MIDWEST MICROBIOME SYMPOSIUM: Creating and responding to change

MAY 8-10, 2023

Nationwide & Ohio Farm Bureau 4-H Center
Columbus, Ohio

PRESENTED BY

THE OHIO STATE UNIVERSITY
CENTER OF MICROBIOME SCIENCE

THE OHIO STATE UNIVERSITY
INFECTIOUS DISEASE INSTITUTE

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COLLEGE OF FOOD, AGRICULTURAL, AND ENVIRONMENTAL SCIENCES

ALL MICROBIOMES WELCOME!

TABLE OF CONTENTS

STEERING COMMITTEE

Faculty

- Vanessa Hale, MAT, DVM, PhD – Ohio State University, College of Veterinary Medicine
- Jiyoung Lee, PhD – Ohio State University, College of Public Health and College of Food, Agricultural, and Environmental Sciences
- Jonathan Jacobs, PhD – Ohio State University, College of Public Health and College of Food, Agricultural, and Environmental Sciences
- Sarah Short, PhD – Ohio State University, College of Food, Agricultural, and Environmental Sciences
- Kris Martens, PhD – Ohio State University, College of Medicine
- Michael Bailey, PhD – Nationwide Children's Hospital Center for Microbial Pathogenesis and Ohio State University, College of Medicine
- Qingfei Zheng, PhD – Ohio State University, College of Medicine
- Caitlin Proctor, MS, PhD – Purdue University, College of Engineering
- Angela Kent, PhD – University of Illinois Urbana-Champaign, College of Agricultural, Consumer and Environmental Sciences

Trainees

- Audra Crouch – PhD Student – Ohio State University, College of Arts and Sciences
- Nora Jean Nealon DVM, PhD – Postdoctoral Fellow – Ohio State University, College of Veterinary Medicine
- Yijing Liu – PhD Student – Ohio State University, College of Engineering
- Zach Lewis – Masters Student – Ohio State University, College of Veterinary Medicine

Administrative support

- Heather Curtis – Senior Project Manager – Ohio State University, Center of Microbiome Science
- Kira Sosnowski - Marketing and Communications Specialist - Ohio State University, Infectious Diseases Institute

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Monday May 8th, 2023	
12:00pm – 12:45pm	Registration
12:45pm – 1:00pm	**Welcome from Gary Pierzynski, PhD** Associate Dean of Research Graduate Education, College of Food, Agriculture, and Environmental Science, The Ohio State University
1:00pm – 1:25pm	**Session: Hosts as a living landscape** **David Thoms,** Florida State University Novel Innate Immune Responses Can Distinguish Beneficial from Pathogenic Root Colonizing Bacteria.
1:27pm – 1:34pm	**Henrique P. Feiler,** Purdue University Rhizosphere Microbiome of Six Soybean Varieties Under Sufficient and Deficient Soil P Conditions: Implications for Plant Mechanisms and Microbiome Interactions
1:36pm – 1:54pm	**Leyao Wang,** Washington University in St. Louis Prenatal maternal exposure to extreme weather events and the offspring microbiome: What can we learn from a birth cohort study after Hurricane Maria in Puerto Rico?
1:56pm – 2:03pm	**Sumita Dutta,** Cleveland Clinic Gut microbiome derived N-acyl serinols regulate postprandial metabolic homeostasis
2:05pm – 2:23pm	**Zakee Sabree,** The Ohio State University Modeling Host-Microbe Interactions
2:25pm – 2:32pm	**Blake Bringhurst,** University of Texas at Tyler Microbial Dimension of Symbiosis and Dysbiosis in Fungus–gardening Ants
2:35pm – 3:00pm	Coffee Break
3:00pm – 3:20pm	**Session: Host-Microbe Interactions: From Basic Mechanisms to Translational Science** **Lihua Ye,** The Ohio State University Enteroendocrine cells: the interface between diet and gut microbiota
3:20pm – 3:40pm	**Brett Loman,** University of Illinois - Urbana Champaign Impacts of psychological stress and nutrition on the microbiota-gut-brain axis
3:40pm – 4:00pm	**Jenessa Winston,** The Ohio State University Clinical utility of fecal microbiota transplant to enhance weight loss in obese dogs
4:00pm	**Eric Martens,** University of Michigan **Keynote**: Opposing roles of commensal bacterial mucus degradation and metabolite production in inflammatory bowel disease
6pm – 8pm	**Trainee Social Event** – PINS Mechanical (141 N 4th St Columbus, OH)

	Tuesday May 9th, 2023
8:50am – 9:00am	**Welcome from Michael Oglesbee, DVM, PhD** Director, Infectious Diseases Institute, The Ohio State University
9:00am – 9:20am	**Session: You are what your microbes eat: Microbiome and Nutrition** **Jasenka Zubcevic,** The University of Toledo Vagal gut-brain axis in cardiovascular homeostasis: role of gut microbiota
9:20am – 9:35am	**Suzanne Alvernaz,** University of Illinois Associations of maternal dietary inflammatory potential & the gut microbiome
9:35am – 9:55am	**Jessica Cooperstone,** The Ohio State University Towards understanding tomato bioactivity using multi-omic approaches
9:55am – 10:10am	**Ethan Hillman,** University of Michigan Using resistant starch to engineer the human microbiome and increase production of indole lactic acid as a therapeutic in the GI tract
10:10am – 10:30am	**Timothy Johnson,** Purdue University Predicting and controlling the swine microbiome
10:30am – 11:00am	Coffee Break
11:00am – 11:25am	**Session: The path of least resistomes** **Skye Fishbein,** Washington University in St. Louis Understanding microbiome-pathogen dynamics during antibiotic exposure in Clostridioides difficile-colonized patients
11:25am – 11:40am	**Gireesh Rajashekara,** The Ohio State University Novel Antimicrobials Discovery – Alternatives to antibiotics to control bacterial pathogens
11:40am – 11:50am	**Marissa Gittrich,** The Ohio State University Unearthing Patterns of *Klebsiella* sp. M5a1 resistome to phage infection
11:50am – 12:00pm	**Paul Oladele,** Purdue University Effect of mode of delivery of fecal microbiota transplants on growth performance and gut microbiome in weaning piglets
12:00pm – 1:30pm	Lunch and **Funding Agency Leadership Panel: The Future and Funding of Microbiome Science** (Panel will be 12:30-1:30pm in main conference room)

	Tuesday May 9th, 2023, continued
1:30pm – 2:30pm	**Poster Session 1** + Coffee
2:30pm – 2:50pm	**Session: One Health and the Environment** **Kelly Baker, University of Iowa** Predicting zoonotic spillover in urban settings: Validation of commercial pet trackers for the study of spatial movement and interactions between infants, domestic animals, and the environment
2:50pm – 3:05pm	**Dae-Wook Kang,** University of Toledo Discovering bacterial biomarkers to strengthen wastewater SARS-CoV-2 surveillance
3:05pm – 3:20pm	**Seungjun Lee**, Pykyong National University Microbial Dysbiosis In Freshwater Environment During Cyanobacterial Blooms Associated With Dissemination Of Antibiotic Resistance Genes
2:20pm – 3:35pm	**Nicholas Nastasi,** The Ohio State University The Indoor Microbiome of Specialized Environments: Controlling Fungal Growth on Aircraft and Spacecraft
3:35pm – 3:45pm	**Angela Kent,** University of Illinois-Urbana Champaign Mining ancient genomes for new strategies for nutrient retention in agroecosystems
4:00pm – 5pm	**Poster Session 2 + Reception**
6:00pm	**Social Event – Funnybiome Improv Show** (Shadowbox Theater – purchase tickets here)
	Wednesday May 10th, 2023
8:50am – 9:00am	**Welcome from David Horn, PhD** Dean, College of Arts and Sciences, The Ohio State University
9:00am – 9:25am	**Session: Friend and foe: Pathogens and the microbiome** **Matt Anderson,** The Ohio State University A metagenomics approach identifies eukaryotes in metazoan-associated microbiomes
9:25am – 9:50am	**Tessa Cannon,** The Ohio State University Monkeys and Microbes: Understanding the role of the gut and oral microbiome in SIV-infected sooty mangabeys
9:50am – 10:02am	**Melanie Medina López,** The Ohio State University Soybean cyst nematode infestation is associated with changes in fungal community composition in agricultural soils of Ohio.
10:03am – 10:15am	**Alexander P. de Porto,** University of Chicago Low fecal short chain fatty acid and secondary bile acid abundances are associated with increased in-hospital mortality in MICU patients

	Wednesday May 10th, 2023, continued
10:15am – 10:30am	Coffee Break
10:30am – 10:45am	**Session: What's in a host?: Host-associated microbiomes** **Jiangjiang (Chris) Zhu,** The Ohio State University Mass spectrometry-based metabolomics in gut microbiome research
10:45am – 11:00am	**Jan Claesen,** Cleveland Clinic Gut Microbial Metabolism of Dietary Polyphenols in Health and Disease
11:00am – 11:15am	**Patricia Wolf,** Purdue University Diversity and distribution of sulfur metabolic genes in the human gut microbiome and their association with colorectal cancer
11:15am – 11:30am	**Matthew Sullivan,** The Ohio State University Viruses: the next chapter in the human microbiome story?
11:30am – 1:00pm	Lunch and **Trainee Career Panel -** (Panel will be 11:45-1pm in rm 110)
1:00pm – 2:00pm	**Kelly Wrighton,** Colorado State University **Keynote**: Amines to Methane
2:00pm – 2:15pm	**Poster Awards and Closing of the Midwest Microbiome Symposium from Matt Sullivan, PhD** Professor of Microbiology and Director, Center of Microbiome Science, The Ohio State University

Trainee Career Panel

Wednesday, May 10th 11:45am - 1pm
Rm 110

Zakee Sabree	Associate Professor Faculty Director	Department of Evolution, Ecology, & Organismal Biology, The Ohio State University Office of Postdoctoral Affairs
Seth A. Faith, PhD, DR-IV, DAF	Medical and Operational BioSciences CTC Lead, Air Force Research Laboratory	711th Human Performance Wing, Airman Biosciences Division (Formerly: Director of Applied Microbiology Services Laboratory at OSU, Research Lead at Battelle, and faculty at NCSU)
Lexie Blalock, PhD	Senior Scientist	Microbial Genomics, Abbott (Former postdoc at Nationwide Children's Hospital)
Dubraska Diaz-Campos, DVM PhD	Assistant Professor	Diagnostic and Clinical Microbiology, The Ohio State University Directs the clinical microbiology laboratory at OSU College of Veterinary Medicine

Funding Agency Leadership Panel: The Future and Funding of Microbiome Science

Tuesday, May 9th 12:30 pm – 1:30pm
Main conference room

Phillip J. Daschner	Program Director	Division of Cancer Biology, National Cancer Institute, NIH
Anika L. Dzierlenga, PhD	Program Director	National Institute of Environmental Health Sciences, NIH, Genes, Environment, and Health Branch
Matthew D. Kane, PhD	Program Director	Division of Environmental Biology, NSF Supports the following programs: Center for Advancement and Synthesis of Open Environmental Data and Sciences Ecosystem Science Cluster (ES) Macrosystems Biology and NEON-Enabled Science (MSB-NES)
Michael Goodson, PhD	Research Biologist	Air Force Research Laboratory, 711th Human Performance Wing
Thomas Mitchell, PhD	Biological Specialist and National Program Leader	National Institute of Food and Agriculture, USDA Oversees the following programs: Plant Biotic Interactions Agricultural Microbiome Biotechnology Risk Assessment IR4 Methylbromide Transition

KEYNOTE BIOGRAPHIES

Dr. Eric Martens, University of Michigan

Dr. Eric Martens is a Professor of Microbiology and Immunology at the University of Michigan Medical School. Dr. Martens obtained his B.A. (1997) from Washington University in St. Louis and his Ph.D. (2005) from the University of Wisconsin-Madison. Dr. Martens began investigating the mechanisms through which human gut bacteria digest diet- and host derived polysaccharides during his postdoctoral work in the laboratory of Jeffrey Gordon at Washington University School of Medicine. He continued to pursue this work at the University of Michigan Medical School in 2009 with a focus on members of the Bacteroidetes, one of only a few numerically dominant phyla of human gut bacteria, which are particularly adept at degrading diet- and host-derived polysaccharides. Current projects in the Martens laboratory are aimed at understanding the role of commensal gut bacteria in triggering inflammatory bowel disease, the dependency of inflammatory outcomes on the amount and variety of dietary fiber, and the mechanisms through which bacterial mucin-degrading enzymes digest the mucosal barrier and promote disease. Additional projects in his lab are focused on lateral gene transfer between bacteria in environments like the ocean and those in the gut, bacteriophage interactions with gut bacteria and the immune system, and cultivation and characterization of the unstudied majority of human gut symbionts.

Dr. Kelly Wrighton, Colorado State University

Kelly Wrighton is an Associate Professor at Colorado State University, where her laboratory uses genomic enabled technologies to uncover how microorganisms control the chemical world in, on, and around us. The Wrighton laboratory research is ecosystem agnostic, with each environment offering a new perspective on the ‘knobs’ that control the chemical transformations microorganisms catalyze. Current focus areas include soil microbiomes in sustainable agriculture (rumen and soil), carbon sequestration, and modulating greenhouse gasses, but her lab also has research relevant to the energy sector and human health as modulated via the gut. Recognizing the impact of her team’s research, Wrighton was awarded the Presidential Early Career Award for Scientist and Engineers in 2020 (one of the highest honors from the US President), was elected to the American Academy of Microbiologists, is a a named fellow of the American Geophysical Union. She has also earned awards from the International Society of Microbial Ecology and International Geobiology Society for her team’s scientific excellence. Wrighton is currently the CSU Bishop Endowed Chair for research excellence. Wrighton actively sits on scientific boards for DOE Knowledge Base (KBase), the Joint Genome Institute (JGI), and Pluton Biosciences.

INVITED SPEAKERS

Matthew Anderson	Associate Professor	Department of Microbiology, College of Arts and Sciences, The Ohio State University
Kelly Baker	Associate Professor	Department of Occupational and Environmental Health, College of Public Health, University of Iowa
Tessa Cannon	Presidential Fellow, PhD Student	Department of Anthropology, College of Arts and Sciences, The Ohio State University
Jan Claesen	Assistant Staff	Lerner Research Institute, Cleveland Clinic
Jessica Cooperstone	Assistant Professor	Department of Horticulture and Crop Science, Department of Food Science and Technology, The Ohio State University
Skye Fishbein	Postdoc Research Scholar	Washington University in St. Louis
Marissa Gittrich	PhD Candidate	Department of Microbiology, College of Arts and Sciences, The Ohio State University
Timothy Johnson	Assistant Professor	Department of Animal Sciences, College of Agriculture, Purdue University
Dae-Wook Kang	Assistant Professor	Department of Civil and Environmental Engineering, The University of Toledo
Seung jun Lee	Professor	Department of Food Science & Nutrition, College of Fisheries Science, Pukyong National University
Brett Loman	Assistant Professor	Department of Animal Sciences, College of Agricultural, Consumer and Environmental Sciences
Nicolas Nastasi	PhD Student	Environmental Sciences Graduate Program, The Ohio State University
Gireesh Rajashekara	Professor, Program Head of Center for Food Animal Health	Ohio Agricultural Research and Development Center College of Food, Agriculture and Environmental Sciences The Ohio State University
Zakee Sabree	Associate Professor	Department of Evolution, Ecology and Organismal Biology, College of Arts and Sciences, The Ohio State University
Matthew Sullivan	Associate Professor	Department of Microbiology, Department of Civil, Environmental, and Geodetic Engineering, The Ohio State University
David Thoms	Assistant Professor	Florida State University
Jenessa Winston	Assistant Professor	Department of Veterinary Clinical Sciences, College of Veterinary Medicine
Patricia Wolf	Assistant Professor	Department of Nutrition Science, College of Health and Human Sciences, Purdue University
Lihua Ye	Assistant Professor	Department of Neuroscience, College of Medicine, The Ohio State University
Chris Zhu	Associate Professor	Department of Human Sciences, College of Education and Human Ecology, The Ohio State University
Jasenka Zubcevic	Associate Professor	Department of Physiology and Pharmacology, The University of Toledo

SPEAKER BIOGRAPHIES

Matthew Anderson, PhD, The Ohio State University

Matt Anderson is an Associate Professor in the Department of Microbiology and the Department of Microbial Infection and Immunity at The Ohio State University. He received his PhD in Genetics working on cell differentiation of Toxoplasma gondii under the supervision of John Boothroyd (Stanford University). As a postdoc, he switched fields to study genetic variation in Candida albicans, the common fungal commensal and opportunistic pathogen of humans. He was trained here by Judy Berman (U. of Minnesota) and Richard Bennett (Brown University).

Investigation of C. albicans in his lab is centered on intraspecies genetic variation and how this contributes to the balance between commensalism and virulence in various niches of the human host. His group uses a combination of experimental and computational approaches to both produce datasets and then mine them for testable hypothesis that can be assessed in the laboratory. More recent efforts have expanded beyond C. albicans to define the microbial eukaryotes associated with humans and understand their contributions to community ecology and the balance between health and disease for the human host. This work is being performed in partnership with Indigenous communities in South Dakota to address health concerns that are identified by the community. Land use interests by our Lakota partners have shifted our realm of responsibility to environmental microbiomes where we are working to identify how ranching alters microbial residents and plant diversity on the Northern Plains.

Kelly Baker, PhD, University of Iowa

Kelly K. Baker is an Associate Professor of Occupational and Environmental Health and Epidemiology at the University of Iowa College of Public Health. Her research focuses on understanding how societal development, especially in urban areas, influences the transmission of enteric pathogens between humans, animals, and the household and community environment, and identifying the most effective developmental strategies for achieving disease control. She leads a large transdisciplinary team on the PAthogen Transmission and Health Outcomes Modeling of Enteric disease (PATHOME) cohort study, which draws upon climate, socio-demographic, behavioral, spatial, environmental, clinical, zoonotic, and statistical disciplines to explore enteric disease ecology dynamics in eastern Africa. Similar research is examining the impact of severe climate events in rural well water quality in Iowa, on food and water security and malnutrition in Ethiopia, and equity in flood vulnerability in urban Kenya. Other research involves developing and evaluating rapid low-cost enteric pathogen/antimicrobial resistance diagnostic assays for disease surveillance and point-of-care decision making domestically and globally. A different area of her research program focuses on measuring the role of water, sanitation, and hygiene access on birth outcomes in low-income populations. She serves on the National Academies Board of Global Health, Chairs the One Health subcommittee for the American Society of Tropical Medicine and Hygiene, is Senior Editor for the CABI One Health Journal, and serves on the Diversity Equity and Inclusion committee for her College.

Tessa Cannon, MSc, The Ohio State University

Tessa Cannon is a PhD Candidate and Presidential Fellow in the Department of Anthropology at The Ohio State University. Cannon’s work focuses on understanding relationship between the natural feeding ecology, gut microbiome and ability of sooty mangabeys to resist AIDS, so we are better able to understand the pathogenesis of SIV, HIV and, ultimately, AIDS in humans.

Her work is first to integrate eco-behavioral information (including data on viral load) on sooty mangabeys in their natural habitat with similar data on these monkeys under laboratory conditions. It has relevance in the domains of public health, primate behavioral ecology and conservation. In support of her PhD project, Cannon received funding form the President's Research Excellence program and several awards from the Infectious Diseases Institute. In 2022, she was awarded a Presidential Fellowship, the most prestigious award given by the graduate school. She founded For the Love of Primates, a non-profit sanctuary for retired research primates, which earned her a President's Buckeye Accelerator award in 2022. Cannon serves as Chair of the Graduate Student in Anthropology Committee, works as a vet tech for the Central Ohio Programs for Animal Welfare and the Humane Society, works as an undergraduate mentor in the Hale Lab, and is an adjunct professor at Columbus State Community College. Cannon earned her bachelor's degree in zoology from Ohio Wesleyan University, her master's degree in primate conservation from Oxford Brookes University and is a certified veterinary technician.

Jan Claesen, PhD, Cleveland Clinic

Jan Claesen is an Assistant Staff faculty member at the Lerner Research Institute at Cleveland Clinic and an Assistant Professor of Molecular Medicine at Case Western Reserve University. Our group was established in November 2017 and we aim to characterize the role of bioactive microbial and dietary small molecules in microbiota-associated diseases. We use a combination of genetic and biochemical techniques, as well as preclinical models to elucidate the molecular mechanisms that drive community dynamics and microbe-host interactions, and engineer commensal bacteria for fundamental and translational applications in the gut and skin microbiome.

Jan obtained a B.S. and M.S. in Biological Engineering, specializing in Cell and Gene Biotechnology, from KU Leuven, Belgium. Next, Jan joined the lab of Prof. Mervyn Bibb and he received his Ph.D. in Molecular Microbiology in 2011 from the John Innes Centre and University of East Anglia, Norwich, United Kingdom, where he studied the genetics and biosynthesis of ribosomally synthesized and post-translationally modified peptide antibiotics produced by Streptomyces bacteria. After his graduate studies, Jan was a postdoctoral scholar in the lab of Dr. Michael Fischbach in the Department of Bioengineering and Therapeutic Sciences at the University of California, San Francisco, USA. There, his work focused on the identification of novel biosynthetic pathways and characterization of bacterial metabolites that mediate microbiota interactions in healthy human gut and skin.

In his free time, Jan enjoys hiking, outdoors activities, cooking, traveling, RPG computer games, heavy and alternative music, Lego, and spending time with his wife and two daughters.

Jessica Cooperstone, PhD, The Ohio State University

www.cooperstonelab.com
Twitter: @CooperstoneLab

Dr. Jessica Cooperstone is an Assistant Professor in the departments of Horticulture and Crop Science, and Food Science and Technology at The Ohio State University, and was hired under OSU's Foods for Health focus area of the Discovery Themes Initiative. She received her B.S. in Food Science from Cornell University and her Ph.D. in Food Science & Technology from The Ohio State University. She and her team are interested in unraveling the chemical basis for the health benefits associated with fruit and vegetable rich diets. From fundamental studies in

crops, to nutrition-based clinical trials, her group works across the plant-food-nutrition-health continuum. Jess and her team are locatedat the interface of plant, food and nutrition sciences, and utilize bioinformatics based approaches, which she will talk about today.

Skye Fishbein, PhD, Washington University in St. Louis

Skye Fishbein, PhD, is a postdoctoral fellow in the laboratory of Dr. Gautam Dantas, in the Department of Pathology & Immunology at Washington University School of Medicine in St. Louis (2019-present). She received her Ph.D. in microbiology at the Harvard T.H. Chan School of Public Health under the guidance of Dr. Eric Rubin (2013-2019). In the Dantas lab, her research focuses on (1) understanding microbiome determinants of Clostridioides difficilecolonization outcomes in the health care setting, (2) identifying strain-level variation in C. difficile that increases pathogenicity, and (3) investigating commensal metabolic relationships in the gut microbiome that impede C. difficile pathogenesis.

Marissa Gittrich, The Ohio State University

Marissa Gittrich is a fifth-year Ph.D. student at Ohio State in the Department of Microbiology. She earned her Bachelor of Science in Microbiology and a minor in Chemistry at Bowling Green State University in the winter of 2017, where she studied ways to reduce harmful *Planktothrix* blooms in Lake Erie. In the fall of 2018, Marissa started her Ph.D. in the Matt Sullivan lab studying how phages interact with bacteria. Since joining the lab, she has worked on several projects, including studying the use of antibiotics and phages to treat *Pseudomonas aeruginosa* infections and using multi-omics to understand how lytic phages reprogram hosts in marine bacteria. Currently, Marissa and her team of undergraduate researchers are testing over 80 phages infecting four diverse plant-growth-promoting rhizobacteria to identify the bacterial genes required for infection. On Tuesday, Marissa will present her work examining the differences in bacterial resistance in highly related phages (>86% similarity) belonging to the same phage genus infecting the soil-derived bacterium *Klebsiella* sp. M5a1.

Timothy Johnson, PhD, Purdue University

Tim Johnson is an Assistant Professor of Food Animal Microbiomes in the Department of Animal Sciences at Purdue University. Tim received his PhD from Michigan State University as a member of the Center for Microbial Ecology. He then went on to complete two postdoctoral positions, the first at McMaster University and then at the Food Safety and Enteric Pathogens Research Unit at the USDA National Animal Disease Center. His work focuses on antibiotic alternative animal feed additives, understanding and controlling microbiome colonization, the impact of antibiotic use on antibiotic resistance gene ecology in the agroecosystem, and the development of rapid bioassays to provide timely information in the selection of an effective antibiotic.

Dae-Wook Kang, PhD, University of Toledo

Dr. Kang received his BS and MS in Civil and Environmental Engineering from the Seoul National University in South Korea and his PhD from the University of Wisconsin-Madison. During his graduate study, he got trained with molecular technologies to understand complex microbial functions in environmental engineering systems. This training allowed him to stretch his research interest from environment to human health as a post-doc and a research scientist in the Biodesign Swette Center for Environmental Biotechnology at the Arizona State University,

where he was involved in groundbreaking work to establish the relationships between human gut microbiome and autism.

Since Dr. Kang joined the University of Toledo in 2019, his research interests are employing multi-omics technologies to advance understanding of the role of microbiome on environmental engineering systems, harmful algal blooms, and human health, and eventually to improve human public health and environment sustainability. He has been awarded several research grants from U.S. Army Corps of Engineers, Ohio Department of Health, and U.S. Environmental Protection Agency.

In addition to research, Dr. Kang has a passion for teaching and mentoring students. He has taught courses, including Microbiome and Multi-omics for both undergraduate and graduate students with different majors. Dr. Kang's research and teaching have been recognized with the President's Award for Excellence in Creative and Scholarly Activity in the University of Toledo, named in a submission to the "Shout Out" for Innovative Instructors and Staff campaign and nominated to receive the Outstanding Adviser Award.

Dr. Kang is active in the professional community as a reviewer for grant proposals and journal papers and is going to serve on the editorial board of Frontiers in cellular and infection microbiology. He is a member of American Society of Microbiology, Association of Environmental Engineering and Science Professors and the American Society of Civil Engineers.

Seungjun Lee, PhD, Pykyong National University

Seungjun Lee is a professor in the Departments of Food Science and Nutrition at the Pukyong National University. He graduated with his mater from the Department of Food Science and Technology and PhD from the Environmental Science at The OSU. He also conducted postdoctoral researcher in the College of Public Health at The OSU. His primary research interests are in food and environmental microbiology for understanding pathogen and antibiotic resistance problems. His group is focused on the application of metagenomics and molecular technique to environmental ecology with potential health risks.

Brett Loman, PhD, University of Illinois at Urbana-Champaign

Dr. Brett Loman earned his PhD in Nutritional Sciences and Registration in Dietetics at the University of Illinois at Urbana-Champaign. His doctoral work focused on the effects of prebiotic and probiotic therapy to enhance enteroendocrine function in a neonatal piglet model of intestinal failure. During his postdoc, he was a T32 Postdoctoral Fellow in the Comprehensive Training in Oral and Craniofacial Sciences program through the Ohio State University and Research Institute at Nationwide Children's Hospital in Columbus, OH. His postdoctoral training focused on microbiota-gut-brain interactions in the context of psychological stress and cancer treatment. As a current Assistant Professor in the Department of Animal Sciences at the University of Illinois at Urbana-Champaign, he is associated with the Division of Nutritional Sciences, Microbial Systems Initiative, and Personalized Nutrition Initiative. Dr. Loman's interdisciplinary research program strives to improve animal and human gastrointestinal and mental health. His team seeks to understand how environmental factors such as nutrition and stress alter communication between the resident microbiota, intestine, and brain. The long-term goal of his research program is to formulate dietary interventions that reduce gastrointestinal symptoms during functional gastrointestinal disorders, psychological stress, and cancer.

Nicholas Nastasi, The Ohio State University

Nicholas Nastasi's research addresses emerging concerns in indoor environmental quality at the intersection of microbiology, exposure assessment, materials degradation, and health outcomes. His work has demonstrated that the amount of fungal growth in carpet is dependent upon moisture availability, dust loading, and flooring material. During the COVID-19 pandemic, he worked on developing novel building-level disease surveillance protocols using dust. Related, he demonstrated that viral persistence on dust and flooring is dependent on the viral envelope and elucidated the efficacy of different disinfection techniques on these materials. His prior work has also elucidated the importance of bacterial taxa on biogeochemical cycles during the early production stages of hydraulic fractured natural gas wells. His current work on a grant funded by NASA aims to create predictive models for microbial growth, community composition, and metabolic function in dust collected from the International Space Station under different environmental conditions. He received his A.S. from Columbus State Community College, a B.S. in Environmental Engineering and M.S. in Environmental Science at The Ohio State University. Currently, he is a PhD candidate at The Ohio State University in the Environmental Science Graduate Program specializing in Environmental Public Health.

Gireesh Rajashekara, DVM, MVSc, PhD, The Ohio State University

Dr. Gireesh Rajashekara received his BVSc (DVM) and MVSc from University of Agricultural Sciences (UAS) Bangalore, India and got his PhD in veterinary microbiology from University of Minnesota. Currently, is a Professor in the Center for Food Animal Health (CFAH), Department of Animal Sciences. Research in Dr. Rajashekara's lab is focused on solving animal health and zoonotic disease problems in food-producing animals using One Health approach. Specifically, his research is focused on the discovery of novel antimicrobials as well as probiotics and antimicrobial peptides (AMPs) to control zoonotic foodborne pathogens, animal pathogens, and phytopathogens. Further studies are focused on elucidating mechanisms of how malnutrition and associated changes in microbiota contribute to gut integrity and intestinal homeostasis and its impact on pathogenesis of enteric pathogens. Dr. Rajashekara has published over 135 peer reviewed articles and holds multiple patents. Dr. Rajashekara is extensively involved in providing service to the professional communities.

Zakee Sabree, PhD, The Ohio State University

Whether free-living in extremely diverse communities in the ocean or residing solitarily in highly specialized tissues of a host organism, microbes exert an immense impact on the way nutrients are acquired, sequestered, recycled and distributed in natural systems. Dr. Zakee Sabree's group is interested in the functional and trophic relationships that forge intimate host-microbe interactions and shape bacterial communities, and the evolutionary outcomes of these symbioses. Two main questions guide Dr. Sabree's current research: 1) how microbes are employed by their hosts to obtain essential nutrients and facilitate trophic niche expansion; and 2) what are the structural and functional impacts of ancient and obligate associations with eukaryotes on the genomes, genes and gene products of their bacterial partners. Insects, specifically cockroaches and termites, are the focus of Dr. Sabree's research because they are ubiquitous, participate significantly in biomass turnover and maintain, often simultaneously, various types of symbioses with microbes. He employs legacy microbiological tools as well as current and emergent molecular and genomics techniques to address several specific aspects of these questions.

Matthew Sullivan, PhD, The Ohio State University

Matthew B. Sullivan studies viruses that infect microbes in their natural settings. The 'microbiome' is increasingly recognized to drive Earth's ecosystems, including in humans, but it does so under constraints imposed by viruses. Sullivan pioneered viral ecogenomics as a means to study viruses in complex communities via quantitative viral metagenomic sample-to-sequence pipelines, new approaches to link viruses and hosts, and developing iVirus, a community-available analytical platform. In the oceans, Sullivan has vastly expanded our understanding of the global virosphere, established automatable scalable taxonomic approaches, and elucidated how 'wild' viruses evolve and even metabolically reprogram the most abundant photosystems on the planet. Outside the oceans, Sullivan has adapted these toolkits for use in extreme environments, soils and humans with each new environment leading to myriad discoveries that place viruses at the core of these microbial ecosystems. Sullivan is a Professor of Microbiology and Civil, Environmental and Geodetic Engineering, a co-founder of the UA Ecosystem Genomics Institute, and is recognized for his work as a co-director of OSU's Infectious Disease Institute Microbial Communities Program, Founding Director of OSU's Center of Microbiome Sciences, leadership of the EMERGE Biology Integration Institute, a Gordon and Betty Moore Foundation Investigator, a Kavli Fellow, a Beckman Mentor, and a senior editor at Nature Publishing Group's ISME Journal.

David Thoms, PhD, Florida State University

Dr. David Thoms uses the plant model system, Arabidopsis thaliana, to study the role of innate immunity in establishing a healthy root microbiome. Hosts rely on a healthy microbiome for optimal growth and development. While the microbiome is crucial for functional immune system development, immunity has also been shown to influence microbiome composition in a manner that prevents dysbiosis. Plant roots are analogous to the animal gut as both are important sites of nutrient acquisition and microbial activity. Dr. Thoms' lab uses a combination of NextGen sequencing, microscopy, and genetics to study the mechanisms required for distinguishing between beneficial and pathogenic bacteria in a manner that modulates bacterial growth.

Jenessa Winston, DVM, PhD, The Ohio State University

Dr. Jenessa Winston is an Assistant Professor at the Ohio State University. She received a Bachelor of Science in Integrated Biology from University of Florida in 2007. She then received her veterinary degree from the North Carolina State University in 2011. She went on to complete a rotating small animal internship and residency training in small animal internal medicine at NC State achieving board certification, as a diplomate in the American College of Veterinary Internal Medicine, in 2015. As a Clinical Investigator and NIH T32 fellow at NC State, Dr. Winston completed a PhD in Comparative Biomedical Sciences with an Infectious Disease concentration in 2019. Her dissertation focused on defining the dynamics between the gut microbiota, microbial derived secondary bile acid ursodeoxycholic acid, and Clostridioides difficile pathogenesis.

As a clinician scientist, Dr. Winston's primary research areas of interest include microbe-host interactions during health and disease. She has a special interest in microbially derived bile acids and rational manipulation of microbial ecosystems including interventions such as fecal microbiota transplantation (FMT). Since starting at the OSU, Dr. Winston has launched the Companion Animal Fecal Bank, which serves as a unique research platform to accelerate our study and translation of microbial community sciences into safe and effective clinical

applications. Currently, there are 4 ongoing veterinary FMT clinical trials. Dr. Winston is also a NIH NIAID K08 award recipient and her research focuses on the impact of inflammation induced alterations to microbially derived bile acids on susceptibility and severity of Clostridioides difficile infection.

Patricia Wolf, PhD, RDN, Purdue University

Dr. Wolf completed her PhD in Nutritional Sciences with a focus on microbial sulfur metabolism at the University of Illinois at Urbana-Champaign. During her graduate training, she simultaneously completed the Didactic Program in Dietetics and became a Registered Dietitian Nutritionist. She then was a postdoctoral fellow in the Cancer Education and Career Development Program NCI T32 at the University of Illinois at Chicago. Her research investigates microbial mechanisms of cancer health disparities related to inequitable food access and quality. To do so, she uses techniques in molecular microbiology and novel enzyme characterization to understand the metabolic capacity of the human gut microbiome. With her expertise in nutrition and dietetics, she then examines whether dietary intake shifts microbial ecology and function toward the formation of deleterious microbial metabolites contributing to cancer risk. Given that dietary behaviors are shaped by the social and structural environment, her future work will explore relationships between the neighborhood food environment and microbial metabolism in order to mitigate the inequitable burden of cancer in certain groups.

Lihua Ye, PhD, The Ohio State University

Lihua Ye is an assistant professor in the Department of Neuroscience at OSU. Her lab is interested in understanding the molecular mechanisms by which intestinal nutrient and microbial signals can be sensed and transmitted to the nervous system.

Dr. Wolf completed her PhD in Nutritional Sciences with a focus on microbial sulfur metabolism at the University of Illinois at Urbana-Champaign. During her graduate training, she simultaneously completed the Didactic Program in Dietetics and became a Registered Dietitian Nutritionist. She then was a postdoctoral fellow in the Cancer Education and Career Development Program NCI T32 at the University of Illinois at Chicago. Her research investigates microbial mechanisms of cancer health disparities related to inequitable food access and quality. To do so, she uses techniques in molecular microbiology and novel enzyme characterization to understand the metabolic capacity of the human gut microbiome. With her expertise in nutrition and dietetics, she then examines whether dietary intake shifts microbial ecology and function toward the formation of deleterious microbial metabolites contributing to cancer risk. Given that dietary behaviors are shaped by the social and structural environment, her future work will explore relationships between the neighborhood food environment and microbial metabolism in order to mitigate the inequitable burden of cancer in certain groups.

Jiangjiang (Chris) Zhu, PhD, MS, The Ohio State University

Chris Zhu, PhD, is an associate professor in the Department of Human Sciences at The Ohio State University and a member of the Molecular Carcinogenesis and Chemoprevention Program at the OSUCCC – James. Dr. Zhu's current research includes studying host-microbiota metabolic interactions and the critical roles of nutritional components in modulating such interactions, as well as investigating the impact of therapeutic modulation of gut microbes to colorectal cancer patients. He is also developing a multiplex mass spectrometry-based metabolomics platform for disease diagnosis and treatment monitoring.

Jasenka Zubcevic, PhD, The Ohio State University

Dr. Jasenka Zubcevic completed her PhD in 2008 at the University of Bristol in England under the mentorship of Dr. Julian Paton. Her graduate training in neurogenic regulation of cardiovascular homeostasis shaped her current research interests, which she continued to expand through her postdoctoral training at North Texas, University of Pennsylvania, and finally the University of Florida. As a new assistant professor in the College of Veterinary Medicine at the University of Florida, Dr. Zubcevic expanded her research questions to include interoceptive mechanisms of physiologic regulation, and specifically the role of the microbiota and the immune system in shaping the neural sensory feedback from the viscera in cardiovascular homeostasis. Her current work at the University of Toledo is focused on gut microbiota-vagal-brain signaling in hypertension.

ABSTRACTS

Short Talks

ASSOCIATIONS OF MATERNAL DIETARY INFLAMMATORY POTENTIAL & THE GUT MICROBIOME

Suzanne Alvernaz*[1], Elizabeth Wenzel[2], Unnathi Nagelli[1], Lacey Peslez[3], Mohit Jain[4], Jack Gilbert[5,6], Pauline Maki[2,7,8], Lisa Tussing-Humphreys[3] , Beatriz Peñalver-Bernabé[1,9]

[1] Department of Biomedical Engineering, University of Illinois, Chicago, IL, USA
[2] Department of Psychology, University of Illinois, Chicago, IL, USA
[3] Department of Kinesiology and Nutrition, University of Illinois, Chicago, IL, USA
[4] Department of Pharmacology, University of California, San Diego, CA, USA
[5] Department of Pediatrics, University of California, San Diego, CA, USA
[6] Scripps Oceanographic Institute, University of California, San Diego, CA, USA
[7] Department of Psychiatry, University of Illinois, Chicago, IL, USA
[8] Department of Obstetrics and Gynecology, University of Illinois, Chicago, IL, USA
[9] Department of Urology, University of Illinois, Chicago, IL, USA

Introduction: Pregnancy is known to involve changes in a wide variety of physiological systems, including the maternal gut microbiota. Dietary intake alters the gut microbiota composition, structure and function and host metabolism. Western diets are particularly characterized by their high levels of inflammatory food, such saturated fatty acids, animal protein and added sugar. Multiple perinatal disorders have been associated with inflammation, maternal metabolic alterations and gut microbiota dysbiosis, including gestational diabetes and mood disorders. However, the effects of high inflammatory diets in the gut microbiota during pregnancy has yet to be thoroughly explored.
Methods: 58 pregnant women were recruited prior to 16 weeks of gestation and were followed through 24-28 gestational weeks. Participants completed a food frequency questionnaire (FFQ) and 46 provided rectal samples. Dietary inflammatory potential was assessed using the Dietary Inflammatory Index (DII) from FFQ data. Rectal samples were analyzed using amplicon 16S rRNA sequencing and processed using DADA2. Differential taxa abundance was identified using a zero-inflated Gaussian model to identify taxa associated with the DII score. Microbial metabolic potential was assessed using PICRUSt2 and gene set enrichment analysis to identify microbial enzymes enriched in terms of DII score
Results: The inflammatory diet associated with the maternal gut microbiome composition showed positive associations with taxa such *Blautia* and *Ruminococcaceae,* and negative associations with taxa such as *Anaerococcus* and *Parvimonas*. Gene set enrichment analysis revealed in increase in microbial genes related to bacterial pathogenesis such as antibiotic resistance and two-component systems and a decrease of genes involved in various metabolic processes including tryptophan, carbon, and butonate metabolism.
Conclusions: Dietary inflammatory potential was associated with changes in the gut microbial composition as well as microbial enzymatic markers with an increase in genes related to bacterial inflammatory processes.

Microbial Dimension of Symbiosis and Dysbiosis in Fungus–gardening Ants

Blake Bringhurst*[1], Jon N. Seal[2]

[1]Ohio State University
[2]University of Texas at Tyler

Higher attine ants (Tribe: Attini) have symbiotic relationships with the fungal cultivars they grow as food and the microbes found in the microbiomes of their fungal gardens and the ants themselves. Among the higher attines, there are two broad groups of fungal symbionts. Most ants in the genus *Trachymyrmex* tend to grow Clade–B fungi, which is a group of undescribed *Leucocoprinus* species. Leaf–cutting ants in the genera *Acromyrmex* and *Atta* tend to grow Clade–A fungi (*Leucocoprinus gongylophorus*). Previous work has shown switching the cultivar grown by some *Trachymyrmex* species, from Clade–B to Clade–A fungus, creates an unstable symbiosis between the ants and their grown cultivar, so that a sudden and catastrophic decrease in the size of their fungal garden invariably results. One hypothesis is that the stability of ant–fungal combinations is maintained by interactions among members of the microbiome of fungus–gardening ants and their fungal gardens. This project explored whether changing fungal partners impacts the microbiomes of the host ants and their symbiotic fungi by performing cross-fostering experiments that forced ants to grow novel fungi. Specifically, these experiments forced ants of three *Trachymyrmex* species that

normally grow Clade–B fungi and a fourth species that has been found growing both clades, to grow Clade–A fungi. The experiments revealed that *Trachymyrmex* ants altered their novel Clade–A garden microbiomes and that these were similar to that of the 'control' or 'sham switched' Clade–B fungal gardens. These results suggest that ants play a role in determining the structure of the microbiome of their fungal gardens. Since these combinations are not stable, it is possible that the 'novel' microbiome structured by the *Trachymyrmex* ants is a factor in driving symbiotic collapse.

Low fecal short chain fatty acid and secondary bile acid abundances are associated with increased in-hospital mortality in MICU patients

Alexander P. de Porto*[1], Nicholas P. Dylla[1], Emerald Adler[1], Maryam Khalid[1], Jessica Little[1], Amber Rose[1], David Moran[1], Michael W. Mullowney[1], Mary McMillin[1], Victoria Burgo[1], Rita Smith[1], Che Woodson[1], Carolyn Metcalfe[1], Eddi Lin[1], Ramanujam Ramanswamy[1], Krysta S. Wolfe[2], Christopher Lehmann[3], Matthew Odenwald[4], Anitha Sundararajan[1], Ashley Sidebottom[1], John P. Kress[2], Eric G. Pamer[1] and Bhakti K. Patel[2]

[1]Duchossois Family Institute, University of Chicago, 900 E. 57th St, Chicago, IL 60637, USA.
[2]Department of Medicine, Section of Pulmonary and Critical Care Medicine, University of Chicago Medicine, 5841 South Maryland Ave, Chicago, IL 60637, USA.
[3]Department of Medicine, Section of Infectious Diseases & Global Health, University of Chicago Medicine, 5841 South Maryland Ave, Chicago, IL 60637, USA.
[4]Department of Medicine, Section of Gastroenterology, Hepatology and Nutrition, University of Chicago, Medicine, 5841 South Maryland Ave, Chicago, IL 60637, USA.

Patients admitted to the medical intensive care unit (MICU) commonly receive antibiotic treatments that reduce microbiota diversity and lead to expanded populations of antibiotic-resistant pathobionts, such as Proteobacteria and Enterococci. Reduced microbiota diversity and increased pathobiont density have been associated with increased mortality in MICU patients. We recently demonstrated that expanded populations of Proteobacteria and reduced concentrations of a subset of fecal metabolites are associated with progressive respiratory failure and death in patients admitted to the MICU with COVID-19. The impact of fecal metabolites on the general MICU population, however, is unknown. We prospectively enrolled 200 patients admitted to the MICU (COVID-19 patients excluded) for respiratory failure or shock and collected fecal specimens, defined microbiome compositions by shotgun metagenomic sequencing, and quantified microbiota-derived fecal metabolites by mass spectrometry. We show that in-hospital mortality is associated with reduced microbiota alpha diversity in the initial fecal sample collected following MICU admission. Patients surviving hospitalization have higher SCFA and secondary bile acid concentrations in their fecal samples. A microbiome metabolomic profile (MMP) accounting for fecal SCFA and secondary bile acid concentrations is independently associated with in-hospital mortality. Our results indicate that fecal microbiota dysbiosis results in low secondary bile acid and SCFA concentrations that identify MICU patients with increased risk of mortality.

Gut microbiome derived N-acyl serinols regulate postprandial metabolic homeostasis

Sumita Dutta*[1,2], William Massey[1,2], Venkateshwari Varadharajan[1,2], Anthony J. Horak[1,2], Rakhee Banerjee[1,2], Amy Burrows[1,2], Danny Orabi[1,2,3], Zeneng Wang[1,2] and J. Mark Brown^[1,2]

[1]Department of Cardiovascular and Metabolic Sciences, Cleveland, OH, USA
[2]Center for Microbiome and Human Health, Lerner Research Institute, Cleveland Clinic, Cleveland, OH, USA
[3]Department of General Surgery, Cleveland Clinic, Cleveland, OH, USA

Commensal gut bacteria expressing the N-acyl synthase (NAS) type VI gene are reported to produce N-acyl serinols, an endocannabinoid-like lipids that signal through the host G-coupled protein receptor, GPR119. Since GPR119 is vital for maintaining postprandial incretin production and systemic host hormone action, a study was designed to understand the role of N-acyl serinols in the regulation of post-prandial metabolic hormonal response. Here wild-type C57BL/6J male mice were subcutaneously implanted with slow-release pellets containing vehicle, N-palmitoyl (16:0) serinol (PS) or N-oleoyl (18:1) serinol (OS), and were maintained at ad libitum for 7 days. Thereafter, mice were either necropsied at ad libitum, 12 h fasted state, or 12 h fasted followed by 3 h of refeeding. LC-MS analysis of plasma and liver showed elevated levels of PS and OS in mouse implanted with these pellets, respectively. However, the levels of endogenous N-acyl amides remained unchanged. N-acyl serinol treated mice showed significantly elevated plasma insulin and leptin levels in response to refeeding. Hepatic gene expression analysis revealed that N-acyl serinol treated mice had significantly decreased levels of lipogenic transcription factors – Bhlhe40, Srebp1c and Srebp2, and their downstream genes involved in lipid/cholesterol synthesis/metabolism, in the refed state. Additionally, monocolonization of germ-free mice with NAS expressing Escherichia coli showed accumulation of N-acyl serinol in the left ventricle of heart. We also

found that the circulating levels of gut microbe-derived PS and OS in HFpEF (heart failure with preserved ejection fraction) patients were significantly reduced compared to healthy controls, suggesting a possible correlation of N-acyl serinols in maintenance of cardiometabolic health. Collectively, we conclude that metabolic consequences of gut microbe derived N-acyl serinols in the host may be an effective therapeutic approach to ameliorate postprandial hormonal response dysregulation in metabolic diseases including type 2 diabetes and obesity, and related heart failure.

Keywords: N-acyl serinol, GPR119, metabolism, insulin, lipogenesis, HFpEF

Rhizosphere Microbiome of Six Soybean Varieties Under Sufficient and Deficient Soil P Conditions: Implications for Plant Mechanisms and Microbiome Interactions

Henrique P. Feiler*[1], Cankui Zhang, Cindy H. Nakatsu

[1]Department of Agronomy, Purdue University

Phosphorus (P) is a vital nutrient for plant growth. In limiting P conditions, plants can recycle the internal P content or associate with rhizosphere microorganisms that can solubilize P to increase its acquisition. We hypothesized during P stress soybean lines with a lower internal phosphorus P recycling depends on its association with rhizosphere microorganism to obtain P. The objectives are (1) to evaluate the phosphorus use efficiency (PUE) as an indicator of the P recycling of six soybean lines, and (2) identify differences in the rhizosphere microbiome (bacteria and mycorrhizal fungi (AMF)) among the soybean lines and relate them to differences in PUE. A randomized block experiment with three replicates and two soil P conditions (-P;+P) was made in a low P soils at PPAC. The rhizosphere was collected for 16S rRNA gene analysis, sequenced and analyzed using the QIIME2. AMF colonization of roots was evaluated following the Trouvelot method. The results indicate four different mechanisms were used to improve PUE. (I) The wildtype species Glycine soja had a high dependency on the microbiome due to higher AMF colonization and 13 genera enriched (LEfSE analysis) on the -P compared to +P soils and a similar PUE in both soil P conditions. (II) The Yellow Chinese landrace line had a higher dependency on the plant mechanism as indicated by higher PUE on the -P compared to +P, low AMF colonization and three genera enriched on the -P). (III) The Japanese Landrace showed had the lowest PUE in the -P, lowest AMF colonization, and only one genus enriched in the -P. (VI) Finally, Korean Landrace had a similar mechanism to the Glycine max for the microbiome, but still the PUE was lower in the -P. These results show different soybean lines appear to use different mechanisms to cope with low P conditions.

Using resistant starch to engineer the human microbiome and increase production of indole lactic acid as a therapeutic in the GI tract

Ethan T. Hillman*[1], Haiyan Tang, Matt Hoostal, Nicole Cady, Amanda L. Photenhauer, Kwi Kim, Alex W. Schmidt, Robert Hein, Kristi Gdanetz, Greg J. Dick, Jonathan L. Golob, Nicole M. Koropatkin, Clegg Waldron, and Thomas M. Schmidt

[1] University of Michigan - Internal Medicine; Microbiology and Immunology

The production of metabolites that promote health in the human gastrointestinal (GI) tract is dependent on the composition and activity of microbes that thrive in it. The activity and composition of the gut microbiome, however, are largely driven by diet – specifically dietary fibers like resistant starch (RS) that escape degradation in the upper GI tract and are metabolized in the colon by specialized bacteria. We are testing the capacity to modulate the production of health-promoting metabolites with supplemental dietary fibers. Here we show that study participants who supplemented their diets with RS commonly experienced blooms of *Bifidobacterium adolescentis* – an RS-degrading specialist. *Bifidobacterium adolescentis 269-1*, a cultivar from the microbiome of a RS-responsive participant, was found to possess a Type IVa sortase-dependent pilus that confers the ability to attach to RS particles. Additionally, RS-consuming individuals also experienced increased levels of short-chain fatty acids and indole lactic acid (ILA), a tryptophan-derived metabolite that modulates the immune system and reduces the permeability of the gut epithelium. To this end, we isolated and screened *Bifidobacterium* strains for production of RS binding and ILA production with varying sources of tryptophan. In coculture with human colonic epithelial cells, we find that media from *Bifidobacterium* or pure ILA modulated barrier function and reduced inflammation as measured by levels of IL-8 and VEGF cytokines. These results suggest that RS combined with a suitable source of tryptophan could be used clinically as an upstream driver of therapeutic concentrations of ILA in the GI tract.

Mining ancient genomes for new strategies for nutrient retention in agroecosystems

Angela D. Kent*[1,2], Alonso Favela[2], Mitra Ghotbi[1], Sierra Raglin[1], Isaac Klimasmith[1], Martin Bohn[3]

[1]Department of Natural Resources & Environmental Sciences, University of Illinois at Urbana-Champaign
[2]Program in Ecology, Evolution and Conservation Biology, University of Illinois at Urbana-Champaign
[3]Department of Crop Science, University of Illinois at Urbana-Champaign

Selection for crop plants based on aboveground traits in high nutrient environments has inadvertently led to large changes to belowground plant physiology and relationships with the soil microbiome, altering microbiome functions that contribute to sustainability and environmental quality (e.g. nutrient acquisition, nutrient retention, and GHG production). We hypothesized that plant genotypes differ in their ability to recruit microbial functional groups, and that microbial community functions can be treated as a selectable plant phenotype and optimized through plant breeding.
We surveyed the rhizosphere microbiome of diverse maize genotypes to compare their capability to recruit microbial nitrogen cycling functional groups and examined rates of nitrogen transformations. Significantly different N cycling microbial communities were observed among maize genotypes that represent the endpoints of directed evolution, as well as among germplasm selected under different levels of fertilization. This differential recruitment affected microbiome function as well. Our results showed significantly lower rates of nitrification and denitrification in ancestral lineages of maize (teosinte). Maize-teosinte near isogenic lines were used to narrow down the genetic region associated with these nutrient retention traits to explore the mechanistic basis for these these microbiome-associated phenotypes. We also explored the combinatorial effect of plant-microbe interactions for their ability to both provision (via N fixation) and retain nutrients, which resulted in elevated nutrient acquisition by the crop as well as sustainable environmental outcomes.
Our results link the host-associated microbiome and ecosystem function, and demonstrated the genetic capacity to optimize recruitment of N cycling functional groups and improve crop sustainability. This will allow selection of crop cultivars that interact with the nitrogen cycle in ways that improve the efficiency and sustainability of agriculture, while protecting environmental quality.

Soybean cyst nematode infestation is associated with changes in fungal community composition in agricultural soils of Ohio.

Melanie Medina López*[1], Soledad Benitez Ponce[1], Horacio D. López-Nicora[2], Timothy I. Ralston[2]

[1]The Ohio State University, Department of Plant Pathology, Wooster OH
[2]The Ohio State University, Department of Plant Pathology, Columbus OH

The soybean cyst nematode (SCN), *Heterodera glycines*, is the most yield-limiting pathogen of soybean, causing losses of over $1.5 billion in the US. Strategies to manage this nematode are limited and have focused on the use of resistant cultivars. Unfortunately, SCN is overcoming the most prevalent genetic source of resistance in commercially available soybean cultivars. Some fungi have shown promise as biocontrol agents against SCN infestation. However, the presence and prevalence of potential nematophagous fungi within field soils in Ohio are underexplored. Therefore, we collected 171 soil samples from soybean fields across 26 Ohio counties in the years 2019 and 2021 to estimate SCN abundance and fungal community composition. From each sample, the abundance of SCN was determined by counting the number of nematode eggs per 100 cm^3 of soil. This abundance ranged from 0 to 15,800 SCN eggs per 100 cm^3 of soil. Using ITS barcoding sequencing the fungal communities of the soil were characterized. We found that SCN abundance and sample location significantly influenced the fungal community composition in the soil. This was further demonstrated using a nearest-neighbor analysis where samples within the same county were significantly assigned as near-neighbors. Core community analysis at different levels of SCN abundance showed that at least two potential soybean pathogens were more prevalent in soils infested by SCN. Further, the nematophagous fungus *Clonostachys rosea* was identified as a core member of all soil samples. However, this fungus was enriched in samples with high levels of SCN abundance. Together, these results suggest that SCN significantly shifts the fungal community composition in field soils. The association of plant pathogens with different levels of SCN abundance could have implications on multi-pathogen interactions in soybean fields. Finally, the prevalence of nematophagous fungi in most of the fields sampled warrants further study for potential biocontrol applications.

Effect of mode of delivery of fecal microbiota transplants on growth performance and gut microbiome in weaning piglets

Paul Oladele*[1], Wenxuan Dong, Brian Richert, Timothy Johnson

[1]Department of Animal Sciences, Purdue University, West Lafayette, Indiana

Weaning is a stressful event for piglets, due to diet change from sow milk to grain-based feed which causes turnover of the microbiome leading to diarrhea. Antibiotics are administered to prevent post-weaning diarrhea (PWD), but increased occurrence of antimicrobial resistance has increased incentives to develop viable alternatives. Previous studies have shown that fecal microbiota transplant (FMT) reduced diarrhea and improved body weight gain in piglets but its adoption in swine production is limited due to the difficulty and labor demand of oral gavage. For FMT to be a viable option in swine management, a simple method is needed to administer the transplant. The objective of this study was to determine the effect of three methods of FMT administration (oral, rectal, and lyophilized in-feed) on growth performance, diarrhea incidence and microbiome. We hypothesize that FMT (in-feed and rectal) will increase colonization efficiency, improve growth performance, and reduce diarrhea incidence compared to control. Forty weaned male piglets were allotted to 4 treatments at 10 piglets per treatment (no FMT - Control, Oral - FMT1, rectal - FMT2 and lyophilized in-feed – FMT3). Feces from 12-week-old pigs was donor material. The study lasted nine days and FMT was for five days. Fecal samples were collected on day 0, 2, 5 and 7 for 16S rRNA sequencing (V4 region) for bacterial community analysis. Data were analyzed with one-way ANOVA in R. FMT3 had significantly higher daily gain between day 0 – 2 ($P < 0.05$) compared to control. There was no effect of FMT on feed intake and diarrhea incidence. FMT3 had higher alpha diversity (Observed features and Faith's phylogenetic) on day 5 ($P < 0.05$) compared to control and beta diversity was different between FMT groups and donor. In conclusion, the three FMT groups has similar colonization pattern but FMT3 increased alpha diversity.

Key words: post-weaning diarrhea, fecal microbiota transplant, piglet microbiome

Prenatal maternal exposure to extreme weather events and the offspring microbiome: What can we learn from a birth cohort study after Hurricane Maria in Puerto Rico?

Leyao Wang*[1], David de Ángel Solá[2], Midnela Acevedo Flores[3], Nicolás Rosario Matos[3], Ai Zhang[1], Sandra Lee[1]

[1]Division of Allergy and Immunology, Department of Medicine, Washington University in St Louis School of Medicine, St Louis, Missouri
[2]Department of Pediatrics, Yale School of Medicine, New Haven, Connecticut
[3]San Juan City Hospital Research Unit, Department of Pediatrics and Obstetrics and Gynecology, San Juan Hospital, San Juan, Puerto Rico

Due to climate change, extreme weather events have been more frequent and intense. Prenatal exposure to weather disasters is strongly associated with increased risks of many diseases. The microbiome may be an important mechanism, but this has not been investigated. To this end, we conducted a birth cohort study named Hurricane as the Origin of Later Alterations in microbiome (HOLA) in the aftermath of Hurricane Maria in Puerto Rico. We recruited term infants aged two to six months, including 29 infants who were exposed *in utero* to Maria and 34 infants who were conceived at least five months after Maria as controls. We performed 16S ribosomal RNA gene sequencing as well as shotgun metagenomic sequencing on infant stool and nasal swab samples. Our results show that infants who were exposed *in utero* to Hurricane Maria had a loss of microbial diversity and a decrease in commensals. Their gut metabolic potential was also altered compared to infants in the control group. The influence of a prenatal disaster exposure on the gut microbiome was the strongest in infants who were exclusively formula-fed. For the infant nasal microbiome, the richness and diversity were significantly higher in the exposure group compared to the control group. Several environmental bacteria usually present in water or soil, including *Rhodocista, Azospirillum, Massilia, Herbaspirillum, Aquabacterium*, and *Pseudomonas* were enriched in the exposure group. Our HOLA study indicated that prenatal exposure to a devastating hurricane is associated with alterations in the offspring gut and nasal microbiome. Further studies are needed to validate our preliminary findings. Importantly, we would like to discuss lessons we learned from this study and recommendations on expanding types of samples collected from the participants and the environment.

Posters

EVEN numbered posters will present during **Poster Session 1**
Tuesday, 5/9/23 1:30pm – 2:30pm

ODD numbered posters will present during **Poster Session 2**
Tuesday, 5/9/23 4:00pm – 5:00pm

Poster #	Presenter	Poster Title
1	M. Alverez Gonzales	Modulation of Structure and Function of Established Wheat-Bran Degrading Bacterial Communities
2	**Shreya Milind Athalye**	**Scope of Spectroscopy and machine learning in viral sample characterization**
3	**Rwiyoo Baruah**	**Purification and characterization of exopolysaccharides from halotolerant unicyanobacterial communities**
4	**Ashleigh Bope**	**Gene expression of fungal communities in dust from the International Space Station (ISS) under varying relative humidity conditions**
5	Patrick H. Bradley	Gut microbial gene clusters with homology to human enzymes can lead to parallel drug metabolism
6	**Kendall Byrd**	**Microbial Community Shifts and Cyanobacteria In Eutrophic Urban Lake: Application of Pathway Analysis & Unmanned Aerial Vehicle Based Multispectral Remote Sensing**
7	Ruth Eunice Centeno Martinez	Identification of Bovine Respiratory Disease in dairy and beef cattle through the nasal microbiome
8	**Kayla Cross**	**Nutritionally unbalanced diets reduce gut microbial diversity yet maintain functional redundancy**
9	**Fabio Cumbo**	**MetaSBT: a scalable reference-based phylogeny-aware framework for characterizing known and yet-to-be-named microbial species with Sequence Bloom Trees**
10	**Josiah Davidson**	**Development of Paper-based diagnostics for targeted characterization of the human respiratory microbiome in clinical settings**
11	Wenxuan Dong	Meta-analysis reveals the dynamic development of the gut microbiome in commercial pigs
12	**Audrey Duff**	**Oral and middle ear delivery of broad-spectrum antibiotics, but not biofilm-targeting antibodies, results in significant alterations to the chinchilla nasopharyngeal and fecal microbiotas**
13	**Taiwo Faloni**	**Development of Azotobacter-phages as a Model System For Understanding Phage-host Interaction Dynamics in the Soil**
14	**Mitra Ghotbi**	**Plant microbiome-associated phenotypes: a promising remedy for mitigating soil microbial mediated nitrogen losses**
15	**Madeline Greene**	**Quantifying Root Traits and their Effects on the Soil Microbiome**
16	**F. E. Guevara**	**Functional characterization of bacteria associated with lettuce hydroponic production systems in Ohio.**
17	**Kristian J Harris**	**Initial steps in testing the Stress Gradient Hypothesis for Selenium exposure in soil bacteria**
18	**Fan He**	**Wastewater SARS-CoV-2 sequencing demonstrates the variant transmission in advance compared to clinical test**
19	Matthew Hymes	Looking beyond DNA and its technical challenges –proof of concept for skin metatranscriptomics
20	**Jayadev Joshi**	**Assessing classical machine learning, neural network, and hyperdimensional computing-based classification techniques on microbiota data for accessible and reproducible biological classification.**
21	**Simerdeep Kaur**	**Nucleic acid detection of live pathogens on contaminated foods**
22	**Minseung Kim**	**Wastewater microbiome as the regional food environment indicator**
23	**Scott Klasek**	**Microbiome comparisons between Nextseq and Miseq sequencing platforms in soil 16S and ITS amplicon community analyses**

24	**Jessica Labella**	**Analysis of soil microbiome community composition in lactate-enriched cultures**
25	**Emma Lancaster**	**Evaluating the public health service role of urban stormwater green infrastructure using microbial source tracking and microbiome analyses**
26	**Zachary J. Lewis**	**Urine limbo: determining minimum urine volume for effective characterization of canine urinary tract microbiota**
27	**Xin Lin**	**Arbuscular Mycorrhizal Fungal Foraging Behaviors in Response to Different Nitrogen Levels**
28	**Yijing Liu**	**Investigation of ultraviolet disinfection and gene damage on different opportunistic pathogenic species of nontuberculous mycobacteria under different light sources**
29	**Kala K. Mahen**	**The Gut Microbe-Derived Metabolite TMA Shapes Host Circadian Metabolic Rhythms Via the Host G Protein-Coupled Receptor TAAR5.**
30	**Makayla Manes**	**Sensing Our Symbionts: A *Saccharomyces cerevisiae* Biosensor for the Human Microbiome**
31	L. Martinez	The microbiome of *Amblyomma americanum* reflects known westward expansion.
32	Miguel Martínez-Mercado	Metabolic relationships inferred between bacterial communities and the toxigenic benthic dinoflagellate *Prorocentrum* in culture
33	**Cindy Mayorga**	**Raman spectroscopy - an analytical tool for biologics**
34	**Molly Mills**	**Household environment contamination and host factors impact the gut microbiome and resistome of infants and young children from rural Nicaragua**
35	**Mohamed Mohssen**	**Microbiome and virome changes after mammalian spinal cord injury**
36	**Sachin Naik**	**Addition of plant growth promoting rhizobacteria to peat-based potting media influences the native rhizosphere microbiome of *Impatiens walleriana***
37	**Nora Jean Nealon**	**To Sample or Not to Sample: Capturing Feline Fecal Microbiome Changes With High-Frequency Sample Collection**
38	**Dinh Duy An Nguyen**	**Exploring The Microbial Contents in Leukemia Initiating Cells**
39	**Anna Clapp Organski**	**Sex hormone deprivation perturbed the gut microbiota in a sex-specific manner**
40	**Lauren Otto**	**Associations among gut permeability, inflammation, and cognitive impairment in female breast cancer patients treated with chemotherapy**
41	**Juan Quijia Pillajo**	**Nutrient limitation influences the rhizosphere bacterial microbiome of *Impatiens walleriana* 'Xtreme Red'**
42	**Valentina Pita-Grisanti**	**Lipocalin-2 Expression Changes Gut Microbiome Composition and Diversity, and Promotes Tumor Growth in a Mouse Model of Pancreatic Ductal Adenocarcinoma**
43	**Akbar Adjie Pratama**	**Diversity patterns and ecological footprint of RNA viruses along a permafrost thaw gradient**
44	**Anurag R. Pujari**	**Metabolic potential of xanthan gum-degrading microbial consortia**
45	**Christian J. Quiles Pérez**	**A comparative study of Lachnospiraceae metabolism and response to oxidative and nitrosative stress**
46	**Adam Quinn**	**Effects of Wheat Genotype on Gut Microbiota Fermentation**
47	**Sierra Raglin**	**What is Lost is not Forgotten: Understanding breeding-driving manipulation in the *Zea mays* microbiome**
48	**Nina Randolph**	**The long-term in vitro bacterial viability of lyophilized and frozen canine and feline fecal microbial transplantation products**
49	Emily Rego	Environmental and genetic regulation of mycotoxin production in *Aspergillus oryzae* isolated from indoor dust
50	**James V Riddell**	**Combining viral identification tools improves virus sequence identification from mixed metagenomic datasets**
51	**John C. Rowe**	**Gut microbiota promoting propionic acid production accompanies diet-induced intentional weight loss in cats**

52	**Kayla Roy**	**The onset and severity of colitis in IL-10 -/- mice is not dependent on fecal microbiota transplantation from ulcerative colitis patients**
53	**Mathias Schneider**	**Host diet, physiology and behaviors set the stage for Lachnospiraceae cladogenesis**
54	**Nivedha Senthil**	**ASSOCIATIONS OF NEUROACTIVE STEROIDS & THE GUT MICROBIOME**
55	Abigayle Simpson	Carbon Source-Specific Regulation of Nitrogen Fixation in *Paraburkholderia xenovorans*
56	**Funing Tian**	**Eco-evolutionary patterns of virus auxiliary metabolic genes throughout the global oceans**
57	**Yonaida Valentine**	**Chemotherapy-induced changes to the gut microbiota mediate fatigue and depression-like behavior and induces neuroinflammation.**
58	**John Van Dusen**	**Sequencing SARS-CoV-2 Variants from Indoor Dust**
59	Jon Van Gray	Disparities in microcosm microbial community response to salinization as the result of ionic specificity.
60	**A. Viji Elango**	**Is There a Core Microbiome of Hydroponic Cultivation Systems?**
61	**Abigail Volk**	**Comparison of cyanobacteria, cyanotoxin, and microbiomes between two harmful algal bloom-impacted drinking water sources in Ohio**
62	Cole Vonder Haar	The gut microbiome is predictive of chronic impaired decision-making after brain injury
63	**James M. Wainaina**	**Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome**
64	**Jiangshan Wang**	**Bacteroidales as a fecal contamination host indicator for accessing environmental fecal pollution**
65	Darryl A. Wesener	Bacterial polysaccharides influence interspecies interactions in the mammalian gut - Research in the Wesener Group at OSU
66	Caroline Wheeler	Intra-tumor microbes identified by RNAseq associated with response to immune checkpoint blockade in metastatic melanoma
67	**Rebecca C Wu**	**Maternal Stress Associated With Infant Gut Microbiota in Cebu, Philippines**
68	Anthony Yarnell	Can causal inference help us ask better questions about microbiomes?
69	**Tianming Yao**	**Different Arabinoxylan Side Chain Branch Density Mixtures Select Dominant *Bifidobacterium* or *Bacteroides* in Human Fecal Microbiota**
70	**Fahren R. Zackery**	**A Meta-Analysis of Diversity-Disease Relationships in the Human Microbiome**
71	ZhiPing Zhong	Glacier preserves ecological and evolutionary history of viruses over the past >45,000 years
72	**Laura Mason**	**Microbial Mechanisms of Millet Drought Stress Mitigation in an Optimized Intercropping Shrub System**

Bold font = Trainee

---------- poster no. 1 ----------

Modulation of Structure and Function of Established Wheat-Bran Degrading Bacterial Communities

M. Alvarez Gonzales*, S. R. Lindemann

Department of Food Science, Purdue University, West Lafayette, IN 47907, USA

Wheat brans are milled using various methods and to various sizes across applications, which may lead to differences in their interactions with gut microbiota. Here, we study the effect of wheat-bran (WB) fractions reduced in size using different methods on the assembly and metabolism of WB-degrading consortia obtained after a 7-day sequential passage fermentation. We performed a crossover experiment in which two particle fractions, coarse and fine, of roller- and stone-milled particles were inoculated with consortia selected either on coarse or fine particles. Fine particles (<180 μm) were inoculated with bacterial communities from consortia consuming roller-milled coarse particles (850-500 μm). Similarly, coarse particles were inoculated with bacterial communities that grew in fine particles. Prior to in-vitro fermentation, WB fractions were digested using α-amyloglucosidase and protease. In-vitro fermentation was performed in phosphate-buffered gut mineral medium, fortified with 10 μM of each proteinogenic amino acid and 1X ATCC vitamin mix. After 6, 12, 24, and 48 hours of cultivation at 35 ºC, samples were collected for short-chain fatty acids (SCFAs) by gas chromatography and microbial community analysis of attached and suspended microbes using 16S rRNA gene sequencing. The structure, composition, and function of all microbial communities rapidly changed as a function of the substrate (i.e. particle size); after a single generation, consortia selected on the opposite fraction accommodated to the new particle size both compositionally and metabolically. A similar effect was observed in the levels of SCFAs produced, which, after 48 hours of cultivation on the switched substrate, mimicked the concentrations measured in the native particle community. Our findings suggest that 1) WB particle damage due to milling increases availability of nutrients and harbors different bacterial communities, 2) bacterial communities selectively settle on various wheat bran particles, and 3) microbial community structure and metabolism of wheat brans is driven by substrate structure.

---------- poster no. 2 ----------

Scope of Spectroscopy and machine learning in viral sample characterization

Shreya Milind Athalye*[1,3], Mohit S. Vermaa[2,3]

[1]Department of Agricultural & Biological Engineering, Purdue University
[2]Weldon School of Biomedical Engineering, Purdue University
[3]Birck Nanotechnology Center, Purdue University

Raman Spectroscopy is a non-invasive technique that can analyze biomolecules qualitatively and quantitatively. We can apply the minimal sample preparation and non-invasive nature of the Raman Spectroscopy in developing a Process analytical technology (PAT) tool and a diagnostic tool. Absorption spectroscopy is a robust technique that, owing to its high sensitivity and large signal-to-noise ratio, has the potential to be implemented as an excellent tool for making predictions. Machine learning methods can aid in the valuable predictions of spectroscopy data. We have implemented different machine-learning methods to predict the concentration of viral particles of interest in biological samples. We utilized both convolutional neural networks (CNNs) and random forests (RFs) to predict the concentration of the samples containing measles, mumps, rubella, and varicella-zoster viruses (ProQuad®) based on Raman and absorption spectroscopy. We demonstrated that both RFs and CNNs could make predictions with R^2 values as high as 95%. We proposed two different networks to use the Raman and absorption spectra jointly. Our results demonstrated that concatenating the Raman and absorption data increases the prediction accuracy compared to using either Raman or absorption spectrum alone. We also verified the advantage of using joint Raman absorption with principal component analysis.

---------- poster no. 3 ----------

Purification and characterization of exopolysaccharides from halotolerant unicyanobacterial communities

Rwivoo Baruah*[1], Tianming Yao, Juan José Juárez García and Stephen R. Lindemann

[1]Department of Food Science, Purdue University

Microbial exopolysaccharides (EPS) are extracellular polysaccharides produced by microbes that aid in survival in adverse environments. These EPS have numerous uses in various industries as hydrocolloids, pharmaceuticals, and

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

bio-flocculants. Recently, microbial EPSs have gained popularity as prebiotic food additives with the ability to modify the texture of the food product. These can be used in combination with probiotic bacteria, such as in functional fermented foods and commercial probiotic capsule contexts. Some cyanobacteria can produce EPS, which can be either in a cell-bound form or in a released form. In the current work we have selected unicyanobacterial consortium (UCC) isolated from halotolerant microbial mats taken from a hypersaline lake in north-central Washington. We purified EPS from 3 unique UCC communities, namely UCC-S, UCC-O and UCC-A; UCC-O and UCC-A produce an attached EPS whereas UCC-S produces a released type. The EPS produced is a heteropolymer containing multiple sugar moieties, such as glucose, galactose glucouronic acid, galactouronic acid, xylose, rhamnose, arabinose, and mannose; fucose was only found in EPS from UCC-S. Molecular weight determination of these EPS revealed their polydisperse nature, having more than one molecular weight fraction. UCC-S had 2 fractions one larger than 2 x 10^6 Da and another 1 x 10^6 Da (approx.). Both UCC-O and UCC-A had 2 fractions with size less than 1 x 10^6 Da (approx.). We plan to structurally characterize these EPS and assess their potential as prebiotic additives, as well as their rheological properties.

---------- poster no. 4 ----------

Gene expression of fungal communities in dust from the International Space Station (ISS) under varying relative humidity conditions

Ashleigh Bope*[1], Nick Nastasi, Sarah R Haines, Bridget Hegarty, John Horack, Marit Meyer, Karen C. Dannemiller

[1]Department of Civil, Environmental and Geodetic Engineering, College of Engineering, The Ohio State University

Microorganisms are inherently present in confined environments, such as an occupied spacecraft like the ISS. Exposure to these microbes have been associated with human health outcomes related to respiratory illnesses and allergies. As we strive to achieve long-term settlements beyond Earth, we need to better understand the qualities of a healthy spacecraft microbiome to inform design decisions and prevent unintended consequences. Thousands of microbial species have been identified aboard the ISS, most of which are similar to those found indoors on Earth. Microbial growth is the factor most strongly associated with negative human health effects in indoor environments. When ambient relative humidity (RH) levels reach a certain threshold, microbial growth will occur within dust. As RH conditions increase, microbes display more diverse secondary metabolic processes which can result in a greater expression of genes that can impact human health. The goal of this study is to characterize microbial function that occurs when dust from the ISS is exposed to elevated moisture conditions. Dust was returned to Earth and incubated under various RH conditions in controlled chamber experiments. The RNA extracted from the dust was sequenced to investigate microbial activity at various RH conditions. Gene quantification and differential expression analysis investigated metabolic activity. Our results indicate that gene expression profiles of microbial communities in dust from the ISS are dominated by RH conditions. Secondary metabolite biosynthetic processes were differentially expressed at higher RH conditions. This includes the regulation of aflatoxin biosynthetic processes that was upregulated at higher moisture conditions which has implications for human health. The ISS is home to many different microbial species that interact in a dynamic relationship with astronauts. Our results should improve our knowledge on how microbes in spacecraft can impact human health, spacecraft integrity as well as how microbes might impact other planets when humans arrive.

---------- poster no. 5 ----------

Gut microbial gene clusters with homology to human enzymes can lead to parallel drug metabolism

Matt Rendina, Peter J. Turnbaugh, Katherine S. Pollard, Patrick H. Bradley*[1]

[1]Department of Microbiology, The Ohio State University

Gut microbes can metabolize a wide variety of ingested compounds, including pharmaceutical drugs. Previous work showed that many prevalent gut Proteobacteria and Firmicutes can inactivate the chemotherapeutic drug 5-fluorouracil, and that they do so in the same way as the human host. Indeed, the proteins encoded by the responsible operon in bacteria (*preTA*) jointly align to the human protein that performs this reaction, dihydropyrimidine dehydrogenase (DPYD). Here, we show that human DPYD is in fact likely the result of an ancient gene fusion and transfer from a bacterial *preTA* operon into early eukaryotes. We then build a pipeline to detect similar cases of operon-to-gene orthology that could relate to drug metabolism. Specifically, we look for clusters of bacterial genes that are close genomic neighbors on the same strand, and whose predicted products jointly align to the same human drug-metabolizing enzyme. Starting with a recent large collection of gut metagenomic assemblies, we build a bioinformatics pipeline that identifies seven high-confidence candidates. Among these is xanthine dehydrogenase (XDH), an enzyme

responsible for metabolizing a range of drugs, including some with narrow therapeutic windows. This suggests that operon-to-gene orthology may be an underappreciated explanation for parallel drug metabolism by humans and their microbiomes.

---------- poster no. 6 ----------

Microbial Community Shifts and Cyanobacteria In Eutrophic Urban Lake: Application of Pathway Analysis & Unmanned Aerial Vehicle Based Multispectral Remote Sensing

Kendall Byrd*[1], Dr. Joyoung Lee[1]

[1]The Ohio State University

As increases in frequency, duration, intensity, and geographical location of harmful algal blooms (HABs) have been observed, more timely monitoring and targeted treatment of HABs and their cyanotoxins are crucial for freshwater bodies that are used for drinking water, recreation, and food production sources. To combat this, new management practices with tools that can handle the spatial and temporal variability of HABs are needed for water treatment plants and other sectors to ensure human health and ecosystem health. Unmanned Aerial Vehicles (UAVs), also known as drones, are a potential solution for near real-time monitoring of HABs. Recently, UAVs have gained increasing interest in research and development due to their many applications, efficiency in data collection, and the ability to customize these systems to specific needs. While research has shown that UAVs can accurately estimate chl-a and phycocyanin values -HAB indicators- little research has been conducted analyzing UAV imagery in parallel with microbiome data. This study aims to accomplish two tasks. The first, is to evaluate how accurate chl-a values gathered from UAV imagery are when compared to chl-a values collected using traditional methods. The second task is to see how shifts in the microbial community may affect UAV aerial imagery data. To accomplish this, twelve field sampling campaigns were conducted at an urban pond known as Schiller Pond in Columbus, OH, USA from April 2022 through September 2022. During each field visit aerial imagery, water samples, meteorological data, and water quality data were collected. Results found that shifts in microbial communities are important factors to consider when evaluating eutrophic water bodies with UAVs. In addition, water quality parameters play a large role in guiding microbial community shifts. This study concludes that UAV imagery is an efficient monitoring tool that can be applied for routine monitoring along with traditional methods.

---------- poster no. 7 ----------

Identification of Bovine Respiratory Disease in dairy and beef cattle through the nasal microbiome

R. E. Centeno Martinez*[1], B. Bitsie[1], C. Suriyapha[1]. A. Richards[1]. J. Davidson[2], S. Mohan[2], A. Ault[3], J. Boerman[1], J. Koziol[4], J. Schoonmaker[1], M. Verma[2], T. A. Johnson[1]

[1]Department of Animal Science, Purdue University, West Lafayette, IN 47907, USA
[2]Department of Agricultural and Biological Engineering, Purdue University, West Lafayette, IN 47907, USA
[3]Department of Electrical and Computer Engineering, Purdue University, West Lafayette, IN, USA
[4]School of Veterinary Medicine, Texas Tech University, Amarillo, TX, 79106, USA

Bovine respiratory disease (BRD) is an ongoing health and economic issue in the dairy and beef industries. Multiple risk factors can make an animal susceptible to BRD and the presence of *Mannheimia haemolytica, Pasteurella multocida, Histophilus somni,* and *Mycoplasma bovis* are commonly observed post-mortem in isolated lung tissue samples of sick cattle. Previous studies have characterized and quantified the abundance of these bacteria in the nasal cavity of cattle, but results remain inconsistent between studies and studies are usually limited to only one farm. Hence, this study aims to determine the diagnostic value of quantifying the prevalence and load density of these four bacterial pathogens in the nasal cavity and compare its nasal bacterial community animals that can be used to discriminate BRD from healthy animals. Samples were collected from four beef (Colorado, Idaho, Indiana and Texas) and dairy (California, Indiana, New York, Texas) farms in the US. Animals were visually examined for signs of respiratory disease. Nasal swabs from visually healthy (n=482) and BRD-affected animals (n=452) were collected at each farm, followed by DNA extraction. Quantitative PCR assays were performed to determine the abundance of the four BRD-pathogens as well as total bacteria. Interestingly, the average abundance of BRD pathobionts was not different between healthy and BRD animals; however, use of random forest (RF) models identified that the difference from the mean abundance of BRD-pathobionts was quite predictive in discriminating healthy and BRD-affected animals in both dairy and beef cattle (Dairy RF error rate: 0 and Beef RF error rate: 0.02). Furthermore, we intend to determine whether there is a difference in the bacterial diversity, composition, and community interaction between the healthy and BRD-affected groups.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 8 ----------

Nutritionally unbalanced diets reduce gut microbial diversity yet maintain functional redundancy

Kayla Cross*[1], Noelle Beckman[2], Benjamin Jahnes[1], Zakee Sabree[1]

[1]Ohio State University
[2]Utah State University

Many animals, including humans, contain a species-rich and diverse gut microbiota that participates in many host-supportive functions that include diet processing and nutrient provisioning. Commensal gut bacterial community composition and diversity respond to changes in diet, but it is less clear to what degree does the metabolic functional capability of the microbiome change as well. To address this knowledge gap, we examined dietary impacts on gut microbiome taxonomic and functional diversity in a model omnivorous invertebrate, the American cockroaches (*Periplaneta americana*). We fed the insects with balanced or unbalanced (protein- or cellulose-enriched) diets for eight weeks, sampled nondestructively, and characterized their microbiomes each week by 16S rRNA gene sequencing. Microbiome functional capacities were inferred from taxonomic censuses using PICRUSt2. Protein- and cellulose-enriched diets altered total family-level phylotypes and resulted in diet-defined community profiles. Unbalanced diets resulted in reductions in predicted functional MetaCyc pathway and KEGG orthologue diversity on microbiome functional capacity; however, less than 15% of pathways in an unbalanced diet were varied in their abundance. While pathway diversity may have declined due to hosts feeding on unbalanced diets, the presence of several pathways with orthologous functions ensured that microbiome functional capacity was less adversely affected. These results suggest that despite diet-induced taxonomic variability, many metabolic features of the gut microbiome remain because they can be performed or produced by several constituent species.

---------- poster no. 9 ----------

MetaSBT: a scalable reference-based phylogeny-aware framework for characterizing known and yet-to-be-named microbial species with Sequence Bloom Trees

Fabio Cumbo*[1] and Daniel Blankenberg^[1,2]

[1] Genomic Medicine Institute, Lerner Research Institute, Cleveland Clinic, Cleveland, OH, USA
[2] Department of Molecular Medicine, Cleveland Clinic Lerner College of Medicine, Case Western Reserve University, Cleveland, OH, USA

Metagenomics allows studying not only well-characterized microbes but also a large number of cultivation-recalcitrant microbes. Recently, metagenomic assembly has been applied to reconstruct genomes from metagenomes, which can then be analyzed with techniques commonly used for whole-genome sequenced isolates. Metagenome-assembled genomes (MAGs) have indeed paved the way for comparative genomics studies of cultivable and uncultivable microbes at strain level resolution, including yet-to-be-characterized ones. Together with the growing number of publicly available metagenomic datasets, this represents an unprecedented opportunity to *de novo* assemble a large catalog of microbial genomes. However, a systematic procedure for organizing and processing hundreds of thousands of MAGs together with all the genomes obtained by isolate sequencing is currently lacking.

Here we leverage the latest development in data structure and algorithm research to create MetaSBT, a general framework to efficiently process and rapidly query such a massive amount of metagenomic data using Sequence Bloom Trees (SBTs). This allows researchers to (i) create, maintain and constantly update an indexed database of microbial MAGs and isolate genomes coming from different hosts and environments, (ii) easily characterize genomes by simply querying the database with the bloom filter representation of the genomes themselves, (iii) identify clusters of potentially novel and yet-to-be-named species, and (iv) unlock potentially relevant insights for investigating host-associated microbes and their relation to particular pathologies among other studies by the integration of metadata about all the involved metagenomic samples.

Our tool is integrated into the Galaxy platform and we are working on distributing constantly updated kingdom-specific versions of SBTs designed over all the publicly available microbial reference genomes from NCBI GenBank, and expanding them with MAGs reconstructed from thousands of public metagenomes. This would finally allow the identification of accurate markers for improving the detection of the abundance of both known and unknown species in kmer-based metagenomic profilers.

Source code: https://github.com/cumbof/MetaSBT

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 10 ----------

Development of Paper-based diagnostics for targeted characterization of the human respiratory microbiome in clinical settings

Josiah Davidson*[1], Mohit S. Verma, Ryan F. Relich

[1] Purdue University, Department of Agricultural and Biological Engineering

Paper-based devices (PBD) are attractive platforms for detection of respiratory pathogens due to their ease of scale-up during manufacturing and their user friendliness. Here, we develop a spatially multiplexed PBD to detect respiratory pathogens at the point-of-care (POC) to enable precise characterization of the respiratory microbiome and guide patient treatment.

Loop mediated isothermal amplification (LAMP) is used to amplify target nucleic acids in the presence of the specific pathogen. This results in a pH drop effecting a color change from red to yellow after including a pH indicator, phenol red. All reagents to conduct LAMP (including primer sets imposing specificity) are dried on 5 x 6 mm chromatography paper grade 222 reaction pads and are annealed to a Melinex backing for structural support via a pH neutral double-sided adhesive. Reaction pads are separated by polystyrene spacers to prevent crosstalk. Patient sample (nasal swabs) is diluted in water and placed on the reaction pad to rehydrate reagents, minimizing preprocessing. Devices are heated for 60 minutes at 65 °C and the color change is visually read out with the naked eye.

We tested our device's ability to detect heat inactivated SARS-CoV-2 in diluted patient saliva on paper. Devices had an accuracy of 98% (97% analytical sensitivity and 100% analytical specificity) when using digital image analysis and 91% when we surveyed users in a color perception survey to account for user perception bias (71% analytical sensitivity and 100% analytical specificity; n=4 users). We anticipate comparable performance characteristics when detecting other respiratory pathogens (i.e. Influenza A/B, Respiratory Syncytial Virus, etc.).

The devices developed allow for the inexpensive POC detection of pathogens potentially disrupting the respiratory microbiome. Along with timely and inexpensive targeted characterization of the respiratory microbiome guiding patient diagnosis and treatment, these devices can be utilized for community surveillance guiding public health measures.

---------- poster no. 11 ----------

Meta-analysis reveals the dynamic development of the gut microbiome in commercial pigs

Wenxuan Dong*[1], Nicole Ricker[2], Devin B. Holman[3], Timothy A. Johnson[1]

[1]Department of Animal Sciences, Purdue University, West Lafayette, IN, USA
[2]Department of Pathobiology, University of Guelph, Guelph, Ontario, Canada
[3]Lacombe Research and Development Centre, Agriculture and Agri-Food Canada, Lacombe, Alberta, Canada

Background: Understanding the mechanisms of microbiome assembly during host development is crucial for successful modulation of the gut microbiome to improve host health and growth. Detailed characterization of the swine gut microbiome through meta-analysis allows us to understand the dynamics of microbial community succession, as well as the transient and natural variations between timepoints and animals.
Results: A total of 3,313 fecal samples from 349 pigs covering 60 time points (from birth to market age) from 14 publications were included in this meta-analysis. Alpha diversity continuously increased during early stages of animal growth and increased more slowly in the following stages. Beta regression analysis revealed that more microbial taxa were recruited while fewer were excluded by the gut microbiome. The microbial community structure also changed significantly between days at early ages and became more similar as pigs aged, as revealed by dissimilarity and distance metrics. Dirichlet multinomial mixtures analysis supported a gradient microbial cluster strategy in analyzing longitudinal pig fecal samples and we found that the early samples spread to more clusters than that from older pigs. Random forest regression identified 30 OTUs as potential microbiota biomarkers for modeling swine gut microbiome development and the external validation proved the generalization and benchmarking role of our models in application to future microbiome studies conducted in suckling and weaning pigs.
Conclusions: By combining multiple datasets, we observed an age-dependent assembly pattern of the swine gut microbiome. Shorter time intervals and a wider range of data sources can provide a clearer understanding of the gut microbiota colonization and succession and their associations with pig growth and development. The rapidly changing microbiome of suckling and weaning pigs implies potential time targets for growth and health regulation through gut microbiome manipulation.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

Keywords: swine gut microbiome, longitudinal, meta-analysis, dynamical development

---------- poster no. 12 ----------

Oral and middle ear delivery of broad-spectrum antibiotics, but not biofilm-targeting antibodies, results in significant alterations to the chinchilla nasopharyngeal and fecal microbiotas

Audrey F. Duff*[1], Joseph A. Jurcisek, Nikola Kurbatfinski, Tendy Chiang, Steven D. Goodman, Lauren O. Bakaletz, Michael T. Bailey

[1]The Abigail Wexner Research Institute at Nationwide Children's Hospital

Otitis media (OM) is a prevalent pediatric disease largely caused by nontypeable Haemophilus influenzae (NTHI). NTHI assimilates into middle-ear polymicrobial biofilms which promote OM pathogenesis and diminish antibiotic efficacy. Oral or tympanostomy tube (TT) broad-spectrum antibiotics are the standard of care (SOC) despite consequences including secondary infections, dysbiosis, and antimicrobial resistance. Antibodies against the biofilm-associated, NTHI-specific type IV pilus PilA (rsPilA) or against a synthetic chimera of peptides in the tip regions of Integration Host Factor (anti-tip-chimer) were previously shown to disrupt biofilms and restore antibiotic sensitivity in vitro. This experiment evaluated whether TT delivery of these antibodies would disrupt nasopharyngeal (NP) or fecal microbiomes, compared to SOC-OM antibiotics. Chinchillas (n=3/treatment cohort) underwent TT insertion prior to treatment. Cohorts included [1.] amoxicillin-clavulanate 10mg/kg (A/C; PO), [2.] A/C 2.5mg/kg BID, [3.] A/C 5mg/kg BID, [4.] anti-rsPilA (5µg), [5.] anti-tip-chimer (5µg), [6.] Ofloxacin (0.3% drops BID), [7.] Trimethoprim-sulfamethoxazole 7.5mg/kg BID (T/S), [8.] T/S 15mg/kg BID, and [9.] Saline. Cohort[1] received 7d of oral treatment; Cohorts[2-9] received 2d of TT treatment. NP lavages (NPL) and fecals were collected prior to treatment, 2-, 5-, 7-, and 9-days post treatment (DPT) for 16S sequencing and QIIME2.0 analysis. Significant differences were observed for UniFrac, Jaccard, and Bray-Curtis beta-diversity across timepoints in fecal and NP samples with distinct clustering of A/C Cohorts (PERMANOVA, $p<0.05$). Differences in Simpson, FaithPD (fecal) and Evenness (fecal and NPL) were found at 7DPT (Kruskal-Wallis, $p<0.05$), and Cohorts[1-3] consistently showed more visibly dramatic changes in alpha diversity over time. Non-parametric microbial interdependence test ($p<0.01$) demonstrated changes in temporal microbial composition for Cohorts[1-3] in contrast to similar clustering for Cohorts[4-9]. Collectively, results show broad-spectrum antibiotics induce the most dramatic NP and fecal microbiome alterations when delivered orally, but also when delivered via TT. Excitingly, biofilm-targeting antibodies had little effect on fecal or NP microbiomes.

---------- poster no. 13 ----------

Development of Azotobacter-phages as a Model System For Understanding Phage-host Interaction Dynamics in the Soil

Taiwo Faloni*, Sarah Bagby

Department of Biology, Case Western Reserve University, Cleveland, OH

Phages have been identified as indirect but crucial drivers of biogeochemical cycles. Understanding soil phage-host dynamics is key for evaluating the role of phages in these cycles and in overall ecosystem functioning. However, our understanding of soil phage ecology is still very limited, in part due to the limited number of soil-derived phage-host model systems. To explore the role of soil phage on N cycling, we sought to develop the globally distributed and genetically tractable diazotroph Azotobacter as a model host.

We aimed to isolate and characterize bacteriophages infecting Azotobacter vinelandii from soil samples collected from northeast Ohio. Phages were isolated with plaque assays and imaged with transmission electron microscopy. Isolates were subsequently sequenced with nanopore flowcells. We present preliminary characterization of this new A. vinelandii bacteriophage library. We have identified unique phages of A. vinelandii. The majority of our phage isolates are temperate, though lytic isolates were also obtained. The identification of temperate phages and the observation of both tailless and tailed phages belonging mostly to the Myoviridae family provide a basis for further investigations into the diversity and ecology of phages associated with Azotobacter. Further study of this library, including characterization of infection dynamics and physiology, will have implications for the understanding of phage-host interactions in soil environments, with the ultimate goal of integrating phages into existing ecosystem modeling tools for improved prediction accuracy.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 14 ----------

Plant microbiome-associated phenotypes: a promising remedy for mitigating soil microbial mediated nitrogen losses

Mitra Ghotbi*[1], Martin Bohn[2], Alonso Favela[1], Logan Woodward[2], Fred Below[2], Isaac M. Klimasmith[1], Angela D. Kent[1]

[1]Department of Natural Resources & Environmental Sciences, University of Illinois at Urbana-Champaign
[2]Department of Crop Sciences, University of Illinois at Urbana-Champaign

Excessive mineral nitrogen (N) input lead to excess of bioavailable N in the soil which if not used by plants will be used by nitrifying and denitrifying microbes and is lost through leaching and gaseous emissions. We have introduced specific maize genotypes that display a promising microbiome-associated phenotype for biological nitrification inhibition (BNI). Synergistically, application of a N-fixing inoculant in a field can add supplemental microbe-mediated N for plants uptake but may also provide additional substrate for nitrification. We compared maize near-isogenic lines with and without the BNI phenotype to evaluate the efficiency of this trait for soil N retention and plant N uptake and N use efficiency under various fertility management schemes: with and without synthetic N and N-fixing inoculants. We anticipated that constitutive N fixation by the inoculant could impact nitrification and N fixation rates by providing additional available nitrogen. DNA amplicon sequencing, soil nitrification rate along with plant yield indices supported the comparison between genotypes efficiency in soil N retention. Among nitrifiers, the Nitrososphaeraceae family was depleted in the BNI inbreds, and the BNI NILs also exhibited greater N use efficiency than the non-BNI control. Contrasting relationships between nitrification rates and relative abundance of nitrifiers suggest that the mechanisms of achieving BNI differ among the near-isogenic lines. Thus, fertility management and genotype selection have to be tailored correspondingly to achieve the most N retention in the soil matrix.

Keywords: microbiome-associated phenotypes, nitrifiers, introgression of Teosinte genes, N-fixing inoculants

---------- poster no. 15 ----------

Quantifying Root Traits and their Effects on the Soil Microbiome

Madeline Greene*[1], Megan A. Rúa

[1]Wright State University

The root microbiome serves as a complex system that contains several thousand fungal and bacterial taxa. Here, microorganisms interact directly with plant roots by promoting growth, defending against pathogens, and cycling nutrients. Despite their deep connection, one important missing link is understanding how varying root trait expression drives changes in the microbial assemblage of the root microbiome. Root traits are the phenotypic variations within a root structure that capture elements of plant health, response, and function. They are divided into functional and structural root traits. Functional root traits, like root carbon (C) and nitrogen (N) concentrations, measure the efficiency of a plant's nutrient cycling and internal signaling mechanisms with respect to overall plant fitness and environmental influence. Structural root traits, like specific root length (SRL) and fine:coarse root ratio, enhance and support the plant structure through varying spatial root growth, emphasizing anchorage and nutrient transport capabilities. While functional and structural root traits fulfill important roles for the plant, the chances of them operating independently from microbial interactions are slim; rather, plant roots have direct connections with microbial communities, thereby influencing microbial colonization, composition, diversity, and function. However, despite the close relationship between roots and microbes, our understanding of how root traits influence the microbiome is lacking. Using a greenhouse experiment, we will measure changes in microbial composition and diversity as a function of changes in SRL, fine roots (<2 mm diameter), coarse roots (>2 mm diameter), root C concentration, and root N concentration. We hypothesize that microbial composition and diversity will increase on roots with high fine:coarse root ratios and high root C concentrations but decrease with low SRL and high root N concentrations. These results will contribute to improving plant adaptability and reforestation efforts for economically important species.

---------- poster no. 16 ----------

Functional characterization of bacteria associated with lettuce hydroponic production systems in Ohio.

F. E. Guevara*[1], Edwin Navarro[1], Christopher Taylor[1], Maria-Soledad Benitez[1]

[1]Department of Plant Pathology, The Ohio State University, Wooster, OH

Hydroponic production is a method of growing plants using soilless substrates, a nutrient solution and oxygen. Different production setups are available, including Nutrient Film Technique (NFT) and Deep-Water Culture (DWC). Microbial communities of hydroponic systems are still understudied and might harbor microbes with the potential to be exploited

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

for increasing plant productivity and reducing pathogen incidence. In 2021, we sampled four NFT and three DWC lettuce hydroponic commercial facilities in Ohio, and isolated bacteria from water sources and nutrient solution. A total of 137 bacterial isolates, representing 57 genera have been recovered and taxonomically classified using 16S rRNA sequencing. We screened 35 bacterial isolates representing the eight most abundant genera recovered from both NFT and DWC (i.e., Pseudomonas, Sphingobium, Novosphingobium, Chryseobacterium, Bacillus, Shinella, Rhizorhabdus and Rhodococcus) for pathogen antagonistic and plant growth promoting properties. Specifically, we tested bioactivity against three lettuce pathogens (Pythium sp., Xanthomonas sp. and Pseudomonas sp.) and for siderophore production and nitrogen fixing capacity. Fourteen of the 35 screened isolates showed bioactivity against at least one pathogen, where an isolate identified as Pseudomonas mediterranea showed biocontrol activity against all tested pathogens. In addition, 14 isolates showed siderophore production activity and 10 are potentially able to fix atmospheric nitrogen. These results suggest that the tested isolates could potentially contribute to plant growth promotion and management of plant pathogens in hydroponics. We also hypothesize that bacteria recovered from hydroponics have adaptations particular to these systems (i.e., biofilm production and/or metabolism of nutrients commonly found in nutrient solutions). Thus, we will use whole genome sequencing of selected isolates to further investigate modes of action and signs of adaptation. By deciphering plant beneficial functions of bacterial communities in hydroponic systems, we could develop efficient microbial inoculants for plant health.

---------- poster no. 17 ----------

Initial steps in testing the Stress Gradient Hypothesis for Selenium exposure in soil bacteria

Kristian J Harris*[1], Alison E. Bennett[1]

[1] EEOB Department, The Ohio State University

The Stress Gradient Hypothesis (SGH) states that interspecific interactions should shift from competitive to facilitative interactions as environmental stress increases. Selenium (Se) is a naturally occurring metalloid that acts as an environmental pollutant and as an essential micronutrient. Due to its metallic properties, Se acts as an oxidative stress and can be toxic to plants and animals. Given this, Se in soil systems acts as an abiotic stress that influences species composition and species interactions. Within soils, bacteria and fungi have evolved to tolerate Se via detoxification and Se processing for respiration and studies show that metal detoxification traits like this can provide community benefits for (i.e. facilitate) non-tolerant species. Thus, this is an opportunity to test whether the SGH applies to microbial systems. First, however, we need to determine thresholds for Se toxicity in microbes. Here we examine the Se toxicity thresholds for bacteria from soils with high and low Se across three geological formations that give rise to different soil types. We collected soil from 18 paired soil sites of naturally high and low Se concentrations across 3 geological formations within the Rocky Mountains and determined soil bulk density, pH, and nitrogen content. We then extracted 10 bacterial isolates from each site and tested their growth rates when exposed to Se at 0 to 500 ppm Se (100 ppm increments) to determine their Se tolerance thresholds and understand if soil pH, soil bulk density, nitrogen, geological formation, and original soil Se (high or low) influence these thresholds. Our data suggests that there is variation in Se tolerance thresholds both within and between sites. This variation may influence a tolerant isolate's capacity to provide facilitative benefits to a non-tolerant neighbor.

---------- poster no. 18 ----------

Wastewater SARS-CoV-2 sequencing demonstrates the variant transmission in advance compared to clinical test

Fan He1, Yuehan Ai1, Michael Sovic2, and Jiyoung Lee1,3,4,*

1 The Department of Food Science and Technology, Ohio State University
2 Center of Applied Plant Sciences, Ohio State University
3 College of Public Health, Division of Environmental Sciences
4 Comprehensive Cancer Center

The severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), as known as the etiology cause of the coronavirus disease 2019 (COVID-19), has resulted in 6.8 million fatalities globally. As the virus has continued to spread globally, new variants of SARS-CoV-2 have emerged. There are several SARS-CoV-2 variants that are continuously circulating, including the B.1.1.7 variant (Alpha), the B.1.351 variant (Beta), and the B.1.1.529 variant (Omicron), with Omicron currently being the most widely reported variety of concern. Monitoring the evolution of SARS-CoV-2 is essential for alerting the public to possible new variants. Previous studies have proved that wastewater SARS-CoV-2 concentration is significantly correlated with human cases in the community, suggesting that wastewater SARS-CoV-2 sequencing is an ideal method for rapidly tracking variant transmission and detecting emerging variants within a community when compared to clinical testing, which is limited by scale, resource, and participation. In this study, SARS-CoV-2 in wastewater was filtered through 0.45 μm filter and concentrated using 0.05 μm Hollow Fiber tips through the Innovaprep concentrating system. RNA was extracted and sent for next-generation sequencing (NGS) by amplicon

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

methods. Wastewater RNA samples were obtained from the Ohio State University and were sequenced 5 times monthly from October 2021 to December 2022, except from May to August 2022. Remarkably, we detected the Omicron variant in the wastewater sample on November 4th, 2021, which is nearly 1 month earlier than the first reported case from clinical on December 7th, 2021. In the meantime, lineage dynamics detected from wastewater showed a clear shift from Omicron BA.1 to BA.2, which became the major lineage of concern. The findings from this study support that wastewater sequencing effectively tracks the transmission and transformation of popular variants, which could provide an early warning of emergent variants in a relatively large community with a controlled and dense environment.

---------- poster no. 19 ----------

Looking beyond DNA and its technical challenges –proof of concept for skin metatranscriptomics

Matthew Hymes*[1], Bitapi Ray[2], Morgan Roos[1], Aaron Garoutte[1], Tasha M. Santiago-Rodriguez[3], Scott Kuersten[1], Brice Le François[2] and Emily Hollister[3]

[1]Illumina, Inc, San Diego, CA USA
[2]DNA Genotek, Ottawa, ON Canada
[3]Diversigen, Inc, Houston, TX USA

Shotgun metagenomic sequencing of skin is challenging due to the high proportion of host DNA associated with skin samples, as well as the bioburden that may be introduced during sample collection and processing. Host depletion, high sequencing depth, short and/or long-read amplicon sequencing, and culture-based approaches are common strategies to overcome some of these challenges in skin microbiome research. However, each technique comes with limitations that can lead to bias and/or loss of valuable information. Skin metatranscriptomics has long been assumed to be limited by the low biomass nature of skin, and the high degree of host material. In this proof-of-concept study, we demonstrate that viable and meaningful metatranscriptomic profiles can be generated from skin samples (n=10 donors), namely, arm, face, scalp, and toe web, collected using swabs. Our results show that libraries are not overwhelmed by host-derived transcripts and can provide insights into the composition and functional outputs of the actively transcribing bacteria present on skin. For example, common skin-associated taxa, including Cutibacterium acnes, Staphylococcus spp., and Corynebacterium spp. are detected across the sampled skin sites, as are the expression of genes associated with lipid and amino acid metabolism, and the metabolism of vitamins and cofactors. These data suggest that metatranscriptomic sequencing is feasible and may be advantageous for low biomass samples. When using the appropriate tools and technology, skin metatranscriptomics can offer new perspectives on the role of the skin microbiome in human health and disease.

---------- poster no. 20 ----------

Assessing classical machine learning, neural network, and hyperdimensional computing-based classification techniques on microbiota data for accessible and reproducible biological classification.

Jayadev Joshi*[1], Fabio Cumbo[1], and Daniel Blankenberg^[1,2]

[1]Genomic Medicine Institute, Lerner Research Institute, Cleveland Clinic, Cleveland OH
[2]Department of Molecular Medicine, Cleveland Clinic Lerner College of Medicine, Case Western Reserve University, Cleveland OH

In the recent past, various studies have shown that machine learning (ML) methods combined with transcriptomic data are effective for the prediction of biological classification problems such as tissue type, sex, age, or diseases, and can unwind these associations. Leveraging ML techniques with microbiome data remains an attractive direction of investigation in metagenomics studies. Recently, several studies have examined the association between microbial communities, host, and environmental conditions. However, the successful exploration of the concordance between metatranscriptomics, metagenomics, and human conditions requires accessible, robust, and extensible data analysis pipelines capable of integrating novel approaches. The presence, absence, or abundance of microbial communities in a system can be represented as a function of one or more variables of the environment, lifestyle, genetics, etc. In this work, we examine classical ML, artificial neural networks, and a brain-inspired classifier based on the hyperdimensional (HD) computing paradigm trained on microbial abundance profiles derived from 8,000 metagenomic samples for a wide range of biological classification tasks, taking into account different types of infection, body sites, sex, age, and other covariates. In this study, we have tested seven different classical supervised ML algorithms, an ANN classifier, an HD computing classifier, four feature selection methods, and two different normalization methods.
Finally, we provide a reproducible data analysis pipeline, integrated into the Galaxy platform which enables researchers to repeat and extend these analyses with their own data regardless of computational skills.
Source Code: https://github.com/jaidevjoshi83/MicroBiomML

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 21 ----------

Nucleic acid detection of live pathogens on contaminated foods

Simerdeep Kaur*, Dr. Mohit S. Verma^

Purdue University, West Lafayette, Indiana

The obstacle for DNA-based techniques is that DNA in the environment can remain stable and can persist for extended periods of time (days to weeks) after cell death. The biosensors based on amplification of target DNA, can detect the DNA from dead cells and lead to overestimation of contamination or false positives. Our goal is to develop a point-of-care biosensor for the detection of live pathogens contaminating beef products. Biosensing of live pathogens is based on isothermal amplification of nucleic acid on a paper-based device. A colorimetric dye is employed as an indicator of the amplification product for visual result. The assay incorporates a compound Propidium monoazide (PMA) that makes the DNA from dead cells inaccessible for amplification. This approach is especially applicable for pathogens that can enter a viable but non-culturable state (VBNC).

---------- poster no. 22 ----------

Wastewater microbiome as the regional food environment indicator

Minseung Kim*[1], Jiyoung Lee^

[1]Department of Food Science & Technology, The Ohio State University, Columbus, OH, USA

The wastewater microbiome has come into the limelight as an effective indicator of public health conditions. However, the wastewater microbiome has not been utilized to assess regional food environments, which play a key role in community health. Thus, we investigated the relationship between food environment and wastewater microbial community structures of 62 U.S. counties. The data were acquired from publicly available sources such as United States Department of Agriculture (USDA), Centers for Disease Control and Prevention (CDC), and the National Center for Biotechnology Information (NCBI). Random forest modeling was then conducted to investigate the association between the wastewater microbiome and county disease rates. The binary classification models indicated that wastewater microbiome data can predict the cardiovascular disease death rate and type2 diabetes rate of the counties well with the area under curve (AUC) 84.20 and 85.00 respectively. Also, five bacterial genera of key importance for the modeling of two diseases were extracted. Finally, principal component analysis of the selected five bacterial genera composition and food environment variables were conducted. The generated two principal components each representing the regional food environment and wastewater microbiome were significantly correlated with each other (Spearman, $r = 0.48$, $p < 0.001$). The result of this study implies that the wastewater microbiome can mirror the regional food environment conditions highly associated with the health status of the regional population.

---------- poster no. 23 ----------

Microbiome comparisons between Nextseq and Miseq sequencing platforms in soil 16S and ITS amplicon community analyses

Scott Klasek*[1], Daryl Gohl, Sophie Wehrkamp-Richter, Diana Lok, Scott Kuersten, Matthew Hymes, Linda Kinkel

[1]Department of Plant Pathology, University of Minnesota

The Illumina Nextseq 2000 platform offers increased throughput and flexibility coupled with cost savings for microbiome researchers compared to the Miseq. To evaluate the validity of cross-platform dataset comparisons, we performed 2x300 bp paired-end sequencing of 16S and ITS amplicons using both platforms on a total of 923 soil samples. Communities from these nine agricultural field sites spanning the northern continental US show distinct regional clustering. In contrast, several biological factors (year, season, plot, potato cultivar grown) explain low but significant proportions of community variance, allowing us to evaluate the extent to which different sequencing platforms can distinguish subtle drivers of community structure.
Quality scores of reverse reads were higher in Nextseq libraries, and did not decline as rapidly with read length compared to Miseq reverse reads. Overall, higher proportions of Nextseq reads passed dada2 amplicon sequence variant (ASV) processing pipelines, particularly after filtering and trimming steps. While 4-7% of Miseq libraries failed

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

to sequence at a cutoff depth of 10k reads, most of the corresponding Nextseq libraries of both amplicons surpassed this threshold.
After rarefying, Nextseq libraries contained 10% higher numbers of observed ASVs. Bacterial 16S libraries, which were more even and rich compared to ITS libraries, showed higher observed ASVs and Shannon alpha diversity indices in Nextseq samples. While the sequencing platform could explain only 0.5% to 1% of ITS community variance, only 54% of the total number of ITS ASVs were detected in libraries sequenced in both platforms. Taken together, these results suggest that the increase in sequence quality offered by the Nextseq 2000 platform can yield higher alpha diversity measurements than corresponding Miseq samples, with the power to identify more rare ASVs. Though we have yet to investigate any sequence-associated biases, overall community composition patterns appear largely similar across platforms.

---------- poster no. 24 ----------

Analysis of soil microbiome community composition in lactate-enriched cultures

Taiwo Mercy Faloni[1,2], Alex Gurgis[1], Sachit Kshatriya[1,2], Jessica LaBella*[1,2], Bowen Man[1], Eric Prileson[1], Alicia Roistacher[3], Fungai Shumba[1,2], Derek Smith[1,2], Fall 2022 members of BIOL410[1]
Sarah Bagby[1,2]

[1]Department of Biology, Case Western Reserve University, Cleveland, OH, USA
[2]EMERGE Biology Integration Institute
[3]Department of Molecular and Microbiology, Case Western Reserve University, Cleveland, OH, USA

As the global climate warms, permafrost peatlands are undergoing rapid changes. Thawing permafrost releases soil organic substrate for microbial communities to use1. The shifts in microbial community activity these substrate stocks enable can feed back to the atmosphere in the form of potent greenhouse gases, thus affecting global climate1,2. Efforts to gauge the effects of thawing permafrost on the changes in environment will be advanced by isolating microbes from thawing permafrost for laboratory study. Stordalen Mire (Abisko, Sweden) is a well-studied model ecosystem with varying stages of permafrost thaw ideal for climate-linked microbiome research. Previous studies in the mire have identified key metabolisms (e.g., lactate fermentation) common among highly represented taxa2. Cultivating representative strains and sequencing their genomes could enable exploration into many aspects of environmental change with climate warming such as microbial community dynamics (species richness, community diversity, competition), mechanisms of acclimation and adaptation (changes in gene expression; production of genetic variants, including by horizontal transfer of genetic material). Moreover, cultivated hosts can be used to isolate phages from the mire to illuminate an important and understudied dimension of soil ecology. We have used soil samples from across Stordalen Mire to seed enrichment cultures targeting five key metabolisms. One fen-derived lactate-amended culture grew green in an unlit incubator, but progeny cultures turned bright pink when transferred to ambient temperatures and indirect natural light. We used nanopore sequencing to investigate the composition of the green and pink cultures. Here, we report the results of assembling and annotating these long-read datasets and place the identified MAGs in the context of existing meta-omic studies of the mire.

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---------- poster no. 25 ----------

Evaluating the public health service role of urban stormwater green infrastructure using microbial source tracking and microbiome analyses

Emma Lancaster*, Jiyoung Lee

The Ohio State University

Bioretention cells (BRCs) serve as one solution to mitigating climate change and extreme precipitation events. Employing a bioretention system as a stormwater control measure is designed to improve overall stormwater quality and reduce stormwater runoff via filtration, sedimentation, and other biological processes. While BRCs are known to effectively reduce pollutant and nutrient load in stormwater runoff, little is known on how bioretention impacts human public health. This study aims to evaluate stormwater microbiome transformation during bioretention treatment to evaluate this stormwater control measure's impact on public health. Following adequate storm events, nine stormwater

sample pairs were collected from a bioretention cell (inlet and outlet) in the Clintonville neighborhood of Columbus, Ohio, USA from October 2021 through March 2022. E. coli quantification was employed to evaluate broad water quality and fecal contamination. Microbial source tracking (MST) was utilized to evaluate major fecal contamination sources (universal fecal, human-, canine-, geese-, and ruminant-specific). Droplet digital PCR was utilized to quantify the level of MST host contamination in addition to three antibiotic resistant genes, tetracycline resistance gene (tetQ), sulfonamide resistance gene (sul1), and Klebsiella pneumoniae carbapenemase resistance gene (blaKPC). Subsequently, 16S rRNA gene sequencing was conducted to characterize microbial community differences. Results found that bioretention does not significantly alter E. coli, MST, and ARG concentrations between inlet and outlet samples. While there are differences in microbial composition by sample type and season, bioretention does not significantly alter pathogenic bacteria composition and abundance. This study shows that existing bioretention technology can sustainably maintain urban microbial water quality and consequently does not threaten human public health. Therefore, this study concludes that bioretention infrastructure can continue to be used as one solution towards mitigating climate change and extreme rainfall events.

---------- poster no. 26 ----------

Urine limbo: determining minimum urine volume for effective characterization of canine urinary tract microbiota

Zachary J. Lewis*[1], Christopher Madden[1], Sheryl S. Justice[2], Adam Rudinsky[3], Jessica Hokamp[4], Vanessa L. Hale[1]

[1]Department of Veterinary Preventive Medicine, The Ohio State University, Columbus, Ohio
[2]College of Nursing, The Ohio State University, Columbus, Ohio
[3]Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, Ohio
[4]Department of Veterinary Biosciences, The Ohio State University, Columbus, Ohio

Until recently, the urinary tracts of healthy individuals were thought to be sterile. However, culture-independent methods have since revealed a distinct and diverse urinary microbiome (“urobiome”). Early studies of the urobiome in humans and dogs have demonstrated important correlations between urobiome composition and disease states such as bladder cancer and incontinence. However, these studies work with urine volumes ranging from 0.5mL to 50mL. Despite growing awareness of the importance of the urobiome, standardized, uniform sampling and analysis pipelines have not been well established for the study of urinary microbiota. Factors like disease states, breed/age, and species may limit available urine for analysis, but it is unknown if there is a minimum volume needed for effective urobiome profiling. That urine is a low-biomass substrate (<105 CFU/mL), making it particularly vulnerable to contamination and introduced community stochasticity, compounds this issue. To determine whether a minimum volume of urine is necessary to obtain consistent urobiome profiles from 16S rRNA gene sequencing, we collected urine from five healthy dogs and fractionated the samples into 0.1, 0.2, 0.5, 1.0, 3.0, and 5.0 mL aliquots before extraction and sequencing. We show that the microbial composition of samples with <1 mL is highly subject to stochastic variability, while samples ≥1mL qualitatively show consistent clustering within dogs. Sample volume negatively correlated with the percent of sequencing reads identified as contaminants ($r = -0.43$, $p = 0.02$) and positively correlated with total reads ($r = 0.63$, $p = 0.0008$) within each sample. Samples ≥1mL tended to have greater microbial diversity than samples with <1mL starting volume ($p = 0.14$). Overall, results indicate that urine samples of <1mL are unlikely to be representative of the urobiome within a dog, while samples ≥1mL show consistent community composition.

---------- poster no. 27 ----------

Arbuscular Mycorrhizal Fungal Foraging Behaviors in Response to Different Nitrogen Levels

Xin Lin*[1], Alison Bennett[1]

[1]Department of Evolution, Ecology and Organismal Biology, The Ohio State University, Columbus, OH, USA

Optimal Foraging Theory has seldom been applied to microbes foraging in soil like arbuscular mycorrhizal (AM) fungi despite the evidence that fungi can perceive signals and respond to their environment. To help address this gap we apply Optimal Foraging Theory to AM fungi foraging for nitrogen. We focus on nitrogen because AM fungi need more nitrogen than their plant hosts and soil nitrogen availability can shift the relationship between AM fungi and their hosts from mutualism to parasitism.

To address this gap, we set up an *in vitro* experiment using carrot (*Daucus carota* L.) hairy root inoculated with AM fungi (*Rhizophagus irregularis*) in bi-compartment plates (with root and hyphal compartments) to study AM fungal hyphal development in response to different nitrogen concentrations. Inoculated roots were cultured in the root compartment on minimal media without nitrogen but in the hyphal compartment we added four concentrations (0 mM, 2.5 mM, 5mM and 10 mM) of ammonium nitrate to minimal media. We focused on two external hyphal types: (1)

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

branched absorbing structures (BAS), which are responsible for nutrient uptake and (2) runner hyphae (RH), which explore the environment. We imaged plates daily and recorded the hyphal extension rate, branching rate (of BAS and RH), branching angle (of BAS and RH), and the ratio of the length of BAS to the length of RH (BAS/RH) in the hyphal compartment.
Results showed variation in both BAS and RH structures and frequency as nitrogen concentration and form changed. We measured the daily change ratio of BAS/RH reflected to provide information on how AM fungi handled patches over time.
This work provides a foundation for studying AM fungal foraging activity and fills an important gap regarding how AM fungi forage for nutrients by applying the framework of Optimal Foraging Theory.

---------- poster no. 28 ----------

Investigation of ultraviolet disinfection and gene damage on different opportunistic pathogenic species of nontuberculous mycobacteria under different light sources

Yijing Liu*, Dr. Natalie Hull

The Ohio State University

Nontuberculous mycobacteria (NTM) are waterborne opportunistic pathogens. NTM have frequently been found in municipally-treated water, especially in drinking water distribution systems, which poses risks of human infections. UV and chlorine have been explored to disinfect Mycobacterium species in different engineered water systems. Distinct colony morphotypes of NTM have different cell structure properties and therefore different resistance to human immune defenses and disinfectants, which has given rise to the need to further explore mechanisms that underlie mycobacterial damage by specific UV wavelengths. This study is investigating the treatment efficiency of different UV wavelengths (222 nm emitted by a KrCl excimer lamp and 254 nm emitted by a low pressure Hg lamp) on inactivating and damaging genes of different NTM species and their morphotypes. We are investigating non-pathogenic Mycobacterium smegmatis (ATCC 19420 and 14468) and morphotypes of pathogenic Mycobacterium avium-intracellulare (MAC) that were isolated from a parent strain (A, smooth opaque morphotype, and B, rough morphotype, were isolated from P, mixed morphotype). Efficacy of inactivation across UV doses is determined by plating. Long amplicon quantitative polymerase chain reaction (qPCR) will be used to quantify the damage of hsp65 genes and rpoB genes. Gene damage will be also explored using Minion nanopore long amplicon sequencing of hsp65 genes and/or rpoB genes. For M. Smegmatis 19420 and 14468, respectively, rate constants fit to the linear portion of the log inactivation curve for 222 nm (0.188 cm2/mJ and 0.176 cm2/mJ) were higher than 254 nm (0.171 cm2/mJ and 0.160 cm2/mJ). UV inactivation of MAC morphotypes and gene damage assays are ongoing. This work will provide mechanistic knowledge on impact of UV wavelengths on different species and morphotypes of NTM at cellular and molecular levels to address the challenge of waterborne opportunistic pathogens residing in wastewater and drinking water to minimize the risks to human health.

---------- poster no. 29 ----------

The Gut Microbe-Derived Metabolite TMA Shapes Host Circadian Metabolic Rhythms Via the Host G Protein-Coupled Receptor TAAR5.

Kala K. Mahen*[1,2,3], Amanda Brown[1,2], Danny Orabi[1,4], William Massey[1,2,3,], Rahkee Banerjee [1,2], Lucas J. Osborn[1,2,3], Pranavi Linga[1], Dev Laungani[1], Anthony J. Horak III[1,2], Sumita Dutta [1,2], Marko Mrdjen [1,2,3], Rachel Hohe[1,2,3], Amy Burrows[1,2], Venkateshwari Varadharajan[1,2], Vinayak Uppin[1,2], Zeneng Wang[1,2], Naseer Sangwan[1,2], J. Mark Brown[1,2,3]

[1]Department of Cardiovascular and Metabolic Sciences, Lerner Research Institute of the Cleveland Clinic; Cleveland, OH, USA
[2]Center for Microbiome and Human Health, Lerner Research Institute of the Cleveland Clinic; Cleveland, OH, USA
[3]Department of Molecular Medicine, Cleveland Clinic Lerner College of Medicine of Case Western Reserve University; Cleveland, Ohio, USA

A transcriptional-translational feedback loop (TTFL) exists in mammalian cells to orchestrate an approximately 24-hour oscillatory rhythm in the expression of thousands of genes. The mammalian circadian clock is coordinated by core transcription factors CLOCK and BMAL1, which peak during light phases, and cryptochromes (CRYs) and period genes (PERs), which are most active during dark phases. The clock regulated TTFL maintains cell autonomous homeostatic responses to external environmental cues, known at zietgebers, including light, food, xenobiotics, and exercise when under normal conditions. However, disruption of normal circadian rhythms induced by abnormal light exposure, sleep-activity, or eating-fasting patterns has been associated with the development of many human diseases including obesity, diabetes, cardiovascular disease, kidney disease, cancer, and neurological disorders. Therefore,

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

"chronotherapies" or therapeutic strategies that prevent circadian disruption hold promise across a wide spectrum of human diseases. It has recently been discovered that circadian disruption is also associated with reorganization of gut microbial communities. However, whether gut microbial factors contribute to circadian disruption is not well understood. Our lab has recently discovered that the gut microbe-derived production of a metabolite called trimethylamine (TMA) can influence the host circadian clock and circadian regulation of host lipid metabolism (Schugar et al. 2022. *Elife*). Here we have extended this to study mice lacking the only known receptor for TMA called trace amine-associated receptor 5 (TAAR5). Mice genetically lacking TAAR5 have alterations in the oscillatory behavior of the gut microbiome as well as the circulating levels of gut microbe-derived metabolites including TMA. Additionally, the biological clock in tissues such as the olfactory bulb, skeletal muscle, and liver are perturbed when TAAR5 is knocked out. Collectively, these studies provide further evidence that the microbial metabolite TMA signals via the host receptor TAAR5 to regulate circadian fluctuations in host phospholipid and energy metabolism.

---------- poster no. 30 ----------

Sensing Our Symbionts: A *Saccharomyces cerevisiae* Biosensor for the Human Microbiome

Makayla Manes*, Dr. Patrick Bradley

The Ohio State University

The interactions between human cells and the gut microbiome are complex, especially when considering the effects of bacterial metabolites on host metabolism and health. Human nuclear receptors (NRs) are one known mechanism of interaction between the host and microbiome systems. Receptors such as Farnesoid X receptor (FXR) and the NR-like aryl hydrocarbon receptor (AHR) interact with bile acids and aromatic amino acid catabolites in the liver and gut. NRs have been linked to changes in host metabolism, host immunomodulation, and cancer. There are forty-nine currently identified NRs, twelve of which are classified as "orphans," meaning their corresponding ligand(s) have not been identified. To determine how the gut microbiome may modulate both known and orphan NR-mediated signaling, we will modify the previously created GEV system in *Saccharomyces cerevisiae* to utilize the ligand-binding domains (LBDs) of other NRs. NRs that are enriched in the liver and gut are promising candidates for aiding our understanding of the interactions between bacterial metabolites and these host systems. The GEV system utilizes a GAL4 DNA binding domain, an estrogen receptor LBD, and a transcriptional activator domain. For each strain in the library, we will swap out the LBD and use either an N-degron system or GFP to create a phenotype that will indicate ligand binding. By creating a library of *S. cerevisiae* strains that express our modified GEV-based reporter system containing alternative NR LBDs, and screening them against cultured isolates, we will be able to identify which microbes produce ligands that activate these receptors, as well as what bacterial genes are involved. By creating a biosensor system in a genetically tractable, easily cultured organism, this work will provide a method of monitoring bacterial metabolites while subsequently increasing our understanding of the interactions between the metabolites and this major class of host receptors.

---------- poster no. 31 ----------

The microbiome of *Amblyomma americanum* reflects known westward expansion.

L. Martinez*[1]; P. Lado[2]; H. Klompen[3]; R.Pesapane[4]; S.M.Short[1]

[1] Department of Entomology, The Ohio State University, 2001 Fyffe Rd., Room 232 Howlett Hall, Columbus, OH 43210, USA
[2] Arthropod-borne and Infectious Diseases Laboratory, Department of Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO, USA
[3]Department of Evolution, Ecology, and Organismal Biology and Museum of Biological Diversity, The Ohio State University, Columbus, Ohio 43212, USA
[4]College of Veterinary Medicine, The Ohio State University,1920 Coffey Rd, A100K Sisson Hall, Columbus, OH 43210, USA

Amblyomma americanum, a vector of human and animal pathogens, has been expanding its range across the United States in recent years. Tick associated microbiomes are under study as they may affect life history traits and the ability of their tick host to transmit pathogens. Furthermore, bacterial communities could be reflecting or enabling the geographic expansion of these ticks. To explore this potential relationship, we examined the microbiota of 189 *A. americanum* ticks from 4 regions spanning their historical and current geographic range (Historical, Northeast, Midwest, West). Using massively parallel sequencing targeting the 16S rRNA V4 region, we analyzed the bacterial community structure of each individual. Consistently, the most prominent members of the community for each sample were either *Coxiella*, *Rickettsia* or *Rickettsiella*. Alpha diversity was significantly driven by the region of origin and tick

sex. Bacterial abundance profiles revealed that ticks from the West harbor communities that significantly differ in structure from those of the historic range. We detected biomarker taxa for each of the populations in the expanded range, whereas none were identified in the communities associated with ticks from the historic range. Additionally, a Mantel correlogram showed that the dissimilarities were structured by the distance between collection sites. Lastly, we quantified the contribution of ecological processes to community turnover. For females and males respectively, we quantified the effects of drift (88.11%; 85.90%), dispersal limitation (11.23%; 12.96%), homogeneous selection (0.61%; 0.10%), and homogeneous dispersal (0.00%; 1.03) on microbial community assembly. Particularly, the detection of spatial autocorrelation and stochastic processes (drift coupled with dispersal limitation) driving turnover, are indicative of geographic isolation. Collectively, our results suggest the microbiome may offer an additional layer of information to study the range expansion of this relevant vector.

---------- poster no. 32 ----------

Metabolic relationships inferred between bacterial communities and the toxigenic benthic dinoflagellate *Prorocentrum* in culture

Miguel Martínez-Mercado*[1], Allan D. Cembella[2,3], Edna Sánchez-Castrejón[2], Anaid Saavedra-Flores[2], Clara Galindo-Sánchez[2], Lorena M. Durán-Riveroll[3,4]

[1] Independent Researcher;
[2] Departamento de Biotecnología Marina, Centro de Investigación Científica y Educación Superior de Ensenada, Baja California, México;
[3] Alfred-Wegener-Institut, Helmholtz-Zentrum für Polar-und Meeresforschung, Bremerhaven, Germany;
[4] CONACyT-Departamento de Biotecnología Marina, Centro de Investigación Científica y Educación Superior de Ensenada, Baja California, México

Bacteria interact with phytoplankton within the cell-surrounding space termed the phycosphere. These bacteria may influence the physiological functions of their host depending on their metabolic capabilities and the environmental conditions. In the toxigenic benthic dinoflagellates of the genus *Prorocentrum* the bacterial communities associated and their potential interactions are poorly understood. The objective of this study was to evaluate inferred functions of the microbiome in the benthic dinoflagellate *Prorocentrum* in culture. *Prorocentrum* isolates from geographically disjunct locations in Mexican coastal waters were established as xenic monoclonal cultures. Bacterial profiles from the two main culture compartments: the culture medium and in close association with the host, were obtained by 16S V3-V4 amplicon sequencing. Alphaproteobacteria, Gammaproteobacteria, and Bacteroidia were the dominant classes among the thirteen classes identified. The isolates showed no difference in diversity between compartments, having only 20 genera exclusive to the culture medium and eight to the host. The grouping of bacterial communities was instead observed by the location of origin. The core members identified in close association with the host belonged to genera *Labrenzia*, *Roseitalea*, *Cohaesibacter*, *Marivita*, *Muricauda*, *Marinobacter*, *Massilia,* and an unclassified member of Rhodobacteraceae. These core members had significant contributions in nine of the top functional pathways inferred in the community. The three broad metabolic categories determined were: stress tolerance, nutrient acquisition, and bioactive molecules. Interactions derived from these metabolic functions suggest that the microbiome of *Prorocentrum* in culture may sustain mainly symbiotic relationships. Detailed characterization of the bacterial members identified will help to confirm or determine the specific relationships and improve the study of this toxigenic dinoflagellate.

---------- poster no. 33 ----------

Raman spectroscopy - an analytical tool for biologics

Cindy Mayorga*[1], Shreya Milind Athalye[2] and Mohit Verma[1,2,3]

[1]Department of Agricultural & Biological Engineering, Purdue University, West Lafayette, Indiana 47906
[2]BirckNanotechnology Center, Purdue University, West Lafayette, Indiana 4906
[3]Weldon School of Biomedical Engineering, Purdue University, West Lafayette, Indiana 47906

Raman Spectroscopy is a non-invasive technique that identifies a variety of microorganisms and small molecules qualitatively and quantitatively. This technique measures the inelastic scattering of light due to molecular vibrations. The versatility of using Raman spectroscopy in liquid, solid, or semi-solid forms of a sample reduces any preparation measures. The minimal sample preparation and non-invasive nature of Raman Spectroscopy can be applied in developing a process analytical technology (PAT) tool and as a diagnostic tool. PAT is used in the pharmaceutical industry because it makes possible real-time and low-cost monitoring of biologics in pharmaceutical industry. PAT is an initiative introduced by the Food and Drug Administration (FDA) in 2004 to develop technologies that can guarantee quality standards of pharmaceutical products in real-time. We have successfully use Raman spectroscopy for

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

qualitative and quantitative measured biologics in our previous work. We have demonstrated that Raman spectroscopy can discriminate among several Gram-positive and Gram- negative bacteria and fungi of interest in the pharmaceutical industry. We have also detected these microbes in a mixture with Chinese hamster ovary (CHO) cells. In addition, Raman spectroscopy can identify the concentration of viral samples. We aim to optimize the sensitivity of Raman spectroscopy by developing in-line probes and by incorporating acoustic devices that can concentrate small particles. We want to further measure biological samples accurately by integrating machine learning tools in the Raman data acquisition as part of our future work.

---------- poster no. 34 ----------

Household environment contamination and host factors impact the gut microbiome and resistome of infants and young children from rural Nicaragua

Molly Mills*[1], Seungjun Lee, Boseung Choi, Barbara A. Piperata, Rebecca Garabed, and Jiyoung Lee

[1]Division of Environmental Health Sciences, College of Public Health, The Ohio State University

Early life plays a vital role in the development of the gut microbiome and subsequent health. While many factors that shape the gut microbiome have been described, including delivery mode, breastfeeding, and antibiotic use, the role of environmental exposures is still unclear. The development of the gut antimicrobial resistome and its role in health and disease is not well characterized, particularly in settings with water insecurity and less sanitation infrastructure. This study investigated the gut microbiomes and resistomes of infants and young children (ages 4 days-6 years) in rural Nicaragua via Oxford Nanopore Technology's MinION long read sequencing using a One Health perspective. Differences in gut microbiome and resistome were tested with host survey factors (age, sex, height for age z-score, weight for height z-score, delivery mode, breastfeeding habits) and household environmental factors (animals inside the home, coliform concentration in drinking water, enteric pathogens in household floors, fecal microbial source tracking (MST) marker genes in household floors). We identified higher gut microbiome diversity with participant age. There were also positive correlations between ruminant and dog fecal contamination of household floors and gut microbiome diversity. However, we identified greater abundances of potential pathogens in the gut microbiomes of participants with greater fecal loading of their household floors. We also found that these children carry diverse gut resistomes, dominated by multidrug, tetracycline, macrolide/lincosamide/streptogramin, and beta-lactam resistance. The abundance of antibiotic resistance genes (ARGs) in the gut decreased with age. The hosts of ARGs were mainly from the family *Enterobacteriaceae*, particularly *Escherichia coli*. This study identified the role of household environmental contamination in the developing gut microbiomes and resistomes of young children and infants. Understanding the impact of the household environment in early life is essential to optimize the relationship between exposure and human health.

---------- poster no. 35 ----------

Microbiome and virome changes after mammalian spinal cord injury

Mohamed Mohssen*[1,2,3], Ahmed A. Zayed[2,3]*, Kristina A. Kigerl[4,5], Jingjie Du[2], Matthew B. Sullivan[1,2,3,6] and Phillip G. Popovich[4,5]

[1]The Interdisciplinary Biophysics Graduate Program, The Ohio State University, Columbus, Ohio 43210, USA

[2]Department of Microbiology, The Ohio State University, Columbus, Ohio 43210, USA

[3]Center of Microbiome Science, The Ohio State University, Columbus, Ohio 43210, USA

[4]Department of Neuroscience, The Ohio State University Wexner Medical Center, Columbus, OH, 43210, USA

[5]Belford Center for Spinal Cord Injury, Center for Brain and Spinal Cord Repair, The Ohio State University Wexner Medical Center, Columbus, OH, 43210, USA

[6]Department of Civil, Environmental and Geodetic Engineering, The Ohio State University, Columbus, OH 43210, USA

Spinal cord injury (SCI) is a debilitating condition that physiologically and neurologically affects millions of individuals in ways that impact gut microbiota in the gastrointestinal (GI) tract. Recent studies posit that gut microbiota may provide a therapeutic avenue for recovery from SCI and/or reducing its comorbidities. Here we take the first step towards assessing "what" microbial taxa most impact SCI and developing hypotheses about "how" they affect SCI using a large-scale time- and genome-resolved metagenomic and ecosystems biology approach across multiple treatments and 59 mice. This resulted in broad "species level" genomic reference data – 245 Metageome-Assembled Genomes (MAGs) and ~65k virus genomes – that were used in a machine learning and ecosystem modeling approach to uncover microbiome-specific sex differences at the level of microbial taxa (species), viruses, and genes representing functions.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

In addition, microbes in male and female mice after injury shift from their original state in a level-dependent manner, implying that the level of injury could dictate how SCI patients receive treatment for microbial dysbiosis. Through these approaches, we provide additional ecological understanding of the microbiota-mouse-SCI nexus and distill thousands of microbial and viral taxa and genes down to the few that likely offer the most promising therapeutic targets for minimizing SCI comorbidities.

---------- poster no. 36 ----------

Addition of plant growth promoting rhizobacteria to peat-based potting media influences the native rhizosphere microbiome of *Impatiens walleriana*

Laura J. Chapin[1], Juan O. Quijia Pillajo[1], Sachin Naik*[1], James E. Altland[2], and Michelle L. Jones[1]

[1]The Ohio State University – Department of Horticulture and Crop Science, 1680 Madison Ave., Wooster OH, 44691
[2]USDA ARS Application Technology Research Unit, Wooster, OH,44691

Microbiomes of containerized floriculture crops produced in soilless substrates have not been well characterized. Our objective was to investigate how the addition of a non-native bacterium influences the native rhizosphere microbiome over time. *Impatiens walleriana* 'Xtreme Red' were produced in peat-based substrate under reduced fertility. Plants were treated at transplant with *Pseudomonas poae* strain 29G9, previously identified as a plant growth promoting rhizobacterium (PGPR). Untreated plants served as a negative control. Plant growth parameters were recorded, chemical composition of potting substrate was analyzed, and rhizosphere substrate was collected at bud-break and fully flowering stages for microbiome analysis. We did not observe differences in plant growth parameters or substrate chemical composition between bacteria-treated and untreated plants. We observed differences in the rhizosphere microbiome. *Impatiens* assembled different bacteria communities at each phenological stage. At bud break, bacterial treatment changed the rhizosphere community structure and increased alpha diversity. The abundance of *P. poae* 29G9 and *Solimonas* spp. were higher in bacteria-treated samples. At flowering, the abundance was reduced and bacterial communities in treated and untreated plants were similar. We conclude that inoculation with a beneficial bacterium influences the rhizosphere microbiome temporarily. Studying the role of abundant bacteria taxa in PGPR-treated containerized ornamental plants may lead to more effective microbe-based biostimulant products.

---------- poster no. 37 ----------

To Sample or Not to Sample: Capturing Feline Fecal Microbiome Changes With High-Frequency Sample Collection

N.J. Nealon*[1], H. Klein[1], M. Salerno[1], V.J. Parker[1], J. Quimby[1], A. Rudinsky[1], J. Howard[1], and J.A. Winston[1]

[1]Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio, 43210

Microbiota-based fecal evaluations are promising feline diagnostic tools. While once-weekly sampling is standard in research, daily fecal microbiota changes make the ideal sampling frequency unknown. The objective of this study is to evaluate how sampling frequency impacts the resolution of fecal microbiota data. Our hypothesis is that daily high frequency fecal sampling is more effective than less frequent sampling at capturing significant microbiota alterations in cats.

Six healthy, sterilized adult laboratory cats (3 male, 3 female) were assessed. To initiate an abrupt microbiota disturbance, a rapid diet change was performed. Feces was collected prior to diet transition and then daily for five weeks. 16s rRNA microbiota analysis (V4 region) was performed using the DADA2 pipeline. To examine impacts of sampling frequency, twelve sampling schemes, representing once-weekly to everyday sampling, were compared for their ability to identify microbial shifts over time. For each scheme, pairwise PERMANOVA and DESeq2 differential abundance testing were used to identify time-dependent microbiota compositional and taxonomic changes respectively. Significance was defined as $p<0.05$ following posthoc corrections.

When comparing sampling schemes, high frequency daily sampling provided the best resolution for identifying microbiota alterations over time ($p<0.01$) compared to low frequency once-weekly sampling ($p = 0.015$). Sampling frequency schemes differentially estimated fold changes in Fusobacteriota, a phylum important in protein metabolism, where daily sampling identified a 5.31-fold reduction in Fusobacteriota abundance between baseline and study week one ($p=9.41E-20$) whereas the once-weekly sampling scheme identified a 3.13-fold decrease ($p=0.0034$).

The results from this study support that high frequency sampling may be needed to accurately capture microbial community shifts occurring in response to an inciting agent, including diet and/or medical treatments. Ongoing analysis will integrate this data with daily feline dysbiosis index values, a widely used feline microbiota diagnostic tool, to further assess the impact of sampling frequency on biologically-relevant taxa.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 38 ----------

Exploring The Microbial Contents in Leukemia Initiating Cells

Dinh Duy An Nguyen*[1], Thomas LaFramboise

Case Western Reserve University, School of Medicine

Acute myeloid leukemia (AML) starts in the bone marrow, the tissue that makes blood cells, causing abnormal development of these cells. Our current and previous work characterized the circulating microbial landscapes of leukemia patients with both DNA and RNA sequencing data extracted from the blood and bone marrow from different cohorts of patients. Together, our analyses indicated that the circulating microbiome is different between leukemia patients and healthy controls. Here, we continue our exploratory work by assessing the microbial contents in leukemia initiating cells (LICs).
It is hypothesized that AML relapse results from the persistence of LICs that escape chemotherapy. Yet, little is currently known about the heterogeneity of LICs and how they evolve during AML disease progression, much less whether there is microbial presence in LICs. We analyzed single cell RNA-seq on 813 LICs isolated from five AML patients' matched diagnosis and relapse bone marrow samples and discovered that there is microbial content within the LICs. We performed a variety of ordination techniques to visualize the data and observed that the microbial contents in pre-treatment LICs are more similar to one another than to post-treatment LICs, and vice-versa. Furthermore, there is a significant shift in the microbial diversity between pre- and post-treatment. Finally, the LICs in each patient were clustered into 2-4 groups based on host gene expression. The microbial content differed from cluster to cluster, and we analyzed bacterial genes and pathways that potentially contribute to the differences in host expression.

---------- poster no. 39 ----------

Sex hormone deprivation perturbed the gut microbiota in a sex-specific manner

Anna Clapp Organski*[1], William G. Schrage[2], Joan S. Jorgensen[3], Tzu-Wen L. Cross[1]

[1]Department of Nutrition Science, Purdue University, West Lafayette, IN, 47907
[2]Department of Kinesiology, University of Wisconsin, Madison, WI, 53706
[3]Department of Comparative Biosciences, University of Wisconsin, Madison, WI, 53706

The hypothalamic-pituitary-gonadal (HPG) axis is critical in regulating sex hormone homeostasis. Medical conditions such as hormone-sensitive cancers can benefit from sex hormone deprivation therapy that suppresses the HPG axis by gonadotropin-releasing hormone (GnRH) analogs. Sex hormone deprivation therapy often results in reduced intestinal motility and increased occurrence of metabolic diseases. The gut microbiota is suggested to be a critical regulator of sex hormone homeostasis, intestinal motility, and metabolic disease risk. However, the role of gut microbiota on the physiological impact of sex hormone deprivation is unclear. Herein, we aim to characterize the impact of sex hormone deprivation on the gut microbiota. **HYPOTHESIS:** We hypothesize that short-term sex hormone deprivation using a GnRH analog, Degarelix, will rapidly perturb the gut microbiota in both sexes. **METHODS:** Male and female C57BL/6J mice (n=10/group) received weekly subcutaneous injections of Degarelix or saline control. Four weeks after initiation of Degarelix treatment, mice were euthanized and body composition, testicular, and uterine weight was determined. Cecal microbiota and longitudinal fecal microbiota was assessed using 16S rRNA gene sequencing. **RESULTS:** As expected, Degarelix treatment resulted in significantly lower testicular and uterine weight. Compared to controls, Degarelix-treated males lost lean mass while females gained fat mass. Community-level assessment showed that Degarelix induced significant shifts of the cecal microbiota in males, but not females. In males, Degarelix treatment diminished the proportion of *Turicibacter* and *Lachnospiraceae* in the cecal microbiota. Metabolites produced by these taxa have been shown to protect against metabolic diseases. Longitudinal sampling revealed shifts in male fecal microbiota occurred one week after Degarelix initiation, suggesting that sex hormone deprivation can rapidly perturb the gut microbiota. **CONCLUSION:** The use of GnRH analog results in gut microbial perturbation only in males. The highly modifiable nature of gut microbiota makes it an excellent therapeutic target for mitigating therapeutic drug side effects.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 40 ----------

Associations among gut permeability, inflammation, and cognitive impairment in female breast cancer patients treated with chemotherapy

Lauren Otto*[1], Lindsay Strehle[1], Corena Grant[1], Olivia Wilcox[1], Ashley Lahoud[1], Nicklaus Halloy[1], Robert Wesolowski[2,3], Rebecca Andridge[1], Leah Pyter[1,4,5]

[1]Institute for Behavioral Medicine Research, The Ohio State University, Columbus, Ohio
[2]The James Cancer Hospital and Solove Research Institute, The Ohio State University, Columbus, Ohio
[3]Stefanie Spielman Comprehensive Breast Center, The Ohio State University, Columbus, Ohio
[4]Department of Psychiatry and Behavioral Health, The Ohio State University, Columbus, Ohio
[5]Department of Neuroscience, The Ohio State University, Columbus, Ohio

Many breast cancer (BC) patients and survivors experience debilitating behavioral side effects during and after chemotherapy treatment, including cognitive impairment. The etiology of these effects is not understood, impeding prevention and treatment. We hypothesize that gut permeability and dysbiosis contribute to the positive relationship between inflammation and cognitive impairments in BC patients treated with chemotherapy. The Intelligut Study was a clinical study of female BC patients treated at Stephanie Spielman Comprehensive Breast Center between 2019 and 2022. Participants were 29-74 years old, with stage IA – IIIB BC, and receiving chemotherapy. Participants completed 3 visits which occurred at their first chemotherapy appointment (pre-chemotherapy), last chemotherapy appointment (during chemotherapy), and after a wash-out period of at least 4 weeks (post-chemotherapy). At each visit, plasma and fecal samples were collected, and participants completed objective cognitive assessments. Several circulating measures of inflammation, gut permeability, and cognitive impairment increased across study visits; post-chemotherapy increases primarily drove these effects. For inflammation, TNF-α increased from pre- to during chemotherapy and increased further from during to post-chemotherapy, while IL-6 and IL-8 were only elevated post-chemotherapy. For gut permeability, sCD14 increased from pre- to during chemotherapy and remained elevated post-chemotherapy. In the Hopkins Verbal Learning Test (HVLT), a letter test of learning and memory, a discrimination index decreased from during to post-chemotherapy, indicating a deficit. In summary, chemotherapy impaired memory and increased markers of gut permeability and inflammation. Analyses are ongoing to explore associations between changes in gut permeability, inflammation, and cognition over chemotherapy treatment, and how stage, type of chemotherapy, radiation, and surgery may modulate these changes. Further, fecal sample sequencing is ongoing to determine measures of microbial diversity, which will be included in correlational analyses with gut permeability, inflammation, and cognition. This work has implications for future prevention and treatment options for chemotherapy-induced behavioral side effects.

---------- poster no. 41 ----------

Nutrient limitation influences the rhizosphere bacterial microbiome of *Impatiens walleriana* 'Xtreme Red'

Juan Quijia Pillajo*[1], Laura Chapin[1], James Altland[2], Michelle Jones[1]

[1] Department of Horticulture and Crop Science, The Ohio State University, Wooster, OH 44691
[2] USDA ARS Application Technology Research Unit, Wooster, OH 44691

Optimum plant development requires adequate levels of nutrients at the rhizosphere. The rhizosphere-associated microbiome can provide additional functions to enhance nutrient availability for plant uptake. While the plant microbiome has been studied extensively in soil-based crop production, less is known about the microbiome of ornamental crops grown in peat-based substrates. We report the rhizosphere bacterial microbiome of *Impatiens walleriana* 'Xtreme Red' cultivated under three fertilization regimes representing limited, optimal, and excess nutrient levels. Phyla Proteobacteria, Bacteroidota, and Actinobacteriota dominates the microbiome of impatiens. The rhizosphere microbiome differs between budding and fully flowering phenological stages. Different fertility levels impacted microbial community composition but not alpha diversity. The abundance of 15 amplicon sequence variants (ASV) at 25 ppm N and 200 ppm N was higher than at 100 ppm N. Plants grown at 25 ppm N were smaller than at higher rates, but they were greener and had higher flower biomass. We have shown that fertilization levels can influence rhizosphere microbiome composition. Shifts in microbial communities can be a strategy used by plants to optimize nutrient availability. Understanding the changes in the plant microbiome in response to limited and excess nutrient levels can facilitate the development of microbial biostimulants targeted to improve ornamental plant nutrition.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 42 ----------

Lipocalin-2 Expression Changes Gut Microbiome Composition and Diversity, and Promotes Tumor Growth in a Mouse Model of Pancreatic Ductal Adenocarcinoma

Valentina Pita-Grisanti MS*[1,2,3]; Kristyn Gumpper-Fedus[2,3]; Zobeida Cruz-Monserrate PhD[2,3]

[1]The Ohio State University Interdisciplinary Nutrition Program, Columbus, OH
[2]Division of Gastroenterology, Hepatology, and Nutrition, The Ohio State University Wexner Medical Center, Columbus, OH
[3]The James Comprehensive Cancer Center, The Ohio State University Wexner Medical Center, Columbus, OH
[4]The Ohio State University, Department of Biomedical Informatics, Columbus, OH

Background: Pancreatic Ductal Adenocarcinoma (PDAC) is a deadly disease. Lipocalin-2 (Lcn2) is a pro-tumorigenic, bacteriostatic molecule, increased in the serum and tumor of PDAC patients. PDAC patients experience microbial dysbiosis which can worsen tumor outcomes. Understanding whether Lcn2 modulates bacteria and PDAC outcomes could generate novel therapies for patients.
Hypothesis: Lack of systemic and tumor derived Lcn2 will decrease PDAC growth and improve microbiome composition and diversity.
Methods: *Lcn2* expression was deleted via CRISPR from PDAC cells (KRas^{G12D}/Trp53$^{-/-}$/PDX-1-CRE; mKPC) to generate *Lcn2*$^{+/+}$ and *Lcn2*$^{-/-}$ mKPC cells that were injected orthotopically into WT and Lcn2 KO mice. Serum Lcn2 was measured via ELISA and *Lcn2* gene expression via RT-qPCR. Tumor growth was monitored over time via the In Vivo Imaging System. Stool was collected before and after PDAC. Microbial DNA extraction and shallow shotgun genome sequencing were performed using the Qiagen DNeasy 96 PowerSoil Pro kit and the Illumina NovaSeq instrument. Data was analyzed using One Codex.
Results: Mice that lack of either tumor or host Lcn2 had less tumor growth compared to control, however tumor weights at endpoint were similar among all groups. Serum and tumor Lcn2 were highest in WT mice with *Lcn2*$^{+/+}$ mKPC cells followed by WT mice with *Lcn2*$^{-/-}$ mKPC cells. Serum Lcn2 levels correlated positively with tumor growth. Tumor *Lcn2* expression modulated microbiome composition in WT mice. After PDAC, beta-diversity differentially clustered WT mice by the tumor *Lcn2* expression, and Gene Ontology analyses showed an upregulation in iron binding processes, glutamate and fatty acid synthesis in mice injected with mKPC Lcn2$^{+/+}$ cells.
Conclusions: Presence of both host and tumor Lcn2 promotes PDAC growth. Lcn2-induced microbiome modulation indicates crosstalk between tumor *Lcn2* and the gut. Additionally, overexpression of LCN2 in PDAC could explain some of the microbial dysbiosis seen in patients.
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---------- poster no. 43 ----------

Diversity patterns and ecological footprint of RNA viruses along a permafrost thaw gradient

Akbar Adjie Pratama*†[1], Guillermo Dominguez-Huerta†[1], Ahmed A. Zayed[1], James M. Wainaina[1], Benjamin Bolduc[1], Funing Tian[1], Jared Ellenbogen[3], Jiarong Guo[1], EMERGE Team, EMERGE Coordinators, Kelly C. Wrighton[3], and Matthew B. Sullivan[1,2]

[1]Department of Microbiology, The Ohio State University, Columbus, Ohio, EMERGE Biology Integration Institute, The Ohio State University, Columbus, Ohio
Center of Microbiome Science, The Ohio State University, Columbus, Ohio
[2]Department of Civil, Environmental, and Geodetic Engineering and Evolution, Ecology and Organismal Biology at The Ohio State University, Ohio State University, Columbus, OH
[3]Department of Soil and Crop Science, Colorado State University, Fort Collins, CO

Rising temperatures can release permafrost soil carbon, accelerating greenhouse gas emissions. The role of RNA viruses in soil eukaryotes is unclear, despite their potential importance in nutrient cycling, as demonstrated in the oceans. (1, 2) and a diversity of forest, mountain, semi- desert, agricultural and sedimentary soils (3). Here we leverage 55 metatranscriptomes (630 Gigabases) collected along a permafrost thaw gradient in the model ecosystem Stordalen Mire to identify, quantify and ecologically contextualize RNA viruses in these soils. Application of analytical approaches optimized for maximal sensitivity and largely-automated systematic classification to these data identified 2,651 “species-like” RNA virus taxa. Though most of these species derive from the 5 known established phyla (4), including 1 vOTUs in the recently suggested phylum “Taraviricota” (1), nearly all represent novel species within these higher taxa and 5 likely represent a novel class in the phylum Lenarviricota (proposed name “Stomiviricetes”). Ecological analyses of the approximately species-level taxa revealed strong habitat specificity, as well as depth trends where RNA virus

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

diversity decreased with depth. To assess the ecological footprint of Stordalen Mire RNA viruses, we predicted hosts and evaluated gene content. This revealed that most (68%) likely infect key nutrient cycling eukaryotes that span multiple levels in the food web (only a few percent RNA viruses were predicted to infect prokaryotes), as well as 96 that carried virus-encoded auxiliary metabolic genes hinting at metabolic reprogramming of hosts' metabolic pathways, cellular and molecular processes. These findings offer essential knowledge on RNA virus diversity and ecology with potential ecosystem impacts for predictive ecological models in the rapidly-changing Arctic.

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---------- poster no. 44 ----------

Metabolic potential of xanthan gum-degrading microbial consortia

Anurag R. Pujari*[1], Dane G. Deemer, Matthew P. Ostrowski, Sabina Leanti La Rosa, Phillip B. Pope, Eric Martens, Stephen R. Lindemann

[1]Diet Microbiome Interactions lab, Department of Food Science, Purdue University

Xanthan gum is a commonly used food additive that is found in a wide range of food products, including sauces, dressings, and baked goods. Despite its widespread use, relatively little is known about how xanthan gum is metabolized by the human gut microbiota and the health implications of its consumption. In this study, we aimed to investigate the metabolic potential of consortia of gut bacteria selected on xanthan gum as a carbon source using genome reconstruction from metagenomes. A group of bacteria belonging to family Ruminococcaceae were found to cleave the xanthan gum backbone. Metagenome Assembled Genomes (MAGs) were analysed using a custom bioinformatic pipeline. We performed gene modeling and draft annotation using RAST and further annotated MAGS using TIGRFAMs, SCG_Taxonomy, COGs, BlastKOALA, and Pfams. Further analysis of these files was conducted using checkM to estimate MAG completeness and contamination, TYGS to search for nearest neighbor strains, CAT/BAT to assign taxonomy, fastANI for average nucleotide identity. Additionally, anvio's anvi-estimate command generated matrix format and long form tables, evaluating KEGG annotation and assigning scores based on the module's completeness. These annotations were used to identify metabolic dependencies of the xanthan-degrading organisms, *R.* sp. UCG-13, with the goal of designing a growth media that can enable R.UCG-13 to be cultivated and isolated. Overall, our study provides new insights into the metabolic potential of gut bacteria involved in xanthan gum degradation. These findings may have implications for the development of new food additives that can promote the targeted growth of beneficial gut bacteria and enhance the production of SCFAs and other metabolites with potential health benefits.

---------- poster no. 45 ----------

A comparative study of Lachnospiraceae metabolism and response to oxidative and nitrosative stress

Christian J. Quiles Pérez*, Dr. Patrick Bradley

Department of Microbiology, The Ohio State University

The human gut microbiome plays a crucial role in maintaining human health. The *Lachnospiraceae* family is one of the most abundant bacterial families in the human gut and is often depleted in disease. They are well known for their production of short-chain fatty acids, antimicrobial compounds, and secondary bile acids. Despite their importance, they are still poorly understood compared to other gut bacterial clades. To address this knowledge gap, we are

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

generating a *Lachnospiraceae* strain collection and developing a defined media that supports their growth across the family. By doing so, we aim to study how these organisms regulate their metabolism in response to nutrient availability, oxidative stress, and nitrative stress. A comparative transcriptomic and metabolomic analysis will provide insight into how *Lachnospiraceae* adapts to different selective pressures and deepen our understanding of this essential gut bacterial family. This knowledge can help us understand the basic nutritional requirements to maintain gut microbes needs to survive in the gut, also it can illuminate why they are being depleted in disease and how we can influence their abundance.

---------- poster no. 46 ----------

Effects of Wheat Genotype on Gut Microbiota Fermentation

Adam Quinn*, Stephen Lindemann

Department of Food Science, Purdue University

Gut microbiomes play important roles in the digestive and overall health of humans and animals and are influenced by dietary fiber. Wheat bran constitutes a major source of dietary fiber in Western diets and is an interesting model for insoluble fiber utilization by gut microbiota. However, effects of wheat genotype on bacterial fermentation have not been addressed in previous research, with many extant studies involving wheat lacking source or class descriptions. The objective of my exploratory research was to determine the extent of microbiota fermentation response variability due to wheat genotype using samples across the genus *Triticum*. Wheat kernels from twenty-one genotypes were milled to obtain whole wheat flour which underwent *in vitro* upper gastrointestinal enzymatic digestion. The remaining whole wheat flour fiber was inoculated with fecal microbiota from three donors in *in vitro* fermentation experiments. After 24-hour incubation, fermentation metabolic outcomes were measured along with microbiota community analysis using 16S rRNA gene sequencing. Results from this work show a broad spectrum in fermentation responses to wheat genotype, such as in pH, gas generation, and short-chain fatty-acid production. Beta-diversity measurements did not identify clear treatment differentiations due to strong initial fecal donor effects. However, wheat genotype effects were observed when looking at growth and promotion of bacteria at the OTU level. Across most fermentation outcomes, wheat genotypes responded more similarly to those from their own taxonomic grouping than those from other groups. These findings suggest wide variability of wheat fiber utilization that cannot be easily represented by one or several genotypes. Wheat genotypes from finer taxonomic levels (e.g. hard wheat, durum, spelt) may follow group trends, but even then, heterogeneity in bacterial utilization within groups appears to be present.

---------- poster no. 47 ----------

What is Lost is not Forgotten: Understanding breeding-driving manipulation in the *Zea mays* microbiome

Sierra Raglin*[1], Dr. Angela Kent[1]

[1]Department of Natural Resources and Environmental Sciences, University of Illinois, Urbana-Champaign

Maize (*Zea mays*) domestication and breeding drastically modified the morphology and physiology of modern germplasm, yet it is uncertain if the directed evolution of maize altered the diversity and complexity of the rhizosphere microbiome. However, as maize was adapted to North American agroecosystems, selection within highly managed environments mitigated pressures from abiotic and biotic stressors. Synthetic additives, such as nitrogen fertilizers and insecticides, became a management crutch now required for industrialized agroecosystems. Selection within these modified environments may have modulated rhizosphere recruitment and filtration mechanisms in modern germplasm. Therefore, we hypothesize that modern breeding within temperate industrial agroecosystems manipulated the structure of the rhizosphere microbiome. This research aims to understand how domestication and northward migration of maize altered the diversity and structure of the rhizosphere microbiome. A chronosequence of maize spanning teosinte to modern inbred germplasm was grown in the greenhouse to sample the rhizosphere microbiome via bacterial 16S rRNA and fungal ITS amplicon sequencing. Multivariate statistics were used to identify breeding-induced changes in bacterial and fungal diversity and composition. Network analysis was used to identify breeding-driven changes in network organization, topology, and complexity. Ultimately this research serves as a stepping-stone to usher in a new era of germplasm development by leveraging the genetic diversity in wild and landrace relatives to understand the microbiome as an extended phenotype.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 48 ----------

The long-term in vitro bacterial viability of lyophilized and frozen canine and feline fecal microbial transplantation products

Nina Randolph*[1,2], Dubra Diaz-Campos[1], Joany van Balen[1], Nora Jean Nealon[1,2], John Rowe[1,2,] Jenessa A. Winston[1,2]

[1]Department of Veterinary Clinical Sciences. The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210
[2]Comparative Hepatobiliary and Intestinal Research Program, The Ohio State University, College of Veterinary Medicine. Columbus, Ohio. 43210

Fecal microbiota transplantation (FMT) is the transfer of feces from a healthy donor into a diseased recipient to confer a health benefit. The precise mechanism in which FMT confers a health benefit is unknown but is linked to the viability and engraftment of microbes. Our study aims to quantitate the colony forming units (CFUs) of microbes within canine and feline FMT products using culture-based techniques in aerobic and anaerobic environments. Three screened canine and feline fecal donors each provided three separate fresh fecal samples for processing. Fecal processing techniques include unprocessed (raw) and three double centrifuged fecal slurries with the following additives: 0.9% saline, 0.9% saline with 10% glycerol, and 0.9% saline with 25% maltodextrin and trehalose (M:D). FMT products were aliquoted for long-term storage at -20C, -80C, and lyophilized for storage at room temperature. Timepoints for CFU/gram quantitation include baseline (immediately following processing), 1 month, 3, 6, and 12 months. At the 3-month timepoint, canine and feline lyophilized products preserved with M:D yielded significantly greater total CFUs compared with other lyophilized products (dogs, $p<.0001$; cats, $p<.0005$). For canine and feline samples frozen at -20C, feces preserved with glycerol and M:D yielded significantly more CFUs than other products (dogs, $p<.0057$; cats, $p<.0022$), with no significant difference between glycerol and M:D (dogs, $p=.6115$; cats, $p=0.999$). In canine and feline samples stored at -80C, 10% glycerol yielded the most CFUs at the 3-month timepoint, however this was not significantly different from samples stored with saline or 25% M:D (dogs, $p>0.1547$; cats, $p>0.999$). One limitation of this study is the unculturability of most fecal microbes. Additionally, the clinical relevance of viability and the CFU/gram "dose" required to confer a benefit for the recipient is unknown. Further research is needed to determine whether increased CFUs translates to microbe engraftment and thus additional clinical benefit.

Key words: Fecal microbiota transplant, canine microbiome, feline microbiome, gut bacterial viability

---------- poster no. 49 ----------

Environmental and genetic regulation of mycotoxin production in *Aspergillus oryzae* isolated from indoor dust

Emily Rego*[1], Bridget Hegarty[1]

[1]Department of Civil and Environmental Engineering, Case Western Reserve University, Cleveland, Ohio

The built environment influences the toxicity of fungi introduced by its occupants, the outdoor air and soil, or structural sources such as plumbing or ventilation. The production of toxic compounds by fungi has been documented since the mid-20th century, yet mycotoxin production by indoor microbes has been ignored in epidemiological studies. Though the effects of temperature and water activity on mycotoxin production and gene expression have been extensively studied in close relative *Aspergillus flavus*, less is known about transcriptional and environmental control of mycotoxin production in *Aspergillus oryzae*. Most well-known for its use in the industrial production of soy sauce and sake, *A. oryzae* also inhabits indoor spaces and poses potential exposure to understudied mycotoxins like *B*-nitropropionic acid. Here, we investigate how humidity impacts mycotoxin production and expression of biosynthesis genes using controlled growth chamber experiments and droplet digital PCR in *A. oryzae* isolated from household dust. We also review the genomic and transcriptomic differences in mycotoxin biosynthesis gene clusters between publicly available sequences of *A. oryzae* RIB40 and *A. flavus* NRRL3557. Our results will help elucidate what genomic, transcriptomic, and environmental factors govern mycotoxin production in *A. oryzae*. Revealing the genetic and transcriptional elements involved in the production of understudied mycotoxins will provide targets for the food industry to create industrial strains with less toxigenic potential. This preliminary research will establish a foundation for future investigations into how the built environment affects toxin production by indoor fungi.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 50 ----------

Combining viral identification tools improves virus sequence identification from mixed metagenomic datasets

Hegarty, Bridget†; Riddell V, James*†; Bastien, Eric; Langenfeld, Kathryn; Lindback, Morgan; Wing, Anthony; Saini, Jaspreet; Duhaime, Melissa

Ohio State University

An enduring challenge in studying the ecology of microbiomes is accurately identifying viral sequences from environmental metagenomes. Current viral identification software tools tend to either identify many possible viruses with a high degree of non-virus contamination, or identify a small fraction of the total viral genomes but with low contamination. Previous studies have attempted to mitigate the tradeoff by combining multiple tool outputs; **this approach assumes combining multiple tools discovers more viruses and improves accuracy, but has not been validated in the literature.**
Here, we benchmarked combinations of four viral identification tools widely used in viral microbiome studies (VirSorter2, VirSorter, VIBRANT, DeepVirFinder) and two additional tools used for quality control (CheckV, Kaiju). We defined rule sets based on each tool's outputs, and two additional multi-tool rule sets to catch false negatives and remove false positives. Rule set combinations were tested on mock environmental metagenomes composed of publically available viral, bacterial, archaeal, fungal, and protist sequences. Next, we applied benchmarked combinations to six different environmental aquatic metagenomes to evaluate the impact of habitat on tool and rule set performance.
We found that combining tools generally increased viral discovery without compromising accuracy. For example, when comparing all combinations of two versus six tools, recall was significantly higher (padj ≤107) and precision stayed constant (padj =0.78). Further, different tool combinations were better suited for long (>5kb) versus short (3-5kb) metagenomic fragments.
In this presentation, I will recommend tool combinations for different experimental setups and types of metagenomes. These recommendations and benchmarking results will help researchers choose which combination of viral ID tools is best suited for their viral microbiome study.

---------- poster no. 51 ----------

Gut microbiota promoting propionic acid production accompanies diet-induced intentional weight loss in cats

J. C. Rowe*[1,2], J. A. Winston[1,2], V. J. Parker[1,2], K. E. McCool[3], J. S. Suchodolski[4], C. Gilor[5], and A. J. Rudinsky[1,2]

[1] Department of Veterinary Clinical Sciences, The Ohio State University, Columbus, Ohio
[2] Comparative Hepatobiliary Intestinal Research Program (CHIRP), The Ohio State University, Columbus, Ohio
[3] Department of Clinical Sciences, North Carolina State University, Raleigh, North Carolina
[4] Gastrointestinal Laboratory, Department of Small Animal Clinical Sciences, Texas A&M University, College Station, Texas
[5] Department of Small Animal Clinical Sciences, University of Florida, Gainesville, Florida

The gut microbiota influence regulation of host metabolic function through microbial-derived metabolite production during states of obesity and weight loss. Specifically, microbiota production of short-chain fatty acids (SCFAs) can become altered in obese people and perpetuate metabolic states associated with obesity, including insulin resistance. These dynamics are minimally explored in feline medicine where it is estimated that 60% of cats in the United States are overweight or obese. In this study, overweight or obese research cats (n = 7) were transitioned from a maintenance diet to a weight-loss diet fed *ad libitum* for seven days, then calories were restricted to achieve 1-2% weight loss per week for an additional 77 days. Cats then received their original maintenance diet again for 14 days. Significant intentional weight loss was noted after the calorie restriction phase (adjusted $p < 0.05$). Fecal samples were collected during the four study phases, and both 16S rRNA amplicon sequencing and targeted SCFA metabolomics were performed. Amplicon sequence variants (ASVs) were generated using DADA2, and taxonomy was assigned using SILVA database. Alpha diversity did not significantly change across study phases; however, beta diversity analysis of Bray-Curtis distances demonstrated differences in microbiota composition between the four study phases (PERMANOVA adjusted $p = 0.011$). Differentially abundant taxa driving the compositional differences were identified using LEfSe, which included four *Blautia* genus ASVs that were significantly enriched either during or following weight-loss diet administration (adjusted $p < 0.05$). During weight-loss diet administration, significantly greater concentrations of the SCFA propionic acid were detected in feces, while branched chain SCFAs were significantly reduced (adjusted $p < 0.05$). These data demonstrate that intentional weight loss in obese or overweight

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

cats in response to dietary intervention is accompanied by shifts in gut microbiota composition promoting production of propionic acid, which is implicated in preventing obesity-associated inflammation.

---------- poster no. 52 ----------

The onset and severity of colitis in IL-10 -/- mice is not dependent on fecal microbiota transplantation from ulcerative colitis patients

Kayla Roy*[1], Edward Moncada, Lavanya Reddivari

[1]Purdue University

Inflammatory bowel disease (IBD) is a chronic inflammatory condition that affects around 1% of the U.S. population. IBD is comprised of Chron's Disease and Ulcerative Colitis (UC), with UC having a higher incidence rate. IBD is believed to be caused by immune dysfunction and several environmental factors. Specifically in UC, bacterial dysbiosis is correlated positively with colitis severity and incidence. Thus, we propose that genetically susceptible mice colonized with human colitis-associated bacteria will exhibit early onset and increased colitis severity. To test this hypothesis, 20-week-old, germ-free IL-10-/- were gavaged orally with fecal samples from healthy individuals and a severe colitis patient with a fecal calprotectin level of 1947 ug/mg. The Disease Activity Index (DAI) was calculated based on occult blood, weight loss, stool consistency, and grimace. DAI was used to assess colitis severity weekly in transplanted mice for eight weeks. 16S rRNA sequencing analysis showed a significant difference in alpha (Shannon Index) and beta diversity (Weighted UniFrac) between the colitis patient and healthy donors indicating dysbiosis (p=.0001; p=.001). The colitis donor had a reduction in species richness. Furthermore, recipient mice clustered with the donors in their bacterial composition, although healthy recipients had a higher colonization efficacy. Compared to mice with healthy individual-associated bacteria, colitic-associated bacteria did not significantly increase the colitis incidence or severity in IL-10 -/- mice. Furthermore, there were no significant differences in DAI scores, intestinal permeability, and fecal lipocalin-2 levels between the treatments. However, female IBD recipient mice had increased colon, spleen, and cecum weights compared to healthy female recipients, while male IBD recipients had no organ weight differences. Additionally, colon mucus thickness was reduced significantly in IBD recipient mice compared to healthy recipients. The results demonstrate that bacterial dysbiosis alone is not sufficient to induce colitis or accelerate disease status in genetically predisposed mice.

---------- poster no. 53 ---------- POSTER WITHDRAWN

Host diet, physiology and behaviors set the stage for Lachnospiraceae cladogenesis

Mathias Schneider*[1], Arturo Vera-Ponce de Leon[1], Benjamin C Jahnes[2], Victoria Sadowski[1], Lennel A Camuy-Vélez[2], Jun Duan[3], Zakee L Sabree[1]

[1]Department of Evolution, Ecology, and Organismal Biology, The Ohio State University
[2]Department of Microbiology, The Ohio State University
[3]Pathology and Laboratory Medicine, University of British Columbia

Diverse bacterial communities are found in the guts of animals of every lifestyle and level of complexity, often contributing to host health through nutrient provision. Lachnospiraceae are a family of anaerobic bacteria that are abundant in mammalian guts. Elsewhere in the environment and in invertebrate guts, Lachnospiraceae are rarer and lacking in characterization. Two Lachnospiraceae isolates cultivated from the gut of the omnivorous model insect *Periplaneta americana* exhibited cladogenesis, with multi-locus phylogenetic and gene content analysis suggesting they diverge significantly from near neighbor taxa within the family and represent two novel genera. Whole genomes of the isolates and a group of relatives were obtained, which underwent detailed gene annotation and comparative genomic analysis. The isolates encode an array of gene products that may facilitate colonization of the insect gut environment and potentially play a role in host diet, such as those involved in plant fiber degradation, short chain fatty acid synthesis, flagellar synthesis, and mucin and chitin catabolism. For oxygen-sensitive commensal microbiota, dispersal outside the gut is largely limited to transmission between insects via coprophagy. We hypothesize that isolation within the host can lead to genetic drift that could drive allopatric speciation (as opposed to coevolution of a mutualistic relationship), resulting in cladogenesis of host-associated bacterial lineages. Further work is currently being conducted to expand the known cultivable constituents of the *P. americana* gut microbiome and their functional capabilities, and to ascertain how lineage and function of microbiota are related to support of the host.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 54 ----------

ASSOCIATIONS OF NEUROACTIVE STEROIDS & THE GUT MICROBIOME

Nivedha Senthil*[1], Elizabeth Wenzel[2], Graziano Pina[3], Unnathi Nagelli[1], Lisa Tussing-Humphreys[4], Jack Gilbert[5,6], Pauline Maki[2,3,7], Beatriz Peñalver-Bernabé[1,8]

[1] Department of Biomedical Engineering, University of Illinois, Chicago, IL, USA
[2] Department of Psychology, University of Illinois, Chicago, IL, USA
[3] Department of Psychiatry, University of Illinois, Chicago, IL, USA
[4] Department of Kinesiology and Nutrition, University of Illinois, Chicago, IL, USA
[5] Department of Pediatrics, University of California, San Diego, CA, USA
[6] Scripps Oceanographic Institute, University of California, San Diego, CA, USA
[7] Department of Obstetrics and Gynecology, University of Illinois, Chicago, IL, USA
[8] Department of Urology, University of Illinois, Chicago, IL, USA

Introduction: Several pregnancy hormones have neurological activity, such as allopregnanolone (ALLO), pregnanolone (PA), progesterone (P4), and isoallopregnanolone (ISOALLO). These hormones are called neuroactive steroids (NAS). Neurological activity and the gut microbiome are interconnected by the gut-brain axis, a bidirectional feedback communication between the brain and the gut microbiota mediated by the immune, endocrine, and neurological systems. Studies from our group show depression associated with inadequate levels of NAS and depression symptom severity associated with the dysregulation of gut microbiota. We aim to study the relationship between the gut microbiome and NAS in the first and second trimesters of pregnancy.

Method: At ~16 weeks and ~28 gestational weeks, forty-two pregnant women completed depression screening using Computerized Adaptive Diagnostic Test for Major Depression Disorder diagnostic screening tool, provided rectal swabs to assess the gut microbiome using amplicon 16S rRNA sequencing and DADA2 processing, and blood serum samples to determine the concentration of ALLO, PA, P4, and ISOALLO using targeted GC-MS. Associations between gut microbiota composition and structure with concentration levels of the NAS were done with zero-inflated generalized mixed models correcting for key covariates, including depression diagnosis, BMI, race, ethnicity, federal income, age, and gestational weeks.

Results: Allopregnanolone showed a negative association with gut microbial richness and a positive association with the volatility of gut microbiota diversity in the first trimester. At a more granular level, allopregnanolone concentrations were negatively associated with the taxa *Prevotella*, and isoallopregnanolone concentrations were negatively associated with the taxa *Ruminiclostridium* and *Subdoligranulum*. These taxa have been previously associated with neurotransmitters related to anxiety and depression, such as GABA, Dopamine, and Serotonin.

Conclusion: Our results reveal a possible association between the maternal gut microbiota and NAS and might indicate a mediation effect of the maternal gut microbiome between NAS levels and depression during pregnancy.

---------- poster no. 55 ----------

Carbon Source-Specific Regulation of Nitrogen Fixation in *Paraburkholderia xenovorans*

Abigayle Simpson*[1], Roland Wilhelm[1]

[1]Purdue University, Department of Agronomy

Paraburkholderia is a genus of metabolically diverse, nitrogen-fixing bacteria with potential use in the manufacture of biofertilizers due to their beneficial effects on plant growth. Previous research suggests that nitrogen fixation is dependent on the carbon source, with aromatics producing higher rates of nitrogen fixation than carbohydrates. This may be due to the consumption of oxygen by oxidative metabolism of aromatics, leading to microaerobic pockets that protect the oxygen-sensitive nitrogenase enzyme. The aim of this study was to determine the effect of carbon source, nitrogen concentration, and oxygen concentration on nitrogen fixation in *Paraburkholderia xenovorans* 4B. Burk's minimal media was supplemented with no nitrogen, low nitrogen, or high nitrogen, and either glucose or *p*-hydroxybenzoic acid (pHB) was provided in equimolar amounts of carbon. Cultures were incubated in sealed serum vials with a headspace of microaerobic or atmospheric oxygen concentration (0.5% and 21%) offset with dinitrogen. *P. xenovorans* growth was monitored over one month in each condition. As expected, microaerobic conditions led to lower final biomass than atmospheric conditions, and growth on pHB source led to lower biomass than glucose. The low nitrogen conditions at atmospheric oxygen concentrations exhibited diauxic growth, potentially due to the switch from ammonium assimilation to nitrogen fixation. Future work will determine the expression of nitrogen fixation genes and

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

nitrogen fixing activity, as well as carbon use efficiency in each condition. We expect there to be significant differences in expression of nitrogen fixation genes based on carbon source, and that nitrogen fixation will be higher when grown on pHB than glucose. This work can be used to develop effective biofertilizers and to provide insights into co-evolution of symbioses between plants and bacteria.

---------- poster no. 56 ----------

Eco-evolutionary patterns of virus auxiliary metabolic genes throughout the global oceans

Funing Tian*†[1,2], James M. Wainaina†[1,2], Cristina Howard-Varona[1,2], Guillermo Dominguez-Huerta[1,2], Benjamin Bolduc[1,2], M. Consuelo Gazitúa[3], Marissa R. Gittrich[1,2], Olivier Zablocki[1,2], Dylan R Cronin[1,2,10], Damien Eveillard[4,5], Kelly C Wrighton[6], Steven J. Hallam[7,8.9], Matthew B. Sullivan [1,2,10,11,12,13]

[1] Department of Microbiology, Ohio State University, Columbus, OH 43210, USA
[2] Center of Microbiome Science, Ohio State University, Columbus, OH, 43210, USA
[3] Viromica Consulting, Santiago, 8320000, Chile
[4] Université de Nantes, CNRS, LS2N, Nantes, France
[5] Research Federation for the study of Global Ocean Systems Ecology and Evolution, FR2022/Tara GO-SEE, Paris, France
[6] Department of Soil and Crop Sciences, Colorado State University, Fort Collins, CO 80523, USA
[7] Department of Microbiology & Immunology, University of British Columbia, Vancouver, BC V6T 1Z1, Canada
[8] Graduate Program in Bioinformatics, University of British Columbia, Vancouver, BC V6T 1Z4, Canada
[9] Genome Sciences Center, BC Cancer Agency, Vancouver, BC V5Z 4S6, Canada
[10] EMERGE Biology Integration Institute, Ohio State University, Columbus, OH 43210, USA
[11] The Interdisciplinary Biophysics Graduate Program, Ohio State University, Columbus, OH 43210, USA
[12] Department of Evolution, Ecology, and Organismal Biology, Ohio State University, Columbus, OH 43210, USA
[13] Department of Civil, Environmental, and Geodetic Engineering, Ohio State University, Columbus, OH 43210, USA

Microbes have impacted marine biogeochemical cycles for billions of years, but their impacts are modulated by viruses through lysis, horizontal gene transfer, and metabolic reprogramming. The latter, though challenging to quantitatively assess, might be qualitatively examined by proxy using virus-encoded auxiliary metabolic genes (AMGs) across large-scale datasets. Though AMGs are increasingly reported, no systematic meta-analysis has been done. Here we screened 7.7 terabases of Tara Oceans sequence data from paired prokaryote- and virus-enriched data to systematically catalog AMGs and placed them into ecological and evolutionary context. Modeled data revealed that two of ten virus populations carried at least one AMG, and ecosystem modeling showed that a tiny subset were predictive of environmental nutrient concentrations, including carbon, nitrate, and iron. Ecologically, the distribution of these AMGs varied largely, and reflected known oceanographic nutrient biogeography and depth stratification - presumably due to viruses being tuned to their hosts' physiologies. Separately, the evolutionary histories of AMGs that mapped to KEGG functions appear to have been acquired, often multiple times, from diverse and abundant marine microbes with most considered broad-spectrum due to being found in >1 microbial phyla. Metabolically, the broad-spectrum and specialized AMGs had comparable functions. Together, these findings improve our eco-evolutionary understanding of virus AMGs and provide baseline data for incorporating such impacts into models to assess ecosystem impacts.

---------- poster no. 57 ----------

Chemotherapy-induced changes to the gut microbiota mediate fatigue and depression-like behavior and induces neuroinflammation.

Yonaida Valentine*[1], Lindsay Strehle[1], Lauren Otto[1], Melina Seng[1], Leah M Pyter[1,2]

[1]Institute for Behavioral Medicine Research
[2]Department of Psychiatry and Behavioral Health, Ohio State University, Columbus, Ohio, USA

Every year, nearly 500,000 cancer patients in the U.S. receive chemotherapy as part of their treatment. Chemotherapy is part of the standard treatment for many cancers, as well as for some autoimmune diseases. However, chemotherapy induces cognitive and behavioral side effects that can reduce treatment compliance and thereby increase mortality. Finding the mechanisms underlying these behavioral changes is essential to identify new treatment strategies. Previously, our lab has associated chemotherapy administration in mice with gut microbial dysbiosis, inflammation, and behavioral deficits. We have shown that chemotherapy-induced changes to the gut microbiota are sufficient to induce anxiety-like behavior and neuroinflammation in germ-free mice. Here, in a more neurodevelopmentally and immunologically healthy mouse model, we ***hypothesize*** that the chemotherapy-transformed gut microbiota induces

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

fatigue, anxiety-like, cognitive dysfunction, and depression-like behavior; and induces neuroinflammation. In the present study, conventional, female, C57/Bl6J mice received an antibiotic knockdown of commensal gut bacteria (2 daily intra-gastric gavages of 1.25g/kg streptomycin) and were then randomized to receive 3 intra-gastric vehicle (Veh-) or chemotherapy (Chemo-) gut-microbial transplants (GMT; i.e., transplant of gut contents from mice that were directly injected with paclitaxel chemotherapy or vehicle treatment) over 7 days. Mice were then assessed for fatigue, cognitive, anxiety-like, and depressive-like behaviors. Brain tissue was collected to assess neuroimmune morphological and gene expression changes. Fecal samples were collected throughout the study for genomic sequencing and 16S rRNA fecal microbial profiles. Preliminary data indicate that antibiotics significantly reduced gut bacterial load, whereas GMTs significantly increased gut bacterial load. Chemo-GMT induced fatigue and depressive-like behaviors in mice. This was accompanied by increased neuroinflammation in the hippocampus (Tnfa, Tlr2, Nlrp3) and a reduction in a neuronal plasticity marker (Psd95) in the hypothalamus as measured by RT-qPCR. These results suggest that the gut microbiota may mediate behavioral deficits after chemotherapy through neuroinflammatory mechanisms.

Keywords: Gut Microbial Transplant, GMT, FMT, Conventional Mice, Antibiotics, Chemotherapy, Paclitaxel, Neuroinflammation, Fatigue, Depression

---------- poster no. 58 ----------

Sequencing SARS-CoV-2 Variants from Indoor Dust

John Van Dusen*[1], Haley LeBlanc[2], Nicole Renninger[3,4], Nicholas Nastasi[3,4,5], Jenny Panescu[4,5,6], Mike Sovic, Amanda Williams[2], Seth Faith[2], Karen C. Dannemiller[4,5,6]

[1]Department of Microbiology, College of Arts and Sciences, Ohio State University, Columbus, OH 43210
[2]AMSL
[3]Environmental Sciences Graduate Program, Ohio State University, Columbus, OH 43210
[4]Department of Civil, Environmental & Geodetic Engineering, College of Engineering, Ohio State University, Columbus, OH 43210
[5]Division of Environmental Health Sciences, College of Public Health, Ohio State University, Columbus, OH 43210
[6]Sustainability Institute, Ohio State University, Columbus, OH 43210

SARS-CoV-2 continues to spread among the global community. Vaccination efforts have reduced the spread of the virus, but SARS-CoV-2 remains a concern in our post-vaccination society. Despite global vaccination efforts, new variants are still emerging among various communities. These new variants have the potential to be more virulent, more transmissible, or even evade host immune systems, resulting in the potential for new health crises to emerge. Continued monitoring is necessary to prevent the emergence of these potential crises. Here we propose the use of indoor bulk dust samples as an effective means for monitoring SARS-CoV-2 variants. Vacuum bags were collected from the Ohio State University's Columbus Campus from April 2021 to March 2022. These samples were examined for three variants of concern: Alpha, Delta, and Omicron. Alpha was found with a 100% frequency in our earliest samples, while Delta became the primary variant from October 2021 to January 2022 with an estimated frequency of 91.09% (±1.33%) across this period. Finally, we detected the shift from Delta to Omicron in early January 2022. Omicron was the primary variant from this point up to the end of our collection period, being detected in samples with an estimated frequency of 87.04% (±3.17%). Comparisons were made between the data obtained from our dust to data collected from OSU's pandemic surveillance efforts and the US weekly confirmed cases report. The trends observed in our dust follow the same patterns observed in the data sets, supporting the hypothesis that dust can be used as an effective method for tracking SARS-CoV-2 in communities.

---------- poster no. 59 ----------

Disparities in microcosm microbial community response to salinization as the result of ionic specificity.

Paul Ayayee[1], Jon Van Gray[2]*

[1] University of Nebraska Omaha
[2]Ohio State University ATI

The salinization of lotic systems is of growing concern for global freshwater resources. The cumulative effects of landscape modifications, climate change, and urbanization have dramatically altered ionic concentrations and composition of affected systems. Due to the complexities of aquatic salt compositions, proxies for salinity, such as specific conductance, are commonly used to characterize dissolved salts concentrations. Such generalizations fail to capture the effects of ionic-specificity on ecosystem processes—many of which are facilitated by in situ microbial communities. When faced with an altered salt regime, halotolerant microbial inhabitants will likely persist and thrive

while more sensitive populations will face extirpation, often resulting in decreased structural and functional diversity of the subsequent microbial community. Whether the resulting community will continue to contribute critical ecosystem services to the impacted stream remains to be seen.
To examine the impact of salt specificity and salinization on microbial community dynamics, sterile sediments were colonized in situ in streams of similar osmotic status in both Nebraska and Ohio. Microcosms were set up in the lab using colonized sediment and stream water that had been amended with one of four salts—NaCl, Na2SO4, MgCl2, or MgSO4—or left unamended. After 4 weeks, shotgun metagenomics were used to compare the effects of salt specificity on microbial response.
Salinization resulted in significant alterations to community profiles. Shannon diversity and richness decreased in all salt treatments and at all taxonomic resolutions. Multivariate analysis identified significant differences in untreated community profiles by state of origin and by amendment type. Surprisingly, the community response to salt amendments was markedly stronger in samples originating from Nebraska. These data suggest that comparable changes in ionic concentration and specificity will result in an incongruent response of microbial communities. Moreover, the initial structural state of the impacted community may affect the strength of community response.

---------- poster no. 60 ----------

Is There a Core Microbiome of Hydroponic Cultivation Systems?

A. Viji Elango*[1], R. C. Wilhelm[1]

[1] Department of Agronomy, Purdue University, West Lafayette, IN 47907, USA

Hydroponics farming is a fast-growing industry in urban areas, providing markets with year-round local and fresh produce with optimized productivity. However, the increased adoption has shed some light on challenges related to plant and human pathogens attack, leading to economic loss and health concerns. To understand the source of undesired microbes and develop mitigation strategies, it is necessary to understand the environmental filters and sources of microbes in hydroponic systems. The microbiome of hydroponics system is expected to vary based on differences in system configuration. However, all hydroponics facilities bring in growth substrates, seed, water, and air, allowing for potential common sources of inoculum. By studying the microbes present in the various components of the system, we show that there is significant overlap between bacteria present on the built environment and plant tissues, and that these organisms commonly occur in multiple environmental reservoirs. A small subset of bacteria were only present on plant tissues. Overall, this suggests the plant microbiome in hydroponics systems is dominated by generalist organisms present in the water, or built environment. In continuation, we performed a meta-analysis of publicly available amplicon sequencing for hydroponic microbial communities to test for the presence of a “core microbiome.” The analysis also includes amplicon sequencing studies from aquaponics, and soil-based cultivation systems as a point of comparison. We consider whether the ready availability of plant nutrient alters the composition of root-associated bacteria relative to traditional soil-based systems and attempt to understand the factors that shape the microbial communities in these systems. We plan to utilize this information towards the creation of strategies to improve the resistance and resilience of these systems to colonization by pathogens.

Keywords: hydroponics, meta-analysis, microbiome

---------- poster no. 61 ----------

Comparison of cyanobacteria, cyanotoxin, and microbiomes between two harmful algal bloom-impacted drinking water sources in Ohio

Abigail Volk*, Dr. Jiyoung Lee

The Ohio State University

Cyanobacterial harmful algal blooms (cyanoHABs) are an environmental and public health threat to Ohio drinking water sources. Freshwater is also a known environmental reservoir of antibiotic resistance genes (ARGs) hosted by bacteria. Recent evidence suggests that cyanobacteria might be associated with and host ARGs. However, the relationships and significance between antibiotic resistance and cyanoHABs are unclear and may vary widely based on location and the dominant cyanobacteria species. To investigate and compare cyanobacteria, cyanotoxin, and ARG profiles in distinct water bodies, source water was collected during 2022 from Grand Lake St. Marys (Celina, OH) and Lake Erie (Toledo, OH), two water bodies with historically persistent cyanoHABs. Concentrations of cyanobacterial genes (PC-IGS for total *Microcystis*, *Microcystis mcy*E, and *Planktothrix mcy*E), ARGs (*sul*1 and *tet*Q), and mobile genetic element *intI1* (MGE) were quantified using droplet digital PCR. Total microcystin was quantified using ELISA. The cyanobacterial

microbial community was also determined using shotgun metagenomic sequencing. There were significant differences in most genes (PC-IGS, *mcy*E genes, *sul*1, and MGE) and microcystin by locations. Specifically, Toledo showed higher *Microcystis* genes, *sul*1 and MGE, while Celina showed higher *Planktothrix mcy*E and microcystin concentrations. The presence of MGE was positively correlated with *Microcystis* cyanobacterial genes. The composition of the cyanobacterial community appeared to vary by location and matched trends observed for PC-IGS and *mcy*E genes. From this analysis, Celina is dominated by *Planktothrix* and high toxin levels, while Toledo has higher *Microcystis* and ARGs. This work suggests that cyanobacteria, ARGs, and cyanotoxin profiles should be monitored together in drinking water sources, and the combined effects studied for drinking water treatment purposes.

---------- poster no. 62 ----------

The gut microbiome is predictive of chronic impaired decision-making after brain injury

Cole Vonder Haar*[1], Carissa Gratzol, Noah Bressler, Reagan L. Speas, Jenna E. McCloskey, Michelle Frankot, Michael T. Bailey, Kris M. Martens

[1]Department of Neuroscience, The Ohio State University

The gut microbiome is involved in regulating a broad variety of host processes. These include many processes that are linked to neurological function: nutrient bioavailability, inflammatory signaling, and vagus nerve communication. Traumatic brain injuries, by their very nature, cause a wide variety of neurological disturbances. However, they also induce dysbiosis in the gut. Thus, a key question is to what degree microbiome changes reflect neural impairments and to what degree they influence the evolution of injury-related pathology. Our laboratory collected several studies in rat subjects after brain injury where risky decision-making behavior was chronically assessed (2+ months, ~8-10% of lifespan). In these studies, we also collected fecal samples at various pre- and post-injury timepoints for 16S rRNA sequencing. The current poster will compare across these studies to better understand how measurements of ecological diversity in the gut can predict the long-term detrimental outcomes associated with TBI. Initial analyses show that gross measures of diversity account for variance in behavioral outcomes, even when accounting for knowledge of injury and other experimental conditions. This is a critical first step in understanding whether gut microbiome measurements may be a reasonable prognostic indicator (i.e., biomarker) and determining if this microbial community could represent a therapeutic target for psychiatric-related impairments.

---------- poster no. 63 ----------

Cryptic and abundant marine viruses at the evolutionary origins of Earth's RNA virome

Ahmed A. Zayed†[1,2,3], James M. Wainaina*†[1,3], Guillermo Dominguez-Huerta†[1,2,3], Eric Pelletier[4,5], Jiarong Guo[1,2,3], Mohamed Mohssen[1,3,6], Funing Tian[1,3], Adjie A. Pratama[1,2], Ben Bolduc[1,2,3], Olivier Zablocki[1,2,3], Dylan Cronin[1,2,3], Lindsey Solden[1], Erwan Delage[5,7], Adriana Alberti[4,5,8], Jean-Marc Aury[4,5], Quentin Carradec[4,5], Corinne da Silva[4,5], Karine Labadie[4,5], Julie Poulain[4,5], Hans-Joachim Ruscheweyh[9], Guillem Salazar[9], Elan Shatoff[10], ***Tara* Oceans Coordinators**‡, Ralf Bundschuh[6,10,11,12], Kurt Fredrick[1], Laura S. Kubatko[13,14], Samuel Chaffron[5,7], Alexander I. Culley[15], Shinichi Sunagawa[9], Jens H. Kuhn[16], Patrick Wincker[4,5], and Matthew B. Sullivan^[1,2,3,6,13]

[1]Department of Microbiology, The Ohio State University; Columbus, Ohio 43210, USA
[2]EMERGE Biology Integration Institute, The Ohio State University; Columbus, Ohio 43210, USA
[3]Center of Microbiome Science, The Ohio State University; Columbus, Ohio 43210, USA
[4]Génomique Métabolique, Genoscope, Institut François-Jacob, CEA, CNRS, Univ Evry, Université Paris-Saclay; 91000 Evry, France
[5]Research Federation for the Study of Global Ocean Systems Ecology and Evolution, FR2022/Tara Oceans GOSEE; 75016 Paris, France
[6]The Interdisciplinary Biophysics Graduate Program, The Ohio State University; Columbus, Ohio 43210, USA
[7]Université de Nantes; CNRS UMR 6004, LS2N, F-44000 Nantes, France
[8§]Université Paris-Saclay, CEA, CNRS, Institute for Integrative Biology of the Cell (I2BC); 91198, Gif-sur-Yvette, France
[9]Department of Biology, Institute of Microbiology and Swiss Institute of Bioinformatics, ETH Zurich; Zurich, Switzerland
[10]Department of Physics, The Ohio State University; Columbus, Ohio 43210, USA
[11]Department of Chemistry and Biochemistry, The Ohio State University; Columbus, Ohio 43210, USA
[12]Division of Hematology, Department of Internal Medicine, The Ohio State University; Columbus, Ohio 43210, USA
[13]Department of Evolution, Ecology, and Organismal Biology, The Ohio State University; Columbus, OH 43210, USA

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

[14]Department of Statistics, The Ohio State University; Columbus, OH 43210, USA
[15]Département de Biochimie, Microbiologie et Bio-informatique, Université Laval; Québec, QC G1V 0A6, Canada
[16]Integrated Research Facility at Fort Detrick. National Institute of Allergy and Infectious Diseases, National Institutes of Health; Fort Detrick, Frederick, MD 21702, USA.

Whereas dsDNA viruses are known to be abundant, diverse, and commonly key ecosystem players, RNA viruses are insufficiently studied outside disease settings. In this study, we analyzed ≈28 terabases of Global Ocean RNA viral sequences to expand Earth's RNA virus catalogs and their taxonomy, investigate their evolutionary origins, and assess their marine biogeography from pole to pole. Using new approaches to optimize discovery and classification, we identified RNA viruses that necessitate substantive revisions of taxonomy (doubling phyla and adding >50% new classes) and evolutionary understanding. "Species"-ranked abundance determination revealed that viruses of the new phyla "*Taraviricota*", a missing link in early RNA virus evolution, and "*Arctiviricota*" are widespread and dominant in the global oceans. These efforts provide foundational knowledge critical to integrating RNA viruses into ecological and epidemiological models.

---------- poster no. 64 ----------

Bacteroidales as a fecal contamination host indicator for accessing environmental fecal pollution

Jiangshan Wang*, Kyungyeon Ra‡

Department of Agricultural & Biological Engineering, Purdue University, West Lafayette, IN 47907

Host-associated microbiomes are essential for host health and play a critical role in various biological processes, including digestion, immune system regulation, and metabolism. Furthermore, host-associated microbiomes can be used as a biomarker to identify the sources of contamination or pollution. *Bacteroidales* is a bacterial order typically found in the animal's gut microbiota. *Bacteroidales* have adapted over time to the particular gut environment and nutrient availability in their host, enabling them to carry out their beneficial activities including generating short-chain fatty acids and digesting complex carbohydrates. Consequently, a particular species of *Bacteroidales* can serve as a fecal indicator bacterium for a certain host.
In the field of food safety, we employed this biomarker to conduct a baseline measurement surveying the background *Bacteroidales* concentration in California's Salinas Valley, a key region for fresh produce production, and to track the source of pollution. Our study discovered extremely low *Bacteroidales* concentrations in the fresh produce fields. We suggest a practical methodology for evaluating the risk of fecal contamination in a real-world setting, complementing current environmental assessment practices. Our findings offer valuable insights into the use of host-associated microbiomes in the field of food safety and can guide the development of effective strategies to prevent foodborne illness outbreaks.

---------- poster no. 65 ----------

Bacterial polysaccharides influence interspecies interactions in the mammalian gut - Research in the Wesener Group at OSU

Darryl A. Wesener*

Department of Microbiology, The Ohio State University

We are a new research group starting in the Department of Microbiology at The Ohio State University. Our research at the interface of glycobiology, microbiology, chemical biology and immunology seeks to uncover how bacterially-derived carbohydrates influence interspecies interactions in the gut. We are particularly interested in: i) whether bacterial cell surface polysaccharides, including those found in probiotic supplements, represent a nutrient reservoir in the mammalian gut that can influence gut microbial community composition, function, and stability, and ii) how specific recognition of bacterial glycans by host immunoregulatory proteins in the gut influences local and systemic immune phenotypes. We will address these questions using a combination of human-derived bacterial isolates, *in vitro* growth assays, microbial genetics, protein biochemistry, next-generation DNA/RNA sequencing, gnotobiotic mouse models, ingestible probes of biochemical function, and mass spectrometry.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 66 ----------

Intra-tumor microbes identified by RNAseq associated with response to immune checkpoint blockade in metastatic melanoma

Caroline Wheeler*[1], Sam Coleman, Rebecca Hoyd, Louis Denko, The exORIEN Consortium, AC Tan^, Dan Spakowicz^, and Ahmad Tarhini^

[1]The Ohio State University Wexner Medical Center Comprehensive Cancer Center

The tumor microbiome has recently been shown to play a key role in the context of oncogenesis, cancer immune phenotype, cancer progression and treatment outcomes in a variety of cancers. We investigated the possible associations between tumor microbiome and successful treatment outcomes with immune checkpoint blockade (ICB) in patients with metastatic melanoma.

We evaluated RNAseq from tumor samples, collected prior to the start of treatment with ICB, from 71 patients with metastatic melanoma. Samples were provided by eight members of the Oncology Research Information Exchange Network (ORIEN). The response to ICB treatment was evaluated as overall survival (>24 versus <24 months).

We applied our custom tool, {exotic} (Exogenous sequences in Tumor and Immune Cells), to carefully identify non-human sequences within the RNAseq data. After filtering reads aligning to the human reference genome, reads were further filtered of common laboratory contaminants, taxa inversely correlated with input RNA quantity, and taxa frequently found in the negative controls of microbiome experiments. A differential abundance analysis was performed on the response groups at every taxonomic level utilizing DESeq2. We calculated expression signatures using {tmesig}, and related them to ICB response using {IOSig}.

We observed significantly enriched taxa (p-value < 0.05) with a high (>1.00) fold-difference in abundance between responders and non-responders found within the tumor RNAseq data, including *Fusobacterium nucleatum* and several viruses in responders, and *Delftia lacustris* and Fungi in non-responders. These microbes were associated with immune cell expression signatures, including Th17 cells and CD8+ T-cells. We constructed a random forest classifier based on the 16 immune-activated gene signatures for which the AUROC value is 0.744. Notably, when we combine the microbe abundance and gene signatures together to develop the random forest classifier the ensemble learning random forest classifier for immune-activated gene signatures plus microbe achieved an AUROC of 0.805.

Combining tumor expression signatures with curated tumor microbiome relative abundances improves the performance of predictive models for treatment outcomes with ICB in melanoma.

---------- poster no. 67 ----------

Maternal Stress Associated With Infant Gut Microbiota in Cebu, Philippines

Rebecca C Wu*[1], Sahana Kuthyar[2], Delia B Carba[3], Thomas W McDade[1], Chris W Kuzawa[1], Katherine R Amato[1]

[1]Department of Anthropology, Northwestern University, Evanston, Illinois
[2]Department of Biological Sciences, University of California, San Diego, San Diego, California
[3]Office of Population Studies Foundation, University of San Carlos, Cebu, Philippines

Infant early-life health outcomes are impacted by maternal health in the pre- and postnatal periods. Stress related to socioeconomic factors can contribute to variable maternal health. Both maternal and infant health are tied to the composition of the gut microbiota, a collection of microorganisms in the human gastrointestinal tract that has been shown to modulate stress through the functioning of the hypothalamus-pituitary adrenal axis. Previous research has linked maternal stress to the infant gut microbiota and infant cognitive developmental issues, which often coexist with physical health problems, but associations between maternal stress, the infant microbiota, and infant physical health have not been explored directly. Using data from the Cebu Longitudinal Health and Nutrition Survey, connections between levels of maternal stress, composition of the maternal and infant gut microbiota, and infant health outcomes were investigated. Maternal stress was measured in 43 mothers using an indexed validated stress survey of 26 variables and C-reactive protein (CRP) levels from dried blood spots. Infant gut microbiota composition was determined at 2 weeks and 6 months of age using 16s rRNA gene sequencing. Results from linear mixed effects models showed a negative correlation between indexed stress levels and the Shannon diversity index at 2 weeks ($p = 0.017$) but not 6 months ($p = 0.288$) of age. Maternal CRP was associated with neither bacterial diversity nor perceived stress, highlighting the complex relationships between CRP, pregnancy, and chronic stress. These results demonstrate that

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

increased maternal perceived psychosocial stress levels are correlated with decreased microbial diversity in infant early life, providing evidence for intergenerational transmission of stress.

---------- poster no. 68 ----------

Can causal inference help us ask better questions about microbiomes?

Anthony Yannarell*

Department of Natural Resources & Environmental Sciences, University of Illinois at Urbana-Champaign

Microbiomes play important functional roles affecting the health of plants, animals, and ecosystems. Microbiome researchers are interested in how these microbial functions respond to variation in microbiome composition, especially when the microbiome changes in response to some external driver. This implies the following causal chain: "driver" " "microbiome" " "function". There is an emerging field of inquiry, called "causal inference," that seeks to understand the implications and effect sizes of these kinds of causal structures that can be expressed in the form of directed acyclic graphs (DAGs). The goal of my presentation is to introduce microbiome researchers to the basic toolkit of causal inference so that they can begin to create and analyze DAGs to help them better understand their systems. I will show that the causal framing of "driver" - "microbiome" " "function" represents a fundamental problem for microbiome research, because information about the "microbiome" blocks the causal linkage between "driver" and "function." In some of these cases, it will be more efficient to just study the "driver" and the "function," and ignore the microbiome composition altogether. This also partially explains why many microbiome studies end up only describing the "driver" " "microbiome" part of the chain. I propose some alternative framings that may lead to more profitable microbiome research. For example, causal inference can help us partition direct "driver" to "function" effects from microbiome-mediated effects, when both causal pathways are present. We can also use DAGs to identify specific microbial taxa that both respond to the "driver" and directly affect the "function." My hope is that increased use of DAGs and other tools of causal inference can help microbiome researchers design more sophisticated studies and lead to more conceptual and theoretical advances in the field.

---------- poster no. 69 ----------

Title: Different Arabinoxylan Side Chain Branch Density Mixtures Select Dominant *Bifidobacterium* or *Bacteroides* in Human Fecal Microbiota

Tianming Yao*, Anurag Pujari, Stephen Lindemann
Whistler Center for Carbohydrate Research, Department of Food Science, Purdue University, West Lafayette, Indiana, USA

Complex glycan linkage structures govern microbial fermentation responses due to the diverse hydrolytic enzymes required and which differ in bacteria from discrete taxa. In a prior study, we demonstrated that an isolated, highly branched sorghum arabinoxylan (NSAX) sustained a consortium dominated by members from family Lachnospiraceae and genus *Bifidobacterium*, whereas a partially debranched sorghum arabinoxylan (DBSAX) promoted a *Bacteroides*-rich community. However, it is unclear whether these stringent microbial selection patterns would be linearly influenced by varying degrees of substrate branching or whether stochastic microbial responses would lead the fermentation outcomes when degree of branching varies (e.g., NSAX and DBSAX offered together). Herein, we performed a 7-day sequential fecal fermentation on NSAX and DBSAX mixtures; namely pure NSAX, 75% NSAX plus 25% DBSAX, 50% NSAX plus 0% DBSAX, 25% NSAX plus 75% DBSAX and pure DBSAX. Our original thought was to employ mixes at varying ratios to represent different branching degrees of fermenting AX substrates. Microbial succession trajectories were then tracked daily by sequencing the 16S rRNA gene to uncover substrate-driven differences in microbial succession. Our findings consistently indicated that a larger proportion of bare xylan backbone AX with fewer branches supports a higher diversity of Bacteroidales spp., and their abundances varies with the initial amount of DBSAX in the combination. On the other hand, higher numbers and populations of *Bifidobacterium* spp. and Firmicutes species were selected by more heavily branched NSAX. Those patterns were demonstrated across the three different donors' initial fecal microbiota investigated. Overall, this study supports the hypothesis that complex polysaccharide fine linkage types can be mixed to deterministically drive the composition and metabolism of human fecal microbiota in a predictable way, forming a foundation for design and development of novel prebiotic fibers that target desired microbial structures in the host.

* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

---------- poster no. 70 ----------

A Meta-Analysis of Diversity-Disease Relationships in the Human Microbiome

Fahren R. Zackery*, Eliza M. Grames, Brian F. Allan

University of Illinois Urbana Champaign

In nature, increased species diversity often leads to a lower prevalence of infectious disease. Many mechanisms have been proposed to explain such diversity-disease relationships in nature, such as transmission reduction by which the probability of a pathogen encountering a susceptible host is reduced with increased species diversity, or susceptible host regulation by which diversity acts to reduce the density of susceptible hosts. The human microbiome has been studied extensively concerning its role in disease outcomes, however, it has not been studied as broadly from an ecological perspective. My research bridges this gap by assessing *evidence for diversity-disease relationships in the human microbiome and if increased microbial diversity is associated with reduced disease in humans?* If diversity-disease relationships operate similarly in the human microbiome as in nature, then I predict to observe more negative relationships than positive relationships between microbial diversity and human health outcomes.
To test this hypothesis, I performed a meta-analysis to quantitatively synthesize the relationship between microbial diversity and human health outcomes across hundreds of individual studies. Preliminary results from a random-effects meta-analysis of studies of the gastrointestinal microbiome show support for negative diversity-disease relationships in the human microbiome, with a mean estimated effect of –0.23 (95% CI: -035, -0.12) for the Shannon index, –0.13 (95% CI: -0.40, 0.15) for Chao1, and –0.18 (95% CI: -0.36, 0.01) for species richness. Understanding whether and how microbial diversity affects human disease will not only help advance our understanding of diversity-disease relationships, but also have implications for human health. In addressing this question, I will advance research into the functional roles of the human microbiome for human health by integrating fundamental principles from community ecology.

---------- poster no. 71 ----------

Glacier preserves ecological and evolutionary history of viruses over the past >45,000 years

ZhiPing Zhong*[1], Olivier Zablocki, Ann C. Gregory, Yueh-Fen Li, James L. Van Etten, Ellen Mosley-Thompson, Virginia I. Rich, Matthew B. Sullivan, & Lonnie G. Thompson

[1]Byrd Polar and Climate Research Center, Ohio State University

Glaciers archive time-structured information, including bacteria and their viruses that illuminate ancient ecosystem functioning and yet are understudied due to methodological challenges. Here we augmented known glacier-preserved ancient viruses (GPAVs) ~51-fold by recovering 1,706 vOTUs (~species-level virus operational taxonomic units) across 9 depths spanning >45,000 years from a 310-meter ice core and assessed their eco-evolutionary stories. Biogeographically, GPAVs appear endemic to glacial regions and to have impacted ecosystems via preying upon dominant microbes, mediating gene transfers, and modulating functions including carbon, amino acid, and cofactor and vitamin metabolisms before being preserved. Meta-community analyses revealed potential community-paleoclimate linkages and an enrichment of historically-persistent viruses, while evolutionary investigations found that species' genetic variations imply generalists/specialists, unveil virus-host arms-races, and may empirically document virus speciation and niche differentiation through time. This study provides a foundation for beginning to understand GPAVs and highlights their potential ecological impacts before being frozen and their evolutionary histories through tens of thousands of years.
Key Words: Ancient virus; Glacier; Evolution; Microdiversity; Ecology; Metagenome; Tibetan Plateau; Guliya ice cap

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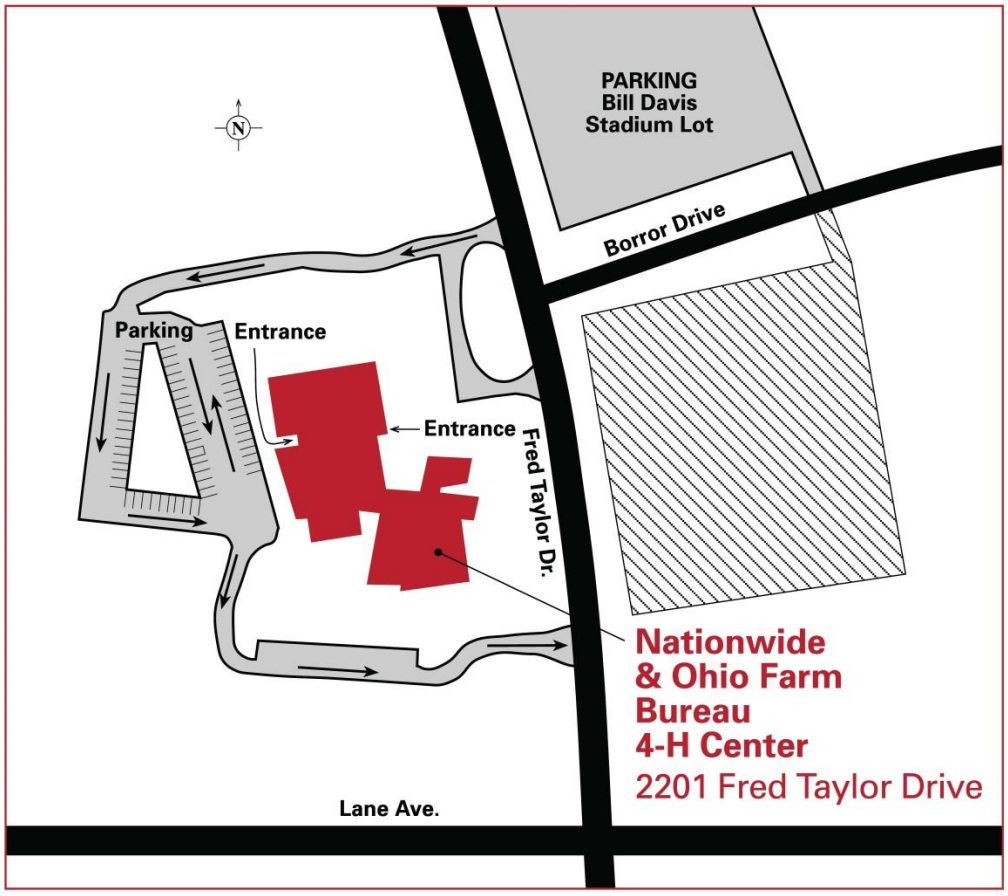
* Presenter
† These authors contributed equally to this work
^ Corresponding author
‡ Co-authors

Nationwide & Ohio Farm Bureau 4-H Center

Parking Information

Ohio State University Extension, 4-H Youth Development
2201 Fred Taylor Dr., Columbus, OH 43210
614-247-6904, www.ohio4-hcenter.org

- Parking is available at the 4-H Center and across Fred Taylor Drive in the Bill Davis Stadium Lot.
- The 4-H Center lot has 57 available parking spaces and 3 handicap spaces.
- Please make sure you completely understand OSU parking restrictions and availability including other events that may be scheduled in the facility and at nearby venues.
- Park only on pavement and in designated spaces. No parking on grass, gravel road or in gated area of arboretum grounds.
- One way only entry at the north driveway and one way exit by use of the south exit.
- Please use the east circular drive for drop off and pick up only. No parking on this drive.
- Your parking permit should be attached to the email from the Midwest Microbiome Symposium. Additional passes will be available in the building.



Wifi and Logins

Ready to Connect? : Technology Services (osu.edu)

Ready to Connect?

Ohio State is pleased to offer both wired and wireless options for connecting a variety of your digital devices.

Follow the simple steps below to connect your device to one of our high speed networks.

Wireless Network Connection

For Laptops, Desktops, Smartphones and Tablets

1. Connect to the **WiFi@OSU** network. A login page should automatically open.
2. Click on **Connect to eduroam** on the login page. (If the login page does launch automatically, open a web browser and go to wireless.osu.edu to be redirected to the login page.)

Exploring Columbus

Getting around:

Uber and Lyft will get you everywhere you need, with average fare around the city of ~$10-$15. A ride share trip to the closest airport (John Glenn International – CMH) to the Ohio Union, goes between $20-$35. There is also a bus service running around Columbus as well as to/from the airport. The bus service is called COTA and you can conveniently pay for rides (~$2) using the 'universal' 'Transit' app directly from your smartphone.

Sightseeing, eats and bars

Thanks to **Experience Columbus** for the following community information:

Ohio's state capital, Columbus, is a vibrant city teeming with things to see and do. There is a strong experimental cuisine scene here, as well as countless microbreweries and coffee shops to experience. Given the short time frame, we encourage you to explore the Short North—the trendiest side of town that has a great diversity of stores and place to eat and drink. Most places are along High Street, and you can easily walk from free campus bus stops (CABS service) to High Street.

Short North Arts District | Neighborhoods in Columbus
Lighted arches over High Street mark the Short North Arts District. From murals to revitalized warehouses, this neighborhood celebrates creative energy.

Campus & Clintonville
The University District, home to The Ohio State University, can be found north of the Short North Arts District. The area is a hub for diverse arts and culture, beloved local bars and restaurants, and sporting and concert facilities, like the Shoe (Ohio Stadium) and the Schott (the Schottenstein Center).

North of the University District lies Clintonville, a residential neighborhood you may recognize as the home of the popular and beautiful Whetstone Park of Roses .
Clintonville's location means its neighborhood-focused community has businesses and love for everyone, from longtime residents and families to young professionals and recent grads. Whether exploring its unique local coffee shops, breweries, restaurants and shops or looking to settle down, Clintonville is a charming area with something for everyone.

Grandview
Just minutes west of downtown but embodying both small-town and urban vibes, the Grandview community is close-knit and friendly, and people of all ages and walks of life call this walkable area home. Grandview boasts many small businesses, from event venues and boutiques to craft beer and coffee.

Local Hotel Accommodations

Red Roof Plus+
441 Ackerman Rd.
Columbus. OH 43202
614-267-9941
redroof.com/property/oh/colum_bus/R_I121

Residence Inn by Marriot - University Area
3100 Olentangy River Road
Columbus. OH 43202
614-261-7994
https://www.marriott.com/search/hotelQuickView.mi?propertyId=CMHRN&brandCode=RI&marshaCode=CMHRN

The Varsity Inn
1445 Olentangy River Rd.
Columbus, OH 43212
614-291-2983
Toll free: 1-886-678-8277
https://www.olentangymotorinn.com.

The Westin Great Southern Columbus
310 S High St
Columbus. OH
43215
614-228-3800
marriott.comfl}otels/trave!Lcmhwi-the-westin-great-southern-_columbus

The Blackwell
2110 Tuttle Park Place
Columbus, OH 43210
614-247-4000
Toll free: 866-247-4003
https://www.theblackwell.com/

Hampton Inn and Suites University Area
3160 Olentangy River Rd.
Columbus, OH 43202
614-268-8700
https://www.hilton.com/en/hotels/cmhunhx-hampton-suites-columbus-university-area/

Hilton Garden Inn - University Area
3232 Olentangy River Road
Columbus, OH 43202
614-263-7200
https://www.hilton.com/en/hotels/cmhuagi-hilton-garden-inn-columbus-university-area/

Holiday Inn Express & Suites
3045 Olentangy River Rd.
Columbus. OH 43202
614-447-1212 Toll Free: 1-888-465-4329
ihg.com/holidayjnnexpress/hotels/_us/eo/CQLIfil'll?Us/cmhol/

Springhill Suites by Marriott
1421 Olentangy River Rd.
Columbus. OH 43212
614-297-9912
https://www.marriott.com/en-us/hotels/cmhos-springhill-suites-

Holiday Inn Express & Suites
3045 Olentangy River Rd.
Columbus. OH 43202
614-447-1212
Toll Free: 1-888-465-4329

Springhill Suites by Marriott
1421 Olentangy River Rd.
Columbus. OH 43212
614-297-9912

Aloft Columbus University District
1295 Olentangy River Road
Columbus, Ohio 43212
614-294-7500
marriott.com/hotels/travel/cmhco-aloft-columbus-university-district

Comfort Suites
1690 Clara ST.
Columbus OH 43211
614-586-1001
_1Joicehotels.c9m/ohio/columbus omfort-suites-hotelsjQ_h2<U?mc=l_lgoxxp

Drury Inn & Suites Columbus Convention Center
88 E Nationwide Blvd
Columbus, OH 43215
614-221-7008
druryhotels.com/locations/columbus-oh/drury-inn-and-suites-columbus-convention-center

Fairfield Inn and Suites by Marriott
3031 Olentangy River Rd. Columbus,
OH 43202
614-267-1111
https://fairfield.marriott.com/

Graduate Columbus
750 N High St Columbus,
OH 43215
614-484-1900
https://www.graduatehotels.com/

Sampling of Area Food, Shopping & Activities

Lennox Town Center

1755 Olentangy River Road .69 miles 1 minute

Go west on Vernon Tharp St. Turn left onto John Herrick Dr. Go to the first light and turn right onto Olentangy River Rd. Go straight into Lennox Town Center.

Food: Bravo! Cucina Italiana
Champps Americana (varied menu)

Shopping:

Barnes & Noble	Old Navy
Bath & Body Works	Petco
Famous Footwear	Staples
Marshall's	Target
Men's Wearhouse	World Market

Activity: Phoenix Theatres Entertainment
IMAX with Laser
phoenixtheatres.com/location/3341/Lennox-Town-Center-24-Theatres

The Shops on Lane Avenue

1585 West Lane Avenue 1.78 miles 4 minutes

Go west on Vernon Tharp St. Turn right onto John Herrick Dr. First light turn left onto Woody Hayes Dr. First light turn right onto Kenny Rd. First light turn left onto Lane Ave. The Shops on Lane are 1.3 miles on the left.

Food:

- Bruegger's Bagels
- Carsonie's Stromboli &Pizza Kitchen
- Cheryl's Cookies Freeze Style Ice Cream
- The Original Pancake House Rusty Bucket
- SOW Plated
- Whole Foods Market
- Piada (Italian)
- Subway
- Starbucks
- Brassica
- Tommy's Pizza
- Graeter's Ice Cream
- La Chatelaine
- Fukuryu Ramen
- Hudson 29 Kitchen
- The Wine Bistro

Restaurants on Olentangy River Road South

Go west on Vernon Tharp St. Turn left onto John Herrick Dr. Go to the first light and turn right onto Olentangy River Rd. At the light turn left which is the continuation of Olentangy River Rd

Brenz Pizza	1.0 miles	4 minutes
Nothing Sundt Cakes	1.0 miles	4 minutes
Starbucks	1.0 miles	4 minutes
Zoup!	1.0 miles	4 minutes
Wendy's & Tim Hortons	1.1 miles	4 minutes
Bob Evans	1.1 miles	4 minutes
Cap City Diner	1.3 miles	6 minutes
Columbus Fish Market	1.4 miles	6 minutes

Restaurants on Lane Avenue

Panera Bread	300 W. Lane Ave. -north side
Tai's Asian Bistro	1285 W. Lane Ave. -south side
Pho Asian Noodle House	1288 W. Lane Ave. -north side
Jersey Mike's Subs	1293 W. Lane Ave. -south side
Moe's Southwest Grill	1305 W. Lane Ave. -south side
Wings Over	1315 W. Lane Ave. -south side

Sampling of Area Food and Shopping, continued

Restaurants on Olentangy River Road

Approximately 8 minutes

Raising Cane's (chicken)	**2823** Olentangy River Rd.
Ali Baba Gyros Food Truck	**2825** Olentangy River Rd.
McDonald's	**2865** Olentangy River Rd.
Skyline Chili	**2995** Olentangy River Rd.
Wingstop	**3005** Olentangy River Rd.
Hy Asian Cuisine	**3011** Olentangy River Rd.
Denny's	**3025** Olentangy River Rd.
El Vaquero (Mexican)	**3230** Olentangy River Rd.
Garden Grill (Hilton)	**3232** Olentangy River Rd.
Sonic	**3250** Olentangy River Rd.
Rooster's	**3370** Olentangy River Rd.

Giant Eagle Market District Grandview Yards

840 W 3rd Avenue 43212 2.2 miles approximately 10 minutes

Unique 97,000 *square foot culinary dining and shopping experience. Offering foods from around the world plus live cooking demonstrations. Departments include bakery, fresh meat, fresh seafood, prepared foods, produce, cheese/ charcuterie (400 varieties), sweets shop, health/beauty/wellness, housewares, beer/microbrews, deli, wine, oil/ vinegar/antipasto bar and the international foods section.*

FUNNYBIOME

An Improv Comedy Show

Tuesday, May 9th, 2023 7:30 pm

Doors open at 7 pm.

Shadowbox Theatre – 503 S Front St #260, Columbus, OH

Love microbes? Wanna learn more about them?? You're in the wrong place. Come for the drinks and stay for the laughs as a panel of (non) experts – The Bunsen Burnouts – engages your funnybiome.

Visit Funnybiome - Up Front Performance Space (upfrontps.org) to purchase tickets ($15).