ONE HEALTH
MICROBIOME SYMPOSIUM
MAY 13 - 14, 2026

OUR UNDIVIDED **DECENNIUM**

Dear Colleagues:

A decade ago, we embarked on a journey rooted in a bold, transformative premise: that the most profound insights of our global future lie within the invisible, interconnected microbial worlds that bind global health. As we mark the keystone decennium of the One Health Microbiome Center in 2026, I ask you to reflect on a decade defined by the relentless pursuit of discovery and the purposeful dissolution of academic silos under the Center's unified umbrella. What began as a grassroots effort across all corners of the campus matured into a world-class destination at Penn State, where our collective defines the landscape of the microbiome sciences and the Center's position in that maturing landscape.

Our community's ethos is written in the spirit of radical, collaborative excellence; it has always been a hallmark. From pioneering breakthroughs in microbiome transplant therapies across ecosystems to critical advancements in microbial stewardship, bioinformatics, education, art, and symbioses abound, you have consistently pushed the boundaries of the known. To honor this storied trajectory, the Center unveils our new 10th-anniversary logo — a visual testament to our interwoven disciplines and the microbial energy that propels us forward. This logo is a tribute to the brilliance and ambition of our scholars, and the enduring impact of a decade of shared stewardship over these vital microscopic frontiers.

The milestone year also finds its ultimate expression at the 2026 One Health Microbiome Symposium. This gathering will be more than a showcase of data; it will be a celebration of the community and the culture of collaboration that has sustained us since our founding. As we converge to share our successes and chart the course for our next decennium, I invite each of you to take immense pride in the legacy you build together with your colleagues. As we've said before, we stand proud but not satisfied at the threshold of a new microbiome era, anchored by our history together and emboldened by the knowledge that our greatest impacts are yet to come.

Happy Anniversary to One Community for One Biosphere.

Yours always,
Seth

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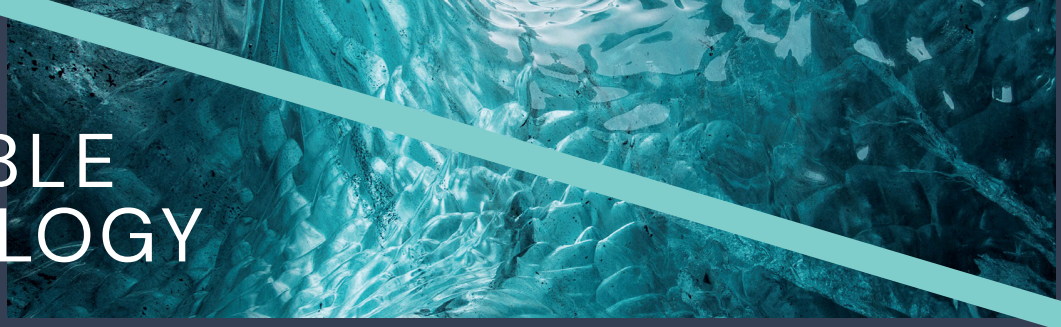

SUSTAINABLE MICROBIOLOGY

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CALL FOR PAPERS

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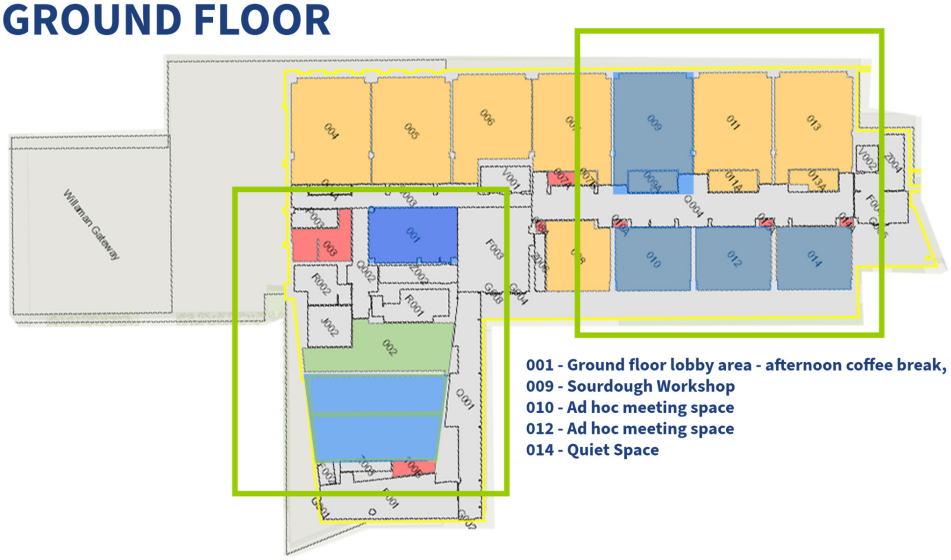
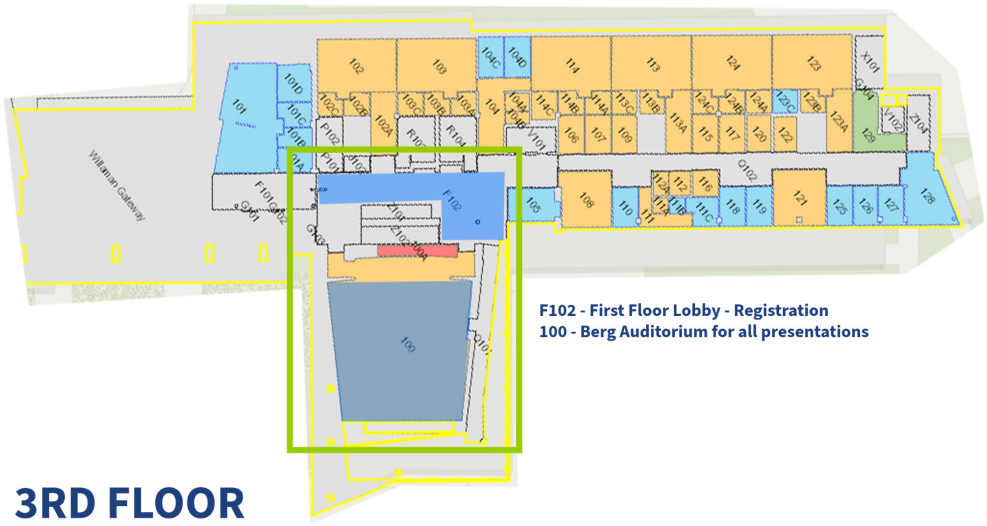
SYMPOSIUM **MAP**

GROUND FLOOR



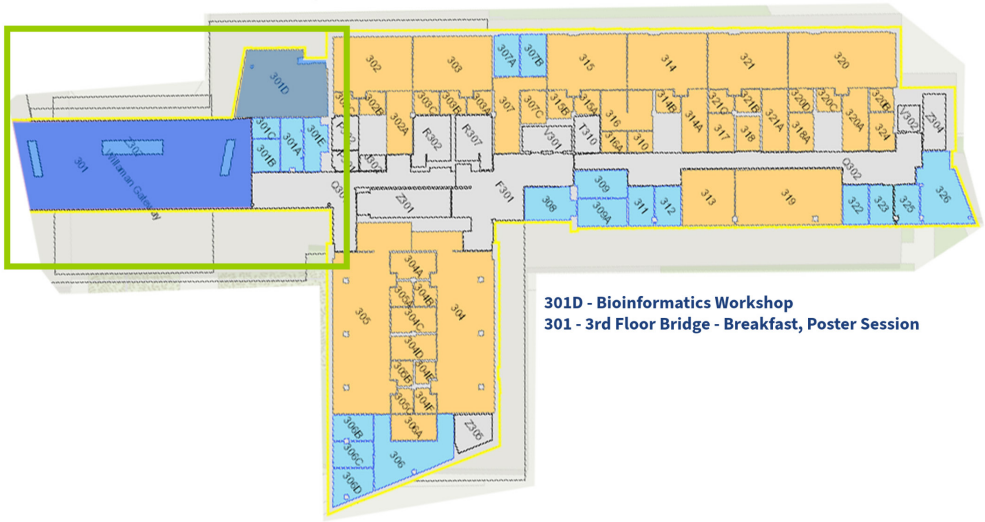
001 - Ground floor lobby area - afternoon coffee break, industry tables
009 - Sourdough Workshop
010 - Ad hoc meeting space
012 - Ad hoc meeting space
014 - Quiet Space

1ST FLOOR



F102 - First Floor Lobby - Registration
100 - Berg Auditorium for all presentations

3RD FLOOR



301D - Bioinformatics Workshop
301 - 3rd Floor Bridge - Breakfast, Poster Session

ONE HEALTH MICROBIOME SYMPOSIUM

MAY 13 - 14, 2026

Huck Life Sciences Building
Penn State University, University Park, PA

Scan for Symposium Website

Wednesday, May 13, 2026 - Day 1

8:00 - 10:00 A.M.	Registration Open - Life Sciences Building First Floor Lobby
8:00 - 8:30 A.M.	Poster Setup - Life Sciences Bridge, Third Floor
8:30 - 9:30 A.M.	Poster Session #1 (Odd Numbered Posters) & Breakfast - Life Sciences Bridge, Third Floor
9:40 - 10:00 A.M.	Opening Remarks from **Penn State President Neeli Bendapudi** and One Health Microbiome Center Leadership - Berg Auditorium

Session 1: Human Health - Berg Auditorium

10:00 - 10:50 A.M.	***Keynote*: Arturo Casadevall, MD PhD** | Johns Hopkins University *The States of Host-Microbe Interactions*
10:50 - 11:10 A.M.	**Keith Crandall, PhD** | George Washington University *Genomic Language Models for Microbiome Characterization*
11:10 - 11:30 A.M.	**Laura Weyrich, PhD** | Penn State University *Oral Microbiome Transplantation Reduces Dental Caries Development and Periodontitis Bone Loss in Preclinical Models*
11:30 - 11:45 A.M.	**QIAGEN**
12:00 - 1:45 P.M.	Lunch - Life Sciences Lawn (provided) & Sourdough Workshop - **Ashley Ohstrom** | Penn State University

Session 2: Environmental Health - Berg Auditorium

1:45 - 2:35 P.M.	***Keynote*: Joy Bergelson, PhD** | New York University *Ecological Drivers of the Microbiome*
2:35 - 2:55 P.M.	**Marta Cerruti, PhD** | Lawrence Berkeley National Laboratory *Integrated Multi-Omics and Machine Learning Approaches to Identify Drivers of Soil Carbon Persistence in Agricultural Soils*
2:55 - 3:15 P.M.	**Talon Jost** | Penn State University *Genomic Characteristics Underpinning Fungal-Inhibiting Functions in Host-Associated Bacteria*
3:15 - 3:20 P.M.	**Applied Microbiology International**
3:30 - 4:15 P.M.	Industry Coffee Break - Life Sciences Building Ground Floor Lobby

Session 3: Trainee Lightning Talks - Berg Auditorium

4:30 - 5:00 P.M.	**Daniela Tizabi, PhD** | Lawrence Berkeley National Laboratory **Jessica Gaydos** | Penn State College of Medicine **Marina Naumova** | Penn State University **Min Soo Kim** | Penn State University **Luana Bresciani** | Penn State University
6:00 - 8:00 P.M.	Reception | Hintz Alumni Center

Thursday, May 14, 2026 - Day 2

8:00 - 9:30 A.M.	Breakfast - Life Sciences Bridge, Third Floor
8:00 - 8:30 A.M.	Poster Setup - Life Sciences Bridge, Third Floor
8:30 - 9:30 A.M.	Poster Session #2 (Even Numbered Posters) - Life Sciences Bridge, Third Floor

Session 4: Integrated One Health - Berg Auditorium

9:45 - 10:30 A.M.	***Keynote Panel*: Joy Bergelson, Martin Wiedmann, Seth Bordenstein, Laura Weyrich** *The Future of One Health and Microbiome Sciences*
10:35 - 10:55 A.M.	**Celeste Allaband, DVM, PhD** | University of California San Diego *Microbes, Metabolites, and Mammals - Tracking Early Life Development in Elephants, Rhinos, and Humans*
10:55 - 11:15 A.M.	**Jeremiah Minich, PhD** | Baylor University *Advances in Long-Read Metagenomics Enabling Temporal, Comparative Genomics Applied to Childhood Undernutrition*
11:15 - 11:30 A.M.	**Eric Antonian** | Penn State University *PFAS Drive Antimicrobial Resistance*
11:45 - 1:15 P.M.	Lunch - Life Sciences Lawn (provided) & Bioinformatics Workshop - **Middle Author Bioinformatics**

Session 5: Agricultural Health - Berg Auditorium

1:30 - 2:20 P.M.	***Keynote*: Martin Wiedmann, DVM, PhD** | Cornell University *A One Health Approach to Building Resilient Food Systems*
2:20 - 2:40 P.M.	**Livleen Kaur** | Penn State University *Microbial Diversity and Disease Relationships in the Phyllosphere Revealed Through Successive Microbiome Passaging*
2:40 - 3:00 P.M.	**Nan Wu, PhD** | Duke University, HHMI *Optimized Gnotobiotic Bag Platform Expands Plant-Microbiome Interaction Research and Agricultural Applications*
3:00 - 3:30 P.M.	Industry Coffee Break - Life Sciences Building Ground Floor Lobby
3:30 - 4:00 P.M.	Awards, Discussions, and Closing Remarks - Berg Auditorium

KEYNOTE SPEAKERS

Arturo Casadevall, MD, PhD | Johns Hopkins University

Arturo Casadevall is a microbiologist and immunologist, serving as Bloomberg Distinguished Professor of Molecular Microbiology & Immunology and Infectious Diseases at Johns Hopkins University, where he also chairs the W. Harry Feinstone Department of Molecular Microbiology and Immunology. He is internationally recognized for his work on infectious diseases and studies host-microbe interactions, with a focus on immune defense mechanisms and how the fungal pathobiont Cryptococcus neoformans evades host immunity. He is a Fellow of the American Academy for the Advancement of Science, the American Academy of Arts and Sciences, the National Academy of Sciences, the National Academy of Medicine, and the American Academy of Microbiology, among others. He earned his M.D., M.S., and Ph.D. from New York University and his B.A. from Queens College, CUNY.

Joy Bergelson, PhD | New York University

Joy Bergelson is the Silver Professor of Biology at New York University and an evolutionary biologist known for her research on plant-pathogen interactions and the ecology of Arabidopsis thaliana. Her lab pioneered the use of genetically manipulated plants to study the selective forces shaping plant-microbe interactions. She is a member of the National Academy of Sciences, the American Academy of Arts and Sciences, and the American Association for the Advancement of Science. Dr. Bergelson also serves as Executive Vice President of Life Sciences at the Simons Foundation and advises several international research organizations and foundations.

Martin Wiedmann, DVM, PhD | Cornell University

Martin Wiedmann is the Gellert Family Professor in Food Safety and Food Science at Cornell University. His research focuses on the pathogenesis of zoonotic and foodborne bacterial diseases, using model organisms such as Listeria monocytogenes and Salmonella to study interactions between pathogens, environments, and hosts. His group also leads an extension program in food safety and dairy microbiology across New York State. He is a Fellow of the American Association for the Advancement of Science and the American Academy of Microbiology, and co-director of the New York State Integrated Food Safety Center of Excellence. He holds a D.V.M. from the University of Munich and a Ph.D. from Cornell University.

ABSTRACT SPEAKERS

Keith Crandall, PhD | George Washington University

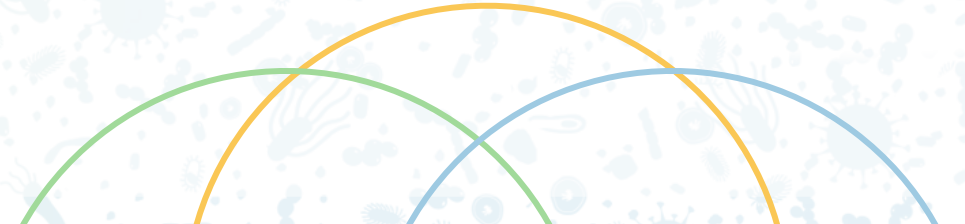
Genomic Language Models for Microbiome Characterization

Understanding evolutionary variation in genomic sequences through the lens of language modeling has the potential to revolutionize biological research. Afterall, DNA is a unique biological language. However, standard Large Language Models have limited applicability to DNA sequences. To maximize the utility of language modeling in genomics, we must develop novel tokenization strategies and model architecture adapted to diverse genomic features across evolutionary timescales. We investigated key elements in genomic language modeling (gLM), including tokenization, pretraining datasets, fine-tuning approaches, pooling methods, and domain adaptation, and applied the language models to diverse genomic data focusing on microbiome characterization and antibiotic resistance detection. We introduce seqLens, a family of models based on disentangled attention with relative positional encoding, which outperforms relatively similar-sized models in 13 of 19 benchmarking phenotypic predictions. We further explore continual pretraining, domain adaptation, and parameter-efficient fine-tuning methods to assess trade-offs between computational efficiency and accuracy. Our findings demonstrate that relevant pretraining data significantly boost performance, alternative pooling techniques can enhance classification, tokenizers with larger vocabulary sizes negatively impact generalization, and gLMs are capable of understanding evolutionary relationships. We further demonstrate the diversity of applications of gLMs with 16S microbiome characterization, metagenomic antibiotic resistance detection, and biosynthetic gene cluster analysis.

Laura Weyrich, PhD | Penn State University

Oral Microbiome Transplantation Reduces Dental Caries Development and Periodontitis Bone Loss in Preclinical Models

Alterations in the oral microbiota are implicated in virtually all major oral diseases. Oral Microbiome Transplants (OMTs) represents a transformative new therapeutic strategy with the potential to shift dental care from reactive to a proactive, using a microbiota-based intervention. Similar to Fecal Microbiome Transplants (FMTs), OMTs introduce beneficial microbial communities to control and out compete disease-causing microbes. OMT can improve oral disease outcomes in mucositis, making it a promising strategy for other oral diseases. Here, we transplanted curated, ultra-healthy donor dental plaque microbiomes using two well-established murine models of dental caries and periodontal disease and assessed disease outcomes. In a rat model of dental caries with Streptococcus mutans, OMT completely eliminated severe caries and prevented moderate caries formation by 54% over 5 weeks. In a mouse model of periodontal disease, OMT significantly protected mice from alveolar bone loss. 16S rRNA amplicon sequencing confirmed significant shifts in diversity and composition of oral microbiota in OMT-treated animals. Importantly, increased inflammation or unintended secondary infections were not observed, suggesting this approach is also safe. These results demonstrate that OMT therapy can shift oral microbiota to promote health, resulting in a novel therapy with applications for caries preventative and periodontal disease treatment.



Marta Cerruti, PhD | Lawrence Berkeley National Laboratory

Integrated Multi-Omics and Machine Learning Approaches to Identify Drivers of Soil Carbon Persistence in Agricultural Soils

Soil carbon (C) persistence, influencing soil nutrient supply and biodiversity, is regulated by the molecular composition of soil organic matter and microbial activity. Crop management practices, such as crop-grass alternation, have been proposed to enhance soil C stability. This study aims to mechanistically link soil C persistence to microbial activities in agricultural soils. Using multi-omics techniques and machine learning, we investigated C-cycling across four soil types (continuous corn field, corn field with a buffer strip, grass within the strip, and uncultivated area) at three depths (0-20, 20-40, 40-60 cm). Targeted metabolomics showed that metabolite signals were higher in deeper layers and clustered according to soil type, with the strongest signals in uncultivated and grass soils. Untargeted HPLC-MS/MS metabolomics showed that metabolite features clustered by soil type. Feature abundance was influenced by both depth and soil type, predominantly including fatty acids and amino acids (hydrophobic) and alkaloids and carbohydrates (hydrophilic). Metagenomic assembly and binning produced 1066 medium/high-quality genomes. Gaiellaceae was the most abundant family across soils, and along with the Thermophylaceae family increased with depth; these families are associated with soil organic matter decomposition. Microbial activity displayed depth-dependent gradients, with fewer metabolic pathways actively transcribed and translated in deeper soils. Multi-omics integration using domain-aware Gaussian Process kernels based on optimal transport is ongoing to correlate microbial and metabolite features. This study provides mechanistic insights into soil microbial activity and C persistence in corn fields. Results will inform agricultural strategies aimed at enhancing carbon stability and long-term soil health.

Talon Jost | Penn State University

Genomic Characteristics Underpinning Fungal-Inhibiting Functions in Host-Associated Bacteria

Host-associated microbes provide numerous benefits for their host, including protection from pathogens. However, the genomic features underpinning these protective characteristics are not fully understood. Comparative genomics allows researchers to characterize and disentangle genetic differences which facilitate these protective actions. The highly virulent amphibian skin fungal pathogen Batrachochytrium dendrobatidis (Bd) has caused declines in numerous amphibian species across the world, but some species tolerate infection. Amphibian skin-associated microbes, particularly those that exhibit antifungal action, are a significant first line of defense that protects species from infection. Over 7,000 isolates have been cultured from the skin of wild amphibians, with ~35% showing Bd-inhibitory function. To investigate genomic composition of Bd-inhibiting microbes, we selected clusters of bacterial strains with identical 16S rRNA sequences but contrasting phenotypic activity to Bd from across the phylogenetic tree. We hypothesize that mutations in key regions of microbial genomes including Type-III polyketide synthase (T3PKS), non-ribosomal peptide synthetases (NRPS), and carbohydrate activate enzymes (CAZymes) producing regions may be associated with fungal-inhibiting behavior. Understanding how differences in genomic composition of host-associated microbes influence phenotypic differences is critical to further understanding the role these microbes have in pathogen defense for their host.

ABSTRACT SPEAKERS

ABSTRACT SPEAKERS

Celeste Allaband, DVM, PhD | University of California San Diego

Microbes, Metabolites, and Mammals - Tracking Early Life Development in Elephants, Rhinos, and Humans

Early-life gut microbial composition is shaped by environment and nutrition, but the role of milk molecular architecture remains unresolved. We longitudinally examined milk and fecal microbiome and metabolome profiles in African elephants (Loxodonta africana; "elephants") and southern white rhinoceros (Ceratotherium simum simum; "rhinos") in human care, as well as humans during early life development in two separate studies. These species have notable differences in digestion strategy, with elephants and rhinos being hindgut-fermenting herbivores and humans being simple-stomach omnivores. Our findings revealed that rhino calves' gut microbiome matured in ~200 days, whereas elephants and humans both required ~1,000 days to reach stability. While rhinos provide metabolic energy primarily through sugar via oligosaccharides, elephants derive the majority of their energy from fat, and humans maintain a 50-50 balance. All three species exhibited rapid functional maturation, with an early rise in microbially-derived metabolites. Furthermore, just as formula milk alters human microbial trajectories, a rhino calf fed milk replacer experienced a maturation delay of ~100 days. In conclusion, milk molecular architecture and environmental exposures constrains microbial and metabolic succession across species. This comparative perspective establishes a mechanistic basis for optimizing nutrition to support gut microbiome developmental assembly in both humans and megafauna.

Jeremiah Minich, PhD | Baylor University

Advances in Long-Read Metagenomics Enabling Temporal, Comparative Genomics Applied to Childhood Undernutrition

Over the past two decades, next-generation sequencing has transformed metagenomics and revealed key roles of the microbiome in human health, including pediatric undernutrition. While links to wasting are established, the microbiome's role in stunting or environmental enteric dysfunction remains unclear. Short-read approaches lack the resolution to assemble complete bacterial genomes, limiting genome-wide and population-level comparisons. We hypothesized that complete metagenome-assembled genomes (cMAGs) from longitudinal long-read metagenomics are essential for pangenome and microbial GWAS analyses of pediatric growth. We benchmarked three leading sequencing platforms—Oxford Nanopore, PacBio, and Illumina synthetic long reads—using 47 pediatric fecal samples collected longitudinally. PacBio produced the most accurate and cost-effective genomes. In a Malawian undernutrition cohort, we generated 986 cMAGs and identified microbial genetic associations with growth-related phenotypes. We further developed the molecular pipeline lowering the per sample cost by about 70% as previously published. We validate this approach by comparing results to a synthetic mock community of ESKAPE pathogens and a complex fecal microbial community pool from 40 participants across six time points (aged 2-3 years old) while addressing potential biased induced from long-range polymerases. We apply this approach to identify microbial genome level associations with environmental enteric dysfunction in a cohort of children from Malawi.

Eric Antonian | Penn State

PFAS Drive Antimicrobial Resistance

Per- and polyfluoroalkyl substances (PFAS) are highly persistent environmental toxicants linked to rising rates of chronic diseases; however, PFAS mechanistic targets remain undercharacterized. We hypothesized that gut microbes may be a target of PFAS. High-throughput screening of gut bacteria demonstrated broad antimicrobial effects of PFAS; however, the opportunistic pathogen E. faecium exhibited significant resistance to the PFAS derivative perfluorooctanesulfonamido amine oxide (PFOSNO). Exposure to PFOSNO was found to drive E. faecium resistance to cell-wall inhibitor antibiotics such as vancomycin and daptomycin, drugs essential for treating Enterococcal infections. To understand how PFOSNO drives antimicrobial resistance, we performed an adaptive evolution experiment of vancomycin-sensitive E. faecium treated with PFOSNO for 10 days of continuous subculture. Genome sequencing of these populations revealed a high mutation frequency in genes associated with fatty acid biosynthesis including fabI. Mutated lines were isolated from the mixed populations and exhibited increased vancomycin resistance up to 32 μg/mL, indicative of vancomycin-resistant enterococci (VRE). By demonstrating that PFAS exposure facilitates VRE development in the absence of horizontally acquired resistance genes, this experiment establishes PFAS as a promoter of antibiotic resistance through de novo mutations. These observations have important ramifications for how environmental toxicants shape microbial genome evolution and antibiotic resistance.

Livleen Kaur | Penn State University

Microbial Diversity and Disease Relationships in the Phyllosphere Revealed Through Successive Microbiome Passaging

The plant microbiome plays an important role in plant health and disease suppression, yet mechanistic understanding of phyllosphere microbial dynamics remains limited. A major limitation is lack of experimentally tractable plant growth systems that allow controlled manipulation of microbial communities. To address this, a microbially controlled plant growth system was developed using microboxes and autoclaved soil amended with activated charcoal (AC) or biochar (BC). Amendments with AC (1% and 2%) and BC (0.6%) restored tomato seedling survival and growth compared to unamended sterilized soil. 16S rRNA sequencing confirmed substantially reduced microbial load relative to non-sterile controls, enabling controlled microbial inoculation and pathogen colonization by Pseudomonas syringae pv. tomato. This system was then used to examine how initial microbial diversity influences disease suppression dynamics. Field-derived phyllosphere microbiomes were manipulated to generate communities with varying diversity and subjected to seven successive passages involving microbial transfer and pathogen inoculation. All microbial community treatments reduced disease compared to the pathogen-only control. Over passages, bacterial diversity increased while fungal diversity decreased. However, there was no significant correlation of bacterial or fungal diversity with the disease. Microbial taxa contributing to disease suppression will be identified and their contribution to disease suppression will be experimentally assessed.

ABSTRACT SPEAKERS

ABSTRACT SPEAKERS

Nan Wu, PhD | Duke University, HHMI

Optimized Gnotobiotic Bag Platform Expands Plant-Microbiome Interaction Research and Agricultural Applications

Plants and their microbial communities form a symbiotic system in which microbiota shape growth, development, and stress resilience, yet the molecular basis of these interactions remains poorly understood. A major barrier is the lack of a consistently sterile growth platform that still supports normal plant development under standard chamber or greenhouse-like conditions. To address this, we developed the "GnotoBag," an improved peat-based gnotobiotic system. GnotoBag features enhanced ventilation and an integrated nutrient and water delivery module that sustains robust plant growth. These upgrades extend Arabidopsis cultivation in gnotobiotic conditions from the typical 4-5 weeks to a full life cycle, enabling seed-to-seed propagation. The expanded headspace also accommodates larger plants, supporting crops such as rice and tomato for at least four weeks. GnotoBag enables studies of microbial effects on long-term phenotypes, including the vegetative-to-reproductive transition, age-dependent senescence, and transgenerational epigenetic regulation. By supporting larger crops and extended growth, GnotoBag provides a scalable platform to investigate microbiome functions relevant to agricultural production.

LIGHTNING TALKS

Daniela Tizabi, PhD | Lawrence Berkeley National Laboratory

Effects of Soil Nitrogen Levels on the Microbiomes of Bioenergy Crop Camelina sativa

Jessica Gaydos | Penn State College of Medicine

The Gut Microbial Role in an Environmental Parkinson's Disease Animal Model

Marina Naumova | Penn State University

Effect of Bacteriocin Production on P. syringae Fitness in Leaf Surface Microbiomes

Min Soo Kim | Penn State University

AI-Enabled Functional Profiling Reveals Hidden Enzymes Driving Microbial Bile Acid Metabolism

Luana Bresciani | Penn State University

Interplay of Ecological Processes Modulates Microbial Community Reassembly Following Coalescence

DAY 1 POSTERS

1. **Kerim Heber,** ***University of Pennsylvania***
   Cysteine Metabolism of Commensal Skin Microbiota Predicts Severity of Atopic Dermatitis Before Flares
3. **Ross Hatlen,** ***Penn State University***
   Temporal Changes in Fungal and Bacterial Communities in Developing Hop Cones and Rhizomes
5. **Naomi E. Huntley,** ***Penn State University***
   Microbiome-Associated Host Variants Act in Tissues Beyond Sampling Sites
7. **Sabrina Elkassas,** ***Penn State University***
   Microbial Activity and Nitrogen Cycling Responses to Prolonged Wetting in Sonoran Desert Soils
9. **Quinn Clarine Burnett,** ***Penn State University***
   Distinct Sourdough Microbiomes Alter FODMAPs of Final Breads
11. **Eunhye Jo,** ***Pusan National University***
    Integrating Relative and Absolute Abundance Metagenomics to Reveal Bacterial–Fungal Interactions in Korean Fermented Soybean, Meju
13. **Sebastian Leon Fallas, Madangchanok Imchen,** ***Penn State University***
    Extracellular Gut Microbiome Alleviates Intracellular Endosymbiotic Reproductive Manipulation
15. **Paula Blanco,** ***Penn State University***
    Variation in Amphibian Immune Metrics Across the Landscape
17. **Rhea Negrón,** ***Penn State University***
    Effects of Carbon Sources and Varying C:N Ratios on Soil Nutrient Cycling and Microbiota Dynamics During Anaerobic Soil Disinfestation
19. **Roger Ort,** ***Penn State University***
    The Mini Gradient Array - A Low Cost In situ Culturing Device to Selectively Tame Microbes From the Environment
21. **Sarah Richards,** ***Penn State University***
    Adaptive Laboratory Evolution of a Soil Bacterium in the Presence of Different Carbon Resources Alters Downstream Fitness
23. **Benjamin Anderson,** ***Penn State University***
    Bidirectional Interactions of Hydroxychloroquine With Gut Microbes Impact its Pharmacokinetics
25. **Jennifer Harris,** ***Penn State University***
    Evaluating Microbial Activity and Functions in Cover Crop Monocultures, Pairwise Combinations, and Mixtures to Better Inform Cover Crop Choice
27. **Caroline J. Nowicki,** ***Penn State University***
    Analyzing Stage Specific Expression of the WO-Mediated Killing (Wmk) Gene and its' Effect on Sex-Ratio Host Distortion

29. **Mankanwal Goraya,** ***Penn State University***
FAIR and Square: How Assembly, Host Genome Processing, and Database Optimization Reshape Potato Metagenomics as a Diagnostic Tool

31. **An-Chi Cheng,** ***University of Pittsburgh***
Microbiome Composition and Dynamics in Tracheal Aspirates during Chronic Critical Illness

33. **Jane Venezia,** ***Penn State University***
Optimizing DNA Extraction of Amphibian Skin Swabs to Maximize Cross-Domain Microbial Diversity

35. **Udeshi I. Wickramarachchige,** ***Penn State University***
Investigating the Interaction Between the Gut Microbiome Dynamics and Host Peroxisome Proliferator-Activated Receptor-alpha Activities.

37. **Luisa Robles Zaragoza,** ***Penn State University***
Long-Term Limestone Mine Legacy Impacts on Soil Physicochemical Properties and Microbial Community Structure in the Páramo of Chingaza (Colombia)

39. **Janhavi J Damani,** ***Penn State University***
The Effect of Replacing Usual Snacks with Pecans on Gut Microbiota Assessed by Shotgun Metagenomics: An Exploratory Analysis of a Randomized Clinical Trial

41. **Angela C. Poole,** ***Cornell University***
The Impact of Whole Grains Versus Fruits and Vegetables on Microbial Metabolites

43. **Joe Ono-Raphel,** ***Penn State University***
Carbon Substrates Modulate Soil Microbiome Dynamics During Anaerobic Soil Disinfestation

45. **Katie Culhane,** ***Penn State University***
Cryo-EM Analysis Reveals Cell-Type Dependent Phosphorylation Patterns and Structural Variability in HBV Capsid

49. **Hanh Tran,** ***Penn State University***
Host-Mycobiome Crosstalk Reveals Site-Specific Patterning Across the Intestinal Mucosa

51. **Kamalesh Verma,** ***Penn State College of Medicine***
A Conserved M16 Peptidase Governs Glucose Homeostasis in Human Gut Bacteroides

53. **Kelsey Mercurio,** ***Penn State University***
Investigating Cowpea Cover Crops and Root Nodule Microbiomes via Farmer Collaborative Research in Semi-Arid Nghumbi, Tanzania

55. **Corien Bakermans,** ***Penn State University***
Preliminary Investigation of the Dragonfly Gut Microbiome

57. **Jie Feng,** ***Penn State University***
Isolation, Persistence and Rapid Detection of Clinically Relevant Salmonella enterica in Wastewater

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59. Gabriela Arp, *University of Maryland*

SpiR is a Gut Microbial Enzyme That Drives Cholesterol Conversion

61. Chutian Chen, *Penn State University*

Protein Scaffolding Expands the Therapeutic Repertoire of An Engineered Gut Commensal

63. Juliana Simas Coutinho Barbosa, *Penn State University*

Improving Dietary DNA Identification From Ancient Dental Calculus Metagenomes

65. Seth Kabonick, *Penn State College of Medicine*

Simple Dietary Sugars Disrupt Bacteroides Gut Fitness and Break Host-Microbe Symbiosis

67. Robert Nichols, *Penn State University*

Elucidating the Relationship Between Evolutionarily Conserved Microbes and the Onset of Disease

69. Jennifer Lausch, *Penn State College of Medicine*

Outer Membrane Vesicles Facilitate Polysaccharide Utilization Between Human Gut Bacteria by Transmitting Intracellular Proteins

71. Daniela Betancurt-Anzola, *Penn State University*

Genomic Dark Matter Drives Metabolic Innovation in High-Altitude Tropical Wetlands

73. Damiana Rojas, *Penn State University*

Assessing Changes in Bacterial Community Assembly in Button Mushroom Casing Alternatives

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4. **Andrew Paff,** ***Penn State University***
   Starchy Food Processing and Prior Diet Effects on the Human Gut Microbiome Community and Metabolites Using a Simulated In vitro Model
6. **Cheyenne Lehman,** ***Penn State University***
   Protamine Expression Levels Influence Cytoplasmic Incompatibility
8. **Marina Naumova,** ***Penn State University***
   Effect of Bacteriocin Production on P. syringae Fitness in Leaf Surface Microbiomes
10. **Jessica Gaydos,** ***Penn State College of Medicine***
    The Gut Microbial Role in an Environmental Parkinson's Disease Animal Model
12. **Dayana Gonzalez Bravo,** ***Millersville University, Manheim Pike Veterinary Hospital***
    Transitions in the Canine Gut Microbiome After Neutering
14. **Erika N. Biernbaum,** ***Penn State University***
    Time and Temperature of Storage Conditions Shape Viability and Molecular Detection of Foodborne Pathogens Salmonella enterica and Shiga Toxin-Producing Escherichia coli in Wastewater
16. **Yara Cavalcante,** ***Penn State University***
    Culture-Independent Detection of Staphylococcus aureus Using Multiple Displacement Amplification and CRISPR-Cas9 Coupled With Nanopore Sequencing
18. **Melanie Medina Lopez,** ***Penn State University***
    Pectobacterium parmentieri and Verticillium dahliae Alter the Functional Genetic Profile of the Potato Microbiome
20. **Yabing Li,** ***University of Arizona***
    Monsoon-Driven Dynamics of Soil Viral Communities and Functional Activities in the Sonoran Desert
22. **Ashley Mae Ohstrom,** ***Penn State University***
    Metagenomic Characterization of Diverse Sourdough Microbiomes and Their Impact on Bread Shelf Life
24. **Min Soo Kim,** ***Penn State University***
    AI-Enabled Functional Profiling Reveals Hidden Enzymes Driving Microbial Bile Acid Metabolism
26. **Shuchi Burad,** ***University at Buffalo***
    Defining Fusobacterium Nucleatum Strain Diversity in Oral Samples
28. **Sabine Hazan,** ***ProgenaBiome, LLC***
    A Potential Gut Microbiome Signature for Cancer
30. **Aditi Bhat,** ***University of Pittsburgh***
    Discovery of Novel Receptor-Like Kinases as Genetic Regulators of Root Microbiome Structure in Arabidopsis thaliana

32. **Pablo Ochoa-Andersen,** ***Penn State University***
Toward Understanding Noncanonical sIgA-Microbiome Interactions

34. **Richard Gonzalez Aquino,** ***Penn State University***
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36. **Alberta Serwaa,** ***Penn State University***
Meta-transcriptomics Analysis and Functional Annotation of Candidatus Phytoplasma ulmi in Elm Yellows Infected Trees

38. **Luana Bresciani,** ***Penn State University***
Interplay of Ecological Processes Modulates Microbial Community Reassembly Following Coalescence

40. **Daniela Tizabi,** ***Lawrence Berkeley National Laboratory***
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42. **Shane Connolly,** ***Penn State University***
Dietary Perturbations Mobilize Bacterial Genes Within the Human Gut Virome

44. **Mackenna Yount,** ***Penn State University***
Impact of Listeria monocytogenes on the EPS Composition in Biofilms With Pseudomonas

46. **Jonah Gray,** ***Penn State University***
Using BONCAT-FACS to Probe the Active Soil Microbial Community During Nitrous Oxide Production

47. **Carly Muletz-Wolz,** ***National Institute of Standards & Technology***
The Effects of PCR Spike-In Standards on Observed Microbiome Structure

48. **Eric Patridge,** ***Viome Life Sciences***
Microbial Oxidative Stress Signatures in Inflammatory Bowel Disease

50. **Emilie Lefoulon,** ***Penn State University***
Challenges in Bacteriophage WO Isolation within Wolbachia-Drosophila Models

52. **Yana Beizman Magen,** ***University of Pittsburgh***
Predicting How Competitive Strategies of a Beneficial Bacterium Shape Rhizosphere Microbiome Structure

54. **Polina Tikhonova,** ***Penn State University***
Mapping Cell-Type-Specific Host-Microbiome Associations in the Distal Lung

56. **Jingcheng Zhao,** ***Penn State University***
Gut Microbes Regulate Dietary Metal Bioavailability

58. **Md Ziaur Rahman,** ***University of California, Santa Cruz***
Plasma Cortisol is Not Associated With Gut Microbiome During Pregnancy in Rural Bangladesh

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60. Landon B Teeter, *Penn State University*

Type 6 Secretion Systems Mediate Interference Competition among Symbiotic Vibrio fischeri Strains

62. Cameron Murray, *Syracuse University*

Nevertheless, Yeast Persisted: Characterizing Pichia in the Sourdough Starter Microbiome

66. Elizabeth Daigle, *Penn State University*

Diversity, Prevalence, and Abundance of dsrAB in the Human Gut

68. Natalie Ford, *Penn State University*

Quantifying the Interactive Effects of Multiple Stressors on Plant-Microbe Interactions

70. Avanti Vairagkar, *Penn State University*

Structural and Functional Characterization of FabI-PFAS Interaction

72. Fernando Flores Lopez, *Penn State University*

Early Microbiome Dynamics Associated with Clavibacter nebraskensis Infection in Maize

74. Alexandra D. Gates, *University of Pittsburgh*

A Beneficial Bacterial Protease Regulates Root Morphology and Protection Against Pathogens

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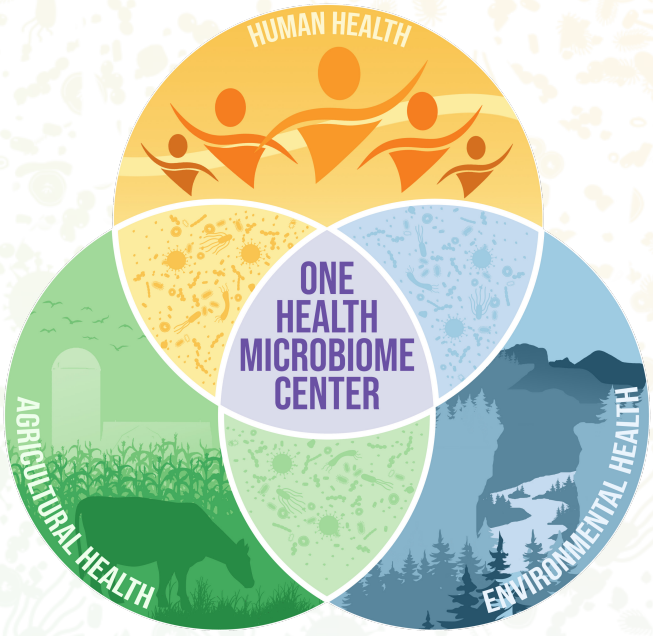

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