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Microbial Sciences Initiative

23rd Annual Microbial Sciences Symposium

Tuesday, December 8, 2026

1:00 - 7:00 pm

Northwest Building | Harvard University

Symposium Program

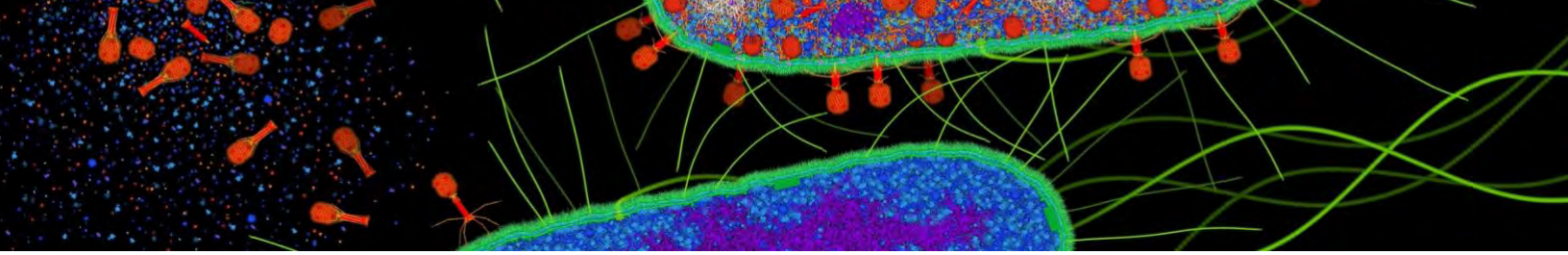
Image: "*Bacteriophage T4 Infection*" by David Goodsell

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Speaker Abstracts & Bios



Image: "*Bacteriophage T4 Infection*" by David Goodsell



Christina Warinner

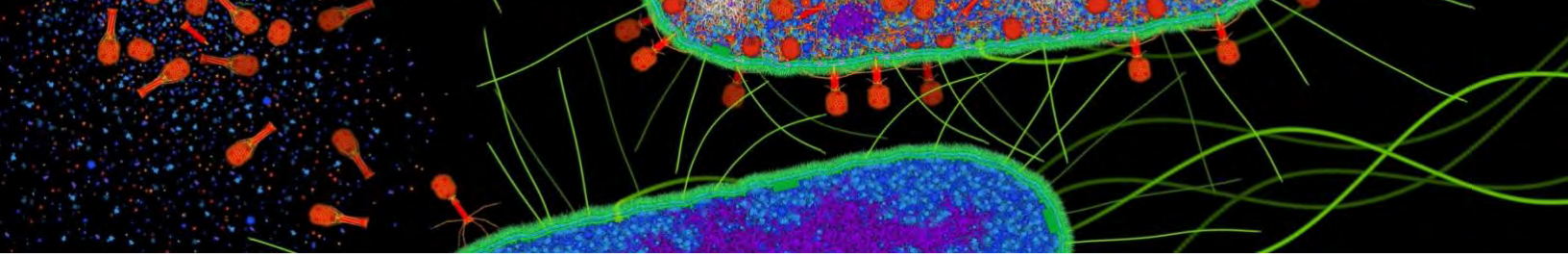


Landon T. Clay Professor of Scientific Archaeology, Departments of Anthropology and Human Evolutionary Biology, Harvard University

The archaeology of microbes and the future of lost genomes

Abstract: Humans have a deep and complex relationship with microbes. Beyond disease, microbes also profoundly shape human health and behavior through their activity in the microbiome and their diverse roles in food and cuisine. And yet we know very little about the origin, evolution, or ecology of the trillions of microorganisms that call us home. Recent advances in genomic and proteomic technologies are opening up dramatic new opportunities to investigate the complex and diverse microbial communities that have long inhabited our human bodies and our food systems - both in sickness and in health. From infectious disease to the microbiome, microbes are the invisible and often overlooked figures that have profoundly shaped human culture and influenced the course of human history. Focusing on the long arc of human-microbial relationships preserved by ancient DNA over the past 100,000 years, this talk explores how emerging research on pathogen evolution and the recent loss of commensal microbes is changing how we understand human health – both today and in the past.

About the speaker: Christina Warinner is the Landon T. Clay Professor of Scientific Archaeology in Departments of Anthropology and Human Evolutionary Biology at Harvard University, and she leads international research groups at the Max Planck Institute for Evolutionary Anthropology in Leipzig, Germany and the Leibniz Institute for Natural Products Research and Infection Biology in Jena, Germany. She is a member of the US National Academy of Sciences and the German National Academy of Sciences Leopoldina, and she is the recipient of the American Association for the Advancement of Science's Sussman Award for Scientific Contributions to Anthropology and the American Anthropological Association's Exemplary Cross-Fields Award. Warinner specializes in the analysis of ancient DNA and proteins, and her research focuses on the study of ancient biomolecules to better understand past human diet, health, and the evolution of the human microbiome. She is passionate about public education and outreach, and she co-created the Introduction to Ancient Metagenomics Summer School and the Adventures in Archaeological Science coloring book, now available in more than sixty languages. Her TED Talks have been viewed more than 2 million times, and she has been featured in documentaries produced by PBS NOVA, Netflix, and the genome sequencing company Illumina. She is engaged in the open science movement, and her research group has been actively involved in improving scholarly communication, data sharing, and research transparency.



Benjamin Wolfe

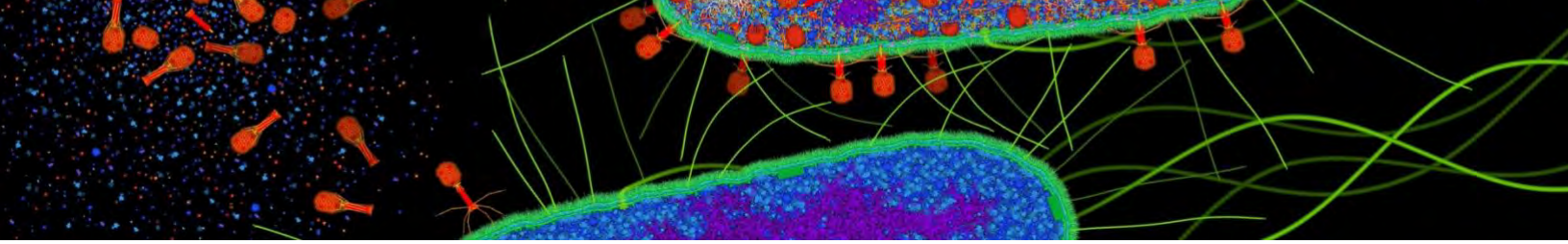


Associate Professor, Department of Biology, Tufts University

Ecology and evolution of fermented food microbiomes

Abstract: Sequencing technologies have allowed microbiologists to rapidly map patterns of microbial diversity across our planet. But we still know surprisingly little about the processes that generate these patterns. My lab uses fermented food microbiomes, simple and reproducible communities that we can take apart and rebuild in the lab, to identify the ecological and evolutionary processes that control microbial diversity. In this seminar, I will describe how dispersal, biotic interactions, and diversification shape microbial community assembly across a range of your favorite ferments, including sourdough bread, kimchi, and cheese. I will highlight how basic ecological and evolutionary principles can help solve quality and safety problems in fermented food production. Finally, I will explore how fermentation can be a powerful platform for improving microbial literacy in the classroom and in our communities.

About the speaker: Benjamin (Ben) Wolfe is an associate professor of microbiology at Tufts University, where he uses cheese, sourdough, kimchi, and other fermented foods to answer big questions in microbial ecology and evolution. Research in the Wolfe lab explores how microbial communities assemble, how species interact, and how microbes adapt to new environments. Ben also works closely with chefs, cheesemakers, and other food producers to understand how microbes shape the quality and safety of fermented foods. A passionate science communicator, Ben has written about food and microbes for Lucky Peach, Boston magazine, The Conversation, and World of Fine Wine. He co-founded the fermented-food education site MicrobialFoods.org with Bronwen Percival. He is co-editor-in-chief of the British Mycological Society journal Fungal Ecology, a senior editor at mSystems, and associate chair of the Department of Biology at Tufts. He earned his B.Sc. at Cornell and his Ph.D. at Harvard and did a postdoc at the Harvard FAS Center for Systems Biology before launching his lab in 2014.



Emily Balskus

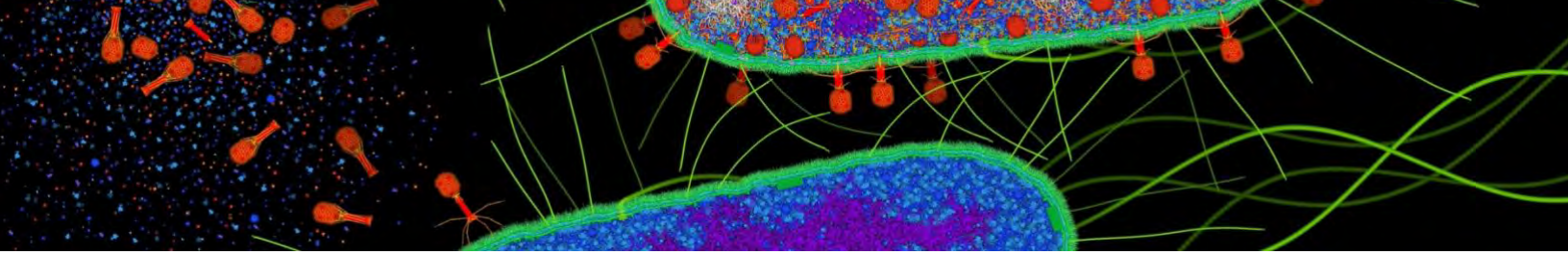


Thomas Dudley Cabot Professor of Chemistry, Department of Chemistry & Chemical Biology, Harvard University

Microbial enzymes: a catalyst for biological discovery

Abstract: The human body is colonized by trillions of microorganisms that exert a profound influence on human biology, in part by providing functional capabilities that extend beyond those of host cells. In particular, there is growing evidence linking chemical processes carried out by the human gut and vaginal microbiomes to various health outcomes ranging from cancer development to preterm birth. However, we still do not understand the vast majority of the molecular mechanisms underlying how the human microbiome influences host biological processes. Major obstacles faced in surmounting this knowledge gap include the difficulty linking functions associated with the human microbiome to specific microbial enzymes and the challenge of controlling these activities in complex microbial communities. This talk will discuss my lab's efforts to characterize metabolic activities from the human microbiome that are linked to health outcomes. I will show how gaining a molecular understanding of microbial metabolism in this setting not only advances our fundamental understanding of biochemistry but is also provides a powerful starting place for biological discovery and therapeutics development.

About the speaker: Emily is originally from Cincinnati, Ohio. She graduated from Williams College in 2002 as valedictorian with highest honors in chemistry. After spending a year at the University of Cambridge as a Churchill Scholar in the lab of Prof. Steven Ley, she pursued graduate studies in the Department of Chemistry and Chemical Biology (CCB) at Harvard University, receiving her PhD in 2008 with Prof. Eric Jacobsen. From 2008–2011 she was an NIH postdoctoral fellow at Harvard Medical School in the lab of Prof. Christopher T. Walsh. She also received training in microbial ecology and environmental microbiology as a member of the Microbial Diversity Summer Course at the Marine Biology Lab at Woods Hole in 2009. Emily joined the CCB faculty in 2011 and is currently the Thomas Dudley Cabot Professor of Chemistry and a Howard Hughes Medical Institute Investigator. She is also an Institute Member of the Broad Institute of Harvard and MIT. Her research focuses on deciphering microbial metabolism and its role in complex microbial ecosystems like the human gut microbiome. Using chemical knowledge and tools, Emily and her group seek to discover new microbial enzymes and metabolites as well as elucidate their biological roles.



Rebecca Sherbo

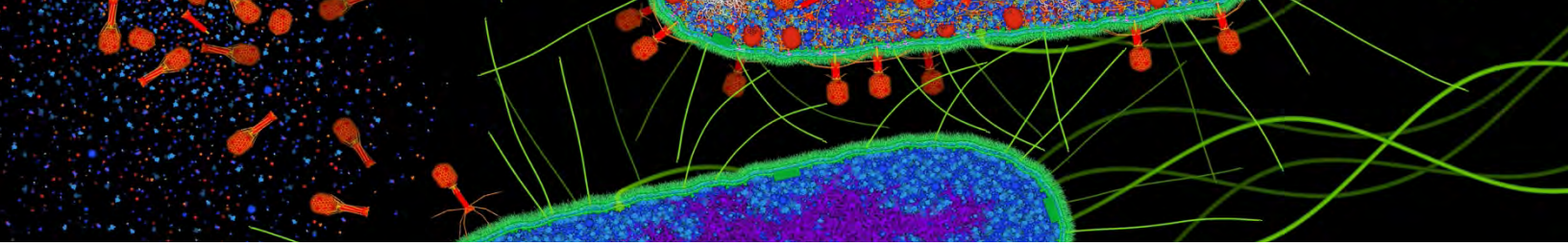


Assistant Professor, Departments of Chemistry & Chemical Biology and Chemical Engineering, Northeastern University

Creating sustainable fertilizers and foods with a Carbon- and Nitrogen-fixing microbe

Abstract: CO2 reduction through the Calvin cycle and N2 reduction by nitrogenase enzymes are essential biological processes that sustain life by converting inorganic gases into biomolecules. Despite their importance, these two pathways rarely coexist in a single organism – carbon fixation depends on O_2 as an electron acceptor while nitrogenase is inactivated by O_2, and both processes have extremely high energy demands. Here, we use the microbe *Xanthobacter autotrophicus*, a hydrogen-oxidizing bacterium capable of both carbon and nitrogen fixation, as a model system to better understand and engineer this unique metabolic capability. I will present a set of genetic engineering tools that allow us to manipulate and probe the metabolism of this organism. I will explore how the bacterium balances these two energy-intensive processes and how its metabolism shifts when fixing CO_2 alone, N_2 alone, or both simultaneously. Finally, I will demonstrate how these pathways can be used for creating valuable products such as sustainable fertilizers and foods.

About the speaker: Rebecca Sherbo is an Assistant Professor of Chemistry & Chemical Biology and Chemical Engineering and Northeastern University. Rebecca received her Ph.D. from the University of British Columbia in electrochemistry and performed postdoctoral research at Harvard University in synthetic biology. Her group focuses on using biological and electrochemical methods to convert waste and abundant starting materials into fertilizers, foods, and fuels.



Jennifer Bhatnagar

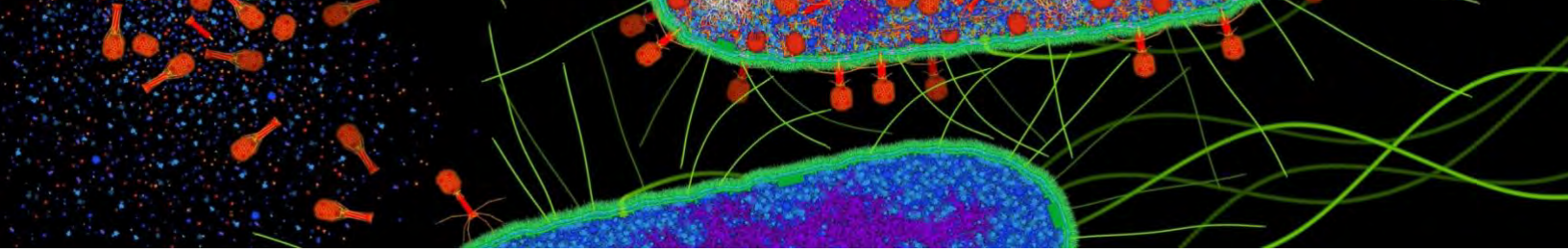


Associate Professor, Department of Biology, Boston University

Disruption of the urban tree microbiome

Abstract: Urban areas have expanded worldwide and are projected to continue growing, causing habitat fragmentation and amplifying already extreme environmental changes, such as high air temperatures, rates of pollution deposition, drought. Tree microbiomes are being reshaped by urbanization and we are just beginning to understand the potential consequences to urban ecosystems, to society, and to the Earth system. This talk will describe what we know about urbanization impacts on the microbiome of trees and what new research is revealing about the alternative rules by which these microorganisms live and shape city ecosystems. We focus on lessons learned from a model urban-to-rural oak tree gradient in the state of Massachusetts, where we have co-analyzed trees, their microbiome, and biogeochemical cycles for the past decade.

About the speaker: Jenny M. Bhatnagar is an Associate Professor in the Department of Biology at Boston University, where she serves as Director of the Biogeoscience Graduate Program and Associate Chair of the Ecology, Behavior, and Evolution research group. Dr. Bhatnagar is a microbial ecologist and biogeochemist, recognized for her work on the biogeography and nutrient cycling activities of soil microorganisms. Her research focuses on identifying patterns of microbial abundance and activity in forests and understanding how human-induced global changes – such as warming, elevated carbon dioxide in the atmosphere, nutrient pollution, and urbanization – impact microbial activity in soils and plants at the molecular, community, and landscape levels. Dr. Bhatnagar serves on the Department of Energy Environmental Molecular Sciences Laboratory Science & Technology Advisory Committee is a member of the Committee of Scientists at the Hubbard Brook Experimental Forest. She has faculty appointments in the Molecular Biology & Biochemistry Ph.D. program at BU and is a core member of the Bioinformatics Ph.D. Program, the URBAN Graduate Program, and the Institute on Global Sustainability. She is a recipient of the Scholar Award from P.E.O. International, the Murray F. Buell Award from the Ecological Society of America, the Early Career Award from the Soil Ecology Society, the Charles Bullard Fellowship in Forest Research from Harvard University, and the Patricia McLellan Leavitt Research Award for the promotion of women in science.



Fatima Aysha Hussain

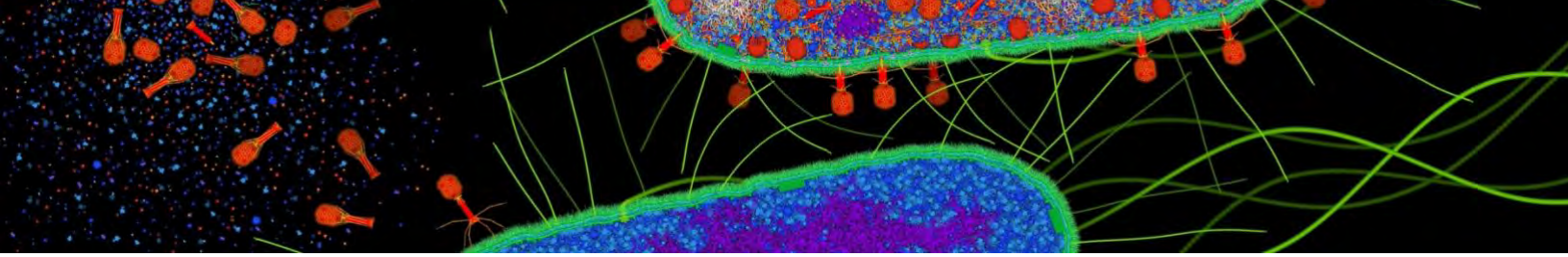


Assistant Professor, Department of Biology, Tufts University

Ecologically-informed microbial therapies for vaginal health

Abstract: *Lactobacillus*-dominant vaginal microbiomes, in contrast to multi-species communities composed of diverse anaerobes, are associated with lower inflammation, reduced risk of sexually transmitted infections, and improved reproductive health outcomes. Despite these strong links to human health, we still do not understand the factors that determine whether vaginal microbial communities remain lacto-dominant or transition to diverse states associated with bacterial vaginosis. Much of what we know about the vaginal microbiome comes from species-level profiling methods that cannot capture the substantial strain-level genomic diversity. In this talk, I present an ecological and evolutionary approach for understanding how microbial interactions shape vaginal microbiome dynamics and how these insights can inform the design of microbial therapies. I will highlight results from the first double-blind, placebo-controlled clinical trial of vaginal microbiota transplantation (VMT) for recurrent bacterial vaginosis, which demonstrates that VMT can shift recipient microbiomes toward donor-like states and restore *Lactobacillus crispatus* dominance in a subset of individuals. I will also present recent work from my lab investigating strain-level ecological interactions among vaginal microbes, including bacteriocin-mediated antagonism and prophage dynamics in *L. crispatus*. Together, these studies illustrate how phage–bacteria and bacteria–bacteria interactions, as well as within-host evolution during colonization, shape microbial diversity. By integrating strain-resolved genomics, experimental microbiology, and clinical studies, our work aims to establish a mechanistic framework for the ecological and evolutionary processes that structure the vaginal microbiome and to inform the development of next-generation, ecologically-informed microbial therapeutics for vaginal health.

About the speaker: Dr. Fatima Aysha Hussain is an Assistant Professor of Biology at Tufts University. She received her PhD from MIT, where she investigated bacteriophage-driven evolution of marine Vibrio. For her postdoctoral work as a Schmidt Science Fellow at the Ragon Institute and Massachusetts General Hospital, she pivoted to clinical human microbiome research, focusing on probiotic design and vaginal microbiota transplants for treating bacterial vaginosis. Now, in her lab at Tufts University, she investigates the ecological and evolutionary mechanisms that shape the vaginal microbiome and leverages these insights to uncover design principles for microbial therapies.



Ruaidhrí Jackson

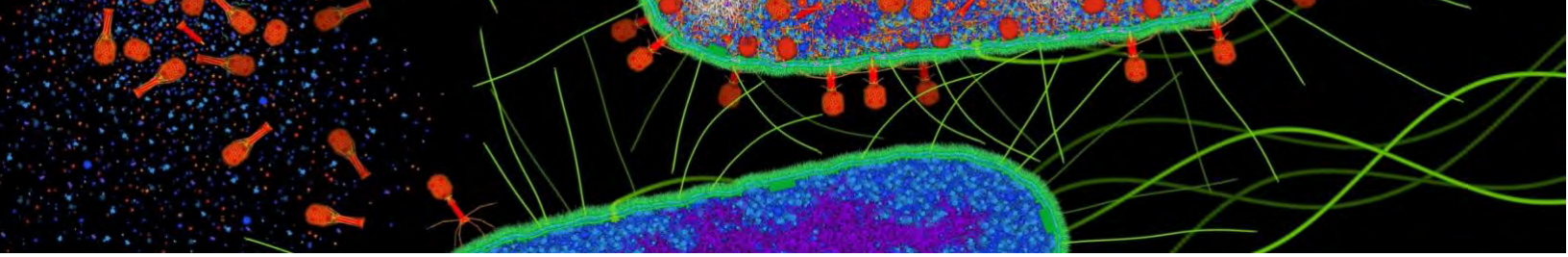


Assistant Professor, Department of Immunology, Harvard Medical School

Intrinsic immunological brains fight microbes at the mucosal barrier

Abstract: The enteric nervous system coordinates gut physiology and regulates local immune responses. We show that enteric neuron–derived IL-18 promotes goblet cell antimicrobial defenses against Salmonella. Mechanosensory enteric neurons adjust gut motility and limit inflammation in experimental colitis, raising the possibility that these circuits also influence autoimmune inflammation. We further identify a role for enteric neurons in shaping immune responses to colorectal tumors.

About the speaker: Ruaidhrí Jackson is an Assistant Professor in the Department of Immunology at Harvard Medical School. He received his Ph.D. in Immunology from the National University of Ireland Maynooth under the mentorship of Dr. Paul Moynagh, where he studied the role of E3 ubiquitin ligases in Toll-like receptor signaling. He completed his postdoctoral fellowship in Dr. Richard Flavell's laboratory at Yale University, investigating non-canonical translation, mechanosensation, cytokine biology, and enteric neuroinflammation in mucosal immunity. Dr. Jackson's independent laboratory focuses on illuminating the immune system's "dark genome" by uncovering previously unannotated transcriptomic and proteomic elements that shape host defense. His work integrates RNA biology, neuroimmunology, and mechanobiology to define how sterile environmental cues, particularly mechanical forces, and novel neuro-immune interactions regulate infection, autoinflammation, and cancer. His research has been recognized with several prestigious awards, including the Paul Allen Distinguished Investigator Award and the NIH Director's New Innovator Award.



Bill Hanage



Professor, Department of Epidemiology, Harvard T.H. Chan School of Public Health

Needles in haystacks: metagenomics for infectious disease epidemiology

Abstract: Many infectious agents are far more common that the headline figures would suggest, because many of them either colonize and transmit without noticeable symptoms or any resulting infections are very mild. This means we find it hard to measure just how often we are exposed to them, and the risk factors that determine the outcome of that exposure. However, interest in the microbiome has led to enormous collections of metagenomic data which can be mined to detect the presence of specific pathogens and offer an alternative measure of exposure. We will discuss ways of doing so, detecting pathogens to the level of individual strains, and how this can be applied to infections from Covid to Strep and beyond.

About the speaker: Bill Hanage is Professor of Epidemiology in the Center for Communicable Disease Dynamics at the Harvard T.H. Chan School of Public Health. His research combines genomic data with theoretical and laboratory approaches to study the evolution and epidemiology of infectious disease, with particular attention to how pathogens respond to interventions such as vaccines and antimicrobials. His work spans bacteria, notably the pneumococcus, and viruses, including SARS-CoV-2, where he has examined transmission, the impact of vaccination in the context of variants, and evolution within individual hosts. He is a frequent public commentator on infectious disease and related topics, for outlets including the New York Times, Washington Post and the Guardian.

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Poster Abstracts

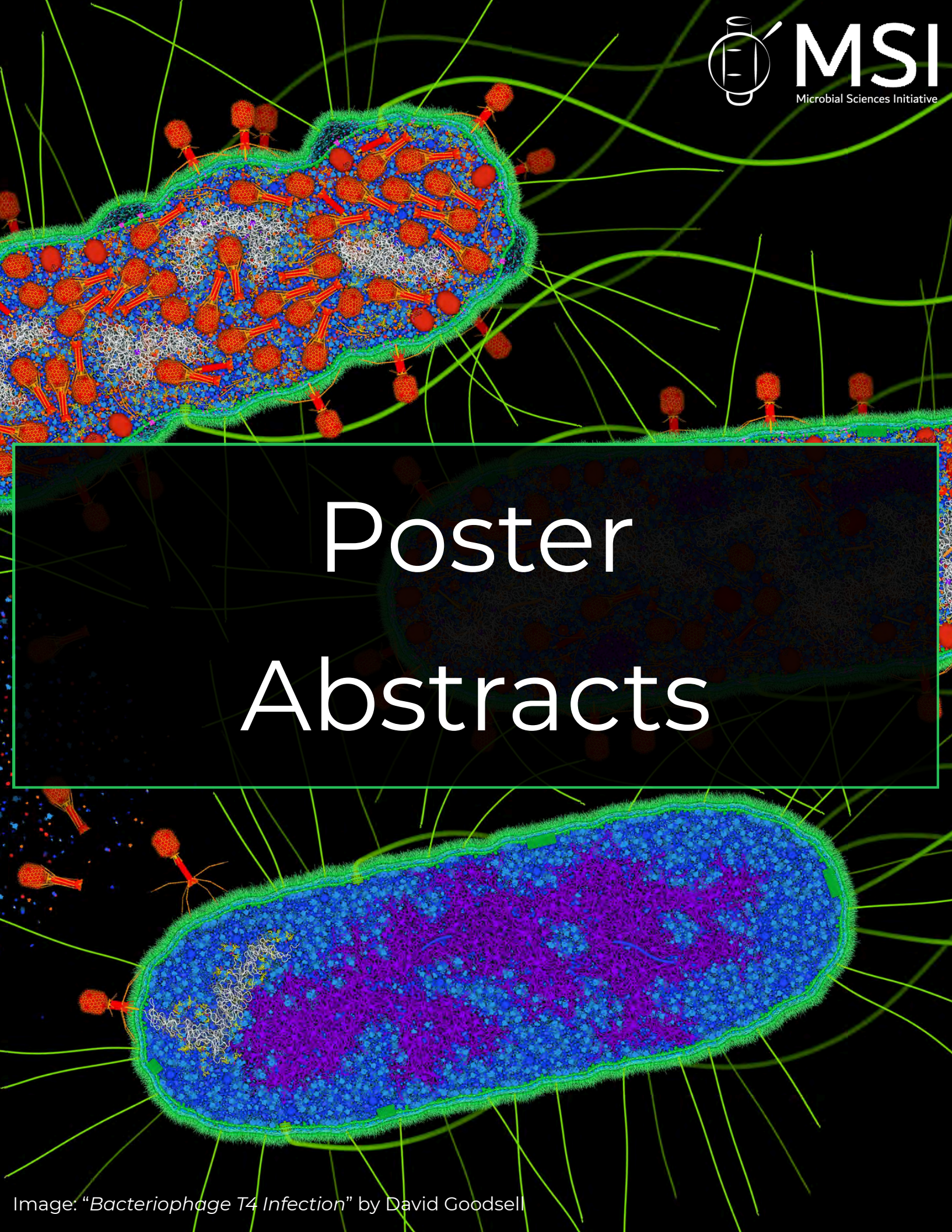


Image: "*Bacteriophage T4 Infection*" by David Goodsell

1. PTPRS mediates invasion of tetanus neurotoxin into the central nervous system

Pengsheng Chen[1,2,3†,] Huan Wang[1,2,3†,] John Manion[1,2,3,4], Jonas Zähringer [5,6], Junjie Liang[1,2,3], Aisha Mohammed[1,2,3], Leo Zhao[1,2,3], Jie Zhang[1,2,3], Yuankai Wang[1,2,3], Kang Wang[1,2,3], Pyung-Gang Lee[1,2,3], Geoffrey Masuyer[7], Karla J.F. Satchell[8,9], Joseph S. Brunzelle[8,10], Taekjip Ha[5,6], Pål Stenmark[7,11], Min Dong[1,2,3]*

1. Department of Urology, Boston Children's Hospital, Boston, MA, USA
2. Department of Surgery, Harvard Medical School, Boston, MA, USA
3. Department of Microbiology, Harvard Medical School, Boston, MA, USA
4. Department of Microbiology and Molecular Genetics, University of Pittsburgh School of Medicine, PA, USA
5. Program in Cellular & Molecular Medicine and Howard Hughes Medical Institute, Boston Children's Hospital, Boston, MA, USA
6. Department of Biological Chemistry and Molecular Pharmacology, Harvard Medical School, Boston, MA, USA
7. Department of Biochemistry and Biophysics, Stockholm University, SE-106 91 Stockholm, Sweden
8. Center for Structural Biology of Infectious Diseases, Northwestern University Feinberg School of Medicine, Chicago, IL, USA
9. Department of Microbiology-Immunology, Northwestern University Feinberg School of Medicine, Chicago, IL, USA
10. Life Sciences Collaborative Access Team, Synchrotron Research Center, Northwestern University, Evanston, IL, USA
11. Science for Life Laboratory (SciLifeLab), Stockholm University, Stockholm, Sweden

Keywords: *Host-microbe interaction; Molecular mechanisms; Pathogenesis; Toxins/virulence factors;*

Other keywords: Tetanus neurotoxin; retrograde transport; central nervous system

Tetanus neurotoxin (TeNT) invades the central nervous system (CNS) via retrograde transport through motoneurons. Whether a host factor is needed to mediate TeNT trafficking has remained unknown. Here, using pull-down and mass spectrometry analysis, and by developing a luciferase-based in vivo transport assay, we identify receptor protein tyrosine phosphatase sigma (PTPRS, PTPσ) as the retrograde transport receptor for TeNT. Global or motoneuron-specific PTPRS knockout (KO) abolishes TeNT entry into the CNS in mouse models. PTPRS-TeNT interactions occur in endosomes, prevent toxin translocation, and direct TeNT trafficking in neurons. Structural studies establish that TeNT light chain and belt region bind to the immunoglobulin domain of PTPRS; disrupting their interactions blocks TeNT trafficking into the spinal cord and a PTPRS-binding-deficient TeNT mutant induces botulism-like flaccid paralysis. Thus, PTPRS is the host factor mediating TeNT trafficking into the CNS, revealing a targetable pathway for post-entry intervention and for drug delivery into the CNS.

2. Host Factors, Genomic Features, and Clinical Outcomes in Bacterial Keratitis

Inès Fenniri, MD, MSc[1, 2, 3]; Andrew Van Camp, MS[4]; Jiyoun Roh, AB[5]; Jiachen Sun, BA[5]; Istabraq Musa, BS[5]; Anjeli Macaranas, AB[5], Michael S. Gilmore, PhD[1,2]; Thomas H. Dohlman, MD[1,3]; Camille André, PharmD, PhD[1],[2]

1. Department of Ophthalmology, Massachusetts Eye and Ear, Harvard Medical School, Boston, MA, USA
2. Infectious Disease Institute, Massachusetts Eye and Ear, Harvard Medical School, Boston, MA, USA
3. Department of Ophthalmology, Boston Children's Hospital, Harvard Medical School, Boston, MA, USA
4. Bioinformatics and Integrative Genomics, Harvard Medical School, Boston, USA
5. Harvard Medical School, Boston, MA, USA

Keywords: *Host-microbe interaction*

Importance: Linking bacterial genomes to clinical records may clarify the host contexts and forms of morbidity associated with bacterial keratitis. Objective: To compare presentation and outcomes across four bacterial species and examine clinical associations with host and genomic features. Design, Setting, and Participants: Retrospective cohort study of 188 distinct adults with culture-confirmed bacterial keratitis at Massachusetts Eye and Ear between 2014 and 2017. Exposures: Bacterial species, documented host risk factors, and within-species genomic features. Logistic regression included age, host risk-factor count, and species. Exploratory genomic comparisons underwent Benjamini–Hochberg correction. Main Outcomes and Measures: Clinical failure, defined as final best-corrected visual acuity (BCVA) ≥1.0 logMAR, post-presentation perforation, therapeutic penetrating keratoplasty, or enucleation/evisceration. Results: The cohort included 71 *Pseudomonas aeruginosa*, 75 *Staphylococcus aureus*, 20 *Streptococcus pneumoniae*, and 22 *Staphylococcus epidermidis* episodes; median age was 58 years, and 110 patients (58.5%) were women. Clinical failure occurred in 61/132 evaluable episodes (46.2%). *S. pneumoniae* had the poorest median final BCVA (2.30 logMAR) and highest observed failure proportion (10/11 [90.9%]); *S. epidermidis* had the highest frequency of structural failure (9/20 [45.0%]) and therapeutic keratoplasty (8/20 [40.0%]). Older age and greater host risk-factor burden were associated with failure after adjustment for species (adjusted odds ratios, 1.66 per decade and 1.51 per additional factor). Exploratory associations retained after multiplicity correction involved mecA detection and failure in *S. epidermidis*, MRSA CC5 and hospitalization and treatment duration, and exoS/exoU profiles and reported swelling in P. aeruginosa. Neither exotoxin gene was significantly associated with clinical failure. Conclusions and Relevance: Integrating clinical and genomic data distinguished species-specific host contexts and patterns of visual loss, structural complications, and treatment burden. Genomic associations identified candidate features for further clinical investigation.

3. Polyethylene nanoplastics impair MSR1-mediated bacterial uptake by macrophages

Fran Prenen[1,2], Madeline Bono[1,2], Veronica Hsu[1,2], Matthew J.G. Eldridge[3], Allie Lipshutz[4,5], Sophie Helaine[3], Edward T. Chouchani[4,5], Evanna Mills[1,2]

1. Department of Cancer Immunology and Virology, Dana-Farber Cancer Institute, Boston, MA, USA
2. Department of Immunology, Harvard Medical School, Boston, MA, USA
3. Department of Microbiology, Harvard Medical School, Boston, MA, USA
4. Department of Cancer Biology, Dana-Farber Cancer Institute, Boston, MA, USA
5. Department of Cell Biology, Harvard Medical school, Boston, MA, USA

Keywords: *Host-microbe interaction; Microscopy/imaging; Pathogenesis*

Nanoplastics are increasingly detected in human tissues, yet how they interact with cells to influence disease remains poorly understood. Here, we show that polyethylene nanoplastics selectively impairs phagocytosis of Gram-positive bacteria by mouse and human macrophages. Proteome integral solubility alteration profiling identified macrophage scavenger receptor 1 as a protein target of polyethylene nanoplastics. Disrupting macrophage scavenger receptor 1 or its bacterial ligand, lipoteichoic acid, abolished the effect of nanoplastics on bacterial uptake. Nanoplastics did not impair bacterial binding but disrupted pathogen-induced actin remodeling and subsequent internalization, revealing a specific defect in phagocytosis. In mice, nanoplastic exposure impaired bacterial uptake by liver macrophages and exacerbated systemic infection. These findings reveal that nanoplastics can perturb specific host–pathogen interactions, providing a mechanism linking environmental nanoplastic exposure to impaired antibacterial defense.

4. A high-throughput method to elucidate mechanisms of microbial competition

Alexandra Surrette, Marcus Tran

Wheaton College, Norton, MA, USA

Keywords: *Antibiotics; Microbial ecology*

Microbes live in constant competition for space and nutrients. Thus, they have evolved several mechanisms by which to kill potential competitors. In this work, we report the development of a high-throughput method to identify genes required for microbial competition. We use *Burkholderia vietnamiensis* as a model to demonstrate this technique. *B. vietnamiensis* is a soil bacterium with an ability to kill the yeast *Saccharomyces paradoxus*. To identify genes responsible for yeast killing, we first performed transposon mutagenesis to generate a mutant library of *B. vietnamiensis*. Next, we developed a replica plating-based system to screen for mutants no longer capable of killing S. paradoxus. Finally, transposon insertion sites were identified using inverse PCR and Sanger sequencing. Assuming plasmid and media compatibility, this method could be easily adapted to study microbial competition in a wide range of microbes.

5. Soil isolates produce antibiotics targeting Gram-positive bacteria

Cole Richardson-Beatty, Oliver Updyke, Noelle Swigor, Destiny Duarte

Wheaton College, Norton, MA, USA

Keywords: *Antibiotics; Microbial Ecology*

Infectious diseases are a global public health challenge, which is exacerbated by the rise of antimicrobial resistance. In this work, we isolate two antibiotic-producing bacteria isolated from a soil sample from Wheaton College. We find that these bacterial strains specifically target Gram-positive bacteria. Furthermore, partial sequencing of the 16S rRNA gene identified these strains as *Streptomyces* and *Kitasatospora* species. Our future goal is to sequence the genome of both strains to identify potential antibiotic production genes.

6. Energy Landscapes Drive Microbial Metabolic Function in a Brine-Dominated Hydrothermal Vent System

Avery H. Fulford[1,2], Teodora Zhivkova[1], Paloma Lopez[1], Matt McIlvin[1], Mak Saito[1], Stefan M. Sievert[1], Jeffrey S. Seewald[1], and Julie A. Huber[1]

1. Woods Hole Oceanographic Institution, Woods Hole, MA, USA
2. Massachusetts Institute of Technology, Cambridge, MA, USA

Keywords: *Anaerobes; Archaea; Bioinformatics; Microbial Ecology; Genomics*

Brine-dominated deep-sea hydrothermal vents form when phase separation generates high-salinity brines that can discharge rapidly or accumulate in subseafloor reservoirs for decades before venting. Elevated chlorinity in hydrothermal fluids results in enhanced mobilization of heavy metals, particularly high dissolved iron concentrations that may precipitate as pyrite upon cooling, generating H2. Despite their distinctive geochemistry, the biogeochemical fluxes and microbial communities at brine-dominated vents remain poorly constrained.

We investigated microbial communities associated with brine-dominated venting along the Northern and Southern Cleft Segment of the Juan de Fuca Ridge (NE Pacific Ocean), where two vent fields with distinct source fluids provide a natural experiment across spatial and temporal scales. Across nine hydrothermal chimneys and nine diffuse-flow vents, we integrated a comprehensive geochemical dataset with 16S rRNA gene sequencing, metagenomics, and metaproteomics to link microbial activity with environmental energetics at mineral-fluid interfaces. Analysis of 16S rRNA gene data showed distinct clustering between Northern and Southern chimney communities. Chimney exteriors hosted sulfur-disproportionating *Dissulfuribacteraceae* and iron-oxidizing *Zetaproteobacteria* and *Gallionellaceae*, while strong geochemical evidence of H2 generated by pyrite formation in the hot inner chimney supported putative methanogenic and sulfate-reducing taxa. Diffuse-flow vent samples were dominated by iron-, sulfur-, and nitrogen-cycling taxa, particularly *Thioglobaceae* (SUP05). Ongoing metagenomic and metaproteomic analyses integrate the prevalence of metabolic genes and proteins expressed at the time of sampling with thermodynamic modeling, linking genetic potential with realized microbial function under in situ geochemical constraints.

7. FILM: AI-Powered Infrared Spectroscopy for Rapid Single-Cell Bacterial Identification

George Abu-Aqil, Meng Zhang, Dashan Dong, Ji-Xin Cheng

Boston University, Boston, MA, USA

Keywords: *Antibiotics; Biophysics; Microscopy/Imaging*

Multidrug-resistant (MDR) bacterial infections represent one of the most pressing global health challenges, driven in part by the widespread empirical use of broad-spectrum antibiotics. Conventional microbiological diagnostics typically require at least 48 hours to identify bacterial pathogens and determine their antimicrobial susceptibilities, with the first 24 hours dedicated solely to species-level identification. This diagnostic delay often necessitates empirical antibiotic treatment, contributing to inappropriate antibiotic use and the emergence of antimicrobial resistance. Here, we demonstrate a rapid, artificial intelligence (AI)-assisted platform that integrates fluorescence-detected infrared photothermal microscopy (FILM) with machine learning for single-cell bacterial identification. By capturing species-specific biochemical fingerprints through infrared vibrational spectroscopy, FILM enables label-based optical detection of molecular signatures that distinguish clinically relevant bacterial pathogens. Coupling these high-dimensional spectral fingerprints with machine-learning algorithms enables accurate classification of bacterial species without relying on conventional culture-based identification workflows. Our results demonstrate approximately 95% classification accuracy across common clinically relevant bacterial species, reducing the time required for species-level identification from approximately 24 hours to less than one hour. This substantial reduction in diagnostic time highlights the potential of AI-powered FILM as a rapid, high-accuracy platform for bacterial identification. By enabling earlier pathogen identification, this approach could facilitate more informed antimicrobial treatment decisions and lay the foundation for integrating rapid antimicrobial susceptibility testing, ultimately improving clinical management and efforts to combat antimicrobial resistance.

8. Robotics-Aided FILM Imaging of D_2O Metabolic Uptake for Rapid Single-Cell Antimicrobial Susceptibility Testing

Xiaoxue Liu, George Abu-Aqil, Dashan Dong, Meng Zhang, Ji-Xin Cheng

Boston University, Boston, MA, USA

Keywords: *Antibiotics; Biochemistry; Engineering; Microscopy/Imaging*

The rapid emergence of multidrug-resistant bacterial infections has created an urgent need for antimicrobial susceptibility testing (AST) methods that can guide treatment substantially faster than conventional culture-based workflows. Current AST methods rely on measurable bacterial growth after antibiotic exposure and typically require 24–48 hours to generate actionable susceptibility results. Here, we present a robotics-aided, single-cell metabolic imaging platform that combines fluorescence-detected infrared photothermal microscopy (FILM) with deuterium oxide (D_2O) incorporation to rapidly assess bacterial response to antibiotics. Bacterial cells are exposed to D_2O-containing media in the presence and absence of antibiotics, where metabolically active cells incorporate deuterium into newly synthesized biomolecules, producing a characteristic carbon–deuterium (C–D) vibrational signal within the cellular silent spectral window. Antibiotic-induced suppression of metabolic activity is quantified by measuring changes in D_2O incorporation at the single-cell level. A robotics-assisted workflow is used for automated sample preparation, antibiotic dispensing, and multi-condition plate handling, enabling standardized and scalable analysis across bacterial species and drug concentrations. Using this approach, we demonstrate rapid discrimination between susceptible and resistant bacterial responses based on metabolic inhibition, without requiring prolonged cell growth. By integrating automated sample processing with FILM-based D_2O metabolic imaging, this platform provides a pathway toward rapid, scalable, and phenotypic AST, with the potential to significantly shorten the time to targeted antibiotic therapy and improve management of multidrug-resistant infections.

9. MicroFuse: Protein-to-Genome Expert Fusion for Microbial Operon Reasoning

Seungik Cho

Department of Physics and Astronomy, Rice University, Houston, TX

Keywords: Bioinformatics; Genetics; Genomics; Microbial Ecology

Other keywords: Multimodal Learning; Biological Foundation Models; Protein Language Models; Operon Prediction; Computational Microbiology

Predicting microbial operon co-membership requires integrating two complementary biological signals: protein-scale molecular identity and genome-context organization. While recent biological foundation models provide powerful representations of each view independently, naive concatenation of these modalities ignores a key biological property -- protein identity and genomic context may agree when adjacent genes form a coherent functional module, or conflict when sequence similarity is misleading but genomic layout indicates independent regulation. We present MicroFuse, a protein-to-genome expert fusion framework that integrates structure-aware protein representations from ProstT5 with genome-context representations from Bacformer through a four-expert Mixture-of-Experts module (protein, genome-context, agreement, and conflict experts) with a learned soft router. Training combines binary cross-entropy with symmetric cross-modal InfoNCE alignment and disagreement-weighted supervised contrastive shaping. We further construct OG-Operon100K, a 100,000-pair scaffold-level benchmark from the OMG metagenomic corpus with biologically grounded positive and negative criteria. On OG-Operon100K, MicroFuse achieves the strongest AUROC, AUPRC, mAP, and mAR among ProstT5-only, Bacformer-only, and Concat MLP baselines. Ablations identify cross-modal contrastive alignment as the dominant component, and a hard sequence-conflict subset reveals MicroFuse's largest gains precisely in biologically ambiguous cases where protein identity alone is misleading.

10. Targeting Host Cells to Clear Infection With (S)-Crizotinib

Andrew Hearst[1,2], Joshua Price[1,2], Cristoph Ernst[3,4], Tianling Ou[6], Li Li[1,2], Shuting Zhang[6], Anne Clatworthy[1,2], Anna Zagieboylo[2,5,6], and Deborah Hung[2,5,6]

1.Department of Molecular and Cellular Biology, Harvard University, Cambridge, MA, USA
2.Department of Molecular Biology and Center for Computational and Integrative Biology, Massachusetts General Hospital, Boston, MA, USA
3. Institute for Medical Microbiology, Immunology and Hygiene, University Hospital Cologne and Faculty of Medicine, University of Cologne, Cologne, Germany
4. German Center for Infection Research (DZIF), Cologne, Germany
5. Department of Genetics, Harvard Medical School, Boston, MA, USA
6. Broad Institute of MIT and Harvard, Cambridge, MA, USA

Keywords: *Genetics; Host-Microbe Interactions; Pathogenesis; Therapeutics*

Antimicrobial Resistance (AMR) is a significant problem that is improperly addressed through the development of traditional therapeutics. As an alternative, Host-Directed Therapeutics (HDTs) offer theoretically unprecedented breadth of spectrum and lower the risk of AMR developing over time. Using a high-throughput screening method, our lab identified (S)-crizotinib, a small molecule that targets the endo-lysosomal pathway of infected hosts and engages with the sterol transporter NPC1 to clear intracellular infection of Gram-negative bacteria that persist in late endosomes. (S)-Crizotinib also clears SARS-CoV-2 viral infection from Vero E6 cells. Currently, it is unclear whether these demonstrated antibacterial and antiviral activities are two distinct phenomena, or if they are due to a single Mechanism of Action (MoA). Using a pseudovirus model of infection, we worked to define the spectrum and MoA of S-Crizotinib in a viral context to evaluate the hypothesis that (S)-crizotinib mediates bacterial and viral clearance through a single set of targets and a unified MoA.

11. Microbes on Mars? *Deinococcus radiodurans* survivability in Mars-like conditions

Yijar Ivy Lin, Rachel Harris, Peter Girguis

Department of Organismic and Evolutionary Biology, Harvard University, Cambridge, MA, USA

Keywords: Microbial Ecology

Other keywords: Extremophiles; Astrobiology

As interest in other worlds' past and present ability to support life has grown, astrobiologists have begun to study the performance of extremophilic Earth microbes in extraterrestrial conditions. One such bacteria is *Deinococcus radiodurans*, a highly radioresistant polyextremophile which has been shown to tolerate several conditions relevant to life on Mars, including: impact pressures associated with Earth-Mars asteroid transit, Martian surface temperature cycling, and Mars-like concentrations of highly oxidizing perchlorate salts. Despite *D. radiodurans'* demonstrated ability to remain viable in these conditions, it remains to be seen whether or not it can sustain growth when subject to the metabolic constraints of a Mars-like environment. We found that *D. radiodurans* maintains growth under several Mars-like conditions, including Mars-like perchlorate concentrations, atmospheric composition, and nutrient profile. However, growth rate and maximum OD were limited by all factors, except that perchlorates seemed to improve growth in a Mars-relevant nutrient profile. These results yield important consequences for planetary protection and Martian biogeoengineering.

12. Enrichment of *Lactobacillus crispatus* in the vaginal microbiome via selective β-glucosidase utilization

Samantha Bozorgzadeh[1], Dominick J. Jenkins[1], Jeremy M. Liang[1], Caroline M. Mitchell[2], Emily P. Balskus[1,3,#]

1. Department of Chemistry and Chemical Biology, Harvard University, Cambridge, MA, USA
2. Vincent Center for Reproductive Biology, Massachusetts General Hospital, Boston, MA, USA; Harvard Medical School, Boston, MA, USA
3. Howard Hughes Medical Institute, Harvard University, Cambridge, MA, USA
Corresponding Author

Keywords: *Anaerobes; Enzymology; Microbial Ecology; Microbiome*

Healthy vaginal microbiomes are typically dominated by non-iners *Lactobacillus* species, including *L. crispatus*. Communities dominated by *L. iners* may transition towards bacterial vaginosis (BV), which is associated with an increased risk of sexually transmitted infections and preterm birth. A prebiotic carbon source that is selectively utilized by health-associated *Lactobacillus* species could help enable probiotic colonization or support growth of endogenous *lactobacilli*. Using growth-based screening and community culture models, we identified prebiotic candidates that enrich beneficial species and shift community composition towards *Lactobacillus* dominance.

We screened nine vaginal isolates on 250 carbohydrates and identified 12 candidates from the β-glucoside, fructooligosaccharide, and raffinose oligosaccharide families that supported growth of non-iners lactobacilli. Genomic analysis with dbCAN3 identified several carbohydrate-active enzymes encoded by *L. crispatus* and absent from dysbiosis-associated species. This provides genotypic support for the selective utilization of these prebiotic candidates by *L. crispatus*.

In nine-member synthetic communities, all candidates increased the relative abundance of *L. crispatus* compared with glucose and glycogen controls. In an *L. iners*-dominated cervicovaginal fluid sample cultured ex vivo, prebiotic conditions selectively enriched endogenous health-associated species, *L. mulieris*, whereas glucose cultures remained *L. iners* dominated. In an ex vivo sample containing BV-associated bacteria, β-glucosides did not support their growth, resulting in lower biomass compared to glucose controls.

These results support leveraging carbohydrate utilization as a mechanism to shift vaginal bacteria community composition. Our prebiotic candidates not only support growth of health-associated lactobacilli but also do not support the growth of many BV-associated microbes.

13. Pan-Ras-In-1 triggers cell wall lysis to eradicate *Staphylococcus aureus*

Weihua Han, Yinjuan Guo, Li Shen, Yu Huang, Xinru Yuan, Bingjie Wang, Can Yang, Rongrong Hu, Yongpeng Shang, Fangyou Yu

Shanghai Institute of Immunity and Infection Chinese Academy of Science, Shanghai, China

Keywords: *Therapeutics*

Other keywords: Staphylococcus aureus; *Cell wall; Pan-Ras-In-1; Programmed cell death; CidA; TarA*

Given the global crisis of antimicrobial resistance, the dual anticancer and antibacterial properties of certain agents have attracted increasing attention as a potential alternative to conventional antimicrobial approaches. In this study, we characterized the bactericidal activity of an anticancer molecule (Pan-Ras-In-1) against *Staphylococcus aureus* (*S. aureus*), a pathogen associated with refractory infection. In vitro assays revealed that Pan-Ras-In-1 has a more pronounced bactericidal effect on *S. aureus* cells than the traditional antibiotics vancomycin and levofloxacin. Furthermore, Pan-Ras-In-1 displayed potential therapeutic efficacy in vivo, as assessed using the murine systemic infection and skin abscess models, suggesting its potential for subsequent clinical applications. Exposure of *S. aureus* to Pan-Ras-In-1 activates CidA-associated peptidoglycan hydrolase systems, which partially mediate bacterial programmed cell death. Peptide-centric local stability analyses revealed that Pan-Ras-In-1 binds to TarA protein, suppressing wall teichoic acid polymer production. The combined action of two mechanisms enables Pan-Ras-In-1 to compromise bacterial cell wall integrity.

14. Intestinal Mucin Architecture as a Driver of Gut Microbiota Health

Daniel Sellers[1], Reuben Allen[1], Olga Sokolovskaya[1], Jason Zhang[2], Katharina Ribbeck[1]

1. Department of Biological Engineering, Massachusetts Institute of Technology, Cambridge, MA, USA
2. Division of Gastroenterology, Hepatology and Nutrition, Boston Children's Hospital, Boston, MA, USA

Keywords: *Engineering; Microbial Ecology; Microbiome; Therapeutics*

Other keywords: Mucus

Gut microbiota composition and metabolic capacity are critical determinants of host health. While dietary carbohydrates are recognized as significant drivers of microbiota assembly, an equally important host-derived carbohydrate source remains underexplored: intestinal mucus. Mucins, the primary structural component of mucus, are carbohydrate-rich glycoproteins and major nutrient sources for the microbiota. Mucins are highly modular structures decorated with diverse glycans that vary in length, branching, linkage patterns, and terminal modifications. However, how mucins alone – in the absence of dietary carbohydrates – govern which microbes colonize and persist within complex communities is unknown. To address this, we developed an ex vivo human gut microbiota culture system with a chemically defined, carbohydrate-free base medium, testing communities from eight independent human donors. Via 16S sequencing, mucins supported substantially greater microbial diversity than individual dietary carbohydrates or mucin monosaccharides. Furthermore, mucins restored diversity to glucose-induced dysbiotic communities. Mucin enriched several health-associated commensals that cannot grow on mucin alone, most notably *Faecalibacterium prausnitzii*, implicating cross-feeding networks. Surprisingly, this *F. prausnitzii* enrichment was highly structure-dependent. *F. prausnitzii* was abundant in all communities fed intact mucins, yet was nearly undetectable in communities fed mucin monosaccharides or degraded commercial mucins. These results demonstrate that mucin glycan presentation, not composition alone, acts as an ecological driver of community assembly. We next aim to identify specific mucin features driving this selective niche, informing mucin-inspired strategies to restore host-microbiome homeostasis.

15. The Enemy of My Host: Evolutionary Conflict Between Mobile Genetic Elements

Mariam Elawady, Shreyas Pai, Kepler S. Mears, Sophia S. Wiesenfeld, Amy D. Zamora, Caspar S. Carson, Arya Kaul, Siân V. Owen, Michael Baym

Department of Biomedical Informatics, Harvard Medical School, Boston, MA, USA

Keywords: Bacteriophages; Microbial Evolution; Microbial Ecology

Evolutionary conflicts are well documented in nature, often between predators and prey, hosts and parasites, and even in intra-species contexts between mates and siblings. These conflicts are observed when the evolutionary interests of one organism are at direct odds with the interests of their competitor. Notably, these conflicts can drive Red Queen dynamics, in which populations undergo frequency-dependent fluctuating selection or a one-directional arms race. In an arms race, selection escalates, likely until the fitness costs of keeping up with one's competitor become too high. Alternatively, competition may favor diversification into multiple strategies, which could eventually contribute to speciation. While these dynamics have been observed in the microbial context, they are not well characterized between mobile genetic elements (MGEs). Two of these MGEs, broad host-range conjugative plasmids and plasmid-dependent bacteriophages, are at direct odds with each other, and thus an ideal system to study the evolutionary conflicts between MGEs. To do this, we utilize experimental evolution and sequence analysis to understand the dynamics and molecular mechanisms of coevolution between plasmids and plasmid dependent phages. This line of questioning involves serially passaging IncP-family plasmid pKJK5 and phage PRD1 through three bacterial hosts without evolving the hosts, isolating the evolution of the MGEs. Through this experiment, we have found instances of one directional arms races, Red Queen dynamics, and even examples of convergent evolution in both the plasmids and the phages. These dynamics have implications for the natural dynamics that exist between these MGEs, namely in the long term evolutionary trajectories of wild populations.

16. Immune imprinting and cross-protective immunity to H5N1

Selin Kubali [1], Passwell Munchooga [2], Hamoobe Munkombwe [2], Catherine Sutcliffe [3], Nichola Hill [1]

1. University of Massachusetts, Boston, Boston, MA, USA
2. Macha Research Trust, Zambia
3. Johns Hopkins University, Baltimore, MD, USA

Keywords: *Host-Microbe Interactions*

Other keywords: Viruses; Immunity

Influenza A is a diverse clade of viruses, and this diversity makes it difficult to predict what immune landscape a given strain will encounter. I am interested in human immunity to H5N1, one of the subtypes of influenza A known as 'bird flu'. H5N1 has caused massive outbreaks among poultry, dairy cattle, and wild animals in recent years. Humans have been infected with H5N1, raising concerns of a pandemic.

Recent evidence indicates that some people have partial immunity to H5N1 due to past infections with the seasonal H1N1 and H3N2 influenza strains. H1N1 has the N1 neuraminidase in common with H5N1, while the H5 and H1 hemagglutinins share a phylogenetic group, so people previously infected with H1N1 have more protection against H5N1 than people previously infected with H3N2. Because antibody response is biased towards the strain of first infection, cohorts who were under five when H1N1 was the dominant strain have better protection than cohorts who were young when H3N2 dominated.

I plan to study this phenomenon, known as immune imprinting, by conducting microneutralization assays with serum from Zambian subsistence farmers who interact frequently with poultry and livestock. Though cross-protective immunity to H5N1 has been studied in high-income countries, H5N1 is most commonly found in low- and middle-income countries (LMICs). I will characterize the extent of cross-protective immunity among Zambian farmers, and ask whether immune imprinting can explain patterns of cross-protective immunity.

17. Phage-phage cooperation: Host range sharing through DNA cross-packaging and chimeric assembly

Blox Bloxham, Michael Baym

Department of Biomedical Informatics, Harvard Medical School, Boston MA, USA

Keywords: Bacteriophages; Bioinformatics; Microbial Ecology; Microbial Evolution

Other keywords: Bacteriophage Ecology

Mutualisms, antagonisms, and parasitisms are rarely rigidly fixed but instead context-dependent and fluidly explored as biological entities co-evolve. Temperate phages, for example, are typically viewed as competitors, yet recent surveys show most phage pairs do not encode defenses against each other, thus allowing other interactions to dominate their dynamics. Here, we explore the potential for phage-phage cooperation driven by genetic mosaicism, as most bacteria contain multiple prophages with a complex mix of shared and unrelated gene modules. In an experimental example, two E. coli temperate phages, mEp237 and mEp332, share DNA packaging machinery and head-tail connecting proteins but have little other homology and different host receptor dependencies. Under cycles of induction and reinfection, if host availability fluctuates between hosts inside one phage's host range but outside the other's and then vice versa, neither phage can survive on its own as each is driven extinct by cycles on which it cannot infect the available host. However, when the two phages are propagated together they survive. This survival may be due to each phage's DNA being packaged into a mix of its own virion and the other phage's or other forms of chimeric assembly, thus giving the phages access to each other's host ranges. Bioinformatic work shows co-occurring prophages often share DNA packaging and head-tail connecting proteins - suggesting this form of cooperation may be common and even eco-evolutionarily selected for. Follow up work will explore whether this cross-packaging could be an important means for complex mosaic phage populations to maintain currently unneeded but later beneficial genes and survive fluctuations in host availability and environmental conditions. This work highlights the eco-evolutionary impact of genetic mosaicism and the importance of viewing phages not only as competitors but also as potential cooperators.