UPDATED: 4-9-2026

Annual Meeting
Ohio Branch of the American Society for Microbiology

BGSU BOWLING GREEN STATE UNIVERSITY

Bowling Green, Ohio
Bowen-Thompson Student Union

April 10 – 11, 2026

Official Meeting Program
and
Conference Abstracts

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Acknowledgements

The assistance and dedication of the following have contributed to the success of OBASM 2026:

OBASM Executive Committee

Christine Weingart
Chet Cooper
D.J. Ferguson
Lubna Abu-Niaaj
Hans Wildschutte
Jennifer Bennett
Stephanie Strand
Shaohua Wang
Laura Tuhela-Reuning
Stephanie Miller
Paul Hyman

Special Thanks to:

Bowling Green State University – for hosting our meeting
Bowling Green State University Department of Biological Science
Bowling Green State University Student ASM Club
The Bowling Green State university Center for Undergraduate Research and Scholarship
Sonia Tiquia-Arashiro – Region 3 Branch Planning Coordinator
Steve Tuhela-Reuning – OBASM Webmaster
ASM Distinguished Lecturer Program
The American Society for Microbiology

Invited Speakers

Davida Smyth
George Bullerjahn
Krithika Rajaram
Rimi Chowdhury
Evan Snitkin
Sarah Bagby
Mengyang Zhang
Justin North
Paul Jensen

Program Schedule for OBASM 2026
All rooms located in Bowen-Thompson Student Union

Friday, April 10

6:00 – 7:00 pm **Registration -** Bowen-Thompson Student Union

7:00 – 7:10 pm **Introduction –** Multipurpose Room (room 228)
D.J. Ferguson, President of OBASM

Welcome Statement

Vice President of Research, Bowling Green State University

7:15 – 8:15 **OBASM Keynote Lecture** – Multipurpose Room (room 228)

"Cyanobacterial blooms in shallow aquatic systems: lessons from Lake Erie and elsewhere"

George Bullerjahn
Emeritus Professor
Bowling Green State University

Saturday, April 11

8:00 am **Registration and Poster Set-up –** Bowen-Thompson Student Union

Poster Set-up – Lenhart Grand Ballroom (room 202)

8:30 am **Introduction and Welcome** – Lenhart Grand Ballroom (room 202)

D.J. Ferguson
President of the Ohio Branch of the American Society for Microbiology

Concurrent Session I, Mylander Room (room 207)

Clinical and Medical Microbiology
Moderator: Andy Wagner

8:45 – 9:15 **Krithika Rajaram** – Room 207
Ohio State University

"Life in darkness: the role of a plastid in malaria parasites"

9:15 – 9:45 **Evan Snitkin**– Room 207
University of Michigan

"Role of genetic background in antibiotic resistance emergence and spread"

9:45 – 10:15 **Rimi Chowdhury**– Room 207
Miami University

“Using inflammation-derived compounds to reduce the source of inflammation”

Concurrent Session II, Skybank Room (room 201A)

Applied and Environmental Microbiology
Moderator: Paul Hyman

8:45 – 9:15 **Sarah Bagby** – Room 201A
Case Western Reserve University

"**Mapping the mobilome in soil communities**"

9:15 – 9:45 **Justin North** – Room 201A
The Ohio State University

"Microbial sulfur acquisition from organic sulfur compounds by nitrogenase-like reductases"

9:45 – 10:15 **Mengyang Zhang** – Room 201A
University of Cincinnati

“Milk, Surfaces, and Influenza: Persistence and Inactivation of Influenza A Virus in the Environment”

10:15 – 10:30 am **Break**

10:30 – 12:00 pm **Podium presentations and judging** – Union Theater (room 206)
Coordinator – Chet Cooper

10:30 – 10:45 am
TaRTLEt: Transcriptionally-active Riboswitch Tracer Leveraging Edge deTection

Sachit Kshatriya*[1] and Sarah C. Bagby[2]
[1]Case Western Reserve University

10:45 – 11:00 am

A Lake Erie isolate of *Pseudomonas fluorescens* is a pathogen of Saprolegnia spp.

Marzie Isavi*, Carren Beurkey, Hsin-Ho Wei, Vipa Phuntumart. Paul F. Morris
Bowling Green State University

11:00 – 11:15 am

Contribution of two T6SSs in *Pseudomonas.fluorescens* LE6_D7 to Virulence against Oomycetes

Arefeh Avestakh*, Paul F. Morris
Biological Science, Bowling Green State University. Bowling Green, OH, 43403

11:15 – 11:30 pm – Break

11:30 – 11:45 am

Validation of shoe sole dust as a microbial sampler reveals changes in diversity along an urbanization gradient

Sadia Marjia Ferdous[1]*, Täubel Martin[2,3], Pekka Taimisto[2], Emma-Reetta Musakka[2,4], Bridget Hegarty[1]
[1]Case Western Reserve University, Cleveland, Ohio, USA
[2]Finnish Institute for Health and Welfare, Kuopio, Finland
[3]Aalto University, Espoo, Finland
[4]University of Eastern Finland, Kuopio, Finland

11:45 – 12:00 pm

Bacteriophage Mediated Control of Aquaculture Pathogen, *Aeromonas salmonicida*

Madison Nichole Altieri*[1], Lauren Goberman[2], Eli Bachman[2], Lauren Greenwell[2], and Raymond Larsen[3]
[1]Bowling Green State University

12:00 – 1:30 pm **Mid-Day Activities:**

Lunch: Box or "on your own"

Box lunches that were pre-purchased during registration will be available in Lenhart Grand Ballroom (room 202)

12:15 – 1:15 pm– **Microbiology Education Session –** Sky Bank (room 201)

Moderator: Jennifer Bennett

"Microbiology Careers in the Age of AI"
Paul Jensen
Associate Professor, Biomedical Engineering, University of Michigan

1:30 – 2:30 pm **ASM Distinguished Lecture** – Union Theater (room 206)

"What Can Microbes Teach Us about the Built Environment?"

Davida Smyth
Professor of Biology
Department of Natural Sciences, Texas A&M University - San Antonio

2:30 – 2:45 pm **Break**

2:45 – 5:15 pm **Poster presentations and judging** – Lenhart Grand Ballroom (room 202)

Coordinator – Chet Cooper

5:15 – 5:45 pm **Meet the Speaker,** Sky Bank (room 201)
An informal meeting with our speakers. Bring your questions and join in the conversation!

5:45 – 7:00 pm **Banquet and Student Awards Presentations** – Lenhart Grand Ballroom (room 202)

D.J. Ferguson – OBASM President

Abstracts of OBASM Poster Presentations
Saturday, April 5
2:45-5:15 pm

BOARD 1

Green Synthesis of Nanoparticles as Supplemental Treatment Against MDR Strains

Keerthana Ashok*[1], Aarushi Bhardwaj*[1], Sriya Talari*[1], Priyusha Pokala[1], Bibi Amena[2], Deekshitha Goud[2], Dr. Roselin Polugari[2], Dr. V. Gayatri[2]
[1]Case Western Reserve University, [2]St. Francis College for Women

Antibiotics are a critical tool for the successful treatment of bacterial infections, but antimicrobial resistance (AMR) has become a major concern in healthcare, creating an urgent need for novel antibiotic therapies. As of late, researchers have explored nanoparticles as a promising solution to address the rise of multidrug-resistant (MDR) bacteria. This study aims to evaluate the effectiveness of different nanoparticle treatments against several strains of MDR bacteria using agar well diffusion. After synthesizing silver oxide nanoparticles using three different methods, we tested the efficacy of three different treatments containing these nanoparticles: nanobiotics, nanoemulsions, and nanoformulations. Additionally, using the crowded plate technique, the synthesized nanoparticles were analyzed with X-ray diffraction (XRD), Fourier-transform infrared spectroscopy (FTIR), and scanning electron microscopy (SEM). The nanobiotic agar well diffusion experiments showed significant inhibition of *Enterobacter* growth with formulations including silver oxide nanoparticles, which had not been previously observed. Nanoemulsions were also shown to have effective antibacterial activity against *Pseudomonas*. Finally, out of the three nanoformulations tested, the calamine lotion formulation seemed to be the most effective antimicrobial agent. Based on the results of this study, we propose future research into synthesis with other plant extracts and zinc oxide nanoparticles, which may also demonstrate antibacterial activity.

BOARD 2

Intestinal Compound Linoleic Acid is utilized by *Shigella flexneri* to regulate virulence

Lindsay Wolverton*, Rimi Chowdhury
Miami University

Enteric pathogens have developed mechanisms to utilize host environments for their own pathogenic benefit. In order to efficiently invade their host, they utilize metabolites found in their host environment in order to upregulate and downregulate their virulence factors. One of the mechanisms used by enteric pathogens is to use compounds found in the intestines to control their regulators of virulence. Regulation of virulence is important for pathogens that reside in the intestines because they must be energetically equipped for invasion. Therefore, they must regulate their virulence in order to time their invasion with the conditions right for their growth. In doing so, they don't expel energy too early or too late, allowing them to therefore optimize their virulence. Enteric pathogens cause infection in the colonic mucosa, which is an environment that contains compounds which are used for these regulatory purposes. In the case of *S. flexneri*, a notorious enteric pathogen, the virulence cascade is triggered with activation of the master regulator, VirF, which controls epithelial invasion. Once activated, VirF initiates the expression of the major regulator VirB, which culminates into the expression of several downstream genes in the pathway, leading to invasion. Here, we show that VirB interacts with the intestinal compound linoleic acid, causing VirB to repress its expression, therefore allowing the pathogen to regulate its virulence. Based on these results, we hypothesize that intestinal metabolites can be utilized by *S. flexneri* to regulate its virulence cascade in the intestinal milieu. If we can understand these mechanisms by which enteric pathogens modulate their pathogenic strategies based on their environment, we can design compounds similar to such signals which can prevent pathogenicity and thus prevent the incidence of shigellosis.

BOARD 3

Revealing high levels of microbial fecal contamination - *E. coli* and *Enterococcus* - in the Huron River, a vital water resource in the southeast Michigan region

Luke Cherian*, Evan Siemienkiewicz, Mary Depowski, Molly Lehn, Zi Jie Gao, and Maitreyee Mukherjee
Eastern Michigan University

The Huron River is a critical freshwater resource in southeastern Michigan, supporting extensive recreational use across a watershed encompassing approximately 900 square miles. Recreational water quality is routinely assessed through quantification of fecal indicator bacteria (FIB), including *Escherichia coli* and *Enterococcus* spp., in accordance with U.S. Environmental Protection Agency (EPA) criteria, which establish thresholds of 126 CFU/100 mL for *E. coli* and 33 CFU/100 mL for *Enterococcus*. The present study evaluated the prevalence and spatial distribution of these indicator organisms across ten sampling locations along the Huron River to characterize fecal contamination patterns and assess potential public health risks. Surface water samples were collected monthly from May through December 2025 and processed within four hours of collection using EPA methods 1603 (*E. coli*) and 1600 (*Enterococcus*). Results demonstrated consistently elevated concentrations of both *E. coli* and *Enterococcus* across all sites, with values frequently exceeding EPA recreational water quality criteria. FIB concentrations exhibited pronounced seasonal variability, with peak levels observed during the summer months and comparatively lower levels during winter and spring. Continued monitoring through 2026 is planned to expand the dataset, followed by microbial source tracking analyses to identify the primary contributors to fecal contamination within the watershed.

BOARD 4

Effect of plastic leachates on the reproduction and survival of *Ceriodaphnia dubia*, a model zooplanktonic organism found in Lake Erie

Ashlynn Malloy*[1], Gillian Champoir[2], Joseph Basden[3], Zach Morris[4], Kevin E. McCluney [5], Christopher Ward[6], James S. Metcalf[7]
[1]Bowing Green State University

Plastic pollution has been ranked the second largest global threat to environmental and human health by the United Nations. Within the Great Lakes, especially Lake Erie, the most documented plastic pollution is from pre-production pellets (PPPs) that are major contaminants of shorelines. The main concern of such pollution is the release of microplastics and leached chemicals from plastic debris that spread into the environment. Out of the seven common plastic types used in consumer goods, five were obtained for leachate experiments and toxicity testing in *C. dubia* bioassays: polyethylene terephthalate (PET, Type 1), high-density polyethylene (HDPE, Type 2), polyvinyl chloride (PVC, Type 3), polypropylene (PP, Type 5), and polystyrene (PS, Type 6). Following the recommended EPA method 1002.0 for conducting bioassays, acute toxicity was not observed in any of the five plastic types. Further evaluation of adverse effects on reproduction and survival of *C. dubia* are underway using chronic toxicity bioassays, measuring heart rate, reproduction, and mortality. It is expected that the results will show indicators of increased stress in *C. dubia* through reduced reproductive capacity, masculinization, and changes in heart rate. With the essential ecosystem and economic services that Lake Erie provides, investigating potential toxicities of plastic pollution, specifically PPP leachates to important components of the food web, will provide insights regarding the consequences of plastic accumulation and their leachates in freshwater ecosystems.

BOARD 5

Assessing *Batrachochytrium dendrobatidis* infections in Invasive and Native frog species in Jamaica and the Inhibitory Potential of *Pseudomonas* Bacteria

Gabrielle Hoo*, Dr. Stephanie Strand, Dr. Rick Lehtinen
The College of Wooster; University of Pittsburgh; University of the West Indies, Mona Campus

Chytridiomycosis is a bacterial skin disease caused by *Batrachochytrium dendrobatidis (Bd)* which has been identified as the main contributor to significant amphibian declines and extinctions globally since its emergence. *Bd* is a fungus that begins its lifecycle as a spore that reproduce asexually and uses a flagellum to move through aqueous or moist environments. This aggressive pathogen burrows into the skin, a critical organ in amphibians, leading to electrolyte imbalance, cardiac arrest, and death. The threat of *Bd* continues to grow, particularly as rising global temperatures provide favorable conditions for *Bd* spread and persistence. Understanding the pathology of chytridiomycosis is crucial for developing effective conservation strategies that can prevent further amphibian extinctions and protect biodiversity. One of the most promising areas of research focuses on the amphibian skin microbiome. Scientists have discovered that some of the naturally occurring microbes on amphibian skin and in the environment can inhibit *Bd* growth, offering a potential line of defense against infection. Evidence suggests that greater relative abundance of *Pseudomonas* on amphibian skin correlates with decreased *Bd* infection intensity. Previous studies have successfully inoculated non-specific *Pseudomonas* bacteria onto the skin on amphibians and noticed a decrease in *Bd* mortality after exposure. My research aims to identify the specific *Pseudomonas* species that inhibit reproduction of *Bd* using *in vitro* inhibitory assays that can be used in future conservation strategies.

BOARD 6

Hidden Beneath Our Feet: Antibiotic Discovery and Native American Culture in Toledo Soil

Mitchell Deller*, TeAnna Thomson*, **Mariam Adams*, Tori Schretter*,** Hans Wildschutte
Bowling Green State University

Antibiotic resistant pathogens have led to devastating impacts on both human health and agriculture. We hypothesized that the soil microbiome presents antagonistic activity against plant and fish pathogens that can be used to advance a One Health approach. Through a Course-Based Undergraduate Research Experience (CURE) over two semesters at Bowling Green State University, we isolated and characterized *Pseudomonas* strain TE_1_2_F24 from a soil sample in Toledo, Ohio. In Biology 3130 Intro. to Microbiology, we found that strain 1_2 had an effective means of inhibiting the growth of plant and fish pathogens through the production of a potentially novel antibiotic. To identify genes involved in antagonistic activity, we performed transposon mutagenesis. Genome sequencing and arbitrary PCR was used to identify the biosynthetic gene cluster that encodes the antagonistic activity. The predicted product was viscosin, a biosurfactant. In the second semester, bioinformatics tools were used to further study strain 1_2 and its origin of isolation. The future of our society relies on soil not only for antibiotic discovery but also for sustained agriculture which was practiced by Native Americans. The soil collected for the study was historically inhabited by Tribal Nations, including the Bodwéwadmi and Myaamia. The sustainable agricultural practices of Tribal Nations such as Three Sisters polyculture and controlled burning historically maintained a complex and healthy soil microbiome. It could also have contributed to natural pathogen suppression. These practices should be reevaluated by modern-day techniques to see if using these methods can assist with the antibiotic resistance issues regarding human health and agriculture.

BOARD 7

Analyzing the Genomic Neighborhood of Unique Mobile Genetic Elements in a Temperature Ramping Microcosm Experiment

Jessica D.V. LaBella*1, Dylan R. Cronin1,2, Derek A. Smith1, Sachit Kshatriya1, Taiwo Mercy Faloni1, Yueh-Fen Li2, Brittany A. Fonner2, Samantha Bosman3, Scott Saleska4, Rachel Wilson3, Jeff Chanton3, Ruth K. Varner5, Virginia Isabel Rich2, and Sarah C. Bagby1
1Case Western Reserve University Department of Biology
2The Ohio State University Department of Microbiology
3Florida State University Department of Earth, Ocean & Atmospheric Science
4University of Arizona Department of Ecology & Evolutionary Biology
5University of New Hampshire Department of Earth Sciences

Mobile genetic elements (MGEs) are genetic sequences capable of moving within or between genomes. MGEs parasitize their hosts for self-propagation but they can also provide host-cell benefits by introducing advantageous genes related to metabolism, photosynthesis, and antibiotic resistance. Due to their mobile nature and potential contributions to niche-specific host fitness, MGEs are thought to play a crucial role in microbial adaptation to changing environments. However, there are several challenges with assessing MGEs in metagenomic data including fragmented assembly, failure of MGEs to bin into metagenomes, difficulty with MGE boundary estimation, and lack of a unified framework for MGE identification. Recent advances in MGE identification have made it possible to identify diverse MGEs types including insertion sequences, transposons, integrons, prophages, and conjugative elements using hidden Markov models that identify hallmark genes used for MGE recombination. Thawing permafrost peatlands offer a unique opportunity to study microbial adaptation in response to environmental change. We conducted a three-month temperature ramping incubation experiment leveraging microcosms of peat sampled from the bog habitat of Stordalen Mire, an actively thawing permafrost model ecosystem. Here, we identify and analyze 475,000 MGEs in metagenomic sequence data from incubation samples across gradients of time and temperature.

BOARD 8

Social environment shapes gut microbiome of sailfin mollies (*Poecilla latipinna*)

Ian M. Sander*, Doyi Kim, Sophia Rohr, Shala J. Hankison, and Andrea M. Suria
Ohio Wesleyan University

The gut microbiome plays a key role in host health, behavior, and stress resilience. In the human gut microbiome, messages are conveyed from the intestines to the central nervous system through the vagus nerve, an association known as the gut-brain axis. In fish, an analogous gut-brain interaction has shown that environmental changes impact the gut microbiome composition and population health. However, little is known about how social structures affect microbiome composition and diversity. Here, we use the social dynamics of the sailfin molly, *Poecilia latipinna*, as a model to examine the effect of social interactions on the gut microbiome. Courting males establish hierarchies with the largest dorsal fins dominating. Males are often aggressive toward each other and oppressive or persistent with females, exhibiting courtship displays from courting males or “sneak and thrust” behaviors from small males. Female sailfin mollies were housed under controlled conditions with and without male conspecifics to isolate the impact of specific social behaviors. Fecal samples were collected, bacterial DNA was purified, and 16S rRNA genes were sequenced. Alpha and beta diversity analyses identified 3,793 unique amplicon sequence variants. Shannon diversity analysis revealed non-courting males exhibited a distinct diversity profile, differing significantly from both females ($p = 0.000239$) and courting males ($p = 0.000932$). Bray-Curtis dissimilarity revealed that gut microbiome composition differed by social condition: females housed with males exhibited shifts in microbial community structure relative to females housed without males, suggesting social interaction-mediated microbial restructuring. These findings highlight social behavior as an important and underexplored driver of microbial community dynamics.

BOARD 9

Transcriptomic analyses of the Antarctic *Chlamydomonas priscui*: impacts of photoacclimation of photosynthetic gene expression

Halie Seifert*, Devon Popson, Tharaka M Alagiyawadu, Rachael Morgan-Kiss
Department of Microbiology, Miami University, Oxford, Ohio

The algae of the McMurdo Dry Valley (MDV) lakes in Antarctica present a unique opportunity to analyze the variety of responses to photosynthetic stress. These lakes are low in nutrients, perennially covered in ice, and exposed to varying light intensities throughout the year. As such, extremophilic organisms like *Chlamydomonas priscui* (isolated from Lake Bonney of the MDV Lakes) may offer alternative solutions to problems created in the photosynthetic apparatuses by fluctuations in light and salt levels as a result of global climate change. Here, we are interested in how these organisms alter gene expression to support survivability of the cell and keep their photosynthetic mechanisms running over a time continuum of stress. Analyzing the RNA will provide additional insight into which genes are expressed, and how they vary at different light and salt levels over a long time period. Samples were collected from continuous cultures at several timepoints and cryopreserved. The continuous cultures were conducted in photobioreactors (FMT150, Photon Systems Instruments) and measurements were taken continuously, every few minutes, or days to verify stress levels in the algae. Once we have validated our RNA and cDNA procedures with practice samples, RNA will be extracted from the preserved samples, converting it to cDNA, then probed with qPCR targeting a suite of key photosynthetic and stress genes. We will also compare the results of *C. priscui* to *Chlamydomonas reinhardtii*, a similar mesophilic strain, so that we can understand how stress adaptation impacts the response to these environmental conditions. We hypothesize that expression of key photosynthetic genes will exhibit species-specific temporal patterns, paralleling results from photobiology measurements All the data related presents interesting insight regarding the responses that extremophilic organisms like *C. priscui* may take to increase their photosynthetic output and sustain their survivability despite significant environmental shifts due to climate change.

BOARD 10

A CURE For Antibiotic Discovery and Understanding Land History

Taylor A. Cundiff*, **Ryanna M. Tuttle***, **Brianna N. Mitchkash***, Hans Wildschutte
Bowling Green State University

Bacterial pathogens are evolving resistance to most antibiotics, causing a global health crisis. Unfortunately, pharmaceutical companies have stopped antibiotic discovery due to low profitability, thus the need for new drugs is urgent. We hypothesize that bacteria from soil could produce antibiotics that inhibit plant and animal pathogens. To test this hypothesis, we contributed to antibiotic discovery through a Course-Based Undergraduate Research Experience (CURE) at BGSU that spans two semesters. In the first semester, Biology 3130 Introduction to Microbiology, soil was collected from our hometown, and bacteria were isolated from it. One strain was identified as *Pseudomonas* sp. TE48-3-F2025 by PCR and sequencing of the 16S rRNA gene. Antibiotic assays were then performed against plant and animal pathogens. Strain TE48-3-F2025 showed inhibition against three *Aeromonas* pathogens which infect fish. Transposon mutagenesis was then optimized at the end of the semester with strain TE48-3-F2025 to identify genes involved in antibiotic production. This research was continued through a second semester in Biology 4260 Pathogenic Microbiology. Whole-genome sequencing, arbitrary PCR, and antiSMASH analysis were used to identify a biosynthetic gene cluster responsible for antagonistic activity. Results suggested an azole-containing ribosomally synthesized and post-translationally modified peptide was the potential product. Altogether, our research addressed the importance of soil ecosystems as they are not only a home for bacteria that produce antibiotics but also serve a greater role in agriculture for human health. To learn about land history, the soil collected in Biology 3130, which was from Cleveland, Ohio, was utilized as a source-location to identify Native Americans who occupied that land and their beliefs in soil and farming practices. Understanding their beliefs can promote the health of our soil for both maintaining global food production and antibiotic discovery.

BOARD 11

Identification of bacteria-derived phytohormone pathways and production from Antarctic lakes and their effects on algae growth

Kavan Jackson*[1], Bradley Kryzsiak[1], Rachael Morgan-Kiss[1]
[1]Miami University

The phycosphere is a prevalent mutualistic interaction in marine ecosystems and a vital part of aquatic ecosystems. Within the phycosphere, algae and bacteria trade organic carbon compounds and nutrients between each other and help facilitate nutrient cycling at the base of the ecosystem. Recent studies have shown that phycosphere-associated bacteria are also able to produce phytohormones. Phytohormones have been shown to improve growth and production in the algae, while also improving their resistance to external stressors, such as temperature and salinity. Antarctic lakes have been chosen due to their stability and reduced outside nutrient input. The lakes are also extreme environments, which will help elucidate some of the roles of phytohormones in these extreme conditions. Because Antarctic lakes are dominated by autothonously-derived organic carbon, we hypothesized that the phycosphere is prevalent and bacteria-algal interactions may be shaped by phytohormones. To test this, we [1] developed algae-bacterial co-cultures from lake water samples collected from Antarctic lakes (McMurdo Dry Valleys, Antarctica); [2] isolated and identified a number of bacteria from the co-cultures, and [3] performed genomic sequencing on the XX strains of bacteria and queried the data for putative phytohormone synthesis pathways. Many of the bacterial isolates have shown the potential to produce auxins, one of the most common classes of phytohormone. After the genomic analyses, algae-bacteria co-cultures will be produced to experimentally determine the potential to produce phytohormones.

BOARD 12

Linking indoor air and surface chemistry with microbial emissions and toxicity

Moumita Mondal*1, Yingxi Lu2, Jenna Ditto2, Bridget Hegarty1
1 (Department of Civil and Environmental Engineering, Case Western Reserve University, Cleveland, OH)
2 (Department of Energy, Environmental & Chemical Engineering, Washington University in St. Louis, St. Louis, MO)

The indoor environment is shaped by a complex interplay between indoor surfaces, microbial communities, and air composition. While each has been shown to shape indoor air quality individually, it is unknown how surface chemistry and environmental pollutants influence microbial emissions. Studying these coupled chemical and biological dynamics is essential for understanding, and hopefully mitigating, the drivers of poor indoor air quality. Here, we will present how surfaces encountered in indoor environments (e.g., glass or oil-coated tile) and common indoor pollutants (e.g., ozone) alter the metabolic activity of microbial communities. Using Proton Transfer Reaction Mass Spectrometry (PTR-MS), we have shown that exposure to ozone fundamentally alters the volatile organic compounds (VOC) emissions profile of *E. coli*, decreasing indole ($C_8H_7NH^+$) production and enhancing the production of a newly formed oxygenated chemical ($C_7H_7NOH^+$), providing evidence of pollutant exposure modifing microbial metabolic activity. To understand whether these changes are related to indole production and/or transport, we are investigating whether *E. coli* varies its gene expression of tnaA and tnaB genes. tnaB transports tryptophan in the cell and tnaA breaks tryptophan into indole. We have successfully amplified both genes using PCR (to confirm the specificity of the primers). We will present these results, as well as how expression of these genes changes between high humidity and high ozone conditions, using reverse transcription polymerase chain reaction (RT-PCR).
Moving forward, we will expand these analyses to microbial communities collected from indoor samples to account for interactions between the diverse fungal and bacterial communities of indoor environments. Together, these findings will lay the groundwork for evidence-based indoor air quality guidelines that account for the fundamental interdependence of surface chemistry, microbial metabolism, and the air we breathe indoors.

BOARD 13

Intestinal fatty acids are exploited by *Shigella flexneri* to optimize virulence strategies

Isabelle Reitz*, Lindsay R. Wolverton, Rimi Chowdhury
Miami University

Enteric pathogens regulate the expression of their virulence and proliferation genes. This regulation is possible because these organisms recognize and exploit environmental metabolites. Pathogens utilize such compounds to increase or decrease transcription of virulence genes, allowing them to choose between energetically expensive virulence programs or gut proliferation based on surrounding conditions. This practice is crucial for pathogen success as it prevents spending valuable resources on invasion genes before optimal population levels and growth conditions are met, while minimizing damage from a host immune response. The enteric bacterial pathogen *Shigella flexneri* is one example of such masterful use of metabolites. However, the role of colonic fatty acids as direct environmental cues to modulate *S. flexneri* virulence is largely unexplored, especially at the level of specific genes that are not global regulators. We hypothesized that *S. flexneri* can utilize intestinal fatty acids as signals to regulate a critical step in the infection strategy: cell-to-cell spread. This movement between colon epithelial cells is mediated by *icsA*, activated by master transcriptional regulator VirF, which has itself been shown to be repressed by fatty acids. Here we show that the dietary and microbially sourced oleic acid can be exploited by *S. flexneri* to reduce the expression of *icsA* and hence cell-to-cell spread, at concentrations significantly below those found in the human colonic environment. This research is crucial to understanding *S. flexneri*'s infection program and discerning possible targets for the prevention of bacillary dysentery.

BOARD 14

THE THERAPEUTIC ROLE OF CCR5Δ32 IN AIDS

Madison Higgins*, Alena Espinosa Alvernia, Dunia Deif, Mallory N. Alvares, Conner Boone, Reece Schindler, Antino Castro, Steven Laing, Jacob Schultz, Hannah Newsome, Gary Dodson, Harry Kestler PhD.

Through the CD4 receptor and one of the co-receptors CCR5 or CXCR4 HIV-1 enters T-cells initiating the first step in AIDS pathogenesis. While most people become seropositive six weeks after exposure, some individuals known as Exposed Seronegative (ESN) do not. Others become seropositive but do not progress to AIDS, they are referred to as Long-Term AIDS Non-Progressors (LTANPs). These outcomes are often linked to a naturally occurring mutation called CCR5Δ32, a 32 base-pair frameshift mutation that produces a truncated protein that is not detected on the cell membrane. This truncated protein may down-modulate the expression of both CCR5 and CXCR4. ESN individuals are often CCR5Δ32 homozygous, while many LTANPs are heterozygotes. The potential for gene therapy is supported by cases where HIV patients with leukemia reached undetectable viral levels after bone marrow transplants from CCR5Δ32 homozygous donors. To evaluate CCR5Δ32 as a therapy, a lentiviral vector system was used to create viral particles. CCR5 wild-type, CCR5Δ32, and a mutagenized version called CCR5Δ33 were compared. The CCR5Δ33 variant was designed to test whether the deletion itself or the frameshift is responsible for down-modulating surface expression. The pLenti-UBKO construct was created to ensure the lentiviral vector was not causing the observed reduction. HEK293-ft packaging cells were co-transferred with the pLenti constructs and helper plasmids psPAX2 and pMD2.G. The resulting pseudotyped viral particles were used to infect H9 and primary lymphocytes. If CCR5Δ32 can successfully down-modulate wild-type CCR5 and CXCR4 in vivo, it may serve as an effective basis for AIDS therapy and effecting neuroinflammation. This research focuses on reducing viral burden by directly targeting the surface expression of the necessary co-receptors.

BOARD 15

Host Range Testing *Bacillus cereus* Bacteriophages

Jillian Hull*, Ayden Mason*, Dr. Paul Hyman
Ashland University

Bacteriophages are viruses that infect different types of bacteria. Many bacteriophage biologists believe that isolating phages using multiple bacterial strains selects phages with broader host ranges. A common belief among bacteriophage biologists is that using several bacterial strains to isolate bacteriophages selects for ones that can infect more kinds of bacteria. However, previous work in our lab suggested that this may not be true. Last year, we expanded on the earlier work with more strains of *Bacillus cereus* group bacteria and more bacteriophages that infect them. This year we have added additional bacteria and bacteriophages for a total of 26 bacteria and 60 bacteriophages. This work started with the isolation of new strains of *Bacillus* bacteria from different soil types using CHROMagar™ isolation, which is a selective differential media, and DNA sequencing to identify different strains. Using these newfound *Bacillus* strains from the wild, bacteriophages were isolated. These bacteriophages were used, along with previously collected bacteriophages, to test their host ranges. Host range testing was done through triplicate repetition on the wild bacterial and lab strains with the different types of bacteriophages in order to find which phages can infect each type of bacteria. Host ranges of bacteriophages are important in medical studies as bacteriophages could be replacements for antibiotics in the future. To learn more about the bacteriophages we've isolated, we have begun genome sequencing of several of them.

BOARD 16

Healing Us: Antibiotic Discovery vs Native American History

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Bacterial pathogens have evolved resistance to most antibiotics, and can devastate human, plant, and animal hosts. Predictions indicate that antibiotic-resistant infections will exceed 10 million deaths per year by 2050, surpassing cancer as the leading cause of mortality. Unfortunately, low profitability from antibiotic discovery has resulted in a lack of effort from pharmaceutical companies, thus necessitating the need for new compounds that are effective against drug-resistant pathogens. We hypothesize that microbes isolated from soil produce antibiotic compounds that inhibit plant and animal pathogens. Utilizing a Course-based Undergraduate Research Experience (CURE) at BGSU in Biology 3130 Intro-to Microbiology, a soil sample was obtained from Bowling Green, Ohio and bacteria were isolated from it. Utilizing PCR and sequencing, one strain was identified as *Pseudomonas* sp. TE 50-2. An antibiotic production assay showed that TE 50-2 was able to inhibit three different fish pathogens. Transposon mutagenesis was then performed to find genes involved in antibiotic production. In a second semester, in Biology 4260 Pathogenic Microbiology, the research was continued. and various bioinformatic tools were used to characterize strain TE 50-2, and we identified a gene cluster involved in antibiotic production. and various bioinformatic tools were used to characterize strain TE 50-2, and we identified a gene cluster involved in antibiotic production. Thus, soil is an environment that can be used for antibiotic discovery. Soil is also important to promote global food production. Current farming practices employ tilling which destroys our topsoil. To understand native practices, the site of soil collection in Biology 3130 was utilized to learn about land history. We identified the native American Indians that occupied that land and their practices. By linking Indigenous soil stewardship with the microbiology research, this project demonstrates that biodiversity-centered land management can promote soil health support drug discovery and reduce dependence on synthetic chemical inputs.

BOARD 17

Conservation of BK polyomavirus immune epitopes in virus-specific T-cell therapy recipients

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BK polyomavirus (BKV) is a double-stranded DNA virus that causes lifelong infection in up to 90% of the population worldwide. While harmless in healthy people, immunocompromised patients are at risk for BKV-related diseases due to robust lytic reactivation of the virus. After hematopoietic stem cell transplant (HSCT), hemorrhagic cystitis (HC) and/or thrombotic microangiopathy (TMA) may develop in 20% of patients. Additionally, BKV-associated nephropathy (BKVAN) occurs in 10% of renal transplant patients. No vaccines or antivirals exist for BKV infection, and reducing immunosuppression risks transplant survival.
Virus-specific T-cell (VST) therapy elicits a strong immune response against BKV reactivation by using peptides to activate T-cells, which are then infused into patients to trigger immunity. Ideally, the peptides utilized should be conserved in patient-derived viral sequences; however, our data show incomplete conservation. This project aims to identify the extent of immune epitope perturbations in post-HSCT patients receiving VSTs to control dsDNA virus reactivation.
Viral DNA was isolated from 63 urine samples of 28 post-HSCT VST recipients, amplified by PCR, and sequenced by next-generation sequencing (NGS). Genotypes were determined by phylogenetic analysis, and the consequences of immune epitope perturbation were assessed *in silico*. Compared to the BKV strain used for VST activation, 35 of 88 [39.8%] VP1 and 120 of 170 [70.6%] Large T antigen peptide sequences were conserved in all patient-derived BKV sequences. This study indicates that standard VSTs may have limited epitope coverage for some BKV strains, suggesting a need to optimize VSTs to achieve their maximum therapeutic potential.

BOARD 18

Methanogenesis from choline, dimethylethanolamine, and tetramethylammonium in *Methanococcoides methylutens* Q3c

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Methane is a powerful greenhouse gas, largely produced by biological processes, including the metabolism of methanogenic archaea. Methylotrophic methanogenesis has been well-studied but many gaps remain in our understanding of methanogenesis from quaternary amines (QAs), such as choline and tetramethylammonium. To provide new insights into archaeal metabolism and to improve models of biogenic methane flux in real ecosystems, our biochemical characterization aims to elucidate the enzymatic processes underlying QA degradation and methane synthesis by Q3c. This study specifically focuses on the catabolism of tetramethylammonium (QMA), choline and dimethylethanolamine (DMEA) by the methanogenic archaeon *Methanococcoides methylutens* Q3C. Recent published work from our laboratory revealed that ACT9XH_04775 (MtqB), a non-pyrrolysine homolog of a monomethylamine methyltransferase, functions as both the QMA and choline methyltransferase. We also identified the putative QMA corrinoid-binding protein ACT9XH_04770 (MtqC), which showed high relative abundance in Q3C cultures cultured on QMA or choline as compared to cells grown on control substrates, trimethylamine (TMA) or methanol. This suggests its involvement in both QMA choline demethylation. Additionally, growth on the intermediate product DMEA revealed increased amounts of the TMA corrinoid protein ACT9XH_10705 (MttC) and the pyrrolysine-containing TMA methyltransferase ACT9XH_10710 (MttB), suggesting these enzymes may be involved in the breakdown of

DMEA, suggesting that MttB in Q3c may be another dual-function methyltransferase. Substrate dependent coenzyme M methylation assays with TMA or QMA grown crude cell lysates support our hypotheses by showing QMA, choline, and DMEA activity in QMA grown cell extracts but, of those, only DMEA activity was observed in TMA grown cell extracts. Our current work is focused on expression, purification, and biochemical characterization of MtqC, MtbA, and RamA to examine their roles in both QMA and choline metabolism, as well as MttB and MttC to examine their potential roles in DMEA metabolism.

BOARD 19

A biomimetic hydrogel system for studying competition of squid reproductive symbionts

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Diverse seawater bacteria compete to colonize the reproductive accessory nidamental gland (ANG) of female Hawaiian bobtail squid (*Euprymna scolopes*). These symbiotic bacteria are deposited into the squid's eggs, where they protect the embryo from environmental fungal pathogens. However, it remains unclear whether this antifungal activity arises from a small number of dominant strains or from interactions among the diverse community. To investigate strain-specific interactions in vitro, we used a biomimetic hydrogel spheroid "egg" model. The alginate-calcium chloride hydrogel system consisted of a yolk sac-like core, an intermediate layer containing bacteria to mimic the jelly coat, and an outer layer that simulated the egg's capsule. Both monocultures and cocultures were tested in the jelly coat layer, with cocultures containing a target strain and a putative inhibitor strain. Bacterial viability and competition were assessed by quantifying colony-forming units (CFUs) recovered from the "eggs", and fluorescence microscopy was used to qualitatively evaluate growth and spatial interactions. Bacteria successfully replicated within the hydrogel model, reaching densities up to 8.00 x 108 CFU/mL. In coculture "eggs," no significant inhibition of target strains was observed, contrasting from previous experiments that showed successful inhibition of target strains in liquid culture and on agar plates. *Fusarium keratoplasticum*, a common marine fungal pathogen, was successfully grown on the hydrogel model in incubated conditions. Future work will focus on exploring fungal quantification methods to assess whether these bacteria within the hydrogel "egg" model can inhibit fungal growth.

BOARD 20

Using Tetranucleotide Frequency to Estimate Mobile Genetic Element Boundaries

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Mobile genetic elements (MGEs) are sequences of DNA that are capable of moving within or between genomes. Among the most prevalent of these elements are bacteriophages, plasmids, integrated conjugative elements, insertion sequences, and transposons. MGEs can promote genomic rearrangements, disrupt genes, or carry cargo genes which provide an adaptive advantage or disadvantage to the host cell. Many of these cargo genes are associated with antimicrobial resistance, virulence factors, metabolic pathways, and altruistic behaviors in the host bacterium. MGEs may be identified bioinformatically by HMM-based detection of the recombinase enzymes that catalyze their movement within and between genomes. While this method allows for the detection of MGEs in metagenomic data, the identification of cargo genes has remained a problem since current bioinformatic approaches have limited accuracy for determining the boundaries of an MGE within the host genome.
Here, we present a bioinformatic tool to detect the boundaries of a MGE using tetranucleotide frequencies. Tetranucleotide frequencies are a conserved and species-specific pattern in the frequency of tetramers throughout a genomic sequence. Since MGEs often originate from outside the host genome, it is expected that the tetranucleotide frequencies of an MGE will differ from the surrounding host genome. We are currently validating this tool to determine whether tetranucleotide frequency analysis can enable accurate boundary assessments across a variety of MGEs.

BOARD 21

B Cell methods of FCRL1 localization to BCR complex

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B Cells are a lymphocyte whose primary purpose is to generate specific antibodies in response to a foreign antigen, and the B cell receptor (BCR) signaling pathway regulates the activation of the B cell. Previous studies have demonstrated that Fc receptor-like protein 1 (FCRL1) is found on B cell plasma membranes, associating with the BCR upon activation. Through this association, FCRL1 either advances or inhibits B cell activation; the pathway is determined by the adapter proteins FCRL1 binds with during localization. FCRL1 may be involved in autoimmunity if unable to bind to inhibitory adapter proteins during localization due to continual stimulation of the BCR pathway. Because it is unknown which region of FCRL1 is responsible for its recruitment to the BCR, the FCRL1 localization pathway is an important topic to further our understanding of B cell activation and autoimmunity. In this study, we used PCR to amplify the DNA pertaining to either the transmembrane and cytoplasmic portion or the transmembrane and extracellular portion of FCRL1 to create two constructs which were then inserted into the genome of A20 mouse B cells using a lentiviral vector. Cells will then be activated and studied under confocal microscopy to determine which region mediates FCRL1 localization to the BCR. Early results include successful PCR amplification and cloning of the relevant regions of FCRL1 into the vector pLenti-CMV-GFP-Puro. The current stage of this study is at the gene transduction step, and future steps include B cell activation and analysis by confocal microscopy. The outcomes will determine if FCRL1 localizes due to the internal protein activation cascade, if it localizes due to an external ligand, or a combination of both. The knowledge gained could be used to help treat those with autoimmune disorders by developing a medication that targets the specific localization pathway.

BOARD 22

OBASM conference abstract AAC

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Bacteria require sulfur for growth, which they acquire from environmental sources. However, when sulfate becomes limited some organisms like *Rhodospirillum rubrum* use volatile organic sulfur compounds (VOSCs). To use VOSCs as sulfur sources, bacteria have evolved enzymes known as methylthio-alkane reductases (MAR). These enzymes are nitrogen fixation-like systems (NFL) which mimic nitrogenases to reduce carbon-sulfur bonds. Furthermore, a second NFL system (NflDK) in *R. rubrum* is also implicated in VOSC utilization. Analogous to nitrogenases, MAR comprises a two-component system of an ATP-dependent reductase called MarH and a catalytic tetramer called MarDK. Notably MarDK possesses complex metallocofactors, mar1 and mar2, analogous to the nitrogenase P-cluster and a catalytic M-cluster, respectively. The nitrogenase M-cluster synthesis begins with the formation of an L-cluster by the radical-SAM protein, NifB. The L-cluster is further matured to the FeMo-co and FeV-co M-cluster by incorporation of homocitrate and molybdenum or vanadium heterometal via the NifEN or VnfEN chaperone scaffold, respectively. In the case of iron-only nitrogenase, maturation of FeFe-co occurs directly on nitrogenase. Here we show that both MarDK and NflDK of *R. rubrum* appear to mature the catalytic metallocofactors in situ via NifB homologs analogous to the iron-only nitrogenase. Through chromosomal gene deletions and plasmid-based complementation in *Rhodospirillum rubrum,* our findings indicate that metallocofactor synthesis for MAR does not utilize assembly scaffold NifEN or the additional NflDK. Furthermore, either the nitrogenase metallocofactor synthesis enzyme NifB or the NifB homolog called MarB is required to mature a functional MAR system. Notably, there is an observable difference in MAR activity profiles for dimethylsulfide versus methylthioethanol, depending on whether MAR was matured by NifB or MarB. Likewise, NflDK requires a maturase for cofactor assembly, and either MarB or NifB can synthesize a functional metallocofactors, each yielding an enzyme with differential activities for methylthioethanol versus mercaptoethanol. In conclusion, these results suggest that L-clusters or L-like clusters are not unique to MAR but play a widespread functional role in nitrogenase-like systems. The second NFL *R. rubrum* appears to be an additional carbon-sulfur lyase involved in sulfur metabolism, being mercaptoethanol its main substrate.

BOARD 23

Osmotic Stress Response in a Novel Microbial Isolate from Thawing Permafrost Peatland

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Biological systems are challenged to cope with stress when physical or chemical changes occur in an environment, including osmotic stress from changes in external solute levels, driving water to flow into or out of cells. As the osmolarity of environments changes, cells are threatened with protein denaturation, severe cell dehydration, and overall metabolic disruption. One major source of osmotic stress is the freezing and thawing of water in soil pores. In arctic permafrost, rising global temperatures affect soil chemistry and water saturation. The Stordalen Mire in northern Sweden serves as a model ecosystem for thawing peatland permafrost, where the thaw gradient extends from a fully intact, dry palsa to a partially thawed bog and a fully thawed, water-saturated fen, with accompanying changes in soil microbial communities. To acclimate and tolerate sharp differences in soil water content across the thaw gradient, microorganisms can produce osmoprotectants and osmoprotectant transport systems to restore ion gradients internally and externally. Here, we aim to characterize the osmotic stress response of a *Caballeronia* strain isolated from a 9–19 cm depth interval in the sphagnum-dominated bog habitat. Long-read genomic sequencing and assembly yielded a near-complete genome, which was annotated to identify osmoprotectant biosynthetic pathways predicted to support acclimation to changes in external osmolarity. Laboratory experiments will manipulate the osmolarity of an enriched arctic medium to examine optical density growth responses and changes in size via microscopic imaging. Future studies will quantify the osmotic stress response by utilizing droplet digital Polymerase Chain Reaction (ddPCR) to quantify single-copy genes transcribed under osmotic stress for various candidate genes. Overall, studying stress patterns of isolates in these ecosystems will improve understanding of tolerances and adaptations in the Stordalen Mire soil and the broader impacts of climate change on arctic soil functions and ecosystems.

BOARD 24

Healing Beneath our Feet: Exploring Antibiotics from Soil Bacteria and Indigenous Perspectives

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The evolution of antibiotic-resistant pathogens is predicted to be the leading cause of death by 2050, surpassing cancer. Unfortunately, pharmaceutical companies have dropped antibiotic discovery due to low profitability, so new antibiotics are at an all-time low. Soil is important in antibiotic discovery because most compounds are isolated from bacteria within this environment. During the past two semesters, we participated in Course-Based Undergraduate Research Experiences (CURE) in Biology 3130 and 4260 for which we performed authentic antibiotic discovery research. We hypothesized that soil bacteria produce antibiotics that inhibit plant and fish pathogens. In Biology 3130, we isolated Pseudomonas species from soil, performed an antibiotic production assay against plant and animal pathogens, and then optimized transposon mutagenesis to identify genes which encoded for the antimicrobial production. Then, in Biology 4260, we used the sequenced genome of the antibiotic producing *Pseudomonas* strain 44-3 to further characterize it. We performed various bioinformatic analyses such as antiSMASH to help identify biosynthetic gene clusters, JGI IMG to generate genome statistics, and the Type Strain Genome Server to identify the bacterial species of 44-3. Altogether, these results have potential biocontrol application in aquaculture since strain 44-3 inhibited pathogens, 1 Aeromonas sobria and 1 Vagococcus salmonarum, which cause disease in fish. Moreover, healthy soil is more than an environment for antibiotic producing bacteria; it sustains human life through agriculture. Thus, the specific soil collection location of strain 44-3 was investigated to learn about Indigenous history and their beliefs of soil. Exploring Native American history allowed us to learn about agriculture stewardship and why it is important to maintain a healthy soil environment. Together, these courses exposed us to authentic antibiotic research, the importance of soil, and Native American history.

BOARD 25

Unmasking the Missing Fungi: Gene-Level Clues to Asthma Triggers from Indoor Dust

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Asthma severity has been linked to environmental microbial exposure, especially indoor fungi, whose diversity and seasonal fluctuations influence respiratory health. Previous work suggests that higher fungal diversity may protect against asthma, while summer peaks in fungal load increase symptoms. However, little is known about how fungal metabolism contributes to these effects. Because fungi in dust have low biomass and large genomes dominated by bacterial and human DNA, genome-centric metagenomics often underrepresents them. This study used a gene-centric metagenomic approach to detect fungal functional signals in indoor dust and explore links to asthma-related environmental factors.
Dust samples (n=81) were collected from New York City households enrolled in the Columbia University Center for Children's Environmental Health birth cohort. Samples were sequenced (~29.5 million reads/sample) and analyzed using metagenomic assembly, fungal genome mapping, and Gene Ontology (GO) annotation.
Although 260 bacterial and one human genome were recovered, no fungal genomes were assembled, reflecting technical challenges. Fungal reads were nonetheless detected in most samples, allowing functional inference despite insufficient genome-level coverage.
Gene-centric analyses showed nominal associations between fungal function and household features—water damage, pet ownership, and maternal ethnicity—all of which lost significance after multiple testing correction. Subtle functional shifts suggested distributed metabolic responses to environmental factors. Mitochondrial-related functions were more abundant in homes with pets, hinting at altered fungal activity.
Overall, gene-level analysis revealed detectable fungal functional signals in indoor dust that genome-centric methods missed. The study highlights the potential of functional metagenomics to assess indoor microbial contributions to asthma risk and calls for deeper sequencing or metatranscriptomics to capture active fungal metabolism.

BOARD 26

Evolution of Double Resistance in Pseudomonas chlororaphis treated with Bacteriophage and Antibiotic Simultaneously

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Antibiotics have long been used to clinically treat bacterial infections, but overuse has led to the emergence of antibiotic-resistant bacteria. Although bacteriophage therapy—using viruses that infect and eliminate bacteria—was put forward as a potential alternative, it can also lead to resistance in bacteria. Scientists have discovered that phage-resistant bacteria often experience increased susceptibility to antibiotics. With limited research on bacterial susceptibility to simultaneous bacteriophage-antibiotic treatment, this project focuses on evolving *Pseudomonas chlororaphis 14B11* strains that become resistant upon simultaneous exposure to bacteriophage and antibiotic. It also aims to investigate mutations that drive this dual resistance. The Minimum Inhibitory Concentration and optimal Multiplicity of Infection were first determined by infecting *P. chlororaphis* bacteria strain with antibiotics and bacteriophage respectively. *P. chlororaphis* was then simultaneously exposed to 2 treatment pairs: PC2 bacteriophage & Geneticin, and PC2 bacteriophage & Tetracycline. Strains that were phage-only resistant, antibiotic- only resistant, phage-antibiotic susceptible and phage-antibiotic resistant were selected in addition to the wild-type control. Their gDNAs were isolated and amplified for sequencing. The amplified gDNA samples will be sequenced and the resulting data will be analyzed to determine how mutations differ in strains resistant to both phage and antibiotic from those resistant to phage-only and antibiotic-only.

BOARD 27

Antimicrobial Activity of Purified Thymol Compared with a Botanical Thymus vulgaris Tincture Against Canine Oral Microbiota

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Natural plant compounds have been investigated as alternative antimicrobial agents for oral bacteria. This study compared the antimicrobial activity of purified thymol with a botanical Thymus vulgaris tincture against bacterial populations from the canine oral microbiota. We hypothesized that purified thymol would produce greater antimicrobial inhibition than the crude botanical tincture due to its higher concentration of the active compound. Oral swabs were cultured under aerobic conditions, and microbial suspensions were standardized to approximately 0.5 McFarland turbidity. Lawn cultures were prepared on Mueller–Hinton agar, and disks containing graded concentrations of purified thymol or thyme tincture were applied. Chlorhexidine served as a positive control and sterile water served as a negative control. Following incubation, inhibition zones were measured using standard disk diffusion methods. Purified thymol produced stronger antimicrobial inhibition and a clearer dose–response pattern than the botanical tincture. These findings support further investigation of plant-derived antimicrobial compounds as potential alternatives for managing oral bacterial communities.

BOARD 28

Under Pressure: Coordinated Regulation of Photoprotective Processes Across a Temporal Continuum in an Antarctic Alga

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Photosynthetic organisms are frequently exposed to fluctuating environments, which disrupt cellular energy homeostasis and compromise photosynthetic performance. Photosynthetic microorganisms, such as green algae, represent tractable genetic models for studying acclimation to environmental stressors. Here, we compared acclimation to two environmentally relevant stressors (light and salt) in the Antarctic polyextremophile *Chlamydomonas priscui*, isolated from Lake Bonney (McMurdo Dry Valleys), with the mesophilic model *Chlamydomonas reinhardtii*. Cultures were maintained under continuous growth conditions in three photobioreactors (FMT150, Photon Systems Instruments) to allow precise evaluation of short- (minutes) and long (days) -term acclimation to high light and salt stress across a temporal continuum. Under high-light stress, both algal strains exhibited a substantial initial loss in photosynthetic performance; however, after 48 hr the Antarctic *C. priscui* exhibited partial recovery while photochemistry remained downregulated in *C. reinhardtii* throughout the treatment. This enhanced photosynthetic performance in *C. priscui* was accompanied by more effective regulation of photosystem II, activation of an alternative electron flow pathway (cyclic electron flow, CEF), and rapid/transient induction of energy dissipation pathways. In parallel experiments, we monitored growth and photobiology in *C. reinhardtii* exposed to a range of salinities: salt-stress acclimation was distinct from that of high-light. Moderate salt stress (50 mM NaCl) caused minimal changes in photosynthetic performance, while 70 mM NaCl induced a substantial yet transient loss in photosynthetic activity, indicating a threshold-dependent response and activation of acclimatory processes. Our results reveal that CEF can be utilized for both ATP production and activation of photoprotective pathways; however, the timing and extent are strain- and stress-specific. Ongoing comparisons with *C. priscui* will clarify how intrinsic stress tolerance influences CEF regulation. Understanding these mechanisms will inform strategies to enhance abiotic stress resilience in crops and photosynthetic production systems.

BOARD 29

Green Nanotechnology and Phytochemicals as Strategies to Combat Multidrug-Resistent Bacteria

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The rise of multidrug-resistant (MDR) bacteria like S*taphylococcus aureus* and *Pseudomonas aeruginosa* makes finding new treatments a priority. This study compares the antibacterial activity of crude plant extracts and their green-synthesized nanoparticles (NPs) derived from nine plant sources: leaves (*Lawsonia inermis*, *Psidium guajava*, *Salvia rosmarinus*), peels (*Punica granatum L.*, *Pyrus malus*, *Citrus sinensis*), and seeds *(Coriandrum sativum, Trigonella foenum-gracecum, Nigella sativa*). Nanoparticles were biosynthesized using zinc and copper precursors, with plant metabolites acting as reducing and stabilizing agents.
The samples were tested against four Gram-positive and three Gram-negative bacterial strains using agar well diffusion assays. Crude extracts generally showed stronger, broader inhibition. Specifically, *Punica granatum L.* and *Nigella sativa* showed the highest activity, reaching zones of 33 mm and 30 mm. Phytochemical screening showed that leaves and peels had a more diverse profile of secondary metabolites (glycosides, tannins, and steroids) compared to seeds. In contrast, the nanoparticles showed more selective activity. *Punica granatum L.* nanoparticles produced the strongest inhibition (52 mm) against *S. aureus*, and *Coriandrum sativum* nanoparticles showed better activity against Gram-negative bacteria than their crude form.
Characterization using FTIR confirmed that phytochemicals were successfully capped on the nanoparticle surfaces. High-performance Liquid Chromatography (HPLC) was employed to separate, identify, and quantify phytochemicals in *Lawsonia inermis, Psidium guajava, Punica granatum L., and Nigella Sativum.* Additionally, X-ray Diffraction (XRD) was used to determine the crystalline phase and purity, and Scanning Electron Microscopy (SEM) was used to observe surface morphology and particle size in *Coriandrum sativum*. Statistical analysis (One-Way ANOVA) confirmed that antimicrobial results significantly depended on the plant source and formulation ($p < 0.05$). These results suggest that while crude extracts provide immediate broad action, optimized green-synthesized nanoparticles offer a way to target specific resistant pathogens. This dual approach provides a versatile strategy for developing sustainable alternatives to conventional antibiotics.

BOARD 30

Investigating Increased Antibiotic Susceptibility in *Pseudomonas chlororaphis* 14B11 Induced by PC2 Bacteriophage Resistance

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The College of Wooster[1]

In the past decades, overuse and misuse of antibiotics have led to an abundance of antimicrobial resistance (AMR), making it harder for scientists to develop new antibiotics. This emergence of AMR has led to an increase in research on alternative therapies to treat antibiotic resistant infections. An alternative method that is currently being assessed is the combined strategy of bacteriophages and antibiotics, known as bacteriophage therapy. Bacteriophages are a type of virus that specifically infects and kills bacterial cells, making them a promising alternative approach to treating AMR infections. Additionally, selective pressure from bacteriophages results in bacterial resistance to phages, thus inducing a fitness trade-off of increased antibiotic sensitivity to the antibiotics the bacteria were once resistant to. There has been much research that studies this fitness trade-off in highly virulent species of bacteria such as *Pseudomonas aeruginosa*, however there is limited research on these interactions in non-pathogenic soil derived species such as *Pseudomonas chlororaphis* 14B11. Furthermore, little understanding of the bacterial protein structures involved in conferring phage resistance and supporting a fitness trade-off. Antibiotic susceptibility to

ampicillin and tetracycline was tested before and after *P. chlororaphis* 14B11 evolved resistance to phage PC2. Minimum Inhibitory Concentration (MIC) assays of the phage resistant mutants showed an increase in antibiotic sensitivity to antibiotic ampicillin however there was a decrease in sensitivity to tetracycline. Additionally, the outer membrane protein (OprM), a part of the MexAB-OprM efflux system, was assessed to determine if this protein structure is altered after phage resistance is induced. Full DNA sequencing will be performed to determine the presence of the *oprM* gene and the presence of mutations in the phage resistant mutants. Future analysis of sequencing data may provide insight into the genomic mechanisms underlying phage-driven fitness trade-offs which could potentially be exploited for therapeutic usage of bacteriophages.

BOARD 31

Unraveling Diversity and Mixotrophic Potential of Dominant Algal Taxa (Cryptophytes) in Lakes Bonney and Fryxell (McMurdo Dry Valleys, Antarctica

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Antarctica's McMurdo Dry Valleys (MDV) have been a site of intensive research for nearly 40 years. One particularly unique feature of this harsh ecosystem are the presence of permanently ice-covered lakes, including Lakes Bonney and Fryxell. The MDV water columns harbor a diversity of extremophilic microorganisms which are adapted to extreme cold, hypersalinity, extreme shade/darkness, nutrient deprivation,, and the polar night - a period of 6 months of complete darkness. Owing to these extreme conditions,these aquatic ecosystems are limited to solely microorganisms. Their communities are dependent upon new carbon production by several algal taxa, including Haptophytes (*Isochrysis*), Cryptophytes (*Geminigera*), and Chlorophytes (*Chlamydomonas*). As part of the Long Term Ecological Research Program, field teams collect a suite of data during the short summer. A diving spectral fluorometer (BBE FluoroProbe) captures depth profiles of major algal taxa, a second moored FluoroProbe monitors the phytoplankton communities year-round.. Furthermore, environmental sequencing of 16S and 18S rRNA has been conducted for the past decade. A comparison between the long-term records of the 18S rRNA and the FluoroProbe has revealed that Cryptophyte sequences overrepresent the eukaryote communities, while the FluoroProbe typically detects relatively low levels of this group. As mixotrophs, Cryptophytes carry a chlorophyll-containing plastid which is detectable by fluorometry; however recent literature has reported widespread loss of plastid in Cryptophyte communities in marine and brackish environments.
We hypothesized that MDV lake Cryptophytes may be under-detected by the FluoroProbe due to a reduction in plastid-carrying taxa. To test this, we sequenced a select set of archived samples from Lake Bonney and Fryxell using a suite of primers targetting different algal groups and functional genes. Molecular estimates of cryptophyte diversity and abundance will be compared with archival FluoroProbe data to evaluate discrepancies and assess whether reduced plastid signal may contribute to fluorometric underrepresentation.

BOARD 32

Examining the Function of a Potential Type VI Secretion System Toxin in a ReproductiveBacterial Symbiont of the Hawaiian Bobtail Squid

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The type VI secretion system (T6SS) is a contact-dependent effector delivery system found in many Gram-negative bacteria, which functions via the mechanical puncturing of neighboring

cells. The T6SS is known to be utilized in interbacterial competition and eukaryotic cell damage. Genomes of several symbiotic bacteria isolated from the accessory nidamental gland (ANG) of *Euprymna scolopes* have been found to possess a T6SS, which may contribute to competition within the organ, or to their symbiotic role in protecting the squid eggs from biofouling. *Leisingera* sp. ANG-M7 in particular was found to contain a second T6SS cluster, and has been shown to kill *Leisingera* sp. ANG-DT *in vitro* despite containing only eight of the 13 core structural genes typical to a T6SS. Cluster 2 of ANG-M7 contains only one potential toxin-antitoxin pair, identifiable by the presence of three conserved PAAR motifs, which does not resemble any effector of cluster 1. To confirm the functionality of these genes, we sought to create disruption mutants of both via homologous recombination. Regions within the suspected toxin and antitoxin genes, as well as a region spanning both, were amplified with PCR and assembled into a plasmid vector. These disruption plasmids were transformed into DH5α *E. coli* for cloning, then transformed into the mobilizer *E. coli* strain RHO3 for conjugation with ANG-M7. The resulting mutants will be screened for loss of T6SS-dependent killing by contact-dependent coculture with ANG-DT. We expect to see loss of T6SS-mediated killing in ANG-M7 mutants where the toxin gene and the pair of genes were disrupted. Disruption of the antitoxin gene may result in self-killing when grown in co-culture with WT ANG-M7. This would validate the role of these genes as a toxin-antitoxin pair, confirm the identity of the toxin, and inform our understanding of this unique T6SS cluster.

BOARD 33

Green Nanotechnology and Phytochemicals as Strategies to Combat Multidrug-Resistent Bacteria

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The rise of multidrug-resistant (MDR) bacteria like S*taphylococcus aureus* and *Pseudomonas aeruginosa* makes finding new treatments a priority. This study compares the antibacterial activity of crude plant extracts and their green-synthesized nanoparticles (NPs) derived from nine plant sources: leaves (*Lawsonia inermis*, *Psidium guajava*, *Salvia rosmarinus*), peels (*Punica granatum L.*, *Pyrus malus*, *Citrus sinensis*), and seeds *(Coriandrum sativum, Trigonella foenum-gracecum, Nigella sativa*). Nanoparticles were biosynthesized using zinc and copper precursors, with plant metabolites acting as reducing and stabilizing agents.
The samples were tested against four Gram-positive and three Gram-negative bacterial strains using agar well diffusion assays. Crude extracts generally showed stronger, broader inhibition. Specifically, *Punica granatum L.* and *Nigella sativa* showed the highest activity, reaching zones of 33 mm and 30 mm. Phytochemical screening showed that leaves and peels had a more diverse profile of secondary metabolites (glycosides, tannins, and steroids) compared to seeds. In contrast, the nanoparticles showed more selective activity. *Punica granatum L.* nanoparticles produced the strongest inhibition (52 mm) against *S. aureus*, and *Coriandrum sativum* nanoparticles showed better activity against Gram-negative bacteria than their crude form.
Characterization using FTIR confirmed that phytochemicals were successfully capped on the nanoparticle surfaces. High-performance Liquid Chromatography (HPLC) was employed to separate, identify, and quantify phytochemicals in *Lawsonia inermis, Psidium guajava, Punica granatum L., and Nigella Sativum.* Additionally, X-ray Diffraction (XRD) was used to determine the crystalline phase and purity, and Scanning Electron Microscopy (SEM) was used to observe surface morphology and particle size in *Coriandrum sativum*. Statistical analysis (One-Way ANOVA) confirmed that antimicrobial results significantly depended on the plant source and formulation ($p < 0.05$). These results suggest that while crude extracts provide immediate broad action, optimized green-synthesized nanoparticles offer a way to target specific resistant pathogens. This dual approach provides a versatile strategy for developing sustainable alternatives to conventional antibiotics.

BOARD 34

Deconstructed Lignin Utilization by *Rhodopseudomonas palustris*

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Lignin is a renewable aromatic carbon-based resource with the potential to replace petroleum-derived products. Its heterogeneous structure presents a barrier to direct biological utilization. Thus, Hydrothermal liquefaction (HTL) is performed to depolymerize lignin into Biocrude transportation fuels, and an aqueous fraction of aromatic acids called the water-soluble organics (WSO). WSO is low-value and environmentally problematic if discarded improperly. The soil bacterium *Rhodopseudomonas palustris* is posed to upscale WSO through its ability to use lignin-derived aromatic acids for growth and production of value-added products. Our objective was to determine the percentage of WSO that is bioavailable to *R. palustris* under anaerobic phototrophic conditions. We tested WSO generated by HTL from four different commercial lignin types (organosolv, lignosulfonate, alkaline, and dealkaline lignin) processed at various temperatures to modulate conversion to Biocrude and WSO. *R. palustris* exhibited growth on WSO from all four types of lignin, with organosolv and lignosulfonate-derived WSO supporting the fastest growth rates (doubling time ~9 h) compared to alkaline and dealkaline-derived WSO (doubling time ~ 18 h). Total organic carbon (TOC) utilization from WSO, total CO_2 fixation, and biomass production by *R. palustris* revealed that WSO from organosolv HTL at 300 – 330 °C was the most efficient growth substrate. Up to 65% of the organosolv-derived WSO was consumed, resulting in ~0.8 g biomass per gram WSO organic carbon consumed, compared to < 0.5 g/g from other WSO types. The higher biomass production on organsolv-derived WSO correlated with increased CO_2 fixation compared to other lignin types. These findings indicated that organosolv-derived WSO is a viable byproduct from the lignin HTL Biocrude production process for decontamination and upscaling to value-added products by *R. palustris*. Further work is needed to identify which WSO compounds are metabolized by *R. palustris*, how this is accomplished, and if compounds inhibit growth and metabolism.

BOARD 35

A culture-dependent DNA analysis of fungal communities in Sandusky Bay

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Despite the pivotal role they play in freshwater ecosystems, freshwater fungi remain an understudied organism. They decompose organic material, cycle nutrients, and have been found to be parasitic towards other organisms, particularly phytoplankton. This includes the cyanobacteria responsible for harmful algal blooms in ecosystems like Lake Erie, releasing cyanotoxins and causing a water quality crisis that impacts both aquatic wildlife and human populations. This understudied state of freshwater fungi is due in part to a lack of consistent methodology. There are debates about the efficacy of culture-dependent versus culture-independent methods, few studies using both, and there is a need for both genome sequences and physiological data to accompany these sequences. We utilized culture-dependent methods and 18S sequencing to identify fungal taxa in Sandusky Bay and determine if fungal communities correlate temporally and with the presence of algal blooms. An isolate library was established by culturing from water samples biweekly on two fungal agar media treated with antibiotics. 67 colonies were isolated in total, with 20 identified as mold and 47 as non-molds based on morphology. All isolates were photo-documented. DNA was extracted from the non-mold isolates, and the 18S rRNA region was amplified using PCR. The PCR products were sent for Sanger Sequencing, and we are awaiting results. Bioinformatics and data analysis tools will be used to identify taxa, construct a phylogenetic tree, and identify potential correlations between taxa and environmental parameters. This project aims to contribute to the limited data on freshwater fungi, providing both sequencing and physiological data. Furthermore, it argues for the importance of studying fungal communities when studying freshwater environments and monitoring water quality.

BOARD 36

Characterizing the Microbiome and Antimicrobial Activity of Mud Crab and Porcelain Crab Eggs

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Defensive symbiosis is a mutualistic interaction where a symbiotic partner provides protection to its host organism from predation or infection by fungal, viral, or bacterial pathogens. Multiple instances of defensive symbiosis have been described where symbiotic bacteria produce secondary metabolites that prevent biofouling of developing eggs. These studies found that bacteria isolated from squid, lobster, and shrimp eggs have antimicrobial activity to protect the eggs from fungal infections, however this activity has yet to be described in crabs. We investigated the microbial community isolated from the eggs of two species of crab collected from Beaufort, North Carolina, the mud crab, *Eurypanopeus depressus,* and porcelain crab, *Petrolisthes armatus*. Microbiome analysis revealed that the *Alphaproteobacteria*, *Bacteroidia*, and *Gammaproteobacteria* were the most abundant groups present in the microbial community of these crab eggs. No significant differences were found between the microbial communities of the two crab species' eggs. Additionally, 61 bacteria from *E. depressus* and 42 bacteria from *P. armatus* were isolated on seawater tryptone media. In total, 95 egg isolates were tested for antimicrobial activity against the marine bacteria, *Roseovarius* sp. TM1035 and *Vibrio fischeri* ES114, using a zone of inhibition assay. We found that 26 isolates inhibited TM1035, 6 isolates inhibited ES114, and 2 isolates inhibited both target strains. These findings suggest that crabs may also have defensive microbial symbioses similar to those found in other marine invertebrates and lays the foundation for future explorations into the function of these egg communities.

BOARD 37

Developing antibacterial wound dressing: Eugenol nanofibers exhibit antibiotic level antibacterial activity

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Bacterial infections at wound sites remain a critical clinical problem and contribute to infection-related mortality worldwide. One strategy to minimize this problem is to utilize wound dressings that not only serve as passive physical barriers but also provide antimicrobial activity. Thus, developing bioactive dressings that deliver antimicrobials directly to the wound site while remaining nontoxic to human tissue is an important goal. Eugenol, a natural compound found in clove oil, has well-documented antibacterial properties and therefore is a promising bioactive candidate for wound dressing materials. However, eugenol is highly volatile and poorly water-soluble, which limits its direct use. Therefore, in collaboration with Dr. Tamer Uyar's lab, we evaluated eugenol-loaded electrospun nanofibers made with either metal–organic frameworks (MOFs) or γ-cyclodextrin (g-CD) in a polylactic acid (PLA) scaffold for antibacterial efficacy and cytotoxicity.
To test antibacterial activity against Gram-positive (*Staphylococcus aureus*) and Gram-negative (*Escherichia coli)*, we analyzed bacterial growth in the presence of these nanofibers. Colony counts from serial dilutions were used to calculate area under the growth curve normalized to untreated controls. All nanofiber formulations supported similar growth during the first 0–2 hours. However, by 4 hours eugenol MOF/PLA nanofibers reduced *S. aureus* counts 298-fold and *E. coli* counts 326-fold compared to control MOF/PLA fibers. In contrast, eugenol g-CD/PLA fibers reduced *S. aureus* growth 5-fold. Notably, 67.5 mg of eugenol MOF/PLA nanofibers performed comparably to 200 µg streptomycin against both species.
To evaluate safety, we exposed HeLa cells to extracts from 70 mg of each nanofiber formulation for 24 hours and measured viability with an MTT assay. All eugenol-loaded and control nanofibers maintained high cell viability, while 0.01% Triton X-100 reduced viability by 85%, confirming assay sensitivity. These findings show that eugenol-loaded MOF/PLA nanofibers provide antibiotic-level antibacterial activity without harming mammalian cells, supporting their promise as natural-compound-based active wound dressings.

BOARD 38

Land use impacts on downstream microbial communities in a coastal Virginia lake

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Drainage area land-use has had a significant impact on aquatic ecosystems. Studies have shown that this runoff provides an excess of certain nutrients such as nitrogen and phosphorus, and this imbalance of nutrients allows for significant alterations in the normal environment for the microbial communities present that can lead to changes in the taxonomic makeup of the area. In this study, we examined the impact of land use on the downstream flow of bacterial communities from streams into a dammed lake. We sampled from three streams flowing into Lake Matoaka in Williamsburg, VA. One stream drains a forest watershed, another one drains the College of William and Mary, and one drains the city. Bacterial diversity and abundance, geochemistry and hydrological parameters were collected. Our results showed that while geochemical and hydrological parameters largely differed in stream sites based on watershed, the lake sites were similar. There were distinct differences in the diversity metrics from the forested site vs. the two more urbanized sites. In addition, bacteria were the most persistent moving downstream from the forested stream. These results further emphasize the importance of studying watershed land use on downstream microbial ecology even in small watersheds, as they can greatly influence microbial communities.

BOARD 39

Plate- and Liquid-Based Growth Methods to Co-culture Cyanobacteria with Environmental *Pseudomonas*

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In August 2014, the city of Toledo, Ohio issued a do-not-drink advisory due to higher concentrations of the cyanotoxin microcystin in the city drinking water caused by the collapse of a cyanobacterial harmful algal bloom, which affected over 400,000 people over the course of 3 days. Currently, bloom control is mainly performed at water treatment plants, as opposed to directly controlling the source of the bloom in this lake. Here, we describe potential ways to co-culture the cyanobacterial strains *Planktothrix* PCC8927 and *Microcystis aeruginosa* LE3 with environmental *Pseudomonas*, for the purpose of testing *Pseudomonas* as an in-lake biocontrol method for cyanobacterial algal blooms. Cyanobacteria were grown on solid agar plates with varying nutrient compositions, and both cyanobacteria and *Pseudomonas* were grown in either liquid BG-11 or BG-11 supplemented with glycerol and glutamine employing different size well plates, with growth being measured as eithe phycocyanin concentration (cyanobacteria) or absorbance at 600nm (*Pseudomonas*). *Pseudomonas* growth was also assessed in spent liquid media that had previously been used to grow cyanobacteria. Plate-based growth conditions were ineffective for growing cyanobacteria, as phycocyanin concentrations did not change across the 4 weeks of growth, and mold growth was severe on many of the plates. Liquid-based growth conditions were much more favorable, as phycocyanin concentration doubled in the supplemented BG-11 as opposed to normal BG-11, and supplemented BG-11 also grew the *Pseudomonas* strains similar to that obtained with *Pseudomonas*' minimal media. Spent cyanobacterial BG-11 also grew *Pseudomonas* similar to that of the minimal media, but growth started to fall after 72 hours. Overall, liquid BG-11 supplemented with glycerol and glutamine could act as a media type in the coculture of cyanobacteria and environmental *Pseudomonas*, which will permit further testing of *Pseudomonas* as a cyanobacterial algal bloom biocontrol agent.

BOARD 40

Cysteine biosynthesis is essential for survival of *Shigella flexneri* under oxidative stress

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Shigella flexneri is a human-adapted enteric pathogen that causes shigellosis, a severe form of infectious diarrhea. Upon ingestion, *S. flexneri* navigates to the colon and invades epithelial cells, triggering a strong inflammatory response by the immune system. Reactive oxygen species (ROS) are a major component of this inflammatory response, aimed at killing the invading pathogen. However, the mechanisms by which *S. flexneri* manages to survive in this hostile environment are poorly understood. Cysteine, an essential amino acid having a free sulfhydryl group, can neutralize ROS. Therefore, we hypothesized that the cysteine biosynthesis pathway may play a crucial role in neutralizing free radicals and ROS. To test this, we first identified the essential genes involved in the cysteine biosynthetic pathway, followed by constructing deletion mutants and testing their growth rate in presence of ROS. Using the bioinformatic tool Biocyc, we scanned the *S. flexneri* genome to identify the putative cysteine biosynthetic operon. Amongst the genes we identified, we selected *cysM* and *cysK* as the primary genes essential for functional production of cysteine in *S. flexneri*. To test their role in promoting survival of *S. flexneri* in ROS rich environments, we first constructed *S. flexneri* strains where we substituted *cysM* with an antibiotic gene (*kan*). Then we compared the ability of the wildtype and the *cysM::kan* strains to survive in an environment replete with ROS by subjecting them to different hydrogen peroxide concentrations. We found that the wildtype *S. flexneri* could survive in moderate amounts of ROS stress, but the mutant strain failed to grow at all. This confirmed our hypothesis that the cysteine biosynthesis gene *cysM* is essential for *S. flexneri*'s survival under oxidative stress. This study advances the field of host-pathogen interactions by uncovering how *S. flexneri* withstands oxidative stress during its infection cycle in the human host.

BOARD 41

Contribution of Kitchen Areas to the Fungal Content of the Dust Microbiome in Homes of Children with Asthma

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Asthma and other respiratory issues are commonly agitated by dust. The dust microbiome is home to various contaminants which inflame these symptoms, and this often includes fungi and its spores. Basements and bathrooms are commonly noted places for fungal growth due to increased moisture present. Which kitchens are not grouped with these rooms as commonly, they also have high moisture areas. Common places for fungal growth in the kitchen include kitchen faucets, drains, and even in the dishwasher, due to constant contact with water. However, we do not yet understand how much these kitchen fungi sources contribute to the overall fungal microbiome in asthmatic children's homes. In this project, these common kitchen locations, as well as any evident mold or water damage, were tested to determine the impact of these spots on the homes' overall fungal content of its dust microbiome in the homes of asthmatic children between the ages of 3 and 15. Swabs of a home's kitchen faucet, kitchen drain, and door trim were taken, along with swabs of the dishwasher, and even mold and water damage if present in the home. The door trim was taken as a control and to compare against to see how these sources contribute to the overall fungal communities in the home's dust. Each swab was stored at -20°C to preserve any fungi present. Swabs were then extracted for fungal DNA and then aliquoted at 20µL undiluted and again stored at -20°C until they were sent for sequencing. This project is currently awaiting sequencing results.

BOARD 42

Cyano-peptide diversity in Sandusky Bay

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Toxic cyanobacterial blooms can cover large expanses of the Western Basin of Lake Erie. With an abundance of species such as *Microcystis aeruginosa* in Sandusky Bay, synthesis of toxic secondary metabolites such as microcystins and other cyano-peptides is likely. Using liquid chromatography-mass spectrometry (LC-MS) with photodiode array (PDA), cyanopeptides were identified using characteristic UV-emission spectra and mass-to-charge (*m/z*) ratios. The following cyano-peptide classes were identified: microcystins, anabaenopeptins, micropeptins, cyanopeptolins, aeruginosins and microginins.

BOARD 43

Seasonal Dynamics of Algal Communities in Lake Fryxell (McMurdo Dry Valleys, Antarctica) Revealed Through Autonomous Sensing

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The McMurdo Dry Valleys (MDV) of Antarctica have been the subject of scientific inquiry for more than four decades, particularly the unique and fragile ecosystems of several permanently ice-covered lakes. The MDV lakes have common physicochemical characteristics, including limited light, low temperatures, and chemically stratified water columns. However, each lake has unique environmental conditions which drive differences in phytoplankton communities. Lake Bonney, one of the most well-studied of these lakes, is oligotrophic and hypersaline and generally dominated by photoautotrophic Chlorophyte species. Lake Fryxell, mesotrophic and brackish and harbors a mixotrophic Cryptophyte population, is slightly less-so.
Previous long-term studies of the MDV lake phytoplankton communities have primarily been restricted to the short summer season (Oct – Feb). The ALPS (Autonomous Lake Profiling System) is a project which utilizes moored sensors and automated sampling to extend into the polar winter. Seasonal trends in Lake Bonney revealed that algal populations are active during the polar night; however, the communities shift from photoautotrophic Chlorophytes to mixotrophic brown phytoplankton species. Given the distinct algal communities between MDV lakes, here we report on seasonal trends in Lake Fryxell using year-round data from a moored spectral fluorometer (bbe FluoroProbe). Our results reveal that seasonal trends in the phytoplankton communities of Lake Fryxell are distinct from those previously reported in Lake Bonney.

BOARD 44

Antimicrobial Properties of Red Oak and White Oak Organic Extracts

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The rise in antimicrobial resistance is a global issue, requiring the discovery of new antimicrobials. Recent studies have begun to revisit native plants as potential sources of new antimicrobials for drug discovery. In this study, we collected the bark of four red oaks, *Quercus rubra*, and four white oaks, *Quercus alba*. Samples were frozen using liquid nitrogen, ground with a mortar and pestle, and extracted using 95% ethanol for 48 hours. Organic extracts were dried using a rotary evaporator and then resuspended in DMSO for zone of inhibition testing. Extracts were tested against six relatives of the ESKAPE pathogens, which are some of the major threats to healthcare due to high rates of antibiotic resistance: *Enterococcus raffinosus, Staphylococcus epidermidis, Escherichia coli, Acinetobacter baylyi, Pseudomonas putida,* and *Enterobacter aerogenes*. During initial testing with 1 mg/mL of extract, only one red oak sample inhibited growth of three bacteria: *P. putida, E. raffinosus,* and *A. baylyi* (average ZOI 1.45cm). During the second round, more highly concentrated extracts were tested (average 93±77.6 mg/ml) against these three bacteria. We found that there was activity in three red oak samples and one white oak sample against *E. raffinosus* (average ZOI 1.09cm). Three red oak and two white oak samples inhibited *A. baylyi*. Finally, two red oak samples inhibited *P. putida*.

Future research will need to screen additional bark samples, collected from different times of the year, to further explore the antimicrobial activity. These findings can further our understanding of antimicrobial activity in native plants that have been used traditionally by indigenous communities and may help fight resistant bacteria.

BOARD 45

Testing a Covalent Inhibitor Scaffold for Antifungal Targeting in *Candida albicans*

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Candida albicans is an opportunistic fungal pathogen responsible for both mucosal and deep tissue infections. Immunocompromised individuals, such as HIV and cancer patients, are particularly vulnerable to Candida infections, with over 40% of nosocomial infection-related mortalities. However, the current arsenal of antifungal drugs is limited due to the challenge of developing selective agents against fungal targets without causing significant human side effects, given the shared biology of fungi and humans as eukaryotes. Moreover, increasing resistance to existing antifungal drugs necessitates the exploration of novel therapeutics. Vinyl sulfones are a well-known chemical scaffold in medicinal chemistry that enables selective and irreversible covalent interactions with diverse biological targets. Current research has highlighted vinyl sulfones as promising antibacterial, antiparasitic, and anticancer agents, yet their antifungal potential remains largely unexplored. Recent structural and enzymatic studies demonstrated that vinyl sulfones rapidly and irreversibly inactivated the Candida enzyme aspartate semialdehyde dehydrogenase (CalASADH). The ASADH enzyme plays a critical role in the aspartate pathway, responsible for the synthesis of almost 40% of essential amino acids in all known microorganisms but is absent in humans. Research in our lab shows that a series of vinyl sulfone derivatives exhibit fungistatic, fungicidal, anti-filamentation, anti-biofilm, and metabolic disruption activity against C. albicans. Moreover, here we show that vinyl sulfones exhibit broad-spectrum antifungal activity against multiple Candida species, including C. auris, a multidrug-resistant pathogen of growing global concern. Our objective is to identify potent vinyl sulfone compounds that selectively inhibit C. albicans via covalent inactivation of CalASADH, offering a novel approach to antifungal therapy.

BOARD 46

Amending agricultural fields with dredged materials enhances soil health, biological cycling of phosphate, and soybean growth

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Phosphorus (P) cycling in soil is crucial for crop productivity and sustainable agriculture, particularly in the face of growing environmental challenges and nutrient depletion. Dredged material (DM) from the Western Lake Erie Basin (Toledo Harbor, Ohio) is a potential soil amendment for replenishing lost topsoil, but its effects on biological phosphate cycling remain unclear. We conducted a greenhouse experiment with soybeans to evaluate how DM application to an agricultural field influences soil nutrient dynamics, plant growth, and microbial P-cycling activity. Soil, plant, and microbial parameters, including the expression of a key P-mineralizing enzyme gene phoD, were measured at various soybean growth stages. Although DM amendment did not substantially increase soil total P, it elevated bioavailable P (70-90 mg kg^{-1}), calcium (Ca) (14,403-17,598 mg kg^{-1}), and magnesium (Mg) (8,916-10,725 mg kg^{-1}), pH (7.3-7.5), cation exchange capacity (29.68-31.07 meq 100g^{-1}), and soybean root and shoot growth relative to an unamended conventional farm soil. However, this growth resulted in lower concentrations of some nutrients in plant tissues, possibly due to a nutrient dilution effect. RT-qPCR analyses indicated that phoD expression increased over time in DM-amended soils. The timing of these increases, along with delayed rises in bioavailable P, suggests that DM may have stimulated microbial P-mineralization indirectly by promoting plant growth and associated rhizosphere activity rather than through a direct chemical effect. Overall, our findings suggest that incorporating DM into farm soil

can improve soil health and crop performance by boosting nutrient cycling processes and stimulating plant growth.

BOARD 47

Identification of mechanisms that govern *Candida albicans - Staphylococcus aureus* polymicrobial interactions

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Candida albicans, an opportunistic fungal pathogen, and the bacterium *Staphylococcus aureus* are among the top causative agents of nosocomial infections worldwide. Both pathogens have high morbidity and mortality rates on their own but are regularly co-isolated from various infectious niches within the human body. Concerningly, polymicrobial interactions between *C.albicans* and *S. aureus* during infection contribute to enhanced virulence, impaired treatment efficacy, and increased patient mortality rates. Fungal processes such as hyphal growth, cell adhesion, and quorum sensing have been implicated in facilitating *C. albicans-S. aureus* interactions, but significant gaps remain in our understanding of how these two microbes co-exist within these various infectious niches. To address this, we sought to identify fungal genes that are necessary for growth in the presence of the methicillin-resistant *S. aureus* (MRSA) strain USA300. We have screened 283 *C. albicans* mutants harboring single gene knockouts for their ability to grow in the presence and absence of USA300. To identify *C. albicans* mutants with altered growth kinetics solely in the presence of MRSA, fungal mutants that showed growth above or below 1 standard deviation of the mean on *S. aureus* co-inoculation plates, but demonstrated growth within 1 standard deviation of the mean on *C. albicans*-only control plates, were identified as candidates for impaired polymicrobial fitness. We have identified 7 mutants that show growth attenuation in the presence of USA300 but grow at wildtype levels on their own. None of these genes have been previously implicated in *C. albicans – S. aureus* synergism. Gene ontology assessment of these hits shows an enrichment in genes involved in *C. albicans* cell wall organization and filamentation (*CDC10, PIR10, DCK2).* Further screening will enhance our understanding of genetic factors that drive *C. albicans* and *S. aureus* interactions and may provide future drug targets to disrupt these processes moving forward.

BOARD 48

Host-Associated Thermal Adaptation and DNA Uptake Sequence Dynamics in *Neisseriaceae* from Ectothermic and Endothermic Hosts

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Host body temperature is a major ecological factor shaping bacterial physiology and genome evolution. However, most research on *Neisseriaceae* has focused on human-associated species, leaving adaptation in non-mammalian hosts less understood. In this study, I will compare conspecific isolates of *Uruburuella suis* recovered from pigs (endothermic hosts) and eastern box turtles (ectothermic hosts). I am examining temperature dependent growth phenotypes across 0–37 °C to define minimum, optimal, and maximum growth temperatures. I'm testing the hypothesis that pig-derived isolates will exhibit higher optimal growth temperatures and greater fitness at elevated temperatures than turtle-derived isolates. Biofilm and auto-aggregation assays will further assess whether reduced temperatures differentially affect adhesion phenotypes. Additionally, comparative genomics is being used to evaluate relatedness and the distribution of a common *Neisseria* repetitive DNA element, the DNA uptake sequence (DUS). Whole-genome sequencing confirms that turtle-derived isolates belong to *U. suis*, sharing species-level ANI (>95%) and high AAI values with pig-derived strains. Genome analyses show a predominant DUS motif in turtle isolates, with variant forms in some strains. Whether DUS variants are linked to functional gene categories, horizontal gene transfer, or strand and reading-frame biases is underway. In parallel, I am investigating the role of DUS sequences in natural transformation in *Neisseria* isolates. Transformation assays will test DUS-dependent and Type IV pilus-dependent competence.

BOARD 49

Genomic Analysis of Penicillin Resistance in Environmental Bacterial Isolates

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Antibiotics are among the most effective tools for treating bacterial infections; however, their widespread use has accelerated the emergence of resistant strains. Resistance to beta-lactam antibiotics, such as penicillin, arises when bacteria acquire genetic changes that allow them to survive exposure to drugs that would normally inhibit cell wall synthesis. These adaptations occur through processes including mutation, natural selection, enabling resistant populations to persist and spread. As a result, antibiotic resistance continues to pose a significant threat to global health.
While antibiotic resistance is a widely recognized problem, the specific genetic basis of penicillin resistance in environmental bacterial isolates remains incompletely understood. This study investigates environmental bacterial isolates from the Tiny Earth course-based undergraduate research experience (CURE) that were assessed to be resistant to penicillin. Genomic sequencing was conducted using long-read nanopore technology (Plasmidsaurus), and the resulting genome sequences were analyzed using bioinformatics approaches to identify mutations linked to resistance. By linking observed resistance patterns to underlying genetic variation, this study aims to provide insight into the molecular mechanism driving resistance and improve understanding of how bacterial populations adapt under antibiotic pressure.

BOARD 50

Mechanistic investigation of phosphonoalamide natural products

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Phosphonoalamides are a recently discovered family of phosphonate oligopeptide natural products (NPs) produced by strains of *Streptomyces* and *Bacillus*. They are defined by the incorporation of l-phoshonoalanine (PnAla) at the *N*- or *C*- terminus of a di- or tripeptide. Although l-PnAla has been isolated previously in marine and freshwater animals, as well as humans, its innate function remains unclear. To understand the mechanisms underlying the antimicrobial activity of the phosphonoalamides, we chemoenzymatically synthesized seven PnAla-tripeptides containing combinations of Ala, Val, Thr, and Gly. Product formation was quantified by ^{31}P NMR spectroscopy. The antibacterial activity of the reaction products was then measured using disc diffusion and microbroth dilution assays. PnAla-Ala-Val, PnAla-Ala-Ala, and PnAla-Thr-Gly displayed the most potent activities, inhibiting growth of both gram-negative and gram-positive bacteria. Free l-PnAla exhibited 8-fold reduced potency against *B. subtilis* 1A1282 and 160-fold reduced potency against *E. coli* K12 in comparison to PnAla-Ala-Val. Based on these results, we hypothesized the phosphonoalamides may function through a 'Trojan-horse' mechanism, in which the composition of the oligopeptides dictates recognition and cellular uptake, and cytoplasmic peptidases subsequently act to release the active l-PnAla pharmacophore. To test this hypothesis, we raised spontaneous mutants of *B. subtilis* 1A1282 and *E. coli* K12 against l-PnAla and PnAla-Ala-Val. The mutants were tested against l-PnAla, PnAla-Ala-Val and other phosphonate natural products including phosphinothricin, aminomethylphosphonate, fosfomycin, and phosphonoacetate. Although several mutants were insensitive to all tested phosphonates, strains that were specifically resistant to l-PnAla or Phosphonoalamide A were obtained. These results pave the way to elucidate the molecular mode of action of phosphonoalamides as well as characterize their chemical properties that modulate the extent of their bioactivity.

BOARD 51

Elucidating the molecular mechanisms of IL-17 receptor signaling in megakaryocytes during oropharyngeal candidiasis

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Megakaryocytes are best known for their role in producing platelets to maintain hemostasis. However, megakaryocytes are also critical for host defense against pathogens including the opportunistic human fungal pathogen Candida albicans, which is the main cause of oropharyngeal candidiasis (OPC). While megakaryocytes are typically found in the bone marrow, there are also distinct populations found in other tissues such as the lung and tongue. Both lung and oral megakaryocytes have been shown to have more of an immune phenotype, expressing higher levels of antigen presenting cell-related molecules (MHCII and B7-2) as compared to megakaryocytes found in the bone marrow. Platelets themselves are also directly involved in antifungal responses through recruitment of neutrophils during inflammation and have also been shown to kill Candida directly. Protection against Candida albicans critically depends on interleukin (IL)-17-mediated immune responses as signaling through the IL-17 receptor (IL-17R) leads to the upregulation of genes that control neutrophil recruitment to the site of infection and the production of antimicrobial peptides that work to clear Candida from the mucosa. Oral megakaryocytes have been shown to respond to IL-17, with IL-17R signaling being required for expansion of megakaryocytes in the context of OPC. In line with this, mice lacking the IL-17RA show reduced platelet levels, suggesting that IL-17R signaling in megakaryocytes contributes to platelet homeostasis and function. Mechanistic studies focused on the IL17 signaling cascade have previously been limited to epithelial and mesenchymal cells and have never been explored in megakaryocytes. We aim to elucidate the downstream molecular mechanisms of IL-17R signaling in megakaryocyte-mediated antifungal immunity during OPC.

BOARD 52

The Effects of Glyphosate on the Growth of *Microcystis aeruginosa*

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Glyphosate is a non-selective herbicide that is often used for agricultural management within the Great Lakes catchment region. As an agricultural herbicide, glyphosate works as an EPSP synthase inhibitor in non-resistant plants, preventing the shikimate pathway from producing vital amino acids that are essential for plant growth and survival. Some degraded forms of glyphosate may contain inorganic phosphates which are known to have beneficial effects on cyanobacterial growth. However, when non-degraded forms of glyphosate are used on cyanobacteria, varying results have been observed. *M. aeruginosa* cultures originally isolated from Lake Erie were exposed to environmentally relevant concentrations of glyphosate. The concentrations were chosen based on the room-temperature solubility of glyphosate in BG-11 growth media, starting at 1.2% (w/v) and reducing the concentration by 0.2% for each experimental group. Absorbance readings were taken every 24 hours for 7 days to measure changes in phycocyanin and total chlorophyll concentrations. The results indicated that as glyphosate concentrations increased, the total chlorophyll and phycocyanin concentrations decreased to undetectable values for each test group in a dose-dependent manner. These results indicate that non-degraded forms of glyphosate present in runoff entering the Great Lakes may lead to decreases in the severity of *M. aeruginosa* blooms.

BOARD 53

Effectiveness of Popular Acne Treatments on Common Acne-Causing Bacteria

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Acne vulgaris, commonly called acne, is categorized as one of the most common chronic skin disorders worldwide. Acne is first caused by hair follicles becoming clogged with sebaceous oils and dead skin. This

condition is then worsened by the bacteria *Cutibacterium acnes*, which thrive on sebaceous oils and dead skin, worsening skin inflammation. *Staphylococcus epidermidis*, another common skin bacteria, also contributes to the formation of acne lesions. Acne may be worsened due to secondary infection by the opportunistic pathogen, *Staphylococcus aureus*. Various topical and oral medications may be used to treat acne based on its severity. Treatments may be recommended by a doctor or dermatologist, or may be home remedies recommended by other sources. In this study, the effectiveness of common topical acne treatments on *C. acnes*, *S. epidermidis*, and *S. aureus* was determined *in vitro*. Common clinical acne treatments benzoyl peroxide (10%) (BPO), hypochlorous acid spray, salicylic acid (2%), and common home remedies tea tree oil, witch hazel, and honey were tested individually on their ability to prevent growth of *C. acnes*, *S. epidermidis*, and *S. aureus*. Combinations of the individual treatments were made and tested to investigate if treatments were more effective in inhibiting bacterial growth alone or combined with another treatment. The effectiveness of the treatments was determined by measuring areas of no bacterial growth, called zones of inhibition, produced by the Kirby-Bauer disc diffusion technique. The treatment that produced the largest zones of inhibition was determined to be most effective in preventing growth of *C. acnes*, *S. epidermidis*, and *S. aureus*. Combination treatments containing benzoyl peroxide or tea tree oil appear to produce the largest zones of inhibition and are most effective for preventing *S. epidermidis* and *S. aureus* growth. Ongoing work will determine the most effective treatment in preventing the growth of *C. acnes.*

BOARD 54

Mitochondrial complex I is required for *Candida albicans* growth within the kidneys

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To cause disease, *Candida albicans* must overcome the nutritional limitations imposed by the host to develop an infectious niche. Each organ infected during systemic candidiasis poses a unique environment that *C. albicans* must adapt to for survival and proliferation. However, we know very little about tissue-specific fitness requirements that are needed for successful fungal colonization during systemic infection. To address this, we have developed an *ex vivo* kidney media composed solely of murine kidney homogenate to determine metabolic pathways that are necessary for fungal growth in this niche. To identify genes necessary for kidney survival, we assessed the growth of 674 mutants harboring single gene knockouts on both kidney and nutrient rich YPD media. We identified 11 mutants that showed kidney-specific growth defects. Surprisingly, 4 of the 11 hits are associated with complex I of the electron transport chain (ETC). We hypothesized that a lack of fermentable carbon sources within the kidney is responsible for the observed ETC requirement for growth. Indeed, supplementing kidney media with fermentable glucose, but not non-fermentable glycerol, restored the growth of the ETC mutants to wildtype (WT) levels. Three of the mutants identified, ORF19.4758, ORF19.2821, and ORF19.1625, have putative NADH dehydrogenase activity, but have yet to be empirically implicated as components of the ETC. Growth in anaerobic conditions or in the presence of rotenone, a complex I inhibitor, had no impact on the growth of the putative ETC mutants but did significantly affect WT growth. All three mutants also showed increased fluconazole susceptibility, and filamentation and virulence defects at comparable levels to *NUO2*, a known NADH dehydrogenase, supporting their involvement in the ETC. Collectively, these findings indicate aerobic respiration is required for fungal survival in the kidney and provide a novel platform for the identification of niche-specific nutritional requirements.

BOARD 55

Discovery of Phosphonate Natural Products from Streptomyces

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Phosphonate natural products are a distinctive class of secondary metabolites defined by a carbon–phosphorus (C–P) bond. Due to their structural similarity to phosphate esters and carboxylates, phosphonates function as

potent enzyme inhibitors, leading to clinically and agriculturally significant compounds. Genes required for phosphonate biosynthesis are broadly distributed across microbes, indicating a substantial reservoir of unexplored chemical diversity. To explore the diversity of these compounds, we employed a genome mining approach to identify microbial strains encoding *pepM*, a gene present in all characterized phosphonate biosynthetic pathways. Through this strategy, we identified a Streptomyces strain containing a biosynthetic gene cluster (BGC) similar to the dehydrophos BGC from *Streptomyces luridus.* Based on sequence identities comparing the proteins of both BGCs, as well as the presence of additional genes, we hypothesize that our *Streptomyces* strain may produce dehydrophos-like compounds with potent antimicrobial activity. To characterize the phosphonates, we cultivated the strain on solid media and applied various chromatographic methods, which ultimately revealed 5 distinct phosphonates produced by this strain. Overall, this work highlights the importance of genome mining to discover unique phosphonate biosynthetic pathways and expanding the chemical diversity of phosphonate natural products.

BOARD 56

Colony count of cultured microbes from decomposing pork loin

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When organic material is decomposed, a community of microbes called a necrobiome helps with decomposition and recycling nutrients. At different stages of decomposition, different microbes are present. Therefore, necrobiomes are useful during forensic investigations of crimes that result in a victim's death. Pork loin was used to simulate how a human would decompose in different locations over time. The pork loin was buried in different locations on the Heidelberg University campus. Throughout the decomposition process, microbes were cultured using agar plates to track the necrobiome and identify the microbes that are present. A plot of the colony count from each location over time was created to observe the change in the necrobiome during decomposition. It was expected that less microbes will be part of the necrobiome at the end of the project than in the beginning because there will be less nutrients for the microbes to consume. Furthermore, there would be a larger variety of microbes participating in the necrobiome in early stages of decomposition than in later stages. The results of this project rejected this claim. The colony count from each location increased, however the control group leveled out in contrast to the experimental group that continued to increase up until the end of the project. This could be due to the decomposition process taking a longer time for the pork loin than anticipated, and microbes still had nutrients to thrive. An area of study for the future could be sequencing the genome of a bacterium to distinguish any mutations, specifically antibiotic-producing mutations that could help with the current antibiotic resistance crisis.

BOARD 57

Analyzing Soil Microbial diversity in Organically Managed Fields Amended with Dredged Material in Northwest Ohio.

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Each year, around 1.5 million tons of sediments are excavated from the federal navigation channels at Toledo Harbor, which used to be disposed in an open lake placement area in Lake Erie. After the ban of open water disposal utilizing this dredged material (DM) as a soil amendment could provide a sustainable approach to managing DM disposal issues. Previous research has shown the DM can improve soil physio chemical properties in the greenhouse setting; current research will focus on investigating the impact of DM on the microbial community in an organic field in northwest Ohio. This study aimed to characterize the taxonomic diversity of microbial communities in the fields amended with DM. Using 16S rRNA gene sequencing analyzed through QIIME2, we profiled the microbial community structure. The study has three organically managed fields. Field 1 and field 3 received 40 tons per acre and 80 tons per acre of DM, respectively, and field 2 received no DM (control treatment). Alpha diversity metrics did not show significant differences among the fields. ($p > 0.05$).

This suggests that the microbial richness and evenness remained relatively stable regardless of the addition of DM. Principal component analysis (PCoA) based on Bray-Curtis dissimilarity revealed clear separation of microbial communities among the three treatments. Each treatment formed a distinct cluster in the emperor plot, indicating compositional differences in microbial communities. PICRUSt 2 based functional predictions further revealed variation in genes associated with phosphorus, nitrogen, and carbon cycling. Notably, phosphorus-cycling genes (phoD and phytase) were enriched in DM amended soils and showed positive associations with soil calcium, suggesting enhanced microbial capacity for organic phosphorus mineralization and solubilization under Ca-enriched conditions. This suggests that while DM influenced microbial structure, functional potential was regulated over time, reflecting adaptation to evolving soil conditions and highlighting the importance of microbial community management for sustainable productivity and environmental health.

BOARD 58

Prevalence and recent activity of an endogenous gammaretroviral lineage in gray fox

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Endogenous retroviruses (ERVs) are the fossilized remnants of ancient retroviral infections in the genome of a host. While generally characterized as defective or inactive, some species contain ERVs whose members have evidence of relatively recent or ongoing activity, as characterized by high sequence similarity, presence of full-length copies with one or more open reading frames, or presence of unfixed ERV loci between individuals, raising the possibility of retained function(s) and/or the potential to impact the host. We previously characterized a chimeric gammaretrovirus-like ERV lineage, CfERV-Fc1(a), or 'ERV-Fc1', identifying five loci present among all extant Canidae, indicating germline entry pre-dating the most recent ancestor of living canids. *Urocyon cinereoargenteus*, colloquially known as the gray fox, is one of two extant members of the basal genus of Canidae that originated ~13 mya. Around ~0.5 mya, the ancestral gray fox diverged into the eastern and western subspecies resulting from geographical isolation. The recent release of an eastern gray fox reference genome from an individual from Vermont offers a unique opportunity to examine ERV-Fc1 activity since speciation following its recent evolution. Here we characterize ~35 ERV-Fc1 copies present in the gray fox reference genome, including a putatively intact provirus dating to within the last ~0.8 mya. By searching publicly available whole genome sequence (WGS) data for 42 gray foxes sampled across the United States, we have additionally identified and characterized ~104 non-reference ERV-Fc1 copies that are variably present across individuals. We implemented a read-based genotyping approach to examine the regional prevalence of these loci across samples, revealing trends among western and eastern sampled individuals. Evaluation of the infective capacity and retained gene functions of this lineage are ongoing. Our findings suggest relatively recent activity and raise the possibility of ongoing spread of ERV-Fc1 within this species.

BOARD 59

Mechanistic Insights into HIV-Associated Cardiovascular Risk: The Interplay of NK Cell Dysfunction, Inflammation, and Gut Microbial Translocation.

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HIV causes persistent inflammation, gut dysbiosis, and immunosenescence that increase cardiovascular disease (CVD) risk despite antiretroviral treatment (ART). Natural killer (NK) cells play a key role in controlling HIV infection and has also been implicated in atherosclerosis development.
We examined the NK cells in HIV-infected adults on ART by comparing those with high versus low coronary artery calcium score, a marker of subclinical atherosclerosis. Age-matched participants included people without HIV (PWoH, n=15), people with HIV (PLWH) with low coronary calcium scores (n=15) and high coronary calcium scores (n=15). High dimensional flow cytometry was used for immune profiling and ELISA for plasma biomarkers. Pearson correlation and one-way ANOVA assessed associations between immune parameters and cardiovascular risk.
Among five NK cell subsets, $CD56^{dim}$ $CD16^{-}$ subset frequency was significantly reduced in PLWH with high coronary calcium compared to those with low coronary calcium, while $CD56^{-}CD16^{+}$ subset was increased. In the

$CD56^{dim}CD16^{-}$ subset, CD57 expression (maturation/memory marker) was lower (P=0.02) and CX3CR1 (P=0.01) (homing receptor for inflamed endothelium) and KLRG1 expression was higher. Plasma IL-6 levels were elevated(P=0.0057) in PLWH with high coronary calcium versus the low coronary calcium group and PWoH and intestinal fatty acid-binding protein(I-FABP) a gut dysbiosis marker, increased in both PLWH groups relative to PWoH. $CD56^{dim}CD16^{-}CD57^{+}$ NK cell frequency negatively correlated with IL-6. Elevated IL-6 has been linked with increased CVD risk. $CD56^{dim}CD16^{-}CX3CR1^{+}$ NK cell frequency positively correlated with plasma I-FABP, suggesting that higher I-FABP may drive CX3CR1-mediated NK migration to the inflamed endothelium.
These findings suggest that NK cell dysfunction, systemic inflammation, and gut microbial translocation are linked and may collectively drive CVD risk in HIV. Targeting these pathways may reduce the CVD in this population.

BOARD 60

Characterization of endogenous retroviral LTR promoter functions of the domestic dog

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During a retroviral infection, the viral genomic RNA is reverse transcribed to produce a double stranded DNA copy that is then permanently integrated into the host cell's genome, referred to as a provirus. Infection of germ tissue may consequently lead to a provirus that is transmitted to offspring, referred to as an endogenous retrovirus (ERV). The full-length provirus possesses a long terminal repeat (LTR) on each end (5' LTR, 3' LTR) of an internal region encoding the genes *gag*, *pol* and *env*. LTR-LTR recombination frequently occurs between the proviral LTRs, leading to a solitary LTR, or solo LTR. The LTR of either allele functions as a promoter for by host RNA Polymerase and encodes sequences to initiate transcription and transcription factor binding sites (TFBSs). As permanent components of the host genome, ERVs are replicated by host DNA Polymerase, during which mutations arise and slowly accumulate over time. Such changes have the potential to impact the LTR promoter activity, for example by affecting regulatory sequences or those of TFBSs. ERVs within the dog genome range in times of integration prior to the Canidae (~14 mya) to recent Canis sp. lineages (<0.4 mya), and many are in genic regions, thus offering the potential to alter host gene expression. We have previously shown dog ERVs are expressed in healthy and tumor tissues and are significantly elevated in the latter. We suggest a scenario in which LTR functions could impact gene expression in this host. To examine their functional potential, we are coupling analysis of TFBS sequence computational predictions with experimental testing using a dual luciferase reporter assay for individually cloned LTRs. Outcomes should shed light on LTR promoter functions still active today and identify candidates for putative exaptation events in the dog.

BOARD 61

Isolation of Virulent Bacteriophage using *Mycobacterium Smegmatis* as a Host

Samia Williams* and Mitchell Deller

Overreliance on antibiotics along with other factors has caused antibiotic resistant bacteria to become a growing threat to global health. Due to the difficulty of discovering novel antibiotics, phage therapy presents a promising alternative for treating these infections. This study used a safe alternative to *Mycobacterium tuberculosis, Mycobacterium smegmatis,* as a host to isolate bacteriophage from soil samples. Through direct and enriched isolation and the uses of plaque assay protocols, we identified a putative lytic phage from a soil sample. Future research will evaluate therapeutic applications of our bacteriophage, including treatment of *Mycobacterium tuberculosis* infections.

BOARD 62

Antibiotic Resistance in Dredged Sediment Bacteria Assessed by Kirby-Bauer Disc Diffusion Technique

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Antibiotic resistance is a growing public health concern (Bengtsson-Palme & Larsson, 2015), which is making infections harder to cure. Bacteria can develop mutations to flush the antibiotics out, thicken their peptidoglycan wall, and have mutations in the antibiotic-targeted area, driven by antibiotic resistance genes (ARGs), which reduce the effectiveness of antibiotics (Muteeb et al., 2023). To address this, our project will venture out the Kirby assay method to see some kind of antibiotic resistance to one or more of the antibiotics tested, ampicillin, tetracycline, and erythromycin, based on reduced or absent zones of inhibition in the Kirby-Bauer assay. We hope to observe different levels of resistance while cultivating a wide variety of bacterial colonies from dredged sedmients of Toledo harbor. This study would highlight patterns of environmental antibiotic resistance, which will be beneficial for the local aquatic ecosystem and for monitoring antimicrobial resistance in it.

BOARD 63

Antibacterial Properties of Honey

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Honey is a combination of various substances such as sugars, amino acids, vitamins, and other organic compounds. Additionally, honey is known to possess antibacterial properties related to low pH, low moisture content, and the production of hydrogen peroxide. It is hypothesized that raw honey samples from across Northwest Ohio will have broad variations in the chemical composition due to variance in botanical species across the region, which will impact the honey samples' antibacterial properties. This procedure aimed to evaluate the antibacterial activity of honey samples using the disk-diffusion method. Cultures of bacteria were introduced to honey of varying dilutions, and antibacterial activity was determined by measuring and comparing zones of inhibition caused by the honey. Results were analyzed to examine the variability of antibacterial activity among honey samples and the potential relationships between the activity and other characteristics of the honey, such as sugar content, free acidity, hydroxymethylfurfural content, pollen content, and moisture content. Overall, the findings of this work support prior research evaluating honey's potential antibacterial properties.

BOARD 64

Distinct endothelial–platelet and fibrinolytic activation in COVID-19 sepsis and implications for long-term atherogenesis risk.

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Sepsis is a major contributor to morbidity and mortality in critical illness and is increasingly recognized as a driver of cardiovascular complications, including myocardial injury, arrhythmias, thromboembolism, and accelerated vascular dysfunction. Across sepsis etiologies, the host response centers on endothelial activation, platelet-leukocyte interactions, and dysregulated coagulation/fibrinolysis pathways linking acute systemic inflammation to both immediate and long-term cardiovascular risk. COVID-19–associated critical illness is marked by prominent vascular pathology, including endothelial injury and immunothrombosis. Building on our prior studies identifying atherogenesis-related immune features in critically ill COVID-19 patients, we investigated whether COVID-19 sepsis exhibits a distinct endothelial–platelet activation signature that could mechanistically link acute SARS-CoV-2–driven critical illness to increased post-recovery atherosclerotic risk. To investigate this, we studied 30 adults with sepsis admitted to the Intensive Care Unit at The Ohio State University Wexner Medical Center during the pre-vaccination period (May–August 2020), including 15 COVID-positive and 15 COVID-negative patients. Clinical data, organ-support requirements, and admission laboratory

variables were abstracted from medical records. Ten plasma biomarkers reflecting coagulation, endothelial and platelet activation, and inflammation were quantified at admission (T1) and discharge (T2) using the LEGENDplex™ Human Thrombosis Panel. Group differences were evaluated using two-tailed tests (α=0.05), and associations with organ dysfunction were assessed using SOFA scores.
COVID-positive sepsis demonstrated greater early organ dysfunction, with significantly higher admission SOFA scores (median [IQR] 4.0 [3.5–4.0] vs. 2.0 [0.0–2.0]; p=0.00028). Biomarker profiling revealed a pronounced endothelial-dominant signature, including significantly elevated tissue plasminogen activator (tPA) that tracked with illness severity. In contrast, non-COVID sepsis exhibited a classical innate-immune–driven immunothrombotic profile characterized by higher PSGL-1, CXCL8/IL-8, and tissue factor (all p<0.05). COVID-19-positive sepsis was defined by elevated tPA alongside reduced IL-8 and tissue factor at T1, indicating an endothelial–fibrinolytic activation phenotype with altered inflammatory–coagulant coupling. Within patient trajectories of IL-8 and PSGL-1, further highlighted divergent leukocyte trafficking biology between COVID-positive and non-COVID sepsis.
We therefore concluded that COVID-19 sepsis exhibits a distinct vascular endotype marked by heightened endothelial activation, dysregulated fibrinolysis, and disrupted leukocyte–platelet–endothelial communication. These mechanisms are strongly linked to microvascular injury, prothrombotic vascular remodeling, and accelerated atherosclerotic development, providing a mechanistic pathway connecting acute critical illness from COVID-19 to increased atherosclerotic risk following recovery. These findings support a cardiovascular risk framework for interpreting COVID-19 sepsis and underscore the urgency of evaluating whether targeted modulation of endothelial- and platelet-mediated pathways can mitigate both acute complications and persistent post-sepsis cardiovascular and atherogenic risk.

BOARD 65

Efficacy of Targeting the AMPK-TOR Pathway in *Naegleria Amoebae*

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This study investigates the effects of target of rapamycin (TOR) kinase inhibitors and AMP-activated protein kinase (AMPK) activators on cellular growth in Naegleria gruberi, a freshwater free-living amoeba that is non-pathogenic and belongs to the same genus as Naegleria fowleri (the brain-eating amoeba), which thrives in warm freshwater environments such as lakes and rivers. If the ameba enters the cranial cavity via the nasal cavity, it can cause primary amebic meningoencephalitis (PAM) by necrotizing brain tissue and inducing inflammation. Although the infection is rare, it is almost always fatal.

In humans, AMPK directly and negatively regulates TOR kinase activity on cellular proliferation. However, this pathway has not been investigated in Naegleria. Therefore, we tested the hypothesis that Naegleria growth can be suppressed by targeting the AMPK-TOR pathway using small-molecule activators of AMPK and inhibitors of TOR.

Cellular viability was measured by an MTS assay, and the data indicated that certain TOR inhibitors and AMPK activators showed efficacy against Naegleria. In silico analyses, identified orthologs of AMPK subunits in Naegleria, and we further analyzed their structures in comparison to human AMPK to identify potential unique binding pockets.

These findings highlight the potential of TOR inhibitors and AMPK activators for modulating cellular activity and provide a foundation for further investigation.

BOARD 66

Structural Analysis of Fatty Acid Desaturase and the Efficacy of a Desaturase Inhibitor on Phagocytosis in Naegleria Amoebae

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Naegleria fowleri is a thermophilic, free-living amoeba known for its pathogenicity in humans. Found in warm freshwater, it can enter the brain via the nasal cavity and cause primary meningoencephalitis (PAM), even in

immunocompetent individuals. While rare, this infection is acute (occurring over 1 to 2 weeks) and almost always fatal, with a ~95% mortality rate across all cases. The long-term objective of our research is to determine drug targets in *N. fowleri* and develop effective pharmaceuticals against it.
Previously, we reported that the fatty acid desaturase inhibitor PluriSIn1 inhibits cell growth in *Naegleria*. Using the nonpathogenic species *Naegleria gruberi* as a model, we investigated PluriSIn1's mechanism of action and tested the hypothesis that it disrupts the homeostasis of unsaturated fatty acids, thereby inhibiting phagocytosis. Phagocytic activity was monitored by tracking *N. gruberi*'s uptake of mRFP-expressing *E. coli* over several days. *N. gruberi* and *E. coli* were co-cultured in well plates in the presence or absence of PluriSIn1, and their cell densities were measured using an MTS assay and OD600, respectively.
Overall, PluriSIn1 did not appear effective in inhibiting phagocytosis. A possible explanation for these results is due to the presence of a secondary organism, with *E. coli* potentially taking up the inhibitor molecules before they could impact *N. gruberi*. The potential PluriSIn1 target, a desaturase in *Naegleria*, was analyzed in silico, with particular focus on a variable domain identified in comparison to human and *Acanthamoeba* desaturases.

BOARD 67

The Hypothetical Protein Dilemma: A Reflection and Prospective on Bacteriophage Genomic Annotation Workflows

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Bacteriophage genomes present unique challenges for annotation due to their high diversity, genetic mosaicism, and ability to perform horizontal gene transfer. Additionally, highly selective evolutionary pressure results in increased divergence of progeny genes, and varying selective pressures on non-canonical replicative factors makes it difficult to use traditional annotation tools and pathways designed for bacterial and eukaryotic systems. A review of current toolkits for analyzing and annotating bacteriophage genomes and a reflection on previous methods will highlight progress and ongoing challenges of bacteriophage genomics, and hopefully provide insight into updating outdated methods.
Another benefit to improving bacteriophage annotation is updating even well annotated and characterized bacteriophage. Utilizing enhanced open reading frame detection and gene calling and predictive protein folding techniques, predicted proteins can be more effectively grouped and associated with function. For example, Phold utilizes the Prokaryotic Virus Remote Homologous Groups (PHROG) database and predicted 3-dimensional protein structure through AlphaFold and ProstT5 to provide increased annotation to bacteriophage genomes and decrease the "hypothetical protein dilemma" (Terzian et. al. 2021, Bouras et. al. 2026).
References
Terzian, P., Olo Ndela, E., Galiez, C., Lossouarn, J., Pérez Bucio, R. E., Mom, R., Toussaint, A., Petit, M.-A., & Enault, F. (2021). PHROG: Families of prokaryotic virus proteins clustered using remote homology. *NAR Genomics and Bioinformatics*, *3*(3), lqab067. https://doi.org/10.1093/nargab/lqab067
Bouras, G., Grigson, S. R., Mirdita, M., Heinzinger, M., Papudeshi, B., Mallawaarachchi, V., Green, R., Kim, R. S., Mihalia, V., Psaltis, A. J., Wormald, P.-J., Vreugde, S., Steinegger, M., & Edwards, R. A. (2026). Protein structure-informed bacteriophage genome annotation with Phold. *Nucleic Acids Research*, *54*(1), gkaf1448. https://doi.org/10.1093/nar/gkaf1448

BOARD 68

Ralstonia pseudosolanacearum uses RprR to orchestrate bacterial fitness in response to host-induced stress

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Bacteria use diverse sensors to integrate environmental stimuli into physiological responses that ensure survival. *Ralstonia pseudosolanacearum* (*Rps*), a soil-borne plant pathogen that causes bacterial wilt, encodes a conserved sensory protein termed RprR (***R****alstonia* **p**lant-**r**esponsive **r**egulator). Initial results revealed that some *in vitro* phenotypes, such as biofilm formation, were only triggered in the presence of *ex vivo* xylem sap,

suggesting RprR requires a plant-derived signal(s) for full cellular functionality. Based on preliminary data from our lab and others, we tested the hypothesis that RprR, which contains multiple sensory and signaling domains, shapes *Rps* biology in response to plant-induced stress. We performed comparative transcriptomics and metabolomics of the model strain *Rps* GMI1000 (wild-type and Δ*rprR*) during infection of a susceptible and quantitatively resistant tomato host. This dual host approach uniquely leverages a natural spectrum of host-induced stress to better understand the biological function of *Rps* RprR. Specifically, the quantitatively resistant line H7996 is known to produce more reactive oxygen species (ROS) and antimicrobial toxins in response to infection. We used these datasets to develop a suite of targeted experiments that define several physiological roles for *Rps* RprR. These include modulating tolerance to ROS and host phenolic compounds, metabolism of sap-relevant compounds, root attachment, stem colonization and, ultimately, virulence in the host plant. Altogether, our work establishes RprR as one of the many sensors that enable *Rps* to cause disease in the dynamic host environment.

BOARD 69

COMPARATIVE ANALYSIS OF MICROBIAL COMMUNITIES IN FUNGAL-INFECTED AND UNINFECTED INDUSTRIAL *HAEMATOCOCCUS* RACEWAYS

Dr. MJ Lashbrook[*1], Margeret Rettig[1], and Dr. Chris Ward[1,2]
[1]Bowling Green State University, [2]University of Massachusetts Dartmouth

Raceway cultures of the microalga *Haematococcus lacustris*, a commercially important producer of the antioxidant astaxanthin, are becoming more common as industrial interest grows. Fungal infections by Chytridiomycota and Blastocladiomycota are devastating to these cultures and can cause complete loss of product. Bacterial community dynamics during infection of these raceways are poorly understood and could inform future detection of fungal infection and monitoring decisions. Microbial samples were collected from parallel outdoor raceways at a commercial cultivation facility over a year-long period. Daily sampling enabled detailed temporal analysis of microbiome dynamics across winter, spring, and summer cultures. Culture raceways included both uninfected and infected cultures associated with parasitic chytrid and blastoclad fungi, which frequently lead to rapid culture collapse.

Bacterial communities were characterized using 16S rRNA amplicon sequencing on the Illumina MiSeq platform, followed by identification of bacterial taxonomic composition analyses across uninfected and infected raceways. Across seasons, infection was consistently associated with shifts in microbial community structure, altered successional trajectories, and changes in taxonomic diversity. Infected raceways exhibited reduced diversity and increased dominance of stress-tolerant or opportunistic bacterial taxa, particularly members of Deinococcota and select Bacillota and Bacteroidota families. Ordination analyses demonstrated significant compositional divergence between uninfected and infected systems, with infection disrupting normal bacterial community successional patterns.

Seasonal variation strongly influenced microbiome responses, with the most pronounced divergence of community composition occurring during summer cultures. Certain taxa were consistently enriched or suppressed under infection conditions, suggesting potential microbial indicators of culture health or increased susceptibility to fungal infection. Uninfected systems generally maintained more stable and diverse communities, supporting the hypothesis that microbial balance may contribute to resistance to fungal invaders.

Overall, these findings demonstrate that fungal infection substantially restructures industrial algal microbiomes and highlight the potential for microbial community monitoring as a tool for early detection and management of these dysbiosis events in commercial algaculture systems.

BOARD 70

Gut microbial translocation may drive NK cell reprogramming in Adolescents Living with Perinatally Acquired HIV

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Natural killer (NK) cell dysregulation contributes to chronic inflammation in people living with HIV, yet underlying mechanisms remain unclear. Gut microbial translocation (GMT), driven by impaired gut barrier integrity in HIV, emerged as a source of systemic immune activation.

We explored the influence of GMT on NK cell phenotype and function in adolescents with perinatally acquired HIV (PHIV, n = 10) on long-term antiretroviral therapy compared to age-matched healthy controls (HC, n = 11). High dimensional flowcytometry was employed for immune profiling, including stimulation with HIV gag peptide pool. Plasma biomarkers were measured by ELISA. UMAP and FlowSOM were used for Phenotypic clustering. Data were analyzed using Mann Wittney U test and Pearson correlation co-efficient.

Six of 15 NK clusters expressing TLR2, TLR4 and HLA-DR were upregulated in PHIV; two KLRG1$^+$ clusters were downregulated ($p < 0.05$). Conventional gating revealed increased TLR2 in CD16$^+$CD56$^-$ NK subset with elevated HLA-DR ($p < 0.05$) alongside NKG2D in CD16$^+$CD56^{bright} subset ($p < 0.005$), indicating persistent activation. KLRG1$^+$ effector memory-like NK cells were downregulated ($p < 0.05$) in three of five NK subsets. Upon stimulation, NK cells from PHIV secreted more TNFα ($p < 0.05$), while KLRG1$^+$ NK cells produced less Granzyme B ($p < 0.005$). This reflects a pro-inflammatory yet less cytotoxic phenotype.

Plasma intestinal fatty acid binding protein (IFABP), a marker of gut integrity, was elevated in PHIV ($p < 0.05$) and positively correlated with TLR2$^+$/TLR4$^+$/HLADR$^+$ NK subsets ($R > 0.5$) and inversely correlated with KLRG1$^+$ NK subsets ($R < -0.5$).

Our findings suggest that GMT may promote NK cell activation via TLR2/TLR4 signaling, driving a pro-inflammatory yet less cytotoxic phenotype. This may contribute to the development of HIV-associated comorbidities. Strategies to restore gut barrier integrity or/and modulation of NK cells could mitigate chronic inflammation and improve long-term outcomes in PHIV.

BOARD 71

Tracking Antibiotic Resistance Genes, Antimicrobial Resistance and Multidrug Resistance in the Huron River

Evan Siemienkiewicz
Eastern Michigan University

Antibiotic resistance arises when bacteria acquire and disseminate genetic determinants that enable survival under antimicrobial selective pressure, frequently through horizontal gene transfer of antibiotic resistance genes (ARGs) among diverse taxa. Despite increasing global concern, the environmental prevalence and distribution of antimicrobial-resistant (AMR) and multidrug-resistant (MDR) bacteria remain insufficiently characterized. The Huron River in southeastern Michigan is a critical freshwater resource subject to substantial anthropogenic influence, raising concerns regarding the environmental persistence and propagation of AMR and MDR bacteria and their associated ARGs. In this ongoing investigation, AMR and MDR phenotypes, along with corresponding ARG profiles, were evaluated over a six-month period (May–October 2025). Surface water samples were collected monthly from ten sites across the river, and *Escherichia coli* and *Enterococcus* spp. were isolated and subjected to antimicrobial susceptibility testing against eight antibiotics using the Kirby–Bauer disk diffusion assay. Quantitative polymerase chain reaction (qPCR) was employed to quantify the presence and relative abundance of targeted ARGs. *Escherichia coli* isolates exhibited resistance to tetracycline and erythromycin and frequently demonstrated multidrug resistance, most commonly involving co-resistance to tetracycline and erythromycin in combination with additional antimicrobial classes. *Enterococcus* isolates showed resistance to ciprofloxacin, with elevated occurrence during June and August, and exhibited lower rates

of multidrug resistance compared to *E. coli*. Molecular analyses revealed consistently high abundance of the *int1* (class 1 integron integrase), *tetW* (tetracycline resistance), *sul1* (sulfonamide resistance), and *ermF* (macrolide resistance) genes across all sampling months. Continued sampling is planned through May 2026 to strengthen spatiotemporal resolution.

BOARD 72

Cultivating CUREiosity: A Study of Possible *Streptomyces* Antibiotic-Regulating Genes

Emily Perrotte*, Gabriella Anzelmo*, and Jennifer A. Bennett
Otterbein University

Undergraduate research is considered a high impact practice in higher education. There are numerous examples of Course-based Undergraduate Research Experiences (CUREs) that are federally funded and used in classrooms across the country. A unique CURE was introduced into the sophomore-level Cell Biology Course at Otterbein University, a small liberal arts college in Central Ohio, that used the instructor's research in *Streptomyces* bacteria phenotyping and genetic engineering. Students in the three laboratory sections worked in groups of three or four to study transposon insertion mutants where the genes of interest were identified previously. Students kept electronic notebooks to record their results for macroscopic phenotypes on agar plates, phase-contrast microscopy, antibiotic resistance assays, bioinformatics, and the construction of plasmids containing the wild-type genes of interest. All groups were able to successfully streak plates, obtain data, and take publication quality photographs, adding to the results from the instructor's research program. As part of the CURE, students also performed numerous math problems and the semester culminated in an abstract and lightning talk for the data collected in this CURE. Here we describe two *Streptomyces coelicolor* developmental mutants that were examined in the class and discovered to overproduce pigmented antibiotics. The two strains also displayed a defect in spore formation, and one of the mutants greatly overproduced antibiotics in response to various antibiotic-containing disks. This research has implications for increasing the yield of antibiotic production for industrial pharmaceutical applications, while simultaneously educating university students in the scientific method, a variety of computational and research skills, and written and oral communication skills.

BOARD 73

The burning questions: elucidating the mechanisms of *Candida albicans* growth in burn wound exudate

Mira Ebersole[*1], Andrew Wagner[1]
[1]Bowling Green State University.

Secondary fungal infection by *Candida albicans* represents a major complication following thermal injuries, as it increases both the morbidity and mortality rates for inflicted individuals. If not quickly resolved, *C. albicans* can form biofilms within the burn wound niche, further complicating disease control while increasing the risk for chronic burn wound infection. Despite this, we know very little about how fungi colonize and persist with the burn niche. To survive, *C. albicans* must metabolize available nutrients from burn wound exudate, a fluid discharge from burned skin, and necrotic tissue in its surrounding environment. To better understand the metabolic requirements for *C. albicans* survival and proliferation within burn wounds, we created a synthetic wound exudate (SWE) that mimics the physiochemical properties of primary human burn wound exudate. Using a single gene knock out library of *C. albicans*, we analyzed the growth of 182 mutants to identify genes that are necessary for fungal survival in SWE. Studies are ongoing, with preliminary growth analyses implicating genes in trace element uptake (*ZRT1, SEF1, PRA1*), metabolic plasticity (*SNF4*), general stress response and mitochondrial respiration as important factors for growth in SWE. Biofilm analyses have linked growth defects in SWE with impaired biofilm formation as well, as *snf4Δ/Δ, dot4Δ/Δ* and *pra1Δ/Δ* mutants all showed attenuated biofilm formation in the synthetic wound exudate when compared to the wildtype. Collectively, the development of SWE has provided a novel platform for the identification of fungal processes needed for growth within the burn wound environment and has generated a list of potential genes for future studies aimed at assessing the role they play during burn wound infection.

BOARD 74

Designing safe and effective phage cocktails for precise microbial control in water systems.

Susan Thapa[a,*], Sadia Marjia Ferdous[a], Bridget Hegarty[a]
[a] Department of Civil and Environmental Engineering, Case Western Reserve University, Cleveland, OH

Persistent biofilm forming and opportunistic bacteria in water systems represent an ongoing public health concern, particularly for immunocompromised individuals. Those bacteria can survive conventional treatment processes. Moreover, reliance on chemical disinfectants contributes to disinfection byproducts with negative health effects, ecological disruption, and antimicrobial resistance (AMR). These limitations highlight the need for precise, sustainable microbial control strategies.

This study seeks to understand the mechanisms behind successful phage cocktails. I will present work showing enhanced bacterial reduction by phage cocktail against *Salmonella enterica* serovar Typhi compared to individual phages, and extend rational phage cocktail design principles to *Mycobacterium smegmatis*, a model for mycobacteria. I will test the hypothesis that synergistic phage cocktails exhibit distinct transcriptomic signatures and infection networks compared to antagonistic or suboptimal combinations, enabling rational and safe cocktail design.

Phage combinations will be experimentally categorized as synergistic or antagonistic based on effects on host growth dynamics. Comparative transcriptomic profiling (RNA sequencing) will characterize bacterial responses to individual phages and optimized cocktails. Differential gene expression and network based analyses will identify shared and distinct stress response pathways, metabolic shifts, and resistance associated mechanisms associated with combinatorial infection. Long term experiments will also evaluate resistance emergence and stability of effective cocktails under simulated drinking and waste water conditions. Safety will be assessed through genomic screening and evaluation of off target infectivity using experimentally validated and predicted infection networks.

By integrating experimental validation, comparative transcriptomics, and resistance evolution assays, this work advances a mechanistically-informed framework for precision phage-based control of bacteria in water systems.

Abstracts of OBASM Podium Presentations

Saturday, April 11
10:30 am – 12:00 pm

10:30 – 10:45 am

TaRTLEt: Transcriptionally-active Riboswitch Tracer Leveraging Edge deTection

Sachit Kshatriya*[1] and Sarah C. Bagby[2]
[1]Case Western Reserve University

Structured RNAs have emerged as a major component of cellular regulatory systems, but their mechanism of action is often poorly understood. Riboswitches are structured RNAs that allosterically regulate gene expression through any of several different mechanisms. *In vitro* approaches to characterizing this mechanism are costly, low-throughput, and must be repeated for each individual riboswitch locus of interest. Bioinformatic methods promise higher throughput; despite robust computational identification of riboswitches, however, computational classification of the riboswitch mechanism has so far been both model-bound, relying on identification of sequence motifs known to be required for specific models of riboswitch activity, and empirically untested, with predictions far outpacing biological validation. Here, we introduce TaRTLEt (Transcriptionally-active Riboswitch Tracer Leveraging Edge deTection), a new high-throughput tool that recovers *in vivo* patterns of riboswitch-mediated transcription termination from paired-end RNA-seq data using edge detection methods. TaRTLEt successfully extracts transcription termination signals despite numerous sources of biological and technical noise. We tested the effectiveness of TaRTLEt on riboswitches identified from a wide range of sequenced bacterial taxa by utilizing publicly available paired-end RNA-seq readsets, finding broad agreement with

previously published *in vitro* characterization results. In addition, we use TaRTLEt to infer the *in vivo* regulatory mechanism of uncharacterized riboswitch loci from existing public data. TaRTLEt is available on GitHub and can be applied to paired-end RNA-seq datasets from isolates or complex communities.

10:45 – 11:00 am

A Lake Erie isolate of *Pseudomonas fluorescens* is a pathogen of Saprolegnia spp.

Marzie Isavi*, Carren Beurkey, Hsin-Ho Wei, Vipa Phuntumart. Paul F. Morris
Bowling Green State University

Saprolegnia is an organism with a hyphal-like growth phenotype that is similar to fungi. Along with *Pythium*, *Saprolegnia* belongs to oomycetes, a class of eukaryotic microorganisms within the kingdom Stramenopiles, which also includes algal protists, diatoms, and brown algae.
Saprolegnia are widely distributed in aquatic environments, especially in cold freshwater, but they are also found in brackish water and moist soil. They are opportunistic pathogens that are able to colonize hosts with weak immune systems, open wounds, and dead or scratched eggs, leading to saprolegniosis. In nature, *Saprolegnia* spp are pathogens of amphibians, crayfish, cladocerans, and fish species that include cyprinids, salmonids, and sturgeons.
In aquaculture, *Saprolegnia* causes significant economic losses by colonizing both juvenile and adult fish, making extensive skin lesions covered with cotton-like mycelial layers. In hatcheries, these infections can result in mass mortality rates up to 80 to 100 percent of infected eggs, making this group of pathogens a significant challenge for fish health management.
In this study, we evaluated the virulence of an isolate of *Pseudomonas fluorescens* from Lake Erie using a collection of *Saprolegnia* isolates collected from northern Ohio and Michigan. The bacterium exhibited contact-based killing in 9 of the 12 tested isolates and suppressed hyphal regrowth and induced structural damage in the remaining samples.
These findings demonstrate broad antagonistic potential against *Saprolegnia* spp., which is consistent with host-pathogen interaction and suggest its potential as a possible biological control agent in aquaculture systems.

11:00 – 11:15 am

Contribution of two T6SSs in *Pseudomonas.fluorescens* LE6_D7 to Virulence against Oomycetes

Arefeh Avestakh*, Paul F. Morris
Biological Science, Bowling Green State University. Bowling Green, OH, 43403

Pythium species, belonging to the class Oomycetes, represent one of the most frustrating challenges facing modern agriculture, particularly in hydroponic systems where their swimming zoospores move freely through recirculating nutrient solutions, rapidly destroying entire crops through damping-off and root rot. The use of bacteria as environmentally safe tools to control plant pathogens has driven the search for effective biocontrol agents. *Pseudomonas fluorescens* LE6_D7, a bacterium isolated from Lake Erie, emerged as a remarkable candidate, capable of killing more than 20 different *Pythium* isolates in laboratory assays. The antagonistic activity of LE6_D7 against *Pythium* is believed to be mediated through two Type VI Secretion Systems (T6SSs) — contact-dependent weapon systems that deliver effector proteins directly into the host cells. *Pseudomonas fluorescens* have two T6SS in different pathogenic islands. To evaluate the importance of T6SS in virulence, we employed a gene replacement strategy in which the TSSB gene was replaced by a GFP genes. Insertion mutagenesis of TssB1 and TssB2 will prevent delivery of Hcp (haemolysin coregulated Protein), vgrG (valine-glycine-repeat protein G), PAAR (Proline-Alanine-Alanine-Arginine-Repeat containing spike protein) and associated effectors delivered by each T6SS. Deletion mutants were demonstrated by PCR and functional expression of GFP in the operon. This mutant shows the diminish virulence.

11:15 – 11:30 pm - Break

11:30 – 11:45 am

Validation of shoe sole dust as a microbial sampler reveals changes in diversity along an urbanization gradient

Sadia Marjia Ferdous1*, Täubel Martin2,3, Pekka Taimisto2, Emma-Reetta Musakka2,4, Bridget Hegarty1
1Case Western Reserve University, Cleveland, Ohio, USA
2Finnish Institute for Health and Welfare, Kuopio, Finland
3Aalto University, Espoo, Finland
4University of Eastern Finland, Kuopio, Finland

Urbanization-driven environmental change has significant implications for human health and wellbeing. A growing body of research highlights that early-life exposure to diverse environmental microbiota supports development of the immune system and may protect against chronic inflammatory diseases such as asthma and allergies. The rising prevalence of these conditions may be linked to the reduced microbial exposure due to increasing urbanization. Understanding these connections, both indoors and outdoors, requires innovative, reproducible methods that accurately reflect human contact with environmental microbiota. While simple and robust methods for assessing microbial exposures indoors exist, no similar approaches exist for outdoor sampling.

In this study, we introduce a novel approach to assess environmental microbiota exposure by measuring microbiota from particulate matter collected from shoe soles. Our central hypothesis is that shoe sole microbial communities serve as a simple, effective, and reliable proxy for environmental microbial encounters. We have validated this approach through repeated walks on routes along an urbanization gradient in the Kuopio region of Finland. DNA was extracted from the shoe sole swabs, microbial concentration was assessed using quantitative PCR (qPCR), and bacterial and fungal community profiling was conducted via amplicon sequencing. Our results show that left and right shoe sole dust from the same walk and same route represent similar microbial communities compared to different walks and routes, confirming shoe sole dust as a dependable method of capturing microbial exposure. We found that fungal and bacterial diversity decreases in urban compared to rural environments, and that NDVI (as a measure of greenness) correlates more strongly with microbial diversity than simple environmental classifications of the path into rural-green, urban-green, and urban-grey.

This method offers a straightforward approach for evaluating microbial exposures, enabling more robust epidemiological studies on the health effects of greenness and environmental biodiversity. By linking outdoor and indoor microbial exposures, researchers can better understand how surrounding greenness can impact indoor air quality and human health.

11:45 – 12:00 pm

Bacteriophage Mediated Control of Aquaculture Pathogen, *Aeromonas salmonicida*

Madison Nichole Altieri*[1], Lauren Goberman[2], Eli Bachman[2], Lauren Greenwell[2], and Raymond Larsen[3]
[1]Bowling Green State University

Aquaculture is a rapidly growing practice to grow farm raised seafood in efforts to meet consumer demand. Benefits that make aquaculture popular, like controlled fish growth, also have their disadvantages. Aquaculture producers often stock their fish at high densities which often leads to disease and death. Infected fish are not permitted to enter the market, so most of these would-be food products must be disposed of. Disease within aquaculture costs the industry a considerable $6 billion dollars per year. One bacterial strain that contributes to this threat to aquaculture is *Aeromonas salmonicida.*
Mitigating disease has proven difficult within aquaculture settings. Standard treatment options, such as antibiotics, are no longer viable as these pathogens gain antibiotic resistance. The usage of antibiotics within aquaculture drives the rise of untreatable pathogens, including *A. salmonicida*. As such, the need for new therapeutics to treat these bacterial pathogens are needed. One alternative that has been promising within the aquaculture industry is bacteriophage (phage), viruses that infect and eliminate bacteria. Otherwise known as bacteriophage (phage) therapy.

Seven phage were isolated from the environment with the ability to infect *A. salmonicida*. These phage were screened for their ability to kill multiple *A. salmonicida* pathogens and environmental *Aeromonas* species. From the data gathered the host range of the phage were determined. A snapshot on the bactericidal ability of the phage within a twenty-four-hour time frame was established *in vitro*. Phage cocktails were performed to determine which pairs of the phage resulted in synergistic or antagonistic outcomes. Multiple of these phage, as individual phage or phage cocktails, could be suitable to treat *A. salmonicida* infections in aquaculture.

Description of Awards for Presentations

N. Paul Hudson Award for Research Excellence

N. Paul Hudson, MD, was chairman of the Microbiology Department at Ohio State University from 1935 – 1950. Dr. Hudson was recruited from the University of Chicago Medical School where he already had established a research/teaching reputation and was told to bring several colleagues with him to serve as faculty members in the department. In 1950 he was appointed Dean of the Graduate School at Ohio State University and served until his retirement in 1957. During the 1930's he was responsible for the successful development of a vaccine against Yellow Fever, which was necessary for the war effort in the tropical countries during the 1940's. Dr. Hudson died at the age of 95 in 1993 in Florida after retiring to his second home in Sarasota in 1970.

Donald C. Cox Award for Research Excellence

Donald C. Cox, PhD, was professor and chair of the Department of Microbiology at Miami University from 1978-1989. After he earned his PhD at University of Michigan in 1965, he joined the microbiology faculty at University of Oklahoma. He later moved to Miami, where he became well known as a charismatic and highly effective teacher, researcher and leader. Dr. Cox received Miami's Distinguished Educator Award, and fostered the growth and development of the Department of Microbiology. Throughout his research career, he focused on the biochemistry and molecular biology of replication of human viruses, and ultimately studied utilization of reovirus in cancer therapy. Dr. Cox was a strong advocate for attracting young people into scientific careers and mentored many students who have gone on to highly significant research careers.

J. Robie Vestal Award for Research Excellence

J. Robie Vestal, PhD, was professor of both biological sciences and environmental health at the University of Cincinnati. He earned his MS in Microbiology at Miami University and his PhD in Microbiology at North Carolina State University. His postdoctoral research at Syracuse University involved the biochemistry of *Thiobacillus ferrooxidans*. Dr. Vestal's research interests focused on how microbial communities function in nature. He studied

microbial communities in Arctic lakes and in soils contaminated with hazardous waste, cryptoendolithic (hidden within rock) communities in Antarctica, mangrove-degrading communities in the Bahamas, and decomposer communities in municipal solid waste compost. He also investigated microbial survival under simulated Martian conditions. Dr. Vestal served on many local and national committees and chaired the Divisional Advisory Committee of the National Science Foundation's Division of Polar Programs.

Ohio Branch ASM Award for Research Excellence

This award traditionally recognizes excellence in graduate research and presentation at the annual Ohio Branch ASM meeting.

Allan A. and Jann M. Ichida Undergraduate Research Award

Allan Ai Ichida, PhD, earned his BA from Ohio Wesleyan University in 1953 and went on to study botany, mycology, and bacteriology at the University of Tennessee where he earned his MS in 1955 and the University of Wisconsin in Madison where he earned his PhD in 1960. Dr. Ichida returned to Ohio Wesleyan in 1961 as a faculty member in the Department of Botany and Microbiology where he taught botany and mycology until he retired in 1995. During his career, Dr. Ichida served as president and advisor of the Ohio Branch of the American Society for Microbiology and on the Olentangy Scenic River Commission where his water quality research helped to secure the river's "Scenic River" status. Dr. Ichida also conducted research in the OWU Bohannan and Kraus nature preserves and mentored numerous undergraduates who went on to become research scientists.

The Ohio Branch ASM Award for Pre-college Research Excellence

Established in 2017, this award recognizes excellence in pre-college research and presentation at the annual Ohio Branch ASM meeting.

UPDATED: 4-9-2026

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