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Mycobacterium tuberculosis causes one in four avoidable deaths in the developing world and kills more adults than malaria, AIDS, and all tropical diseases combined. Tuberculosis was named a global health emergency by the World Health Organization, a distinction no other disease has received. Although the study of mycobacterial genetics has expanded dramatically, with new investigations into mycobacterial growth, replication, metabolism, physiology, drug susceptibility, and virulence, most of the problems in tuberculosis control that existed in 2000 remain today.

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FEATURES

55 Climate Change Broadly Increases Infectious Disease Risks
Shannon Weiman
Climate change could prove damaging to individual plant and animal species, to complex ecosystems, and of course to humans

61 After Horizontal Gene Transfer, Metabolic Pathways May Need Further Optimization
Joshua K. Michener and Christopher J. Marx
Effective use of a horizontally transferred pathway can require co-evolutionary changes in the host or pathway

68 Encouraging Microbiology Students To Think Like Scientists
Erica Suchman
Instead of urging students to memorize new materials, teach them to understand concepts fully and then put them to use

FORUM

46 Passing the Torch and the Samples
Lynn W. Enquist
When microbiologists retire, what happens—or should happen—to the resources they have amassed over their careers?

CURRENT TOPICS

RESEARCH ADVANCES

48 Vector-Borne Plant Pathogens Cost Plenty, Know No Boundaries
49 Unusual Biosynthesis for Nisin Depends on Adding, Deleting Glutamyl-tRNA
51 In Wave Tanks, Microbial Fragments Wrangle Sands into Wrinkle Structures
52 Source-Based Media Helps To Identify Bacteria in Nutrient-Poor Power Plant

NEW IN ASM JOURNALS

50 Polymicrobial Infections Abound: Synergies and Greater Complexities
53 Highlights from Recent ASM Journals

DEPARTMENTS

83 Reviews and Resources
84 Application Deadlines
85 Calendar
86 Employment
88 Small Things Considered
ASM NEWS

74 2014 ASM Election Results
75 Sansalone Named ASM Interim Executive Director
75 ASM Strategic Alliances Department

SECTIONS

77 ASM Report
79 ASM Public Affairs
80 Education Board
81 International Affairs

NEXT MONTH

Microbial Extension Cords: Nanowires in *Shewanella oneidensis*
Sarah E. Barchinger

To connect with external electron acceptors, these bacterial cells extrude membrane vesicles that extend to form filaments called nanowires.

The CREATE Strategy Benefits Students and Is a Natural Fit for Faculty
Sally G. Hoskins and Alison Krufka

Analysis of scientific literature using the CREATE approach allows students to learn microbiology while engaging with the process of science.

Point-of-Care Diagnostic Testing in Global Health: What Is the Point?
Madhukar Pai, Marzieh Ghiasi, and Nitika Pant Pai

The main goal of such testing is to inform caregivers in ways that lead rapidly to their starting correct treatments for patients.

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Passing the Torch and the Samples

When microbiologists retire, what happens—or should happen—to the resources they have amassed over their careers?

Lynn W. Enquist

I was at a meeting recently and one of my younger colleagues referred to a group of us as "microbiologists of a certain age"—a polite way of saying that many of us not only are getting older, but that several are clearly in that category. It is true: a surprising number of currently active microbiologists were born between 1940 and 1950. We lived through the heyday of molecular biology. As a former department chairman, this group showed up on my radar screen as a large group of faculty who could retire en masse over the next few years. As I talked to other department chairs around the country, it was clear we all were looking at a similar situation. While various administrative buzz phrases were used to describe this phenomenon (e.g., changing of the guard, energizing the faculty, removing dead wood), many people began to realize that this group of a "certain age" had amassed some valuable resources that could disappear with them. I refer not only to knowledge and experience, but also to culture and mutant collections, virus stocks, plasmid and vector collections, and information of their provenance and curation.

What happens to all these reagents when someone retires or moves on? There are some options: the American Type Culture Collection will agree to take a few samples. You can use the E. coli Genetic Resources Center, the Salmonella Genetic Stock Centre, or various yeast resource centers in the United States and Canada. We also have the Agricultural Research Service Culture Collection for U.S. Department of Agriculture research programs in the United States. The United Kingdom has the National Collection of Industrial, Marine, and Food Bacteria, the National Collection of Type Cultures, and the National Collection of Pathogenic Fungi. Other countries have their own collection centers, and some institutions have set up type culture collections from some key individuals.

The fact is that making arrangements for long-term storage of your biological samples takes time and money, resources that are not always easily available. Of course storage is only half the battle; how do we identify and retrieve these materials once they are put away? The elephants in the room are these simple questions: how do we know what to store, how do we verify what we have in storage, and what do we just let fade to black?

The reality is that keeping all your samples safe and accessible indefinitely is essentially impossible. They will most certainly disappear along with those microbiologists of a "certain age." I don’t know the number of strains, mutants, and other biological samples that reside in the labs of microbiologists older than 60, but I suspect it is a large number. Many of these collections represent one-of-a-kind samples that define a process, pathway, or function. Some are characterized by phenotype and not genotype. The salient point is that these collections represent the history of a generation; older folks might say they are their life. The reality today is that if it isn’t published and sequenced, it is "off the grid."

I suppose we could sequence everything, deposit the sequences in some large database, and turn the freezers off to let the biological remnants decay. I wonder about the practicality of that option. Who will take charge of this sequencing operation, who will pay for, edit, curate, and validate the information? Maybe this sequencing adventure represents a business opportunity for some enterprising individual. A quick poll of some colleagues indicates that the most common fall-back plan is to open their freezers to their students and lab alumni and autoclave what isn’t taken.

The situation represents a personal dilemma for me, as I hold a modest collection of bacteriophage lambda and herpesvirus mutants con-
structured over my career. I know my collection is small compared to others. I know that many microbiologists don’t really care about my mutant collection. But I can’t be the only one who is thinking about this. I’m curious—what are other microbiologists’ plans for their collections? Some of us of that “certain age” would like to know.

Lynn W. Enquist is Henry L. Hillman Professor in Molecular Biology and Professor in the Princeton Neuroscience Institute at Princeton University, Princeton, N.J., and was Editor in Chief of the Journal of Virology from 2002–2012.

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RESEARCH ADVANCES

Vector-Borne Plant Pathogens Cost Plenty, Know No Boundaries

Jeffrey L. Fox

Large numbers of commercially important plants are subject to a wide range of vector-borne diseases, some already wreaking havoc in orchards and vineyards in Europe and the United States (US), according to Rodrigo Almeida of the University of California, Berkeley. He was one of several experts who spoke last September during a workshop, “Vector-Borne Diseases: Exploring the Environmental, Ecological, and Health Connections,” convened by the Forum on Microbial Threats, which operates under the auspices of the Institute of Medicine (IOM) in Washington, D.C.

More than 70% of plant-infecting viruses are transmitted from one host to another by arthropod vectors, according to Anna Whitfield of Kansas State University in Manhattan. Moreover, insect vectors may carry fungal or bacterial pathogens. For instance, a beetle serves as vector for the fungus responsible for thousand canker disease of black walnuts, a malady that appears to be traveling east with those insects and in lumber in which they may be carried.

Aphids transmit the majority of plant-infecting viruses, but thrips, nematodes, and mites also play important roles, according to Whitfield. Although vector-borne diseases are blamed for $1 billion in crop losses each year in the US, little is known about the interactions between plant viral pathogens and their insect vectors, she says. One line of research to reduce those losses calls for disrupting replication of viral pathogens within their respective insect vectors, hoping to head off damage before they reach the crop plants themselves, she says, cautioning: “We don’t view these solutions as silver bullets.”

Meanwhile, Xylella fastidiosa bacteria colonize more than 300 plant species, dwelling in the xylem of their hosts, mostly without causing them harm, according to Almeida. These sometime pathogens depend on sap-feeding insects to deliver and distribute them to those plant hosts, and those insects make up a “very wide range of vectors,” he says. Although X. fastidiosa “usually does not cause disease,” the consequences can prove monumental when it does. Pathogenesis appears to be pretty simple. The bacteria occlude the xylem system of their hosts, blocking the flow of water and starving the upper parts of the plant of water and nutrients.

In the US, this plant pathogen is damaging to a wide variety of valuable crops, including grapes, citrus, olives, peaches, almonds, and plums, as well as ornamental trees and shrubs. Delivered by the glassy-winged sharp-shooter insect (Homalodisca vitripennis) to cause Pierce’s disease in grapevines, the pathogen is blamed for causing more than $500 million in damage in California.

More recently in 2013, this plant pathogen began causing disease in olive groves in the Puglia region of Italy, where it is now accorded the “highest quarantine level and is subject to select agent handling,” Almeida says. Olive trees in Puglia and elsewhere in Italy...
typically are 100 years old, and local economies depend on them. Although the pathogen poses a threat to nearby vineyards, so far they appear not to be infested. One possibility is that there is no suitable insect vector in Italy to deliver the pathogen to grapevines.

“There is no such thing as a plant vector being purely mechanical,” Almeida says. Instead, the interplay among plant, insect vector, and microbial pathogen appears to be determined at the molecular level, suggesting that biotechnology-based strategies might help to solve some of these agricultural problems, he adds, pointing to “exciting work” that seeks to use RNAi to block plant pathogens or vectors from feeding on plants.”

Jeffrey L. Fox is the Microbe Current Topics and Features Editor.

RESEARCH ADVANCES

Unusual Biosynthesis for Nisin Depends on Adding, Deleting Glutamyl-tRNA

Carol Potera

Glutamate, carried by transfer RNA (tRNA) molecules, plays a key but unexpected role in transforming nisin from a linear peptide into an active, five-membered ring structure with antimicrobial properties, according to Wilfred van der Donk, Satish Nair, and their collaborators at the University of Illinois (UI) at Urbana-Champaign. This long-mysterious final stage of nisin biosynthesis, featuring such an unusual role for glutamyl-t-RNA molecules, could help to explain not only how lantibiotics but also other important classes of natural products are anticipated to supply during the final stages of nisin biosynthesis.

Finding that tRNA molecules furnish the glutamate needed for the biosynthesis of nisin was a considerable surprise, according to van der Donk’s colleague Nair. “This is a very unusual use for tRNA,” he says, noting that amino acid-charged tRNA molecules typically insert amino acids into polypeptides as they form along ribosomes. “But in this case, glutamate carried by tRNA is used to make an antibiotic.”

In a second reaction, that same dehydratase eliminates glutamate residues that were linked to the serine and threonine side chains of the nisin precursor. X-ray crystallography analysis reveals that these residues are expelled at two different active sites of that enzyme. “One site adds glutamate, and the other removes it,” Nair says. The painstaking efforts of graduate students Manuel Ortega and Yue Hao helped to sort out this unusual two-step process, he adds.

“This is a landmark paper,” says Hans-Georg Sahl of the University of Bonn in Bonn, Germany. Researchers have long puzzled over the mechanisms underlying the synthesis of this peptide, particularly how its serine and threonine residues were modified once the initial peptide was made along ribosomes, he says. “Now it’s clear that a unique catalytic glutamylation with tRNA is involved.”

When Lactococcus lactis cells ferment milk, they produce nisin as a metabolic by-product, one with valuable antimicrobial properties. For more than 50 years, nisin has been added to meat, cheese, and other foods to prevent spoilage. It is considered a broad-spectrum natural antibiotic, one that punches holes in bacterial cell walls and also shuts down peptidoglycan biosynthesis. Despite its widespread use in the food industry, however, there is little evidence of resistance to nisin, suggesting it may be a worthy template for designing additional antimicrobial agents better suited for treating infectious diseases, according to Nair. “Other natural products with

MINITOPIC

Federal Officials Complete Inventory of Misplaced Select Agents, Promise Reforms

Following disclosures of biosafety lapses from several federal agencies in the middle of 2014, the President’s science advisor and other federal officials called for a comprehensive inventory of such items and also for those affected federal agencies to devise and institute reforms. By December, some 4,000 facilities were inspected, uncovering 27 instances in which cultures of select biological agents (microorganisms) and toxins “were not properly registered.” Despite these formal lapses, however, officials report “no indications of human exposure, including staff or the general public.”

**MINITOPIC**

**More Hints of Life from Mars, Rover Senses Methane, other Organics**

The Curiosity rover on Mars detected changing levels of methane, a teaser result that could be consistent with microbial life on the red planet, but not a finding that is considered definitive, according to scientists from the National Aeronautics and Space Administration (NASA) and their collaborators, who reported their findings during the annual American Geophysical Union convention, held in San Francisco last December.

“This temporary increase in methane—sharply up and then back down—tells us there must be some relatively localized source,” says Sushil Atreya of the University of Michigan, Ann Arbor, and a member of the Curiosity rover science team. “There are many possible sources, biological or nonbiological, such as interaction of water and rock.” The rover also detected other organic chemicals in powder drilled from a rock on the surface of Mars, the first definitive detection of organics there, the scientists say. “These Martian organics could either have formed on Mars or been delivered to Mars by meteorites.”

**NEW IN ASM JOURNALS**

**Polymicrobial Infections Abound: Synergies and Greater Complexities**

**David C. Holzman**

Polymicrobial infections exert a profound impact on both outcomes and responses to treatment, says W. Edward Swords of Wake Forest School of Medicine, Winston-Salem, N.C. Efforts to study such infections grew considerably during the last decade, due to “faster and more comprehensive [genomic] sequencing that makes it possible to identify every organism in a sample without having to grow anything in culture.” Three recent reports illustrate the breadth of this phenomenon, its importance for public health, and some of the practical challenges it poses.

Conventional culture-based diagnostic tests sometimes fail to uncover some of the culprits underlying infections in individual patients, according to Swords. “Lots of infections aren’t merely new colonization by an overt pathogen, but rather a shift in the population to a dysbiotic state, where the proportion of different species changes, resulting in disease,” he says. For example, in periodontal disease, microbial community structures vary less from one case of disease to another than they do among healthy individuals, according to Gary Wang of the University of Florida, Gainesville, and his collaborators. “Samples from individuals with periodontal disease are characterized by high levels of *Fusobacterium* and *Porphyromonas*, while in healthy gums, subgingival bacterial communities have high levels of *Rothia* and *Streptococcus*,” he says. “Genes and functions related to bacterial motility, energy metabolism, lipopolysaccharide biosynthesis, flagellar assembly, methane metabolism, bacterial chemotaxis, and peptidase, are abundant in chronic periodontitis compared to healthy controls.” Details appeared 14 November 2014 in *Applied and Environmental Microbiology* (doi: 10.1128/AEM.02712-14).

“There is increasing appreciation that human indigenous microbial communities are a critical component of human biology,” Wang says. “In some disease states, we need to think of microbial communities, rather than specific bacteria, as pathogens.”

The effects of one pathogen can influence what happens with successor pathogens, according to Mary Ann Jabra-Rizk of the University of Maryland Dental School in Baltimore, and her collaborators. For instance, after...
Candida albicans invades the oral tissues of mice, the animals become more vulnerable to Staphylococcus aureus, she says. “In some of our scanning electron microscopy images, red blood cells could be seen around the hyphae and S. aureus as they co-invaded the tissue,” indicating that vascular injury caused by hyphae enabled entry by S. aureus, she and her collaborators note. “Importantly, antifungal therapy was effective in impeding the development of bacterial dissemination” in mice, she adds. Details appeared 24 November 2014 in Infection and Immunity (doi: 10.1128/IAI.02843-14).

Similarly, an influenza virus infection can render a host more susceptible to a pneumococcal infection, according to Swords. “Influenza shifts the immune response such that the response necessary to clear or contain pneumococci is impaired or even ablated, thus predisposing to more serious disease,” he says.

In mice, pneumococcal infection following influenza “is associated with reduction of B cells and T cells in lymphoid organs such as the spleen and mediastinal lymph node, which is needed to support antibody production,” says Yu-Lung Lau of the Li Ka Shing Faculty of Medicine, University of Hong Kong. All mice that were co-infected with influenza and pneumococci died, he notes. Details appeared 26 November 2014 in the Journal of Virology (doi:10.1128/JVI.02455-14).

David C. Holzman is the Microbe Journal Highlights Editor

RESEARCH ADVANCES

In Wave Tanks, Microbial Fragments Wrangle Sands into Wrinkle Structures

Barry E. DiGregorio

Wrinkle structures, found in ancient sedimentary environments along the surfaces of sandy beds, can be formed experimentally by adding microbial fragments to sand layers within wave tanks, according to Giulio Mariotti of the Massachusetts Institute of Technology (MIT) in Cambridge and his collaborators there and at Smith College in Northampton, Mass. They say that wrinkle structures in natural sediments are “morphological biosignatures” of microbial fragments—inscribed at the sediment–water interface.

MINITOPIC

Another Set of Gut Microbiota Highlights from Microbe in 2015

Efforts to understand how microorganisms in the gut affect the host continue to be part of the news. Microbe’s second set of examples for 2015 include:

- The blood-brain barrier is “leaky” in newborn mice that were carried by germ-free mothers, but remains normal in those whose mothers’ gut microbiota was intact, according to Viorica Braniste and Sven Pettersson at Karolinska Institutet in Stockholm, Sweden, and their collaborators. Details appeared 19 November 2014 in Science Translational Medicine (doi:10.1126/scitranslmed.3009759).
- The ordinarily benign gut bacterium Bacteroides thetaiotaomicron can enhance virulence gene expression in enterohemorrhagic Escherichia coli and also change the metabolite environment at infection sites, perhaps explaining how resident microbiota can influence an individual’s susceptibility to pathogens, according to Vanessa Sperandio of the University of Texas Southwestern Medical Center in Dallas and her collaborators. Details appeared 10 December 2014 in Cell Host Microbe (doi:10.1016/j.chom.2014.11.005).
- Bacterial biofilms are associated with colorectal cancers, suggesting that the gut microbial community contributes to this type of cancer, according to Christine M. Dejea and Cynthia L. Sears of Johns Hopkins Medical Institutions in Baltimore, Md., and their collaborators there and at several other institutions. Details appeared 8 December 2014 in Proceedings of the National Academy of Sciences (doi:10.1073/pnas.1406199111).
- Consuming fiber increases the relative abundance of Bacteroidetes by about 12% compared to Firmicutes in the human gut and, along with that shift, the abundances of many microbial genes, including those associated with carbohydrate, amino acid, and lipid metabolism, according to Kelly Swanson of the University of Illinois, Urbana, and his collaborators. Those fiber-related changes in diet are associated with weight loss. Details appeared 12 November 2014 in the American Journal of Clinical Nutrition (doi:10.3945/ajcn.114.092064).
- Ingested nanosilver particles can upset the gut microbiome, shifting bacterial populations there and reducing their metabolic activity, according to Virginia Walker and Pranab Das at Queen’s University in Kingston, Ontario, Canada, and their collaborators. Details appeared October 18, 2014 in the Journal of Nanomedicine and Nanotechnology (doi:10.4172/2157-7439.1000235).
- Kissing, which strictly speaking is not about the gut microbiota, can lead to the exchange of some 80 million bacteria between two individuals, leading them to share “similar communities” of oral bacteria, according to Remco Kort of the Netherlands Organisation for Applied Scientific Research, or TNO, in Zeist, and his collaborators. However, because the “similarity does not clearly correlate to kissing,” there appears to be an “important role for specific selection mechanisms resulting from a shared lifestyle, environment, or genetic factors from the host.” Details appeared 17 November 2014 in Microbiome (doi:10.1186/2049-2618-2-41).
MINITOPIC
Updated Estimate for Bringing a New Drug to Market: $2.6 Billion

The costs for developing a new drug and gaining regulatory approval to market it are now estimated to be $2.6 billion, according to Joseph A. DiMasi of the Tufts Center for the Study of Drug Development in Boston, Mass., and his collaborators. “Drug development remains a costly undertaking despite ongoing efforts across the full spectrum of pharmaceutical and biotech companies to rein in growing R&D costs,” he says. “Our estimate links the costs of unsuccessful projects to those that are successful in obtaining marketing approval from regulatory authorities.” In an earlier study by the Tufts from 2003, those drug development costs were said to be $802 million, the equivalent of $1,044 million in 2013, indicating a 145% increase in such costs since then. Rising drug development costs were driven mainly by increases in out-of-pocket costs for individual drugs and higher failure rates for drugs tested in human subjects, he and his collaborators note. For additional information about the November 2014 study, “Cost of Developing a New Drug,” see http://csdd.tufts.edu/news/complete_story/pr_tufts_csdd_2014_cost_study.

in wave-dominated environments, and not beneath larger microbial mats as previously thought. Those wrinkle structures likely formed early during the evolution of animals, possibly while they were grazing on microbial fragments. Details appeared 31 August 2014 in Nature Geoscience Letters (doi: 10.1038/geo2229).

Outside wave tanks, such wrinkle structures—fossilized millimeter-to-centimeter wavy-ripple patterns—appear to be distributed only as part of the fossil record and are not found in modern sediments. By using a wave tank, the MIT and Smith College scientists could control hydrodynamics well enough to do experiments on a fine scale capturing what might have occurred in ancient sediments, according to Mariotti. “This decision was driven by the observation that many stromatolites form in wave-dominated environments,” he says. “I initially explored how microbial mats reduce sediment mobility. The results on wrinkle structures [were] unexpected.”

By themselves, small waves are not effective at moving sand grains directly, according to Mariotti and his collaborators. However, the waves can move millimeter-sized microbial fragments, which then rapidly help organize the sand into forming linear ridges and rounded scour pits, typically within a few hours, the researchers find. In that sense, wrinkle structures in ancient sediments appear to be “biosignatures,” evidence left by organisms that once moved through those sites whether still alive or already dead.

“They present a wonderful documentation of the formation of the wrinkle structures considering the effect of microbial aggregates,” says Nora Noffke of Old Dominion University in Norfolk, Va., referring to the findings of Mariotti and his collaborators. “The quantitative explanation is well thought through, and the complex interconnection between biofilm-coated grains, hydraulics, and sediment had never been shown.” However, she is not willing to go quite so far as they do in drawing conclusions. “The relation of wrinkle structures to the rise of microscopic organisms by the beginning of the Phanerozoic is a bit ambitious,” she says. “We do not have enough data on the distribution of wrinkle structures throughout Earth history to allow any firm conclusion at this time.”

“I am confident that the mechanisms we described can occur in nature and very likely formed the wrinkle structures,” Mariotti says. “I have more doubts regarding the origin of the microbial aggregates needed to create wrinkle structures. We are suggesting that grazers, early animals, might have contributed to the production of microbial aggregates. If so, the presence of wrinkle structures might be an indirect measurement of grazing pressure. However this hypothesis needs further testing.”

Barry E. DiGregorio is a freelance writer in Middleport, N.Y.

RESEARCH ADVANCES
Source-Based Medium Helps To Identify Bacteria in Nutrient-Poor Power Plant

John Otrompke

A new culturing technique enabled scientists to identify three novel microbes from the nutrient-poor waters of a power plant in rural Hungary. All three strains are alphaproteobacteria, and comprise a new species, which is being called Phreatobacter oligotrophus, according to Erika Toth from Eötvös Loránd University of Sciences in Budapest, Hungary, and her collaborators. “In these environments, bacteria survive only if they live in consortia and produce things for one another,” she says. Details appear March 2014 in the International Journal of Systematic and Evolutionary Microbiology (doi: 10.1099/ijs.0.053843-0).

To culture, the bacteria, Toth and colleagues used water from the power plant, which is near the town of Paks, and consider it an integral part of the growth medium, she says. It contains “exactly the same water, instead of distilled water,” that is found in the power plant. In other respects, the medium being used to grow P. oligotrophus is intentionally carbon-poor, Toth says. Moreover, the medium supports growth by more types of alphaproteobacteria, including Mesorhizobium, Ancylobacter, and Methylobacterium, as well as many Actinobacteria, than would grow using more conventional media she adds.
Several years ago, Toth and her collaborators isolated a gram-positive bacterium, called Aquipuribacter Hungaricus, from the same power plant, which is near the town of Paks. The more recently isolated strains of P. oligotrophus from the same plant grow on different nutrients, she says. Relatives of these strains also can be isolated from a lake in Sovata, Romania, about 600 km or 375 miles from the power plant.

“The greatest discovery in this research is not just the description of a new genus, but the highly original way of approaching the problem of ‘non-culturable’ bacteria,” says Máriá Vargha, who directs the Department of Water Hygiene at the National Institute for Environmental Health in Hungary. “Toth’s novel approach to cultivation will lead to the discovery of many new or previously uncultured organisms. The cultivation of bacteria that contribute to biofouling processes allows for identifying and testing potential treatments—something that cannot be done if we rely solely on molecular methods.”

“I am surprised that they had not used an even more oligotrophic medium, such as the frequently used RAVAN medium for microorganisms adapted to extremely low organic concentrations,” says Christine Moissl-Eichinger at the Medical University of Graz in Austria. “Most oligotrophs that we cultured in our laboratory were heterotrophic microorganisms, and that means they were using organic compounds as a carbon source.”

“If there is carbon dissolved in the water in such environments, as there almost certainly is, then organisms can fix carbon,” says Jonathan A. Eisen at the University of California, Davis. “If there is some nitrogen gas in the water, then organisms could fix that, too. Then to get everything else, [a microbe] has two choices: concentrate in some way, or just grow really slowly.”

John Otrompke is a freelance writer in Chicago, Ill.

NEW IN ASM JOURNALS

Chemical Family Targets Every Stage of Plasmodium Infection Cycle

Malaria causes more than 200 million cases annually, killing around 600 thousand, mostly African children. Ana Rodriguez of New York University School of Medicine et al. found that Xenomycins, currently in clinical trials against cancer, can eradicate the Plasmodium parasite at every stage of its life cycle: the liver stage, where it abides following infection, and the blood, where it replicates. “Xenomycins also inhibit transmission to mosquitoes, says Rodriguez. “Multiple stage-targeting drugs would be beneficial because they would have increased efficacy and lower risk of developing resistance as compared to single stage-targeted drugs,” says Rodriguez. “Additionally, a single medicine could be used for preventive and curative treatments, and for eradication campaigns to eliminate transmission from those infected to others in the community.”


NEW IN ASM JOURNALS

Two Antibiotic Alternatives for Livestock

Livestock consume the majority of antibiotic production, and are a major source of resistant pathogens. Two new studies in ASM journals focus on alternatives to antibiotics. Swine production consumes copious antibiotics, particularly during weaning. Mikel Lenz Strube, of the Technical University of Denmark, Lyngby, et al. show in an in vitro piglet gut system that providing crude potato pulp feed impregnated with specific enzymes produces prebiotics, encouraging growth of beneficial lactic acid bacteria during fermentation. Deep sequencing showed increases in Lactobacillus and Veillonella and reduced Streptococcus. Strube plans to test the supplement in a large scale animal study. The in-animal prebiotic production bypasses additional steps of transport, dedicated reaction chambers, and purification.

Meanwhile, Evelien Kieckens of Ghent University, Belgium, et al. show that bovine lactoferrin, an antimicrobial protein, applied to the rectum of calves can clear enterohemorrhagic Escherichia coli (EHEC) infections and prevent subsequent re-infection. Rec-
potentially infectious viruses from 20,000 (similar to what would be found on a surface touched by a norovirus-infected person) to 500 after 15 minutes. The results suggest that the method could be used for continuous disinfection of contaminated surfaces, says Klein.


NEW IN ASM JOURNALS

First Study of Pumice-Associated Microbial Communities

Scientific studies of newly created ecosystems following volcanism are difficult, given the short duration and the often distant locations. Following the June 2011 eruption of the Puyehue-Cordon Caulle volcanic complex in southern Chile, James Elser of Arizona State et al. found that microbial communities on pumice floating in nearby lakes were different from those in the water column, but similar from lake to lake, suggesting similar selection among the pumice communities. Microbes growing on the pumice showed high demand for the key limiting nutrients, nitrogen and phosphorus, he says, “taking those elements up from the lake water at rates similar to those of water-dwelling microbes,” and shifting pumice from its initial impact as a nutrient source due to leaching of phosphorus, to a sink. This is the first study to characterize the ecological composition of pumice-associated microbial communities, as well as the first to examine the microbes’ biogeochemical impact, says Elser.


The pathogen *Escherichia coli* O157:H7 can spread, likely airborne, more than one-tenth of a mile downwind from a cattle feedlot onto nearby produce, according to Elaine D. Berry of the U.S. Department of Agriculture, Agricultural Research Service, U.S. Meat Animal Research Center, in Clay Center, Neb. “The high percentages of leafy greens contaminated with *E. coli* suggest great risk for planting fresh produce 180 m [590 feet] or less from a feedlot,” she writes. That suggests that current buffer zone guidelines of 120 meters [400 feet] from a feedlot may be inadequate, she says. In the study, the investigators sampled leafy greens growing in nine plots, at 60, 120, and 180 m downwind from the cattle feedlot at the research center, testing them six times during June through September, over two years. The rate of contamination with *E. coli* O157:H7 varied widely, up to 92%, but on average declined with distance from 3.5% of samples per plot at 60 meters to 1.8% at 180 meters. This is likely the first comprehensive and long-term study of its kind, says Berry.


NEW IN ASM JOURNALS

Buffer Zone Guidelines May Be Inadequate to Protect Produce From Feedlot Contamination

The cold atmospheric pressure (CAPP) plasma may reduce transmission of norovirus. CAPP significantly reduced the number of virus particles in norovirus samples. CAPP, which is actually close to room temperature, is a gas used to kill bacteria without harming surfaces or human tissues. Medical applications include wound healing, and scientists are investigating its potential to remove bacteria from fruits, vegetables, and meats. The finding is exciting because noroviruses are resistant to detergents, chlorine, freezing, and heating, says senior study author Günter Klein, head of the Institute of Food Quality and Food Safety at the University Veterinary Medicine Hanover in Germany. In the study, Klein et al. grew norovirus from an infected stool sample on Petri dishes, and then treated them with CAPP for varying lengths of time. CAPP reduced the numbers of potentially infectious viruses from 20,000 (similar to what would be found on a surface touched by a norovirus-infected person) to 500 after 15 minutes. The results suggest that the method could be used for continuous disinfection of contaminated surfaces, says Klein.


Climate Change Broadly Increases Infectious Disease Risks

Climate change could prove damaging to individual plant and animal species, to complex ecosystems, and of course to humans

Shannon Weiman

By favoring the growth of pathogens, climate change will make infectious disease outbreaks more likely and more frequent, according to researchers who gathered during the 2014 ASM General Meeting (GM), held in Boston last May. Those pathogens threaten not only food sources and human health, but also entire ecosystems, they say. Rising temperatures are a major factor in this forecast, allowing many pathogens to expand their geographic ranges and prolong seasonal risks. Higher temperatures also promote pathogen growth and virulence, particularly in Vibrio species that infect a wide range of marine organisms and humans. In addition, changing climate conditions can stress host plant and animal species, making them more susceptible to infections.

Taken together, they warn, climate change is tipping the balance between host and pathogen, a shift in favor of pathogens that will lead to more frequent and severe outbreaks of bacterial, viral, and fungal diseases across diverse ecosystems.

Plant Pathogens Threaten Crops along with National Economies

Climate change will affect crop yields by altering rainfall and temperatures, but also by enhancing the growth of plant pathogens, according to Caitilyn Allen of the University of Wisconsin, Madison, who spoke during the 2014 ASM GM plenary session “Global Change Microbiology: Anthropogenic Pressures and Microbial Response.” For example, rising temperatures threaten coffee tree plantations by boosting the fungal pathogen Hemileia vastatrix. Commonly known as coffee rust, H. vastatrix infiltrates the leaves of coffee trees, defoliating them and often killing the tree. However, because the fungus cannot survive below 10°C, trees planted at higher elevations have historically been safe from this blight. “Until recently, rust only appeared below 1,300 m altitude; cooler temperatures protected higher altitude plantings from the disease,” she says.

Temperatures in tropical highlands are increasing and this terrain is experiencing earlier and heavier rainfall, allowing H. vastatrix to grow at higher altitudes than ever before, according to Allen. Since 2012, Central America has been struck with an epidemic of coffee rust that is badly damaging trees and undercutting local coffee-dependent economies, she says. “Rust has been in the Americas for over 40 years, but never affected more than 5% of the crop. Last year’s incidence was 53%.”

This striking increase could indicate the emergence of a new, more virulent strain of H. vastatrix, but genetic analysis reveals that the pathogen itself has not changed, Allen continues. Instead, average temperatures increased a mere 1.5°C. “Rust was the explosive, but climate change was the detonator,” she says.

If average temperatures continue to rise by another 1–1.5°C, as expected, land suitable for coffee production will be drastically reduced, ac-

SUMMARY

- By favoring the growth of pathogens, climate change will make infectious disease outbreaks more likely and more frequent.
- Climate change can affect crops by altering rainfall and temperatures, but also by enhancing the growth of plant pathogens.
- Rising sea surface temperatures are linked with increasing levels and ranges of diseases in humans and in marine life.
- Marine bacterial pathogens, particularly Vibrio species, can disrupt ecosystems such as those that are anchored by coral reefs.
ccording to the Intergovernmental Panel on Climate Change. As it is, rust reduced coffee yields 20% across Central America in 2013, costing 500,000 jobs and $500 million. These losses are hitting local economies hard, with coffee as the most valuable commodity and main driver of the economy in many Latin American countries. Guatemala, Nicaragua, Honduras, and Costa Rica all declared states of emergency in 2013 due to rust-associated losses, Allen says.

While coffee rust is the first plant disease epidemic clearly attributable to global warming, others may soon follow, according to Allen. Changing weather conditions not only may favor particular plant pathogens, but can also stress the host plants, making them less resilient and more vulnerable to attack. Monoculture crops, which account for much of the world food supply, are particularly susceptible to pathogens due to their lack of genetic diversity. For example, the bacterial pathogen *Xanthomonas campestris* pathovar *musacearum*, which causes wilt, is running rampant through banana plantations because the trees, which are genetically identical clones, carry no natural resistance to this pathogen. “Production losses are estimated at 53%, with $8 billion in economic costs over the past 10 years,” Allen says.

Bananas are a dietary staple in nations where food is scarce, and a driver of the economy in many developing nations. The impact of this plant pathogen could prove catastrophic, particularly if forthcoming climate changes shift the balance to favor its growth even more than it already has. “As many host-pathogen interactions are highly vulnerable to changes in environment, climate change can alter the likelihood of disease outbreaks [and] has altered terrestrial ag-

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**FIGURE 1**

Coffee leaf rust caused by the fungus *Hemileia vastatrix*. This disease has spread rapidly through growing areas previously immune to it because of rising temperatures. (Image credit: Smartse—Own work. Licensed under CC BY-SA 3.0 via Wikimedia Commons [http://commons.wikimedia.org/wiki/File:Hemileia_vastatrix_-_coffee_leaf_rust.jpg#mediaviewer/File:Hemileia_vastatrix_-_coffee_leaf_rust.jpg].)
ricultural disease risk,” says Colleen Burge of the University of Washington, Seattle.

Pathogens of Fish and Shellfish Threaten Seafood Industries

Climate change-associated outbreaks of infectious diseases attributable to marine pathogens are also on the rise, posing an increased threat to seafood industries, according to Burge, who spoke during the 2014 ASM GM symposium “Small Change, Big Change: the Growing Challenge of Climate Change in the Ocean.” Cultured and wild harvests of fish and shellfish are affected, including salmon, abalone, bivalves, and crustaceans. “Rising sea surface temperatures have been linked with increasing levels and ranges of diseases in humans and in marine life, including corals, abalones, oysters, fishes, and marine mammals,” she says. “Climate shifts can impair the immune response of a host and increase the frequency of disease. This is especially true for ectothermic organisms such as shellfish, corals, and finfish.” Other climate-related factors contributing to these problems include ocean acidification, caused by increasing levels of dissolved carbon dioxide, as well as changes in salinity and stratification.

Finfish, including salmon and rainbow trout, are susceptible to infection by Icthyophonus, a protozoan species that invades muscle tissue, impairs swimming ability, which leads to death. Elevated water temperatures promote disease progression, which impairs spawning and further increases mortality rates. “In addition to its population-level effects on marine fish resources, ichtyophiosis affects human societies by reducing the market value of fish. . . . resulting in unsightly and aromatic lesions in the skeletal muscles of infected fish, rendering the affected fillets unmarketable,” Burge says. The fishing industries based in Alaska and Nova Scotia are being hit hardest by Icthyophonus outbreaks as warmer waters creep northwards.

Vibrio species are prevalent among the pathogens that infect and are carried by shellfish. Vibrio harveyi, a pathogen of many marine organisms, including prawns, lobsters, and fin fishes, is threatening the European abalone, Haliotis tuberculata. “Significant alterations in abalone host-bacterial parasite dynamics in recent years are associated with increased seawater temperature,” Burge says. During spawning season, increasing the seawater temperature from 17 to 18°C can tip the balance to favor V. harveyi, leading to 80% losses in abalone harvests, she says. Along the California coast, Candidatus Xenohaliotis californiensis, which infects the abalone gut and interferes with nutrient absorption, has been moving northwards, with particularly damaging outbreaks during warmer El Niño years.

Meanwhile, Vibrio tubiashi, a pathogen that infects larval oysters and which is linked to ocean acidification, is damaging the oyster industry along the west coast of the United States. Other oyster pathogens, such as the protozoans Perkinsus marinus and Haplosporidium nelsoni, are increasingly problematic along the east coast, moving into economically important regions such as the Chesapeake Bay. “The prevalence and intensity of these diseases are subject to influence by cyclical climate patterns, such as the El Niño–Southern Oscillation (ENSO) and North Atlantic Oscillation, which modify regional and local temperature and rainfall (salinity) conditions,” says Burge.

Marine Vibrio Species Threaten Human Health

Climate change and its impact on ocean conditions promote the growth of other Vibrio species that more directly threaten human health, according to Burge. Vibrio parahaemolyticus, a shellfish pathogen that causes food poisoning in humans, has expanded its range northwards in recent years, invading major seafood-producing regions such as the Chesapeake Bay and Prince William Sound in North America and the Baltic Sea in Europe.

Vibrio vulnificus, a species that causes necrotizing wound infections, also expanded its geographic range. Regional outbreaks among humans infected with these and similar Vibrio species correlate with local sea surface temperatures, with the number of cases nearly doubling for every 1°C increase in the Baltic Sea, says Burge, citing work by Craig Baker-Austin of the Centre for Environment, Fisheries and Aquaculture Science in Weymouth, Dorset, United Kingdom. With warmer ocean temperatures stretching earlier into spring and later into autumn, seasonal risk has expanded as well.

“Pathogenic Vibrio bacteria pose a significant human health risk,” Burge says. “In the United States alone, there are approximately
4,600 cases of *Vibrio* infection each year, of which approximately 90 are *V. vulnificus* cases and 4,500 are *V. parahaemolyticus* cases.” These highly invasive pathogens can cause septicemia and death.

Warming temperatures and changes in rainfall can also make the environment more hospitable for *Vibrio cholerae* growth, and can lead to increases in human infections, according to Rita Colwell of the University of Maryland, College Park. “Cholera outbreaks have been linked to environmental and climate variables including precipitation, flooding, river levels, sea surface temperatures, and coastal salinity,” she says. Warm air temperatures combined with springtime drought, which increases water salinity in estuaries, provide optimal conditions for *V. cholerae* growth, setting the stage for outbreaks when rains come. “Heavy rainfall, followed by inundation and destruction of sanitation infrastructure, accelerates interactions between contaminated water and human activities, resulting in an epidemic,” she says. Rising global temperatures and more extreme weather patterns can result in more droughts and flooding, suggesting cholera outbreaks could increase in frequency and intensity.

From data collected for 26 years from northern India, Colwell generated climate-based early warning systems to identify high-risk areas and to predict cholera outbreaks months ahead of time. “Location and intensity of cholera outbreaks can be predicted up to 3 months in advance in the Bengal Delta region with understanding of underlying hydroclimatology and satellite-derived environmental variables,” she says. Other, similar models help to predict such outbreaks in Mozambique, Pakistan, and Haiti, giving those communities and governments time to prepare for outbreaks, with the goal of reducing the cholera disease burden and related deaths, she says.

![FIGURE 2](image_url)
Marine Pathogens Disrupt Important Ecosystems

Marine bacterial pathogens, particularly *Vibrio* species, can disrupt ecosystems by infecting species that provide essential functions within those communities. For example, oysters help to maintain reef habitats, filter water, and serve as food sources for other organisms within such ecosystems. “Hence, in addition to being economically devastating, oyster diseases affect overall ecosystem productivity and health,” says Burge. Terrestrial examples of species-specific diseases disrupting forests include Dutch elm disease and chestnut blight. Although such cases of infectious disease-driven ecosystem restructuring are well documented, researchers are only beginning to understand how climate-associated infectious diseases affect marine ecosystem dynamics.

Coral reefs appear to be the hardest hit so far for a number of reasons, according to Colwell. “Coral reefs, in particular, are already experiencing unprecedented degradation worldwide due in part to infectious disease outbreaks and bleaching episodes that are exacerbated by increasing sea-surface temperatures,” she says. *Vibrio* species are causing mass mortalities in coral species throughout the Mediterranean, while yellow band disease, also caused by *Vibrio* spp., threatens corals in the Caribbean and Pacific. “*Vibrio coralliilyticus*, a globally distributed bacterium associated with multiple coral diseases, infects corals at temperatures above 27°C,” she says. Further contributing to the problem, at higher temperatures virulence factors that affect motility, host degradation, secretion, antimicrobial resistance, and transcriptional regulation are up-regulated.

*V. coralliilyticus* also takes advantage of climate-stressed, immune-compromised corals, responding to stress signals that they emit, according to Roman Stocker, Melissa Garen, and their colleagues at the Massachusetts Institute of Technology in Cambridge. In response to heat stress, some corals secrete dimethylsulfoniopropionate (DMSP), a chemical that attracts *V. coralliilyticus*. “In heat-stressed coral fragments, DMSP concentrations increase fivefold and the pathogen’s chemotactic response was correspondingly enhanced,” says Stocker.

Corals are highly sensitive to climate-change stress due to their reliance on microbial symbionts, namely dinoflagellates of the genus *Symbiodinium*. In nutrient-poor tropical waters, corals rely on carbon-containing nutrients generated by these photosynthetic algae. “*Symbiodinium* trap solar energy and nutrients, providing more than 95% of the metabolic requirements of the coral host,” says Ove Hoegh-Guldberg of the University of Queensland, Australia, who spoke during the 2014 ASM GM session “Microbes in Symbiosis, Signaling and at Sea.”

However, these symbionts are compromised by both ocean acidification and rising ocean temperatures, Hoegh-Guldberg continues. “Coralline algae are among the most sensitive calcifying organisms to ocean acidification as a result of increased atmospheric carbon dioxide,” he says. “Under high carbon dioxide conditions, corals at the phenotype level lost over half their *Symbiodinium* populations, and had a decrease in both photosynthesis and respiration.”

Rising temperatures make matters worse; increases of only 1–2°C in water temperature further disrupts symbiosis, according to Hoegh-Guldberg. “Previous experiments that focused on ocean acidification alone may have underestimated the impact of future conditions on coralline algae,” he says. “Given the central role that coralline algae play within coral reefs, these conclusions have serious ramifications for the integrity of coral reef ecosystems.”

Loss of algal symbionts, which leads to bleaching, leaves corals struggling for survival and highly susceptible to infectious disease. “Over the past four decades, increasing environmental stress from rapidly changing climate . . . has disrupted the balance between hosts, agents, and the environment that underpins coral health,” Burge says. “Disruption of coral-microbial symbioses and concomitant reduced resistance to opportunistic pathogens have been major factors in the deterioration of coral reef communities worldwide.”

Overall, higher ocean temperatures and acidification favor pathogens, resulting in more frequent and severe outbreaks of infectious diseases in corals across the globe, according to Burge. “The host range and abundance of one of the most temperature- and nutrient-sensitive coral diseases, black band disease, have increased worldwide, likely reflecting the combined impacts of compromised host resistance and enhanced pathogen virulence associated with increasing seawater temperature and declining water quality,” she says.
Other temperature-dependent coral diseases include white syndrome, white patch disease, white plague, and yellow band disease, responsible for decimating coral populations in the Caribbean, Mediterranean, and Indo-Pacific regions. While some corals recover from these outbreaks, their resilience is being tested by continuing warming trends that do not provide adequate recovery time between heat stresses, according to Hoegh-Guldberg. Thus, 50% of corals in the Great Barrier Reef have disappeared since bleaching events began several decades ago. Similarly alarming statistics are reported for the Caribbean and other tropical reef regions.

The loss of coral reefs and other marine ecosystems can have far-reaching impacts, according to Burge. “Marine ecosystems are among the most valuable and heavily used natural systems worldwide and provide critical ecosystem services, including shoreline protection, water filtration, nursery grounds, food from fisheries and aquaculture, and revenue from tourism,” she says. Hoegh-Gulberg adds, “Climate change and ocean acidification are already... threatening the ability of the oceans to continue providing economic resources and environmental services on which we so critically depend.”
After Horizontal Gene Transfers, Metabolic Pathways May Need Further Optimization

Effective use of a horizontally transferred pathway can require co-evolutionary changes in the host or pathway

Joshua K. Michener and Christopher J. Marx

One surprising discovery of the genome sequencing era is the sheer ubiquity of horizontal gene transfers (HGT), particularly among bacteria. Genetic material encoding single enzymes and entire metabolic pathways has moved between distantly related species, with important consequences for microbial evolution, physiology, and ecology. HGT facilitated the rise of antibiotic resistance, the emergence of new bacterial species, and the adaptation of microbes to new ecological niches. By drawing on the metabolic potential of this “flexible genome,” novel microorganisms are capable of adopting a diverse array of phenotypes.

However, the frequency of HGT should not obscure the challenges involved for recipient cells trying to accommodate their new genes. After all, we observe the results of only those rare successful transfers that led to improved cells, rather than the vastly more common cases of unfit recombinant cells that failed to survive.

HGT Succeeds Only Rarely

To transfer a gene or genes successfully from one cell to another, a DNA molecule must first move into its new host by means of transduction, conjugation, or natural competence. Next, the transferred DNA must elude any recipient-cell defense mechanisms that target incoming genes, including CRISPR/Cas or restriction/modification systems, and then stably replicate within the recipient cell. Depending on the source of the DNA, the transferred gene may need to acquire appropriate transcription and translation signals if it is to become active in its new environment. Any necessary posttranslational interactions, including localization or chaperone-assisted folding, must be maintained in or adapted to the new host. Even if all of these challenges are overcome, a gene may still fail to function effectively.

Because cells contain complex, interconnected metabolic and regulatory networks, perturbing such systems by adding new genes can prove harmful, compromising both the horizontally transferred pathway and the native pathways of the new host cell. Many of the genes that we believe were successfully transferred are predicted to lie at the periphery of these networks, minimizing the chances for deleterious interactions. However, even genes that interact with few partners can be highly disruptive, and transfers of core functions may endow recipients with strong selective benefits that overcome transient fitness costs. In these cases, effective use of newly acquired pathways may depend on post-transfer refining mutations to minimize deleterious interactions and their costs to the recipient cells.

Experimental Evolution and Metabolic Engineering Highlight the Challenges of HGT

Studying transient post-transfer refinements in natural isolates can be challenging, since natural selection quickly eliminates any cells with de-

SUMMARY

> Pathways acquired through horizontal gene transfer (HGT) may impose new stresses on recipient cells.
> HGT-related stresses can limit the utility of newly acquired genes.
> Effective use of horizontally transferred genes may require refining mutations to both the recipient and the transferred genes.
> Synthetic biologists deliberately transfer genes between species and seek to determine how such genes can be optimized to function properly within recipient cells.
Josh Michener had not planned to study biology. “I had an empty slot in my schedule for my senior year of high school, and took a genetics class,” he says. “I had a great teacher, really enjoyed the class, but still was leaning towards majoring in computer science.” As a college freshman, “I signed up for another genetics class. One thing led to another, and I eventually added a major in biology.”

Today, Michener, a postdoctoral fellow at the Massachusetts Institute of Technology (MIT), studies how microbes evolve after gaining new functions either through horizontal gene transfer or genetic engineering. His research has moved from engineered to natural systems, “looking at how nature solves similar problems when they occur during horizontal gene transfer,” he says.

Michener, 30, grew up in Chapel Hill, N.C., where his parents work at the Duke University Medical Center. His father is Chair of the Department of Community and Family Medicine, while his mother is an assistant consulting professor with the Division of Community Health. An older sister teaches high school science in Charlottesville, Va.

His parents nurtured his love of math and science, even to the point of teaching him algebra at home. He made the U.S. Physics Olympiad team when he was a high school junior. He spent his final two years of high school at the North Carolina School for Science and Math, a public boarding school in Durham, an experience he calls one of the most influential of his young life. Later, he earned his Bachelor of Science degree in 2006 from MIT, and his Ph.D. in Bioengineering in 2012 from the California Institute of Technology.

What really “kick started” his career was the opportunity to conduct research as an undergraduate with Drew Endy, a synthetic biologist and bioengineer, now at Stanford University, but earlier at MIT, Michener says. “As both a biologist and an engineer, the idea of deliberately making biology easier to engineer was extremely attractive. I sent him an e-mail, cold, asking if I could work in his lab. He agreed, and I ended up spending much of the rest of my time in college working in the Endy Lab.” A research fellowship took Michener to Sweden in 2011 to work with Jens Nielsen at Chalmers University of Technology. “Working with Jens, we tried to look at my strains more holistically, to see all the different ways in which my engineered pathway was interacting with the host microbe.”

Michener’s wife is a physical therapy assistant at Massachusetts General Hospital, who plans to return to school for her doctorate in physical therapy. Michener, an enthusiastic cyclist, also enjoys cooking, sometimes incorporating fermentation steps into his culinary efforts—for example, by making sauerkraut and kombucha tea. “Friends have tried to convince me to brew my own beer, but that’s probably not going to happen any time soon,” he says.

Marlene Cimons
Marlene Cimons lives and writes in Bethesda, Md.

creased fitness. However, synthetic biologists and metabolic engineers are effectively conducting HGT by moving genes between distantly related organisms. Some of these engineering projects have yielded microbes that can produce pharmaceuticals, specialty chemicals, and biofuels, and these efforts offer an opportunity to appreciate the challenges of HGT.

Unfortunately, for every successful metabolic engineering project, many more unreported attempts fail, when enzymes and pathways that function well in their original host cells are ineffective in the recipient strain. In some cases—for instance, when genes encoding membrane-bound eukaryotic enzymes are transferred into bacteria—these failures are not surprising. In many others, however, the reasons for failure are neither expected nor explained, forcing investigators to change their experimental approaches. Consequently, to rapidly engineer metabolic pathways, we need to confront these barriers to HGT and learn how to overcome them.

At the same time that we develop improved engineering strategies, we also wish to understand natural evolutionary processes. Since engineers use different strategies than nature does, a pure engineering approach offers limited insights into natural processes. An alternative approach combines aspects of synthetic biology and experimental evolution. We can deliberately recreate HGT in the laboratory by transferring pathways into hosts and then selecting for use of the new ability. If a newly acquired pathway functions poorly, mutations that increase pathway effectiveness will provide a selective advantage to their host. Working backwards from these mutations allows us to identify both the challenges that previously limited the effectiveness of the pathway and the biochemical mechanisms for overcoming those challenges.
These evolutionary solutions also begin to develop a toolbox of design strategies for engineering applications.

**Fitness Costs May Accompany Antibiotic Resistance Gene Transfers**

One of the most dramatic consequences of HGT is the rapid spread of antibiotic resistance determinants among bacterial species and strains. Acquisition of a new resistance determinant often carries a fitness cost to the recipient cell. When patients are being treated with antibiotics, the benefits of resistance outweigh these costs. In the absence of the antibiotic, however, strains frequently acquire compensatory mutations that enable them to maintain resistance while minimizing those fitness costs.

When resistance determinants are carried on plasmids, mutations that lessen the plasmid carriage costs can occur in the host bacterium, the plasmid, or both. Similarly, resistance genes with an inherent fitness cost may acquire regulatory segments that block expression until the bacterial cell becomes exposed to that antibiotic, thus minimizing costs to the cells. In other cases, mutations that disrupt antibiotic binding can provide resistance but at a substantial fitness cost, until compensatory mutations restore fitness while maintaining resistance. These kinds of post-transfer refinements within the pathogen have significant medical consequences, since eliminating the fitness cost of resistance can prevent such bacteria from reverting to antibiotic sensitivity in the absence of antibiotic treatment.

**Genes for Other Horizontally Transferred Pathways May Undergo Refinements**

By introducing metabolic pathways for degrading novel substrates into new host microbes, HGT can enable recipients to occupy new environmental niches. For example, several bacterial strains can grow naturally on dichloromethane (DCM) as the sole source of carbon and energy. In the first step of this catabolic pathway, DCM is converted into formaldehyde plus two molecules of hydrochloric acid. The associated dehaloge-
nase gene, dcmA, is found in distantly related strains and is usually flanked by IS elements, observations that are consistent with ready dissemination by HGT.

Although the DCM catabolic pathway is found in several different bacterial strains, it is very difficult for recipients to exploit their new ability. Among other challenges, this catabolic pathway produces toxic formaldehyde and hydrochloric acid, as well as a highly mutagenic intermediate, S-(chloromethyl) glutathione.

To learn more about what makes such transfers difficult and how to overcome those difficulties, we transferred the dcmA gene from Methylobacterium extorquens DM4 into six other Methylobacterium strains. When the transconjugants were fed DCM, none grew as well as the reference strain, and one of those strains was completely unable to grow on DCM. Each strain functionally expressed the dehalogenase, suggesting that pathway-related stresses of some kind limit growth on DCM.

We then used experimental evolution procedures to identify mutations that could improve the ability of the dcmA-containing strains to grow on DCM. Mutations in four loci improve the
fitness of transconjugants during growth on DCM, and all of these mutations are linked to increased chloride efflux. Of note, several mutations increase expression of the chloride/proton antiporter, ClcA. Using this knowledge, we demonstrated that two independent DCM-degrading environmental isolates of *M. extorquens* both contain mutations in the *clcA* promoter. These promoter mutations are necessary and sufficient to permit effective growth on DCM.

Thus, for a *Methylobacterium* strain to grow on DCM requires not only a functional version of *dcmA* but also appropriate refining mutations. Remarkably, the adaptive steps we observed in our experiments appear to be the same as those that arose on multiple, independent occasions in nature. Putting this finding in engineering terms, organisms that are designed to degrade organochloride compounds are also likely to benefit from mutations that increase chloride export. More specifically, overexpressing ClcA appears to satisfy this goal without compromising viability in natural environments.
Replacing Metabolic Pathways Involves Co-Evolution of the Host and Pathway

Beyond transfers of novel pathways, examples of HGT include the replacement of a viable, functioning pathway with a homologous or orthologous alternative. Strikingly, these transfers can include highly-connected housekeeping functions such as RNA polymerase subunits, ribosomal proteins, or core metabolic enzymes. We constructed an example of this process by replacing a portion of the pathway for methanol catabolism in *M. extorquens* AM1 with an alternate metabolic route. Thus, instead of oxidizing methanol via the native tetrahydromethanopterin-dependent pathway, our modified strain contains genes for a glutathione-dependent pathway from *Paracoccus denitrificans*. Initially, this change led to a strain with a roughly threefold decrease in growth rate on methanol. Laboratory evolution of the modified strain yielded isolates that closed this fitness gap.

Analysis of one improved glutathione-dependent isolate revealed three main adaptations that enable it to better accommodate its new pathway for degrading methanol. One mutation reduces expression of the novel pathway, and subsequent work demonstrated that these enzymes are produced at unnecessarily high levels, with a substantial fitness cost for the modified cells. Another host mutation led to increased glutathione biosynthesis, accommodating increased demands for glutathione by the new pathway. The third mutation led to increased expression of a transhydrogenase, which interconverts NADH and NADPH. The methanol pathway in the parent strain produces a mixture of NADH and NADPH when methanol is oxidized, while the new pathway produces just NADH, and the transhydrogenase apparently adjusts for this difference. Similar to post-transfer refinement of DCM catabolism, replacement of a portion of the core methanol oxidation pathway requires significant refinement of both the host and the new pathway in order to function efficiently. As will be discussed below, similar strategies for balancing enzyme expression or increasing cofactor biosynthesis are common in metabolic engineering.

Overexpression of Promiscuous Enzymes Mimics Some Challenges of HGT

In addition to acquiring new metabolic pathways through HGT, microbes are hypothesized to extend their metabolic networks by coopting promiscuous catalytic activities of native enzymes. In *Escherichia coli*, several knockouts of genes that are otherwise essential for growth on minimal media can be complemented by overexpression of enzymes from unrelated pathways. Promiscuous catalysis by these overexpressed enzymes produces novel metabolic pathways that bypass the deleted reactions. However, these new pathways lead to many of the same challenges that are seen in cases of HGT, since in both situations the host cells may be unprepared for the new regulatory and metabolic interactions that result.

For example, overexpressing either YeaB or ThrB, the former from an unknown metabolic pathway and the latter involved in threonine biosynthesis, enables *E. coli* cells to grow after deletion of *pdxB*, a gene encoding an enzyme involved in pyridoxal phosphate (PLP) biosynthesis. Overproducing either enzyme enables mutants to grow by redirecting intermediates from serine biosynthesis into the PLP biosynthetic pathway, downstream from the reaction catalyzed by PdxB. However, that growth is limited because the novel pathway introduces two new intermediates, 3-hydroxypyruvate and 4-hydroxythreonine, that inhibit enzymes involved in amino acid biosynthesis. Moreover, ThrB continues to be regulated by threonine, even when this regulation conflicts with its new role in PLP biosynthesis. Finally, native enzymes such as IlvH can react with these new intermediates and reduce PLP production.

In cases involving HGT, enzyme amplification, or synthetic biology, introducing new metabolites and enzyme activities can disrupt both the novel function and the native pathways of the host. Developing new tools to identify and eliminate these deleterious interactions would aid in both the analysis of HGT and the construction of synthetic organisms.

Heterologous Enzymes Put New Stresses on Host Cells

Metabolic engineers frequently transfer genes from natural isolates into recipient bacterial species that are considered more genetically tractable but may be only distantly related to the source species. Just as in HGT, the metabolic intermediates being produced in such engineered pathways can impose stresses on the recipient strains that
interfere with production of the target metabolite. For example, transfer of the gene encoding an engineered P450 monooxygenase from *Bacillus megaterium* into *Saccharomyces cerevisiae* led to only moderate conversion of caffeine into the bronchodilator theophylline. Decreasing expression of that enzyme, however, increased both the growth rate and levels of theophylline in the engineered yeast strain, suggesting that the pathway was placing a stress on this host. Measurements of mRNA transcript levels confirmed that enzyme expression severely depletes heme in such cells. Accordingly, boosting heme biosynthesis in the yeast host increases both monooxygenase levels and theophylline yields.

Heterologous enzymes, whether transferred by HGT or synthetic biology, often increase demand for native cofactors or require the introduction of new cofactors. Learning to recognize the signatures of increased cofactor demand will aid in the analysis of environmental isolates, while identifying mutations that increase cofactor production without overly burdening the host will be valuable tools for metabolic engineering.

Similar to the enzyme amplification example discussed above, deliberately introducing an engineered metabolic pathway may produce intermediates that interfere with the native metabolism of the new host. For example, several genes were introduced into *E. coli* cells, enabling them to make a precursor for artemisinin, a valuable drug for treating malaria. However, when the first three genes in the pathway are overexpressed, a non-native intermediate, 3-hydroxy-3-methylglutaryl-CoA (HMG-CoA) quickly accumulates and inhibits growth. Further analysis shows that elevated levels of HMG-CoA inhibit fatty acid biosynthesis in the engineered cells. This problem can be overcome, however, by supplementing the growth medium with fatty acids or by modifying expression of the enzymes in the pathway to prevent accumulation of HMG-CoA.

In both natural and engineered systems, including these examples of artemisinin production and glutathione-dependent methanol oxidation, differences between donor and recipient cells may lead to metabolic pathway imbalances in the new host cells. In some cases, reducing the levels of the introduced enzymes will overcome the burden of protein overexpression and also avoid any accumulation of toxic intermediates.

Joshua K. Michener is a postdoctoral fellow in the Department of Biological Engineering at the Massachusetts Institute of Technology, Cambridge. Christopher J. Marx is an Associate Professor in the Department of Biological Sciences at the University of Idaho, Moscow.

**Suggested Reading**


Encouraging Microbiology Students To Think Like Scientists

Instead of urging students to memorize new materials, teach them to understand concepts fully and then put them to use

Erica Suchman

Like many instructors, I went to a university where lectures were the norm. Because that strategy seemed to work so well, I emulated that approach when I began teaching microbiology to college students.

After many years of teaching, however, I had an epiphany. It came while reviewing a diagram with one of my lecture students. She drew it perfectly on her last exam, yet realized that she did not fully understand parts of what she had drawn so expertly. I soon realized that my star student—someone whose urge to understand material was so strong that she visited me to discuss material she supposedly had mastered—did not genuinely understand diagrams that she could perfectly reproduce.

I found myself wondering how many other students merely reproduce but do not understand diagrams or other materials from lectures. Soon, I began questioning students about these diagrams and other items that were described in lectures. To my dismay, although the vast majority of my students could draw those diagrams, they did not understand them. Thus began my quest to determine how better to teach my students what the diagrams mean, how to move them past merely memorizing the information from lectures, and how to assess authentically their understanding of the materials in the course. By authentic I mean testing their ability to understand the diagrams and know when and how to apply the material to new situations—not their ability to memorize diagrams.

Searching for Solutions

All teachers should have great mentors. One of mine, Spencer Benson, currently at the University of Macau in China, taught me about backwards design. Following this method, a teacher first decides what skills, abilities, and knowledge he or she wants students to have at the end of a learning activity and then develops the means for determining whether the students have acquired those skills. Only then does the teacher develop a curriculum that will help students achieve the intended outcomes.

This process was opposite to how I was designing my courses. I followed a more conventional approach by developing a list of topics, lectures to cover those topics, and assessments to determine how well students mastered those materials. Upon reflection, however, I realized that I was not teaching my students the skills that I wanted them to have, primarily the ability to think critically about the material I was teaching. Furthermore, my assessments did not really evaluate what I thought was most important.

I strive to follow the advice of many experts, including recent ASM President Jo Handelsman of Yale University and the U.S. Office of Science and Technology Policy, who recommend using scientific evidence to drive one’s teaching methods and to identify which approaches really work.

SUMMARY

Teachers can benefit from attending workshops, reading about teaching, and having mentors.

Instructors should use evidence-based teaching strategies.

Backwards design can be used to determine whether learning outcomes, classroom activity design, and assignments are aligned.

Student-centered learning forces students to practice thinking like scientists, while building their confidence in their ability to do so.

Unless classroom activities and student assessments reflect the skills that a teacher is trying to impart to his or her students, they will not realize that these are important skills for them to develop.
A tremendous amount of evidence indicates that students learn more when teaching is more student-centered, meaning the students are not simply listening to lectures but that they are also interacting with information during class periods.

My department invests heavily in professional development and sends me each year to the ASM Conference for Undergraduate Educators (ASMCUE). Participating in these annual conferences enables me to explore alternative teaching techniques that are described by many great biology teachers who attend the meeting. Each year I return from ASMCUE with ideas that help me to improve the learning experiences of my students.

Thus I gladly adopt ideas from others that help my students learn to think like scientists, meaning that I owe a great deal of thanks to ASM for creating this venue for exchanging ideas about teaching and learning. I encourage all educators to attend this conference or others like it because doing so can help to improve the student-learning environment. Indeed, after nearly 20 years of attending ASMCUE, I still gain new ideas each year for making such improvements.

Furthermore, access to education journals such as the ASM Journal of Microbiology & Biology Education (JMBE) (http://jmbe.asm.org/index.php/jmbe) and CBE Life Science Education (http://www.lifescied.org/), which is published by the American Society for Cell Biology, can help microbiology, cell biology, and other specialty biology teachers explore new ideas without having to leave their offices. I would argue that teaching without revisiting the newest information on teaching and learning is equivalent to performing research without keeping up on the literature in your field of study.

**Implementing Significant Change Gradually**

Importantly, I did not immediately change everything in my approach to teaching. Instead, every semester I try to improve or add at least one thing to each of my courses to address my most challenging teaching issues. I always keep a list of things to improve, and I seek constantly...
for new ways to address these issues. If I tried to implement all such improvements in one semester, it would have overwhelmed me and my students. So my suggestion is change something every semester. I view teaching as a work in progress.

The first additions to my courses were problem-based, group projects. Topics my students struggled with the most—for example, metabolism and protein translation—became the subject matter for “group exams,” in which groups of students work on data-driven problems for a week and then take an in-class examination when all members of each group decide together on the best answers to turn in. This approach allows me to grade 20 to 30 group papers rather than 80 to 120 individual exams. The exam questions are designed so students must develop their own answers: all data are fabricated, and there is nowhere to look up answers. I do not use real data to avoid students searching for expert opinions, rather than taking the risk of being wrong.

Over the years, this student-centered learning activity has been improved in response to perceived weaknesses. Earlier, many students complained that other members of their groups would not listen and chose instead to record incorrect answers that penalized them. So I added a page on which to record dissents, enabling individual students to disagree with the answers submitted by their groups. Although they rarely submit such dissents, adding the option eliminated this complaint.

To deal with students who allowed other students do all the work, I first asked each student to evaluate all other members of his or her group. However, students found it awkward to evaluate each other and rarely used this approach to identify or correct those who were not doing their fair share of the work. Luckily, in 2004, I learned about a new technology, called classroom response systems or clickers, through which students may answer questions anonymously (to one another) during class. The next semester I added clicker questions to my lectures and clicker quizzes to the end of each group exam. Once the group exams are turned in, everyone in the class takes a quiz covering the same material but now using their clickers. Individual students must score more than 70% correct to earn the score that their group does, or else they get 70% of the group’s score, because they obviously were not an active participant. This approach has greatly improved student participation.

**Importance of Clickers, Inducing Individuals To Think for Themselves**

The clickers are a very important, maybe even revolutionary, tool in my teaching. I repeatedly tell students that I do not want them to memorize material, that they need to know how to use it and apply it to new situations. However, some students, who do not appreciate what I mean, continue to memorize material and assume that means they can use it. If we do not give them practice applying those concepts, they may never gain that skill.

Although lectures and occasional homework assignments in which students practice applying concepts are preferable to confronting students during exams with their weaknesses, the lectures and homework are only marginally better. Instead, students must practice skills regularly. Indeed, my students now understand the importance of applying concepts to new situations because they are asked to do so in every class period, as well as outside class every week.

Generally I present a concept, often with a diagram exemplifying that concept—for example, regulation of the Lac operon. Then I ask students questions about a different gene and its regulation, again, often including fabricated data. Students use their clickers to answer the new questions. If the majority cannot answer correctly, I say to them, “Turn to your neighbor and convince them your answer is correct, and if you agree, explain your rationale to one another.” By simply doing this, the percentage of correct answers goes up dramatically—on average, 22% in my class—without me saying anything else.

This peer-to-peer teaching allows students to develop a deeper understanding of the material while affording them opportunities to articulate new concepts. Furthermore, it shows them different ways in which I expect them to use the material being taught. These clicker questions are not worth credit, hence students feel free to answer with whatever answers that they believe are correct. Three times during each the semester, I teach “flipped classes” where my students watch a 15-minute lecture before the class after which we do active learning activities for the entire class, using their clickers to gauge their understanding.
Randomly chosen class periods where students receive extra credit if present in class, as demonstrated by their having answered questions with their clickers, provides an incentive to regularly attend classes and participate in them.

I wanted a way to encourage students to study more but did not want more grading to do. Because students benefit from frequent low-stakes opportunities to apply knowledge to new situations, I have my students take five online quizzes individually, in addition to the five group exams that they all take. Thus, they have a group exam, online quiz, or midterm test almost every week. They can take each online quiz up to 10 times and will get credit for their highest score (20 points out of 700). These quizzes have 20 pools of questions. Each pool tests a different concept (e.g., determine the mRNA produced from a given piece of DNA) and contains multiple questions. Each time students take the exam, they get a different randomly chosen question from each pool, and all 20 concepts will be tested, but with slightly different questions each time.

Students are given their scores and told which questions they missed, but not the correct answers. While I realize that the nature of these online quizzes allows students to get answers from other students, my goal is not to test them on these concept, but to make them practice them so they will perform better on exams and have greater long-term retention of material. The beauty of these online assessments is that I do not do any grading, and each student’s scores automatically load into my learning management center’s grade book. After the initial and not trivial time commitment required to develop these assessments, very little work is required to make this resource available.

Another Teaching Epiphany

My exams have changed dramatically over the years. While listening to Robert Duke of the University of Texas, Austin, a music professor and expert on learning, I had another epiphany about teaching. He posed a simple question. If it is not an important point, why is it on your exam?

I realized that my exams were full of questions that promoted memorization instead of understanding. If there is one thing I learned
from my own teaching, students will try to learn what they believe they will be tested on. Previously, my exams were teaching them that if they memorized diagrams and trivial information, they could succeed in courses I taught. If I wanted to change how my students learned, I was going to have to change how I assessed them. My students now know that I will never ask them to draw a diagram that we have gone over in class. In fact I allow my students to bring to exams one 8½-by-11 handwritten sheet that includes anything we talked about in class, to prove to them I will not ask them any memorization questions. I ask questions about systems that we never discussed, forcing them to apply the concepts that we did discuss.

After many years of following this practice, I believe that my intended learning outcomes are being clearly articulated to my students, my classroom sessions are designed to teach them the skills I value, and the students know that I will assess their learning in ways that require more than memorization. Does that mean that my approach to teaching is perfect? Of course not, there is a long list of things to improve. One of the things I love about teaching is that, if you are doing it right, there is always another challenge to face.

Erica Suchman is a Professor in the Department of Microbiology, Immunology, and Pathology at Colorado State University, Fort Collins, and was the 2014 Carski Foundation Distinguished Undergraduate Teaching Award winner.

Suggested Reading


One Health: People, Animals, and the Environment

Editors: Ronald M. Atlas, University of Louisville; Stanley Maloy, San Diego State University

One Health is a global strategy that represents a paradigm shift in how we must respond to the threat of infectious diseases. One Health, rather than identifying and treating infections in focuses on a collaborative, holistic surveillance of the environment, animals, and humans to predict an outbreak of disease before it happens. This approach accelerates biomedical advances by integrating environmental, veterinary, and human medical science in understanding the development and transmission of infectious diseases.

In One Health: People, Animals, and the Environment, editors Ron Atlas and Stanley Maloy have compiled 20 chapters written by interdisciplinary experts that present core concepts, compelling evidence, successful applications, and the remaining challenges of One Health approaches to thwarting the threat of emerging infectious disease.

This book is a valuable resource for physicians, veterinarians, environmental scientists, microbiologists, public health workers and policy makers, and others who want to understand the interdependence of human, animal, and ecosystem health.

March 2014. 330 pages, full-color illustrations, index.
List Price: $90.00 | ASM Member Price: $72.00

When you buy books from the ASM Press, you support the society that supports the science of microbiology

Topics Include

• the interconnectedness of human and animal pathogens
• emerging diseases in animals and humans
• case histories of notable recent zoonotic infections, including West Nile virus, hantavirus, Lyme disease, SARS, and salmonella
• epidemic zoonoses and corresponding environmental factors
• insight into the mechanisms of microbial evolution toward pathogenicity
• causes behind the emergence of antibiotic resistance
• new technologies and approaches for public health disease surveillance
• political and bureaucratic strategies for promoting the global acceptance of One Health
2014 Election Results


Lynn W. Enquist, Princeton University, Princeton, N.J., is the new president of ASM for a 1-year term beginning 1 July 2015.

Susan E. Sharp, Kaiser Permanente Northwest, Portland, Oreg., is the new president-elect of ASM for a 1-year term beginning 1 July 2015.

Joseph Campos, Children’s National Medical Center, Washington, D.C., has been elected as secretary of ASM for his ninth term beginning 1 July 2015.

James Tiedje, Michigan State University, East Lansing, has been elected as treasurer of ASM for his eighth term beginning 1 July 2015.

Divisional Group Representatives, 2015–2017

Two of the four divisional groups elected group representatives for 2-year terms beginning 1 July 2015.

Divisional Group I—Diagnostic Microbiology and Epidemiology (Divisions C, F, L, V, Y, and AA)

Barbara Robinson-Dunn
William Beaumont/Oakland University School of Medicine
Royal Oak, MI

Divisional Group IV—Molecular Microbiology, Physiology, and Virology (Divisions H, J, K, M, S, T, and X)

Gail E. Christie
Virginia Commonwealth University
Richmond, VA

At Large Division Councilors

Kirsten St. George (reelection to a 2nd term)
New York State Department of Health
Albany, N.Y.

Yvonne Salfinger (reelection to a 2nd term)
Florida Department of Agriculture and Consumer Services
Tallahassee, FL

Janice Matthews-Greer (re-election to a 2nd term)
Louisiana State University Health Science Center Shreveport, LA

Suzanne Fleiszig (re-election to a 2nd term)
University of California Berkeley, CA

Michael Donnenberg (re-election to a 2nd term)
University of Maryland
Baltimore, MD

Mike McInerney (re-election to a 2nd term)
University of Oklahoma
Norman, OK

Anita Wright
University of Florida
Gainesville, FL

Erin Lipp
University of Georgia
Athens, GA

Bylaws Amendments

The amendment to the ASM Bylaws regarding the establishment of international student chapters was approved by the membership. See the ASM website effective January 2015 for a revised copy of the Constitution and Bylaws.

Honorary Membership

Michael Goldberg has been elected for honorary membership in the Society by the membership.

Divisional Officers, 2015

The members of ASM’s 27 divisions elected officers for terms beginning 1 July 2015. Chairs and chairs-elect serve a one-year term. The Table of Divisional Officers for 2015 is on page 77.
Sansalone Named ASM Interim Executive Director

Nancy A. Sansalone has been named Interim Executive Director of ASM effective 1 January 2015. She steps in for Michael Goldberg, who retired at the end of 2014 after 30 years of stellar leadership. She has been asked by the ASM Officers to lead the staff, to steward the operations and finances, and to prepare the organization for change while the Society conducts an international search for a permanent Executive Director/CEO. The search is expected to begin in January 2015.

Sansalone joined ASM in 2010 as the Deputy Executive Director. In this role, she provides leadership and management expertise to the board leadership and staff to ensure the fulfillment of the Society’s mission and strategic plan and provides leadership direction for the Society’s operational, programmatic, and business activities.

Sansalone has spent her entire career in association management and higher education administration. Prior to joining ASM, she served as the CFO and Chief Operating Officer at the Special Libraries Association (SLA) and Vice President and CFO of the American Association for Higher Education (AAHE). Previously, Sansalone worked for 10 years with the Council of Graduate Schools (CGS), serving as Vice President for Finance and Administration and Treasurer for the Council’s Board of Directors.

She also has served as a volunteer leader on numerous nonprofit boards such as the National Association for Women in Education, where she served as the elected President, the Washington Higher Education Secretariat Metropolitan Employer Trust as an Advisory Board member, the Capital Association for Women in Education as President, the National Conference for College Women Student Leaders as Chair, the National Center for Higher Education Meeting Professionals as Chair, the American Society for Association Executives as a member of the Finance and Administration Advisory Board, and as a member of the ERIC Clearing House on Higher Education Coordinating Board. She also has held administrative posts at both Harvard University working with international programs at the Kennedy School of Government and at Northeastern University in the Cooperative Education Division.

Sansalone is a graduate of Northeastern University with a Master’s Degree in Public Administration and a Bachelor’s of Science Degree in Political Science and Public Administration. She completed work at Harvard University in their advanced graduate study in management program. She lives in Arlington, Va., with her spouse Jim and their four dogs.

ASM Strategic Alliances Department

ASM has always had a rich history of strong partnerships and alliances that have moved the organization forward and assisted with positioning ASM as a leader in the microbiology community. However, the majority of these relationships have historically been managed through the various departments and leadership of ASM, and the entire impact of the affiliations were not always realized. This decentralized approach brought into question whether ASM’s relationships were being leveraged to their full potential.

The 2013 ASM Strategic Issues and Objectives also highlighted that uncoordinated, decentralized programs contribute to mixed messages, inefficiency, and redundancy. The historic separation of service and products by program (e.g., meetings, journals, books, education) limits flexibility in responding to customer needs. It was also recognized that increased financial pressure on the health care industry affects the viability of ASM products and services. The health care industry is destabilized, and the future availability of revenue is uncertain. ASM must adapt to the changing environment and forge new relationships. Finally, it was agreed that there is a need to expand strategic partnerships (e.g., commercial, professional, national, and international organizations). ASM will develop and propose a strategy for the high-level management of relationships with our corporate sponsors (advertising, exhibitors, and donors) across the Society.

To create a more unified and comprehensive approach to developing, managing, analyzing, and executing ASM’s business relationships, the Society established the Strategic Alliances Department in October 2014. The department, staffed by Connie Herndon, Director of Strategic Alliances, and Gregg McGrath, Manager of Strategic Alliances, will lead ASM’s effort to form a centralized program that will provide a dedicated
staff person to efficiently track the budget cycles, product development/research pipelines, patent deadlines, and other company-specific information instrumental in determining appropriate funding sources. Having a single ASM contact will ensure a strong relationship with the funding decision-makers. The new department will allow a reduction of duplicate efforts among the departments and provide opportunities to encourage cross-departmental initiatives, creating synergies that do not currently exist.

A more proactive approach will help create programs and projects to serve the needs of the members and provide greater potential for securing the necessary funding and help achieve the goal of increased recognition and potential revenue based on supported, strategic relationships. Overall, the establishment of the Strategic Alliance Department is an investment in the organization with the primary goal of establishing, fostering, and maintaining the essential partnerships that will contribute to increased success. It is ASM’s first step in leveraging relationships to build sustainability for the future.

Join ASM Speakers’ Bureau!

Interested in sharing your microbiology or immunology career experience with ASM Student Chapters? ASM is looking for members employed in the clinical lab or industry, such as —

- Bioremediation
- Biosafety
- Biotechnology
- Dairy
- Food Safety
- Indoor Air Quality
- Medical Device
- Pharmaceuticals
- Policy
- Public Health
- Tech Sales
- Water Quality

The Speakers’ Bureau is designed to attract students to microbiology career opportunities. Speakers share with ASM Student Chapters information about their careers, how they got started and tips for success. Speakers can give a live, recorded or video call presentation!

ASM Members can visit http://bit.ly/ASMspeakers to learn more and sign up!
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<th>Divisions</th>
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| Antimicrobial Chemotherapy     | Gerry Wright  
McMaster University  
Hamilton, Ontario, Canada  | Jared A. Silverman  
Cubist Pharmaceuticals Inc.  
Lexington, MA  |
| Microbial Pathogens           | H. (Hank) Steven Seifert  
Northwestern University  
Chicago, IL  | Denise Monack  
Stanford University School of Medicine  
Stanford, CA  |
| Clinical Microbiology         | Eileen Burd  
Emory University Hospital  
Atlanta, GA  | Karen C. Carroll  
Johns Hopkins Hospital  
Baltimore, MD  |
| Microbe-Host Interactions     | Vanessa Sperandio  
UT Southwestern Medical Center  
Dallas, TX  | Eric P. Skaar  
Vanderbilt University Medical Center  
Nashville, TN  |
| Immunology                    | John MacMicking  
Yale University School of Medicine  
New Haven, CT  | Thirumala-Devi Kanneganti  
St. Jude Children’s Research Hospital  
Memphis, TN  |
| Medical Mycology              | Marta Feldmesser  
Albert Einstein College of Medicine  
Bronx, NY  | Deborah A. Hogan  
Dartmouth University School of Medicine  
Hanover, NH  |
| Mycoplasmology                | Li Xiao  
University of Alabama in Birmingham  
Birmingham, AL  | Christopher McGowin  
LSU Health Sciences Center  
New Orleans, LA  |
| Genetics & Molecular Biology  | Susan Lovett  
Brandeis University  
Waltham, MA  | Jade Wang  
University of Wisconsin-Madison  
Madison, WI  |
| General Microbiology          | Larry Halverson  
Iowa State University  
Ames, IA  | Thomas M. Schmidt  
Michigan State University  
Ann Arbor, MI  |
| Cell & Structural Biology     | Elizabeth Wright  
Emory University  
Atlanta, GA  | Erin Goley  
Johns Hopkins University School of Medicine  
Baltimore, MD  |
| Microbial Physiology & Metabolism | Anne K. Dunn  
University of Oklahoma  
Norman, OK  | Julie L. Zilles  
University of Illinois at Urbana–Champaign  
Urbana, IL  |
| Healthcare Epidemiology       | Keith Kaye  
Detroit Medical Center  
Detroit, MI  | Jesse Jacob  
Emory University  
Atlanta, GA  |
| Bacteriophage                 | Mya Breitbart  
University of South Florida  
Saint Petersburg, FL  | Gerald Koudelka  
University at Buffalo  
Buffalo, NY  |
| Microbial Ecology             | Barbara Campbell  
Clemson University  
Clemson, SC  | Dionysios A. Antonopoulos  
Institute for Genomics and Systems Biology  
Argonne, IL  |
## Division Officers 2015 (continued)

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<thead>
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<th>Division</th>
<th>Chair</th>
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<tr>
<td><strong>O</strong> Fermentation &amp; Biotechnology</td>
<td>Aindrila Mukhopadhyay</td>
<td>Daniel K. Y. Solaiman</td>
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<td>Lawrence Berkeley National Laboratories</td>
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<td>Wyndmoor, PA</td>
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<td>Edward G. Dudley</td>
<td>Rebecca Bell</td>
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<td>Pennsylvania State University</td>
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<td>Morgan Langille</td>
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<td>Bobbi Pritt</td>
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ASM Public Affairs

FY 2015 Funding Bill Completed

In mid-December Congress passed the fiscal year (FY) 2015 “Cromnibus” bill (H.R. 83) which funds federal agencies for the full FY through 30 September 2015, except for the Homeland Security Department, which is funded through 27 February 2015 on a continuing resolution. Highlights of provisions related to research and public health include the following:

National Institutes of Health (NIH). The bill includes $30.08 billion for the NIH, $150 million above the FY 2014 level (a 0.5% increase). NIH receives an additional $238 million for Ebola activities. The bill reforms the Public Health Service evaluation transfer or “tap” so that NIH will receive $715 million in return for its contribution of $700 million. The appropriations report encourages the National Institute of Allergy and Infectious Disease, the Centers for Disease Control and Prevention (CDC), and other federal partners to conduct a workshop to develop a coordinated action plan to address antibiotic resistance issues. The report directs NIH to develop a new approach to reduce the average age at which an investigator first obtains R01 funding and legislative language mandates NIH to submit a 5-year scientific strategic plan.

Centers for Disease Control and Prevention. The bill appropriates $6.9 billion for the CDC, $43 million above the FY 2014 program level. CDC will also receive $1.2 billion for Emerging and Zoonotic Infectious Diseases; $30 million to support the Advanced Molecular Detection Initiative; an increase of $8 million for food safety; an increase of $7.3 million for CDC’s internal lab capacity, including rapid diagnostics and high containment safety. The proposed CDC Detect and Protect Against Antibiotic Resistance Initiative was excluded from the bill.

Food and Drug Administration (FDA). FDA will receive $2.6 billion, a $37 million increase from last year. Included is $27 million in new funding for the Food Safety Modernization Act.

National Science Foundation (NSF). NSF will receive $7.344 billion, about $172 million over FY 2014 (a 2.4% increase).

Department of Energy Science Research. Funding is set at $5.1 billion, the same as FY 2014;

USDA Research. The National Institute of Food and Agriculture is funded at $1.3 billion and the Agriculture Research Service is funded at $1.1 billion; the bill includes $325 million for the Agriculture and Food Research Initiative for competitive grants.

Ebola supplemental funding. The bill includes $5.4 billion in supplemental funding to combat Ebola.


ASM Meets with Officials from WRAIR

On 4 December, Ronald Atlas, Chair of the Public and Scientific Affairs Board; Charles Rice, Chair, Committee on Agricultural and Food Microbiology; Janet Shoemaker, Director, ASM Office of Public Affairs; and Meghan O’Brien, Manager, ASM Public Affairs, met at the National Science Foundation (NSF) with James Olds, Assistant Director, Directorate for Biological Sciences (BIO); Jane Silverthorne, Deputy Assistant Director for BIO; Sonya Mallinoff, Senior Advisor, Planning, Analysis and Operations for BIO; and Charles Liarakos, Senior Advisor for Strategic Planning, Policy and Analysis. The meeting focused on microbiology and funding for research within BIO as well as on ways that the ASM could continue to work with the NSF to support microbiology research and development. Olds was appointed in September (http://nsf.gov/news/news_summ.jsp?org=BIO&cntn_id=132477&preview=false).

ASM Endorses Letter to the FDA the Regarding Collection and Reporting of Antimicrobial Data

ASM joined 27 other organizations in sending a letter to Margaret Hamburg, Commissioner of the Food and Drug Administration (FDA), regarding implementation of the National Action Plan on Combating Antimicrobial Resistance. The letter requested FDA move quickly to (i) release already-collected data on the sales of antibiotics for use in food-producing animals from 2013; (ii) make public the FDA’s plans for collecting data on how antibiotics are used on farms; and (iii) identify any gaps or barriers to collecting these data. To read the entire letter go to http://www.asm.org/images/PSAB/FinalDataCollection.pdf.

ASM Signs Letter Regarding FY 2015 DOE Appropriations

ASM cosigned a letter from the Energy Sciences Coalition urging Congress to complete work on the fiscal year 2015 Appropriations process and to increase
ASM NEWS

funding for critical scientific research supported by the Department of Energy’s Office of Science and the Advanced Research Projects Agency for Energy (ARPA-E). ASM is a member of the Energy Sciences Coalition. To read the letter, go to http://www.asm.org/images/pdf/ESC-FY15.pdf.

ASM Attends December CCCLW Meeting

On 8 December, Janice Matthews-Greer, member of the ASM Public and Scientific Affairs Board Professional Affairs Committee, represented ASM at the Coordinating Council on the Clinical Laboratory Workforce (CCCLW) meeting in Chicago, Ill. CCCLW is currently focusing on the value of laboratory testing in patient outcomes. The CCCLW is a coalition of laboratory organizations working together to ensure a high-quality workforce, and ASM is one of nearly 20 long-term members. You can read more about their past projects by going to http://www.cclcw.org/default.html.

ASM Attends FDA Anti-Infective Drugs Advisory Committee Meeting

ASM staff attended the 4 December meeting of the Food and Drug Administration (FDA) Anti-Infective Drugs Advisory Committee. FDA officials focused on the history of antibacterial drug development, current approaches to unmet medical needs, statistical considerations in evaluation of unmet medical needs, and trial considerations. Later, members of the public addressed the committee and several stakeholders, such as the Infectious Diseases Society of America and the American Thoracic Society, presented before the committee. To see the materials from this meeting, please go to http://www.fda.gov/AdvisoryCommittees/CommitteeMeetingMaterials/Drugs/Anti-InfectiveDrugsAdvisoryCommittee/ucm385739.htm

Education Board

ASM Represented at National Student and Educator Meetings in Fall 2014

The strategic directions of the ASM Education Board include collaborating with national organizations to promote microbiology education at all levels. In fall 2014, the Board sponsored the Society’s participation in the following conferences for science students and educators:

SACNAS National Conference. Education staff members Tiffani Fonseca and Irene Hulede represented ASM at the Society for the Advancement of Chicanos and Native Americans in Science (SACNAS) National Conference held 15–19 October in Los Angeles, Calif. The conference featured career workshops, scientific symposia, exhibits, and student research presentations, along with speakers highlighting resources designed to help Chicano/Latino and Native American students pursue advanced degrees in the sciences. During the exhibits program, Fonseca and Hulede shared information about ASM education resources and student programs.

Compact Annual Institute on Teaching and Mentoring. Hulede represented ASM at the 19th Annual Institute on Teaching and Mentoring sponsored by the Compact for Faculty Diversity. Held 30 October to 2 November in Atlanta, Ga., the invitation-only institute was designed to help minority scholars with the strategies necessary to survive the rigors of graduate school, earn doctoral degrees, and succeed as members of the professoriate. During the exhibits program, Hulede shared information about ASM faculty and student resources.

POD Network Annual Meeting. Education staff member Kelly Gull represented ASM at the Annual Meeting of the Professional and Organizational Development (POD) Network in Higher Education held 5–9 November in Dallas, Tex. The POD Network aims to improve teaching and learning in postsecondary education. At the meeting, Gull promoted ASM Faculty Programs as professional development models that help faculty develop skills to improve student learning and become agents of change on their campuses, in their Scholar communities, and in their professional societies.

NABT Annual Meeting. Committee for K-12 Outreach chair Dave Westenberg and Education staff members Kelly Gull and Lyndsey Van Druff represented the Society at the National Association of Biology Teachers Annual Meeting (NABT) held 12–15 November in Cleveland, Ohio. ASM sponsored the symposium “STEM and the Clinical Microbiologist,” which featured talks by Jon Kallay (Ben Venue Laboratories) on “Microbiology Testing in the Pharmaceutical Industry,” Sandra Richter (Cleveland Clinic) on “Antimicrobial Resistance Detection in the Clinical Laboratory,” and Christopher Wooterton (Kent State University) on “Lab Safety and Bioterrorism Readiness Curricula.” In the exhibits program, Education staff shared information about the Society’s K-12 outreach activities, along with other ASM faculty and student resources.

Coming this Spring: New Online Mentor Training Course for Research Investigators

This spring, the ASM-NSF Leaders Inspiring Networks and Knowledge (LINK) initiative, Mentoring Mondays, returns with ASMentors, an online mentor training course for researchers. ASMentors is a three-month professional development series that blends instructional webinars with an interactive discussion forum and mentoring resources. The program is designed for research investigators who are currently training early-career scientists (i.e., undergraduate, graduate, or postdoctoral researchers) and are interested in enhancing research productivity through quality mentoring.
Through this series, participants will learn the benefits of effective mentoring, develop skills to establish beneficial mentoring relationships, and discuss strategies to support a diverse research program. The webinars will cover themes, including:

- Research Relationship Primer: Maintaining Effective Communication, Setting Goals, and Aligning Expectations (March)
- Equity and Inclusion in the Research Enterprise: Challenges, Issues, and Resolutions (April)
- Accelerating Trainee Progress: Fostering Independence and Scientific Confidence (May)

Registration is now available online. This series is provided as a complimentary benefit with your ASM membership. To learn more, visit the ASM Mentoring Mondays web page at http://www.asmlink.org.

**International Affairs**

**ASM at the Second African Society for Laboratory Medicine International Conference**

Since its launch in 2011, the African Society for Laboratory Medicine (ASLM) has served as a continent-wide professional society advocating for the role and needs of laboratory medicine. ASM has contributed to the ASLM since its inception by facilitating the creation of a clinical laboratory interface framework and contributing to the development and launch of the ASLM website.

Five ASM International team members attended the second ASLM International Conference in Cape Town, South Africa, between 28 November through 4 December 2014, to provide on-site volunteer support at the conference and to increase awareness about ASM through an exhibition booth, poster, and seminar presentations.

The ASM delegation team presented a seminar session entitled “Sharing Success: Laboratory Mentoring Program 2.0,” which highlighted ASM’s unique approach to strengthening quality-assured diagnosis of infectious diseases through structure mentoring. The session attracted more than 20 attendees. ASM’s oral poster entitled “Quantification of Microbiology Laboratory Mentoring Progress in Tanzania” won second place in its category. There were four other posters showcasing ASM’s Mozambique and Namibia Microbiology and EQA successful laboratory mentoring programs. While these posters gained publicity with attendees, the ASM booth also attracted a lot of traffic, and many ASLM2014 participants were interested in ASM’s international endeavors. The booth helped to recruit more than 70 new members as well as promote ASM journals and resources.

The conference theme, “Innovation and Integration of Laboratory and Clinical Systems: Reshaping the Future of HIV, TB, Malaria, Flu, Neglected Tropical Diseases and Emerging Pathogens in Africa,” highlighted the need to maintain the current commitment to ensuring improvement in quality patient care and disease control through strengthened laboratory systems in Africa. The third ASLM International Conference will be held in 2016 in Cape Town, South Africa.

**Asia-Pacific Biosafety Association Conference, Partnering to Advance Safety in Science**

The Asia-Pacific Biosafety Association (A-PBA) Conference convened 3–6 November 2014 in Bangkok, Thailand. The conference provided a valuable forum for scientists from the region and around the world to share experiences and discuss biosafety capability and capacity building. This was a particularly timely event, as the Ebola outbreak in West Africa has brought biosafety and the transnational threat of infectious diseases to the forefront of many discussions, as well as reinforced the importance of international scientific cooperation.

Twenty-six microbiologists from India, Pakistan, Malaysia, and Yemen were awarded ASM travel grants to support their participation in the A-PBA Conference and post-conference courses. This respected international forum on biosafety and biosecurity offered many opportunities for network building with regional peers and professional development. Grantees participated in sessions and post-conference workshops which explored the theme of the conference: “Biosafety and Biosecurity Collective Partnership towards One World One Health.”

ASM member and former director of the U.S. Army Medical Research Institute of Infectious Diseases, David Franz, spoke on cultivating a sustainable biosafety and biosecurity
culture in organizations. Officials from ministries of health throughout the Asia-Pacific region spoke of their individual experiences, challenges, and solutions. Post-conference courses gave participants the opportunity to delve deeper into high-containment facility design, biosafety cabinet design and function, biorisk assessment, and many other useful topics. The event included participants from the research, healthcare, veterinary and industry sectors.

ASM also hosted preconference training for select travel grantees who serve as the BioResource Center (BRC) Coordinators at their home institutions. The workshop provided the coordinators with tools to support the BRCs as robust platforms for training, scientific exchange, and education. BRCs are established through partnerships between ASM and local institutions; they are dedicated spaces for the local scientific and health communities to access up-to-date resources and participate in continuing education opportunities and exchanges across the globe.

A prime example of an active BRC is the center at Mahidol University in Bangkok, Thailand. Under the leadership of the ASM Ambassador to Thailand, Chanwit Tribuddharat, and BRC Fellow Tossawan Jitwasinkul, the BRC hosts monthly virtual scientific lectures on current topics to engage the university community. While at A-PBA, ASM staff had the pleasure of visiting this BRC and meeting with Tribuddharat and Jitwasinkul. ASM was honored to participate in the Conference and continues to foster strong relationships with A-PBA and its member societies in support of ASM’s mission.
Reviews and Resources

BOOK

Philosophy of Microbiology

Is there really such an animal as a philosophy of microbiology? I am not convinced, but fortunately that is not what this book is about. Instead Maureen O’Malley, a philosopher with credentials in molecular science based at the University of Sydney, takes us on a tour of the “interdisciplinary space” where the interests of microbiologists meet and mesh with those of philosophers. The book is well written, not excessively technical, informative and at times eye-opening.

Historically, microbes played but a minor part in the formulation of biological concepts, and they are still apt to be regarded as marginal relative to the plants and animals. But that is changing, or ought to be. Half a century ago, microbes supplied powerful model systems for the most basic activities of living things, including heredity, energetics, and evolution. Today, developments emanating from microbiology are transforming the way we understand matters that have long been the concern of philosophers of science. Among the topics considered here in some detail are the classification of living things, the new tree of life with its three primary domains, the meaning of species, the enigmatic status of viruses, and what lateral gene transfer means for evolution. Some even argue that magnetotactic bacteria supply an elementary model for the way the mind holds a representation of the external world. Microbial ecology is opening new windows on biodiversity and on the role of communities in the operation of ecosystems. Our world is indeed microbial through and through, and on the role of communities in the operation of ecosystems. Our world is indeed microbial through and through, and therefore “philosophy should start with microbes as the entry point into biological reflection, and only subsequently focus on larger organisms” (p. 173). Amen! All this deserves to be much more widely appreciated, even by microbiologists, who tend to see their occupation chiefly in material terms.

If I may register a quibble, it would be that only in the final chapter does O’Malley take notice of the elephant in the room, and that most gingerly. If ours is a microbial world, with the higher organisms but relatively late accretions, then it must be microbes that hold the key to the deepest questions—what is life, is it a cosmic phenomenon or unique to this planet, how did it originate, and what meaning does it hold? It seems that modern philosophers, no less than microbiologists, prefer to see themselves as hard-headed, techno-savvy professionals that keep “free-floating cogitations” where they belong, down in the bar. The trouble is that if you persist in asking simple questions, it won’t be long before you reach the edge of the incomprehensible. Isn’t that what philosophy is ultimately about, to tackle the Big Questions? Perhaps in some future effort, Maureen O’Malley will take a deep breath and plunge in.

Franklin Harold
Seattle, Wash.
ASM-CDC Postdoctoral Research Fellowship. Postdoctoral scientists are encouraged to submit applications for 2014 ASM-CDC Postdoctoral Research Fellowships. Offered through the ASM-CDC Program in Infectious Disease and Public Health Microbiology, each fellowship is a two-year research experience under the mentorship of CDC scientists. The goal of the fellowship is to support the development of new approaches, methodologies, and knowledge in infectious disease prevention and control in areas within the public health mission of the CDC. All fellows perform research at a CDC location. Available fields of study include bacterial and mycotic diseases, viral and rickettsial infections, and HIV/AIDS.


American Board of Medical Microbiology (ABMM) Certification. Certifies the expertise of doctoral-level microbiologists seeking to direct public health or clinical microbiology laboratories. ABMM certification is achieved by passing an online multiple-choice exam that is offered daily in the month of June at testing centers worldwide.


ASM Robert D. Watkins Graduate Research Fellowship. Senior-level graduate students are invited to apply for the 2015 ASM Robert D. Watkins Graduate Research Fellowship. As part of its goal to increase the number of students from underrepresented minority groups who complete doctoral degrees in the microbiological sciences, the Watkins fellowship provides students with support to complete and present microbiology research. Fellows attend the ASM Kadner Institute for Graduate Students and Postdoctoral Scientists in Preparation for Careers in Microbiology (see below) or the ASM Scientific Writing and Publishing Institute (http://www.asmgap.org/) and, dependent on abstract submission and acceptance, are supported to present research at the ASM General Meeting.


ASM Kadner Institute. Senior-level graduate students and early-career postdoctoral scientists are invited to apply for the 2015 ASM Kadner Institute for Graduate Students and Postdoctoral Scientists in Preparation for Careers in Microbiology. Sponsored by the National Institute of Allergy and Infectious Diseases and the Burroughs Wellcome Fund, the institute will be held on 24–27 July in Washington, DC. Participants receive careful guidance and mentoring in key topics important for succeeding in the microbiological sciences: (i) career preparation and opportunities; (ii) preparation, review, and critique of research proposals; (iii) scientific presentations and communication; (iv) effective teaching methods; and (v) professional ethics development.


American Board of Medical Laboratory Immunology (ABMLI) Certification. Certifies the expertise of doctoral-level scientists seeking to direct laboratories engaged in the immunological diagnosis of human disease. ABMLI certification is the highest credential available to practicing medical laboratory immunologists and is recognized under CLIA ‘88 as one of the acceptable personnel requirements for high complexity laboratory directors. ABMLI certification is achieved by passing an online multiple-choice exam that is offered daily in the month of August at over 700 testing centers worldwide.


About Application Deadlines

The Application Deadlines section provides ASM members with information about certification programs, awards, and fellowships sponsored by ASM. More resources are available to members on the website at http://www.asm.org/index.php/awards-grants/whats-new-in-asm-awards-grants-fellowships-and-professorships.html. The website provides direct links to program Web pages for complete details, including eligibility requirements and application information.
ASM Meetings Calendar

9–11 February 2015.
ASM Biodefense and Emerging Diseases Research Meeting.
Washington, D.C.
WWW, http://www.asmbiodefense.org/

13–16 March 2015.
Mechanisms of Intercellular Cooperation and Competition.
Washington, D.C.
WWW, http://conferences.asm.org/

26–29 April 2015.
31st Clinical Virology Symposium.
Daytona Beach, Fla.
WWW, http://wwwclinicalvirology symposium.org/

8–11 May 2015.
Antimicrobial Resistance in Zoonotic Bacteria and Foodborne Pathogens.
WWW, http://conferences.asm.org/

ASM Conference for Undergraduate Educators.
Austin, Tex.
WWW, http://www.asmcue.org/

30 May–2 June 2015.
ASM General Meeting.
New Orleans, La.
WWW, http://gm.asm.org/

12–16 June 2015.
Prokaryotic Cell Biology and Development.
WWW, http://conferences.asm.org/

8–12 September 2015.
ASM Conference on Pseudomonas 2015.
Washington, D.C.
WWW, http://conferences.asm.org/

17–21 September 2015.
ICAAC/ICC Meeting.
San Diego, Calif.

1st ASM Conference on Rapid Next-Generation Sequencing and Bioinformatic Pipelines for Enhanced Molecular Epidemiologic Investigation of Pathogens.
Washington, D.C.
WWW, http://conferences.asm.org/

24–29 October 2015.
7th ASM Conference on Biofilms.
Chicago, Ill.
WWW, http://conferences.asm.org/

2–5 November 2015.
Chicago, Ill.
WWW, http://conferences.asm.org/

About the Calendar

The ASM Meetings Calendar is provided as a service to readers of Microbe. It includes annual meetings and conferences organized by the Society. Detailed information for these events is published in the ASM Meetings and Conferences insert, which appears bimonthly in the center of Microbe.

As an added benefit of membership in ASM, an online calendar of microbiology-related meetings hosted by ASM and by other organizations is available through the ASM website. Any organization may submit items for the online calendar provided that submissions are of obvious interest to microbiologists. ASM will not permit announcements to appear in the calendar when the subject matter and dates conflict with ASM meetings or workshops. The calendar is located at https://info.asm.org/index.php/meeting-and-event-calendar. All entries in the online calendar are limited to conference name, dates, location, website, and contact information (person, address, telephone, fax, and/or e-mail). When websites and e-mail addresses are provided, links to them will be established. Because of the volume of submissions received, ASM staff is unable to provide proofs or other confirmation of receipt of each listing. Submit items for the online calendar through the “Add a new event/deadline” link on the Meeting and Event Calendar page.
Employment

Employment Advertising

Microbe is published monthly and available to nearly 40,000 ASM members and institutional subscribers. Lead time for employment ads is about 3 weeks. Microbe is mailed around the 8th of the month of issue, but the delivery date is not guaranteed. Please consider delivery dates when setting application deadlines.

ASM does not accept classified advertisements that indicate a limitation, specification, or discrimination on the basis of race, religion, national origin, sex, mental or physical disability, age, or any other matters which may not be lawfully considered in making employment decisions. Employment notices that discriminate against microbiologists on the basis of a particular board certification or doctoral degree will not be accepted. Such advertisements will be rejected unless it can be established that the position by state or federal law or regulation requires a specific board certification or doctoral degree.

Classified

Classified ads must be typed, double spaced, with normal sentence capitalization (capital and lowercase letters). Microbe cannot accommodate requests for extra capitalization, boldface type, or other text or layout enhancements in classified ads.

Include the name and telephone and fax numbers of a contact person for questions about your ad copy. Incorrectly typed ads or ads with application deadlines earlier than the 15th of the publication month requested cannot be guaranteed placement in that issue.

Classified ads should be sent (with payment) to Walchli-Tauber Group, 2225 Old Emmorton Road, Suite 201, Bel Air, MD 21015, attn: Rhonda Beamer, tel. (443) 512-8899x106; fax, (443) 512-8909; e-mail, rhonda.beamer@wt-group.com.

Rates:

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- 151–200 words $720
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- 301 words $3.45 per word

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For display ad Internet posting costs, please contact Rhonda Beamer at the address given above.

Display

Display advertising closes the 1st of the month preceding publication. For specifications, rates, and deadlines for display ads, contact Rhonda Beamer at the address given above.
Cases in Medical Microbiology and Infectious Diseases

Fourth Edition

Authors: Peter H. Gilligan, Daniel S. Shapiro, and Melissa B. Miller

Cases in Medical Microbiology and Infectious Diseases challenges students to develop a working knowledge of the variety of microorganisms that cause infections in humans. The cases are presented as “unknowns” and represent actual case presentations of patients the authors have encountered. Each case is accompanied by several questions to test knowledge in broad areas.

Cases in Medical Microbiology and Infectious Diseases is a proven resource for preparing for Part I of the National Board of Medical Examiners Exam and an excellent reference for infectious disease rotations.

This new fourth edition includes:

- An entirely new section, “Advanced Cases,” which includes newly recognized disease agents as well as highly complex cases where the interaction of the immune system and human pathogens can be more closely examined
- A revised “Primer on the Laboratory Diagnosis of Infectious Diseases” section that reflects the increasing importance of molecular-based assays
- Forty-two new cases that explore the myriad advances in the study of infectious disease in the past decade
- Thirty-two updated cases that reflect the current state of the art as it relates to the organism causing the infection

“A uniquely practical text that presents the diagnostic, pathogenic, prevention, therapeutic and public health aspects of clinical microbiology in the context of case based presentations. An essential resource for training the clinical microbiologist, pathology resident and infectious disease fellow.”

- David W. Craft PhD, Medical Director of Microbiology, Penn State Milton S. Hershey Medical Center

Sep 2014. 604 pages, full-color illustrations, index.  
List and ASM member price: $80

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Self-Assembly For Me
http://schaechter.asmblog.org/schaechter/2014/08/self-assembly-for-me.html
by Elio

I have the grating feeling that the subject of self-assembly of complex biological structures may not always amass the level of respect it deserves, even though its importance is generally appreciated. This is one of the most magnificent aspects of biology, one that beautifully combines logic with mechanics and attests forcibly to the power of evolution. And it goes back a ways. The pioneering study on the self-assembly of phages played an integral role in the development of molecular biology.

Today, the assembly of the bacterial flagellar motor rates high on the list of exciting self-assembly phenomena, possibly vying with that of viral structure. The motor, a key constituent of bacterial flagella, is located at the flagellar base, where it both anchors and rotates the flagellum. The assembly of its many components constitutes an amazing engineering feat. One of the earliest indications of its complexity goes back to a 1971 paper by DePamphilis and Adler in which they convincingly showed that flagella have an intricate base, consisting of several rings presumed to anchor the flagellum to the bacterial envelopes in a rotor-stator arrangement. This structural design for a molecular machine delightfully explained how flagella could both rotate and remain in place.

Later came imaging techniques of previously unimaginable power, such as electron cryotomography, a way to reveal the 3D arrangements in unfixed biological material under the electron microscope. This is somewhat analogous to a CAT scan but instead of the optical sections being parallel, they are produced by tilting the specimen at various angles. When combined with computerized analysis of single images (electron cryotomography and subtomography averaging), one can observe structures at “macromolecular” (several nanometer) resolution. In other words, in exquisite molecular detail. The elements of the flagellar motor, the various rings, the center rod, the stator component, and what is known as the export apparatus, are now revealed in glorious detail. It’s like looking at the wheel assembly of a car reduced about 10 million-fold.

Now comes a surprise. One would expect such a complex structure to be the product of a single uncommon event in evolution, consequently to be alike in different bacterial species. Not so. A most exciting detailed analysis of 11 different species shows that although the basic plan is the same, these tiny machines vary considerably in detail. Their elements differ in curvature and in positioning relative to the axis. True, the species chosen included an assortment of flagellar arrangements, the flagella being polar in some, peritrichous in others, and in yet others encased in the periplasm. One can well imagine that such variations might require specially adapted machinery. Nevertheless, this finding does reveal a great degree of plasticity in the way flagellar motors are structured. Isn’t this amazing?

Self-assembly requires a high degree of “smartness” by the molecules involved—a higher degree than found in our “smartphones” that are all but self-assembled. Not only must the whole bunch of molecules carry out their intended function, they must be able to join with others to form highly sophisticated, ultra-tiny machines. Even more fascinating is that this self assembling ability is self-evolved! If I were starting over and wanted to dedicate myself to molecular mechanisms, I would likely turn to the study of such smart molecules.

Talmudic Question of the Month*

Of the ~10^{30} prokaryotic cells on Earth, what proportion would you guess are viable (using your favorite criterion for viability)?


*We use this term to denote questions whose answers cannot be found by a Google search.
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From the American Society for Microbiology Press:

**PRINCIPLES OF MICROBIAL DIVERSITY**

JAMES W. BROWN, NORTH CAROLINA STATE UNIVERSITY

“Every speck of dust, drop of water, and grain of soil and each part of every plant and animal contain their own worlds of microbes.”

Designed as a key text for upper-level undergraduates majoring in microbiology, genetics, or biology, *Principles of Microbial Diversity* provides a solid curriculum for students to explore the enormous range of biological diversity in the microbial world. Within these richly illustrated pages, author and professor James W. Brown provides a practical guide to microbial diversity from a phylogenetic perspective in which students learn to construct and interpret evolutionary trees from DNA sequences. He then offers a survey of the “tree of life” that establishes the necessary basic knowledge about the microbial world. Finally, the author draws the student’s attention to the universe of microbial diversity with focused studies of the contributions that specific organisms make to the ecosystem.

**AVAILABLE:** January 2015.
Paperback, 406 pages, full-color illustrations, glossary, index.
**PRINT:** 978-1-55581-442-7
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“We desperately needed a book that climbs the big tree, branch by branch, written both for undergraduates and as a reference. *Principles of Microbial Diversity* is that book!”

– JO HANDELSMAN
Howard Hughes Medical Institute Professor, Frederick Phineas Rose Professor, Department of Molecular, Cellular and Developmental Biology, Yale University

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