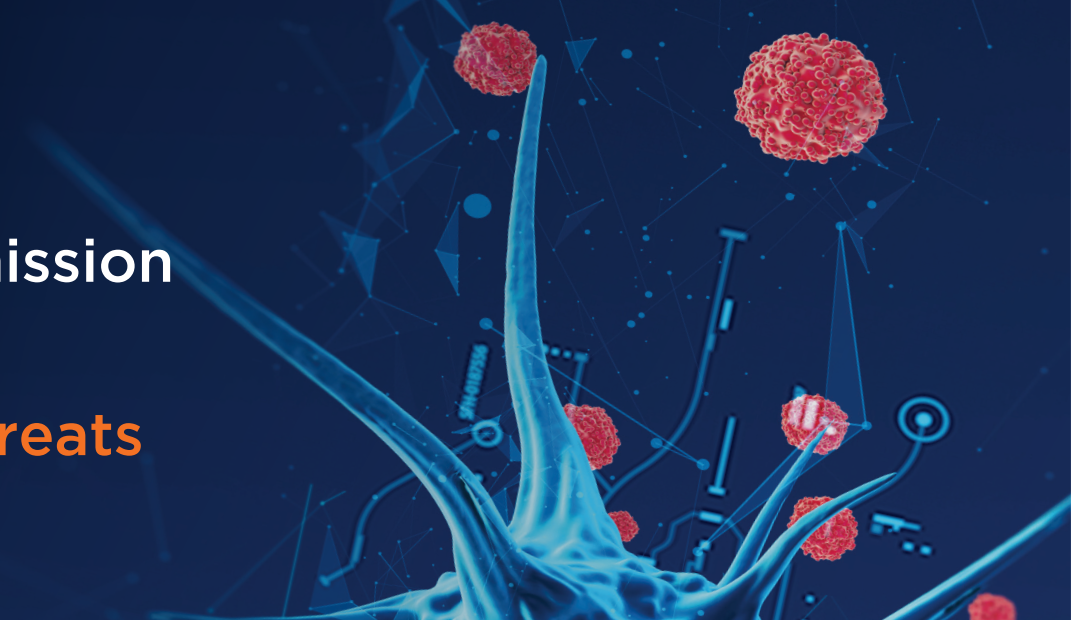
What's new in high consequence pathogen research?

You tell us!

2020 ASM

BIOTHREATS

January 28–30, 2020 | ARLINGTON, VIRGINIA



Abstract submission opens Sept. 9

asm.org/biothreats