

EVENT PROGRAM

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2018 Nebraska Research & Innovation Conference

**MICROBIOMES FROM
DIFFERENT HABITATS:
SOIL, WATER AND GUT**

OCTOBER 16-17 | LINCOLN, NEBRASKA





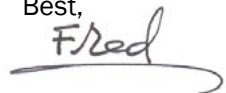
Message from the Nebraska EPSCoR Director

Welcome to the 2018 Nebraska Research & Innovation Conference (NRIC)! Thank you to our speakers for sharing their time and expertise with us, and thanks to program chair Daniel Schachtman for recruiting this excellent slate of speakers.

This event extends an annual series of conferences and symposia that Nebraska EPSCoR has been organizing to advance research activities in this state. This year's conference connects to Nebraska's Center for Root & Rhizobiome Innovation (CRRRI), a five-year project funded by the National Science Foundation.

In CRRRI's Year 3, this symposium gathers leaders from academia and industry, with international perspectives and regional connections at the forefront.

Please enjoy NRIC's knowledge transfer and networking opportunities, and be sure to visit Tuesday's poster session for a look at this area's exciting future.

Best,


F. Fred Choobineh, Ph.D., P.E.
 Director, Nebraska EPSCoR
 Blackman Distinguished Professor of Electrical Engineering, UNL

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NRIC 2018 | MICROBIOMES FROM DIFFERENT HABITATS: SOIL, WATER AND GUT

AGENDA

WiFi Network: Embassy Mtg | Username: microbiomes | Password: neepscor

DAY 1 - Tuesday, October 16

7:30 am Conference materials pick up and continental breakfast
8:30 am WELCOME | Fred Choobineh & Daniel Schachtman

8:50 am - 12:30 pm | Sessions Chair: Daniel Schachtman, University of Nebraska-Lincoln

8:50 am I contain multitudes: Telling stories about microbes and the people who study them | Ed Yong
9:40 am Searching for simplicity amidst the complexity of the soil microbiome | Noah Fierer
10:30 am BREAK
10:50 am A web of interactions shapes the soil microbiome | Mary Firestone
11:40 am Microbial life in soil and deciphering the signatures of niche adaptation | Eoin Brodie
12:30 pm LUNCH

1:30 - 4:25 pm | Sessions Chair: Karrie Weber, UNL

1:30 pm Forming a groundwater microbiome: Go with the flow and find a niche | Kirsten Küsel
2:20 pm BREAK
2:45 pm Microbes, fluids and rocks: Life beneath the seafloor | Julie Huber
3:35 pm Methanogenesis in soils: It may not be as deep as we all thought | Kelly Wrighton
4:30-6:30 pm POSTER SESSION AND RECEPTION

On Twitter, follow #NRIC18, @NebraskaEPSCoR and @NE_CRRI.

FOR DAY 2 (WEDNESDAY) AGENDA, SEE NEXT PAGE



NRIC 2018 | MICROBIOMES FROM DIFFERENT HABITATS: SOIL, WATER AND GUT

AGENDA

WiFi Network: Embassy Mtg | Username: microbiomes | Password: neepscor

DAY 2 - Wednesday, October 17

7:30 am Conference materials pick up and continental breakfast

8:40 am Opening Remarks | Mike Boehm

8:50 am - 10:30 am | Sessions Chair: Karin van Dijk, University of Nebraska-Lincoln

8:50-9:35 am Perturbing the microbiota of early life and its consequences | Martin Blaser

9:40 am Can we use bugs as drugs? Restoring the gut microbiota with 'Microbial Ecosystem Therapeutics' | Emma Allen-Vercoe

10:30 am BREAK

10:50 am - 12:30 pm | Sessions Chair: Erin Doyle, Doane University

10:50 am The effects of antibiotics and pesticides on the gut microbiome and health of honeybees | Kasie Raymann

11:40 am Can the plant mycobiome serve as a tool for improving grass stress resistance? | Christine Hawkes

12:30 pm LUNCH

1:30 - 4:00 pm | INTERACTIVE SCIENCE COMMUNICATION WORKSHOP

Critical skills for talking to the media: How to prepare for an interview and win public trust
Sandra Blakeslee & Mary-Charlotte Domandi

On Twitter, follow #NRIC18, @NebraskaEPSCoR and @NE_CRRI.



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TUESDAY, OCTOBER 16

WELCOME

FRED CHOUBINEH, Nebraska EPSCoR

DANIEL SCHACHTMAN, University of Nebraska-Lincoln

8:30 A.M.

8:50 - 12:30 P.M.

SESSIONS CHAIR

DANIEL SCHACHTMAN, UNL

I contain multitudes: Telling stories about microbes and the people who study them

ED YONG, The Atlantic

8:50 A.M.

ABSTRACT: The microbial world is endlessly fascinating to those who study it, but a source of fear and disgust to most people. Ed Yong, author of the New York Times bestselling book *I Contain Multitudes* will show how to bridge that gap by telling stories about the microbiome, providing an insider's look at how science writers craft their pieces, and examining why storytelling is crucial to science.

BIO: Ed Yong is a science journalist who reports for The Atlantic, and is based in Washington DC. His work appears several times a week on The Atlantic's website, and has also featured in National Geographic, the New Yorker, Wired, Nature, New Scientist, Scientific American, and many more. He has won a variety of awards, including the Byron H. Waksman Award for Excellence in the Public Communication of Life Sciences in 2016, and the National Academies Keck Science Communication Award in 2010. *I CONTAIN MULTITUDES*, his first book, became a New York Times bestseller and inspired an online film series, an anthology of plays, and a clue on Jeopardy! Ed has a Chatham Island black robin named after him.

Searching for simplicity amidst the complexity of the soil microbiome

NOAH FIERER, University of Colorado at Boulder

9:40 A.M.

ABSTRACT: Soils harbor diverse microbial communities, including large numbers of taxa that remain undescribed despite their importance to terrestrial biogeochemical cycles and other ecosystem properties. With recent methodological advances, we can gain unprecedented insight into the diversity of soil microbial communities. I will discuss a series of studies where we have been exploring the structure and function of soil microbial communities, and specific microbial taxa, across spatial scales ranging from the local scale (Central Park in New York City) to the continental scale (all of North America). These studies demonstrate that, despite their complexity, soil microbial communities and their functional attributes are often predictable. We can now begin charting the enormous amount of biodiversity that exists belowground and identifying the specific traits that allow microbes to cope with the biotic and abiotic challenges of living in the soil environment.

BIO: Noah Fierer, Ph.D., is an Associate Professor in the Department of Ecology and Evolutionary Biology, and a Fellow of the Cooperative Institute for Research in Environmental Sciences, at the University of Colorado at Boulder. He is a microbial ecologist and his research program focuses on microbes living in a range of environments, including those bacteria, fungi, and protists living inside our homes, in soil, on plants, and in the atmosphere. His group uses various approaches, including DNA sequencing and high-throughput cultivation, to explore the diversity and structure of microbial communities, identify the fundamental controls on microbial processes, and examine the mechanisms by which microorganisms influence the health of ecosystems, plants, and animals (including humans). For more information, see: <http://fiererlab.org>.



NRIC 2018 | MICROBIOMES FROM DIFFERENT HABITATS: SOIL, WATER AND GUT

A web of interactions shapes the soil microbiome

MARY FIRESTONE, University of California, Berkeley

10:50 A.M.

ABSTRACT: Soil microbiomes comprise the most diverse and complex assemblages of organisms on earth reflecting the heterogeneity of their habitat and the array of interactions that shape them. Introduction of ^{13}C into soil facilitates definition of complex web of biotic interactions through isotope-enabled genomics and genome-resolved metagenomics that reveal phage, bacterial, fungal, and faunal participants; food-web and network modeling identify and quantify guilds. Resulting data indicate that the development of rhizosphere-competent bacterial consortia support production of “rhizosphere” phage populations. The physical separation of nematodes and protists from soil requires gradient centrifugation and size selection by differential filtration. DNA extraction and barcode analyses have yielded 50-70% faunal sequences. Nematode and protist densities have been assessed in bulk and rhizosphere. Predicted functional roles of these guilds suggest direct root feeding and bacterial and fungal predation. Functional predictions are being evaluated using isotopic methods.

BIO: Mary Firestone, Ph.D., is a microbial ecologist who has worked extensively on the roles of soil microorganisms in terrestrial ecosystem function. She is known for her work on nitrogen oxidation and reduction processes, adaptation of microbes to the soil drying, and carbon- and nitrogen-based interactions among plant roots and soil organisms. The extreme heterogeneity of soil and the scale at which microorganisms interact with their habitat has made understanding the ecology of soil microbes a challenge. Her program has brought to bear expertise in microbiology, biogeochemistry, ecosystem science, and community ecology; her work has been recognized by a range of disciplines: she is a fellow of the Soil Science Society of America, American Academy of Microbiology, Ecological Society of America, and American Geophysical Union. Mary was elected to the National Academy of Sciences in 2017.

Microbial life in soil and deciphering the signatures of niche adaptation

EWIN BRODIE, Lawrence Berkeley National Laboratory

11:40 A.M.

ABSTRACT: Soil is an archetypal complex system, with physical and chemical heterogeneity co-evolving with biology to create abundant metabolic and physiological niches for soil microorganisms to survive and thrive. Recognizing the genetic complexity of soil microbiomes, there is a need to derive generalizable principles regarding the drivers of microbial functional diversity in soil and their interactions with microbial traits. Deriving these principles and approaches to evaluate them is a necessary step towards building predictive models of soil microbiome activity. In this presentation I will discuss several advances in illuminating microbial functional traits in soil and a framework to incorporate this new knowledge into mechanistic models of soil biogeochemistry.

BIO: Eoin Brodie obtained his Ph.D. from University College Dublin in Ireland and joined Berkeley Lab following postdoctoral research at the University of California, Berkeley. At Berkeley Lab he is Deputy Director of the Climate and Ecosystem Sciences Division. His research focuses on the feedbacks between microorganisms and their natural environments, with a primary focus on soil and subsurface systems scaling from microbial mechanisms to ecosystem scale processes.

1:30 - 4:25 P.M.

SESSIONS CHAIR

KARRIE WEBER, UNIVERSITY OF NEBRASKA-LINCOLN



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Forming a groundwater microbiome: Go with the flow and find a niche

KRISTEN KÜSEL, University of Jena

1:30 P.M.

ABSTRACT: The terrestrial deep biosphere hosts up to 20% of the earth's biomass. Within AquaDiva, we aim to understand the links between the surface and subsurface biogeosphere. To achieve this, we have constructed a novel infrastructure, the Hainich Critical Zone Exploratory, which allows us to access groundwater and aquifer rock material from oligotrophic limestone aquifers along with soil and seepage from the respective groundwater recharge areas. We tracked the formation of the groundwater microbiome and the differentiation of the predominant Cand. Patescibacteria. Network and correlation analysis allowed us to postulate different biological and hydrochemical drivers for community assembly. By comparing the stable and radiogenic carbon isotope compositions of phospholipid-derived fatty acids (PLFAs) with those of the potential microbial carbon sources, we determined that subsurface microbiomes appeared to assimilate up to 70% ancient organic matter. These signatures challenge the current paradigm and point to an intensive internal cycling of carbon independent of surface input.

BIO: Kristen Küsel studied Geocology with a focus on hydrology, geochemistry and soil science before she entered the fascinating field of environmental microbiology to start a Ph.D. under the supervision of Harold L. Drake at University of Bayreuth, Germany, in 1992. During her postdoc time she focused on diversity, function and adaptation strategies of anaerobic bacteria at oxic-anoxic gradients in soils, freshwater and marine sediments. In 2004 she became Professor for Limnology and later Full Professor for Aquatic Geomicrobiology at University of Jena which allows her to combine the fields of microbiology and geoscience. She is also a founding Director of the German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, a research centre with approximately 300 employees and members with the mission to establish the scientific basis for the sustainable management of our planet's biodiversity.

Microbes, fluids and rocks: Life beneath the seafloor

JULIE HUBER, Woods Hole Oceanographic Institution;
NSF Science and Technology Center for Dark Energy
Biosphere Investigations

2:45 P.M.

ABSTRACT: Exploration of the sea over the last 40 years has resulted in astounding discoveries about the extent and diversity of life in the deep ocean, pushing our understanding of the intimate connections between the biosphere and geosphere to the extremes, including the discovery of chemosynthetic ecosystems at hydrothermal vents and active microbes buried in sediments, kilometers beneath the seafloor. This lecture will focus on microbial communities in the largest actively flowing aquifer system on Earth, the fluids circulating through oceanic crust underlying the oceans and sediments, and include recent discoveries and the technology that enabled such discoveries at both well-studied underwater volcanoes and completely novel and unexplored systems, including the worlds' deepest hydrothermal vents.

BIO: Julie Huber, Ph.D., is an oceanographer by training and is broadly interested in how basic earth processes- rocks forming, fluids moving, sediments accumulating- interact to create and maintain life in the oceans. Her research addresses some of the most central questions about the nature and extent of microbial life on Earth in one of its least explored corners, the subseafloor habitat beneath the ocean floor. Julie received her B.S in Marine Science from Eckerd College in 1998 and her Ph.D. from the University of Washington in 2004. In 2007, she received the L'Oréal USA Fellowship for Women in Science. Beyond her duties as an Associate Scientist in Marine Chemistry and Geochemistry at Woods Hole Oceanographic Institution, Julie also serves as the Associate Director of the NSF Science and Technology Center for Dark Energy Biosphere Investigations (C-DEBI), whose mission is to explore life beneath the seafloor and make transformative discoveries that advance science, benefit society, and inform and inspire the general public about discoveries in ocean sciences and related disciplines. You can find her on Twitter @julesdeep.



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Methanogenesis in soils: It may not be as deep as we all thought

KELLY WRIGHTON, Colorado State University

3:35 P.M.

ABSTRACT: The current paradigm, widely incorporated in soil biogeochemical models, is that microbial methanogenesis can only occur in anoxic habitats. In contrast, here we use porewater and greenhouse-gas flux measurements to show clear evidence for methane production in well-oxygenated wetland soils. A comparison of oxic to anoxic soils revealed up to ten times greater methane production and nine times more methanogenesis activity in oxygenated soils. Metagenomic and metatranscriptomic sequencing recovered the first near complete genomes for a novel methanogen species, and showed acetoclastic production from this organism was the dominant methanogenesis pathway in oxygenated soils. This organism, *Candidatus Methanosaeta oxydurans*, is prevalent across methane emitting ecosystems, suggesting a global significance. Moreover, in this wetland, we estimated that a dominant fraction of methane fluxes could be attributed to methanogenesis in oxygenated soils. Together our genomic enabled findings challenge a widely-held assumption about methanogenesis, with significant ramifications for global methane estimates and Earth system modeling.

BIO: Kelly Wrighton is an Assistant Professor of Soil and Crop Science at Colorado State University. Her laboratory uses multi-omic data coupled with anaerobic physiological methods to interrogate microbial metabolic interactions in soils, subsurface, and gut ecosystems.

POSTER SESSION & RECEPTION

4:30- 6:30 P.M.

FOR A LIST OF PRESENTERS, PLEASE SEE LATTER PAGES OF THIS PROGRAM.

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NEBRASKA INNOVATION CAMPUS

WEDNESDAY, OCTOBER 17

DAY 2 OPENING REMARKS

MIKE BOEHM, University of Nebraska-Lincoln

8:40 A.M.

8:50 A.M. - 10:30 A.M.

SESSIONS CHAIR

KARIN VAN DIJK, University of Nebraska-Lincoln



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Perturbing the microbiota of early life and its consequences

MARTIN BLASER, New York University School of Medicine

8:50 A.M.

ABSTRACT: There is strong evidence for inheritance of an important proportion of the microbiota. These early life organisms play roles in the host's metabolic, immunological, and cognitive development. Antibiotics perturb both the microbiome and development, which may lead to long term consequences. We are studying the nature of the perturbations, and their effects, and examining ways to restore healthy development. This continues to grow as an innovative STEM learning tool in the nation's P12 schools, with many projects funded by the National Science Foundation to bring new ideas and creativity into this powerful learning platform. Many instructional applications are "bioinspired", such using mechanical linkages to model animal movement, using swarming robots to represent bird flocking behavior, and monitoring wildlife with robots. New 3D printing capabilities have also facilitated connections to P12 STEM learning. This presentation will tour various NSF funded educational robotics efforts that may well open the doors to an increased student interest in biomechanics study and careers.

BIO: Martin J. Blaser is the Muriel and George Singer Professor of Medicine, Professor of Microbiology, and Director of the Human Microbiome Program at the NYU School of Medicine. He served as Chair of the Department of Medicine at NYU from 2000-2012. He is both a doctor and a scientist. Over the course of his career, Dr. Blaser has served as the advisor for a large number of students, post-doctoral fellows, and junior faculty. In his scientific work, Dr. Blaser has been studying the relationships we have with the bacteria that live in the human body as well as invaders that make us ill. Over the last 20 years, he has been actively studying the relationship of these bacteria with such important diseases as asthma, obesity, diabetes, allergies, kidney stones, and cancer. He served as the President of the Infectious Diseases Society of America, Chair of the Board of Scientific Counselors of the National Cancer Institute, and as Chair of the Advisory Board for Clinical Research of the National Institutes of Health. Appointed by President Obama, he is the Chair of the Presidential Advisory Council for Combating Antibiotic Bacteria (PACCARB). He was elected to the National Academy of Medicine and to the American Academy for Arts and Sciences. He holds 28 U.S. patents relating to his research, and has authored over 500 original scientific and medical articles. Recently, he wrote *Missing Microbes*, a book targeted to general audiences, now being translated into 20 languages, and the recipient of the 2017 Wenjin Book Award from the National Library of China.

Can we use bugs as drugs? Restoring the gut microbiota with 'Microbial Ecosystem Therapeutics'

EMMA ALLEN-VERCOE, University of Guelph; NuBiyota

9:40 A.M.

ABSTRACT: The human gut microbiota is now recognized to be extremely important in the maintenance of human health, yet there are many aspects of modern living that erode its diversity and function with potential implications in many diseases. Fecal microbial transplants are quickly gaining attention in the clinical sphere as a way to replace missing microbes and restore functions that may have been lost. However, it is extremely difficult to regulate stool-based medicine, and the practice is not without risk. In this talk I will discuss our efforts to create pure microbial ecosystems derived from the gut and to develop these as novel therapeutics, as a potential way to improve the safety and palatability of the approach.

BIO: Emma Allen-Vercoe, Ph.D., obtained her BSc (Hons) in Biochemistry from the University of London, and her Ph.D. in Molecular Microbiology through an industrial partnership with what is now Public Health England. Her lab at the University of Guelph focuses on trying to culture the so-called 'unculturable' microbes of the human gut in order to better understand their biology. To do this, she developed a lab specializing in anaerobic bacteriology along with a model gut system (dubbed 'Robogut') to emulate the conditions of the human gut and allow communities of microbes to grow together, as they do naturally. Emma holds a University Research Leadership Chair and her lab currently runs many projects that are broad in nature, but united under the banner of human microbiome research. In 2013, Emma co-founded NuBiyota, a research spin-off company that aims to create therapeutic ecosystems as biologic drugs, on a commercial scale. The research enterprise for this company is also based in Guelph.

10:50 A.M. - 12:30 P.M.

SESSIONS CHAIR

ERIN DOYLE, Doane University



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The effects of antibiotics and pesticides on the gut microbiome and health of honeybees

KASIE RAYMANN, University of North Carolina at Greensboro

10:50 A.M.

ABSTRACT: Since 2006, the world's honeybee colonies have undergone elevated mortality, and annual colony losses continue to rise. The reasons for this phenomenon are not fully understood, but several possible causes have been suggested, such as pesticides, habitat fragmentation, climate change, and various diseases and parasites. However, no single stressor has been shown to account for the declines. Gut microbial communities influence animal health, and perturbed gut communities can be detrimental to host health. Honeybees are exposed to a number of chemicals, such as pesticides and antibiotics, which are potent sources of disturbance to microbial communities. In view of growing evidence for the importance of the gut microbial communities in animal health and the largely unexplained decline of honeybee colonies, the effects of chemical exposure on the honeybee gut microbiome are of major interest. My research aims to determine how exposure to chemicals affects the composition of the gut microbiome of honeybees and, in turn, how this impacts honeybee health. Additionally, I am interested in how microbiome perturbations affect susceptibility to pathogens. My results show that chemically induced gut microbial community imbalances can decrease the survival rate of honeybees and suggest that this reflects increased susceptibility to pathogens.

BIO: Kasie Raymann is an Assistant Professor at the University of North Carolina at Greensboro. As an evolutionary biologist, Kasie's broad interest is in understanding how microbes evolve and adapt as populations and communities. Her research has addressed microbial evolution both at the broad-scale (e.g. ancient evolutionary relationships) and fine-scale (e.g. microbial community response to perturbation). Currently, the Raymann lab uses the honeybee, an important agricultural and environmental pollinator, as a model system to study the evolution and dynamics of host-associated microbial communities. Kasie is interested in understanding how chemical and environmental perturbations impact the population dynamics of the honeybee gut microbial communities and how these perturbations impact honeybee health. In addition, she is also using the honey bee model system to study how microbial community imbalance influences pathogen susceptibility, what role resident microbes play in protecting their host, and how and when opportunistic pathogens become virulent.

Can the plant mycobiome serve as a tool for improving grass stress resistance?

CHRISTINE HAWKES, North Carolina State University

11:40 A.M.

ABSTRACT: Plant symbiotic fungi can mediate plant stress physiology and thus provide a potential tool for increasing the sustainability of agricultural ecosystems. The development of such novel tools will be particularly important in the future given expectations of increasing drought and water scarcity. We focus on widespread foliar fungal endophytes in C4 grasses, where we have discovered a wide array of host-fungal relationships and traits to predict those functions. However, the observed benefits of individual fungi vary with the abiotic environment and biotic interactions, suggesting that implementation in real-world systems requires a mechanistic understanding with ecological context.

BIO: Christine Hawkes received her B.A. in Environmental Studies from Bucknell University in 1993 and her Ph.D. in Biology in 2000 from the University of Pennsylvania. This was followed by a Smith Postdoctoral Fellowship in Conservation Biology at the University of California Berkeley and a NSF Postdoctoral Fellowship in Microbial Biology at the University of York in the UK. Since 2018, she has been a Professor in the Department of Plant and Microbial Biology at NC State University. Dr. Hawkes' research encompasses both basic and applied aspects of plant-microbe interactions and their role in communities and ecosystems. Current projects include understanding the role of plant symbionts in plant drought physiology, historical contingencies in soil microbial responses to climate change that affect carbon cycling, and drivers of microbial community assembly.



NRIC 2018 | MICROBIOMES FROM DIFFERENT HABITATS: SOIL, WATER AND GUT

INTERACTIVE WORKSHOP ON SCIENCE COMMUNICATION

Critical skills for talking to the media: Prepare for an interview and win public trust

SANDRA BLAKESLEE, *New York Times*

MARY-CHARLOTTE DOMANDI, *RadioCafe.org*

1:30 - 4:00 P.M.

ABSTRACT: On April 22, 2017, more than a million people in over 600 locations around the world marched in support of science. For thousands of researchers, it was a call to defend their values and to demonstrate the importance of their work. It felt good – but arguably it’s not enough.

Now more than ever, scientists need to explain what they do—and why it matters—to the general public. When they fail to step up, we see measles epidemics because parents no longer believe in vaccines, among other serious problems.

This workshop will help you learn how to prepare for interviews with print, radio and television journalists. Through role playing exercises, you’ll see what works and doesn’t work. You’ll have effective tools that promote the understanding of science. And you’ll have the confidence to interact with the media.

BIOS:

Sandra Blakeslee is a science journalist based in Santa Fe, New Mexico. She has spent nearly all of her career writing for the *New York Times*, both on staff and on contract. She is an author or co-author for ten books, including two on the microbiome, “Missing Microbes” and “Dirt is Good.” She was rewarded a fellowship from the Templeton Foundation to spend several weeks in Cambridge, England, discussing science and religion. She is a fellow of the American Association for the Advancement of Science, a fellow of the Committee for Skeptical Inquiry and was the first journalism fellow at the Santa Fe Institute. She is entranced by microbes and microbiomes.

Mary-Charlotte Domandi is producer and host of the Radio Cafe (radiocafe.org), a long-time public radio program and now a podcast on the Santa Fe New Mexican. She covers science, the arts, politics, the environment, books, films, and many local and Southwestern topics. She’s also the host of Down to Earth (downtoearth.media), a podcast on sustainable and regenerative agriculture. Her program was voted “best radio program” in Santa Fe many years running, and she’s the recipient of several journalism awards, and of the Mayor’s Award for Excellence in the Arts.

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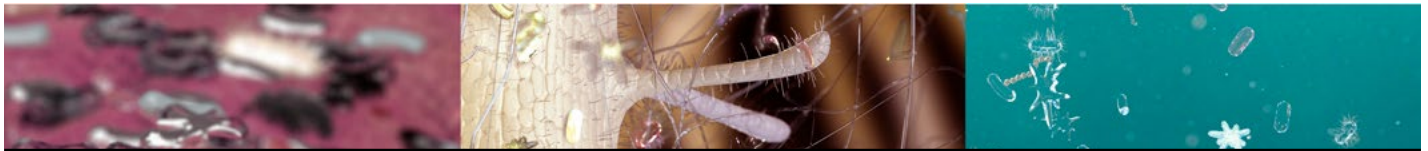
POSTERS

SESSION BEGINS AT 4:30 P.M. ON TUESDAY, OCTOBER 16

#1 --- **Margarita Marroquin-Guzman, Christopher Proctor, Justin McMechan, Anthony Adesemoye, Sydney Everhart | SOIL MICROBIAL DIVERSITY DURING A SOYBEAN-COVER CROP ROTATION USING COMMUNITY SEQUENCING** | Cover crops represent an important rotational benefit to field crop production systems. In the Midwest, over-wintering cover crops such as oats (*Avena sativa* L.) and rye (*Secale cereale* L.) are known to improve disease management, soil properties, and provide an economic benefit from forage production. However, how cover crops impact soil microbial communities and whether longer periods of cover crop provide greater benefit is understudied. Here, our aim is to characterize soil microbial community diversity in a soybean- oat/rye system in three experimental trials in Nebraska. A fallow control treatment was utilized at each location and cover crops consisted of a 50:50 mixture of oats and cereal rye. The soil was sampled at planting and at termination. Bulk DNA was purified and the ITS and 16S regions were sequenced using the Illumina Mi-Seq platform. We used a community sequencing approach to characterize the dynamics of the soil microbial communities associated with cover crops within and across locations. Results will contribute to understanding how cover crops impact microbial communities in Nebraskan soils and identify microorganisms that may be potential indicators of disease incidence and yields.

#2 --- **Serkan Tokgoz, Dilip Lakshman, Bakhyt Yertayeva, Mahmoud H. Ghozlan, George Biliarski and Amitava Mitra | EVALUATION OF SOYBEAN NODULE MICROBIOME FOR BIOCONTROL APPLICATIONS** | Legume nodules are known to harbor a host of bacteria besides the Rhizobia. In an effort to identify beneficial bacteria for plant disease control, we are studying soybean nodules as the source of these bacteria as our metagenomics analysis of a single soybean nodule identified a large number of diverse bacterial species. Surface sterilized single soybean nodules were used to isolate nodule associated bacterial species. A total of 500 colonies were tested individually against two bacterial and one fungal pathogen on solid media plates for inhibition of pathogen growth. From the initial screening, 54 colonies were selected based on significant growth inhibition of selected plant pathogens. These colonies were further tested on three other bacterial and two fungal pathogens on solid plates. Fifteen colonies from these were also tested in tomato seedlings against two bacterial pathogens. Both soil and stem inoculation methods were used to infect tomato plants. Bacterial metabolites were extracted from 15 colonies with ethanol and ethyl-acetate and used to treat tomato seeds. Treated seeds were tested for resistance against two bacterial pathogens. Results show that many soybean nodule associated bacteria strongly inhibit the growth of plant pathogens in both in vitro and in vivo assays. Furthermore, the treated plants grew better than untreated control plants. All 54 colonies are being identified by 16s RNA sequencing and MALDI-TOF assays. Efforts are being made to establish a cocktail of these bacteria that can be used for a broad-spectrum disease management.

#3 --- **Morgan R. McPherson, Peng Wang, Yen Ning Chai, Ellen Marsh, George Graef, and Daniel Schachtman | MICROBIAL COMMUNITIES OF THE ROOTS OF UNIQUE SOYBEAN (GLYCINE MAX.) GERMPLASM IN ALKALINE AND NON-ALKALINE SOILS** | Plant roots are essential for nutrient and water uptake. Microbial communities present within the endosphere, rhizosphere, and soil play a vital role in plant development, nutrient acquisition, and in some instances promote growth. This research aims to discover and characterize functional interactions between soil microorganisms and soybean roots. Due to limited iron availability in alkaline soils, iron deficiency causes decreased growth and yield. Endosphere, rhizosphere, and soil of eight genotypes from a soybean population segregating for iron deficiency chlorosis tolerance were grown near Valley, Nebraska. Genotypes consisted of two parent lines and six recombinant inbred lines that showed more extreme phenotypes than the parent lines in alkaline soils. The field has naturally occurring streaks of higher pH with lower available iron and more neutral pH areas. This provides an ideal site to make comparisons between the microbial communities due to pH and sensitive and tolerant soybean genotypes. The V4 region of the 16s rRNA gene was sequenced using Illumina MiSeq and multiple bioinformatics analyses were utilized to provide data on the presence, absence, and abundance of microbial taxa. These data provide insight into the identity and composition of microbial communities associated with the endosphere, rhizosphere, and soil of soybean plants.



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#4 --- **Michael A. Meier, Martha G. Lopez-Guerrero, Raghuprakash K. Ramamurthy, Brandi A. Sigmon, Kent M. Eskridge, Joshua R. Herr, Karin van Dijk, Jinliang Yang, James R. Alfano, James C. Schnable | USING A LARGE MAIZE DIVERSITY PANEL TO IDENTIFY GENETIC LOCI THAT SHAPE ROOT MICROBIAL COMMUNITIES UNDER NUTRIENT STRESS** | Root microbiomes, if affected by plant genetics, may be a trait that can be used in plant breeding to improve tolerance to nutrient stress. In this study, we aim to link genomic differences between 266 corn genotypes derived from the Buckler-Goodman diversity panel to changes in rhizosphere microbial communities under control and nitrogen stress treatments. Root samples were collected from a total of 1152 field plots before flowering and again after flowering. Extra replicates as well as soil samples were collected for a subset of 26 genotypes to estimate sample to sample variance in rhizobiome composition. DNA is being isolated from rhizosphere and bulk soil and microbial communities will be analyzed through sequencing of the 16S ribosomal DNA V4 region. GWAS analysis using several million SNP markers from whole genome resequencing will be employed in an attempt to identify genetic loci that shape the maize rhizobiome.

#5 --- **Paul Twigg, Renee Roebke, Katie Arndt, Carmen Pavlik | SUBSTRATE EFFECTS ON THE MAIZE ROOT MICROBIOME AND PLANT GROWTH** | In this project, our group of undergraduate researchers aims to correlate prescribed changes to the soil substrate with alterations of the maize root microbiome including persistence of the changes that can be applied to soil microbial inocula. We used a high clay soil with approximately 3% organic matter as a starting point. We also used 2 prescribed variants of our initial soil each with 6% organic matter. In the first variation all of the added organic matter was biodegradable and in the second half of the added organic matter was biologically inert. For each soil type, DNA was extracted from control soil samples and from soil adherent to the maize roots throughout the growing season. In addition, phenotypic measurements of canopy closure using Canopeo and chlorophyll content were also collected. We will present our results to date. The authors wish to acknowledge financial support provided by NSF EPSCoR grant number OIA-155741, a grant from the University of Nebraska Foundation, and a grant from the UNK URF.

#6 --- **Siwen Deng, Jinliang Yang, Devin Coleman-Derr | HOST GENETIC REGULATION OF THE SORGHUM ROOT MICROBIOME** | The interaction of plant roots and soil microbes is essential for plant health and plant productivity. These microbes exist as part of complex microbial communities and can adhere to the root surfaces (rhizosphere) and colonize internal root tissue (endosphere). Recent studies in various plant species have shown that both environmental factors and host genetics can impact root microbiome development; however, it is challenging to identify specific host genetic variants that affect the root microbiome. Here, we describe a population-level microbiome study using a sorghum diversity panel in a replicated field trial. To dissect the host genetic architecture in determining the root microbiome variation, we employed a genome-wide association study (GWAS) approach. The experiment design enabled us to estimate the broad sense heritability for individual microbes and microbiome diversities. As a result, a number of highly heritable microbes were discovered. Further analysis of highly heritable microbes identified plant loci that are associated with variation in sorghum root microbiome. Understanding the host genetic regulation of the plant root microbiome can provide insights into how best to control beneficial interactions between plants and microbes that could be adapted for agricultural improvement..

#7 --- **Yen Ning Chai, E.L. Marsh, V. Stoerger, D. Schachtman | INTEGRATING HIGH-THROUGHPUT PHENOTYPING TO MONITOR NITROGEN STRESS MITIGATION PROCESSES INDUCED BY DIAZOTROPHS IN SORGHUM** | Diazotrophs are the microbes that are capable of reducing gaseous nitrogen (N) into ammonia, making N available for plant uptake. Diazotrophs mitigate N stress in plants by interacting intimately with plants, yet the mechanisms for how diazotrophs relieve N stress may go beyond just N fixation. This research aims to study the changes in plant traits and N accumulation induced by a diverse set of diazotrophs over time and ultimately establish a stable relationship between plants and diazotrophic microbes under N stress. Sorghum bicolor is used in this study because it is widely grown in developing countries and its increasing importance in biofuel production. To determine if diazotrophs enhance sorghum growth under low N conditions, plants were inoculated with synthetic communities (SynComs) consisting of at least nine different diazotrophs and grown in an automated high-throughput phenotyping facility. The diazotrophs were originally isolated from the roots and soil of field-grown sorghum. Acetylene reduction assays were used to verify isolates with N fixation abilities. A SynCom consisting of non-diazotrophic strains and a nonmicrobe treatment were included as the controls. Sorghum morphological and physiological traits were monitored daily using RGB (Red Green Blue) and hyperspectral cameras. After two months of growth, the DNA from roots and rhizosphere was isolated and prepared for 16S amplicon sequencing to determine the microbes that colonized sorghum roots and rhizosphere. The transcriptional responses in roots will be studied to assess the changes in transcript level from the microbial and N treatments. Selected microbes from these SynComs will be genome sequenced to determine other mechanisms of growth promotion in addition to N fixation. This study will allow for a deeper understanding of both plant- and microbe-based mechanisms behind the N stress mitigation that result from diazotroph inoculation.



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#8 --- **Sanjay Antony-Babu, Karrie A. Weber | MINING MICROBIOME AND GENOMIC DATA FOR THE IDENTIFICATION OF NOVEL ANAEROBIC PLANT GROWTH PROMOTING BACTERIA** | Plant growth promoting bacteria contribute to the health, development and productivity of plants. To date primarily aerobic organisms have been described as plant growth promoting bacteria despite identification of anoxic microsites near or at the plant root. Here we demonstrate identification of common anaerobic, metal-reducing bacteria, genus *Geobacter*, in the rhizosphere of *Oryza sativa* and *Typha angustifolia* (saturated soils) as well as *Gossypium* sp., *Arachis hypogaea*, *Pinus patula* and *Saccharum* sp. (unsaturated soils) from mining of microbiome databases. This in silico analysis demonstrates *Geobacter* spp. in wide range of natural and crop rhizospheres. The rhizosphere sequences of this genus formed distinct clades of uncultivated species demonstrating a knowledge gap in understanding this widespread rhizosphere organism. Comparative in silico genomics reveal plant growth promoting properties such as auxin (tryptophan synthase and nitrilase) and terpene production (terpene cyclase), nitrogen fixation (nitrogenase), phosphate mobilization (phosphate-responsive transcriptional regulator and phosphate specific transport) and sulfur dissimilation (sulfate permease, 3'-phosphoadenosine 5'-phosphosulfate synthase and cysteine synthase A) throughout sequenced *Geobacter* spp. genomes. Together with the ability of this genus to reductively dissolve iron oxide minerals which would increase iron availability in soils, members of the *Geobacter* genus have genomic potential to contribute to plant growth promotion.

#9 --- **Yuguo Yang, Yuqing Geng | INFLUENCE OF UNDERSTORY GROUND COVER TYPES ON SOIL MICROBIAL COMMUNITIES AND ENZYME ACTIVITIES** | Changes in understory ground cover types may affect soil microbial communities through influencing microenvironment and plant-derived carbon input (litter and root exudates), which will further influence the soil biochemical cycle. The purpose of this study was to evaluate the effect of changed understory vegetation and ground cover types on soil biological quality. Organic layer samples and 0-5 cm underground soil samples were taken from three understory vegetation types (moss patches, herb patches and shrub) and one ground cover type (litter patches) in a *P. crassifolia* forest and a *P. wilsonii* forest. We estimated soil microbial community structure and measured five key hydrolase activities. Soil chemical properties were also analyzed. The results showed that moss patches and litter patches had higher microbial phospholipid fatty acid content and overall soil enzyme activities than herb patches and shrubs, whereas herb patches and shrubs had higher bacterial/fungal ratio. Changed organic matters and phenolic compounds were responsible for it, and dissolved organic carbon and dissolved organic nitrogen were major driven factor of the overall variation in microbial communities and enzyme activities. The results of this study may provide data reference for the ecological management of understory soil.

#10 --- **Ashley Stengel, Megan Franklin, Joshua Herr, Elizabeth S. Jeske, Virginia Jin, Marty Schmer, Rhae Drijber | CROP DIVERSITY AT A LONG-TERM FIELD SITE: DO RECRUITMENT POOLS MATTER?** | Sustainable management of agricultural lands is a pressing concern as human populations continue to grow, while arable lands remain finite. Diversification of crops is one strategy for promoting agronomic yields to meet food demands. With these management practices come physical and chemical changes in the soil environment which can in turn shape the structure and function of microbial communities. Incorporating an ecological perspective, our research seeks to explore the maize-associated soil microbiome and elucidate the long-term effects of crop rotation and nitrogen addition. To address questions related to the assembly of microbial communities in maize seedlings, we conducted a greenhouse experiment using soil collected from an agricultural field site that has been maintained for over 40 years. Our analysis includes agronomic properties, soil nutrient pools, microbial community structure via amplicon sequencing, and functional capabilities through enzyme assays and metagenomic sequencing.

#11 --- **Thais Egreja, Joshua R. Herr | DETECTION AND QUANTIFICATION OF XANTHOMONAS VASICOLA PV VASCULORUM WITHIN THE MAIZE MICROBIOME USING DROPLET-DIGITAL PCR** | The aim of this study was to develop a rapid and sensitive assay using droplet digital PCR (ddPCR) for detection and absolute quantification of *Xanthomonas vasicola pv vasculorum* (Xvv), causal agent of Bacterial Leaf Streak (BLS) of maize and other economically important crops. We analyzed bacterial suspensions and plant material and a 10-fold serial dilution was prepared to evaluate the sensitivity and detection limit of the ddPCR method. We also evaluated resistant and susceptible inoculated maize inbred lines at 24, 72, and 168 hours after inoculation to monitor pathogen growth inside the host. Based on preliminary results, ddPCR can be used as a diagnostic tool for sensitive, accurate, fast, and quantitative detection of Xvv. Moreover, quantification of the pathogen in different maize genotypes, suggested this assay can also be used for evaluation of BLS resistance.

#12 --- **Oskar Siemianowski, Kara R. Lind, Ludovico Cademartiri | MODEL ECOSYSTEMS FOR PLANTS AND MICROBES, A PHENOTYPING APPROACH WITH QUANTITATIVE CONTROL OF SIGNALING BETWEEN ORGANISMS AND THEIR ENVIRONMENTAL CONDITIONS** | One of the issues in the quantitative study of organismal interactions in ecosystems such as the rhizosphere is that signaling is strongly dependent on



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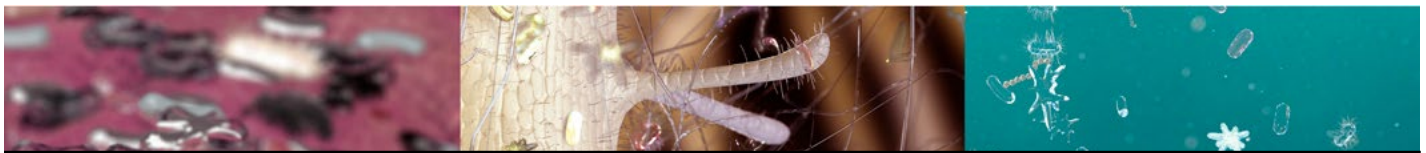
distance and usually requires distances smaller than most bacteria cultures and root systems. This issue has led to the widespread use of mesocosms/microcosms where organisms are in proximity but where the control/monitoring of signaling kinetics between individual organisms is difficult. Detangling this problem requires control over mass transport that is beyond the capabilities of the commonly used growth environments (e.g., Petri dishes). We developed a simple approach to the creation of networks of independently controlled habitats for plant and microbe growth. We show that oscillatory flows of nutrient solutions in these networks produce mass transport that is quantitatively analogous to diffusion but controllable in rate over three orders of magnitude, thereby effectively allowing to control the signaling distance between organisms in the network between 10 cm and less than 1 mm. This finding allows for the creation of rhizosphere models where each component of the rhizosphere can be grown and monitored in independently controlled habitats. We use the model ecosystem to study plant - microbial interactions to deliver new perspective for agriculture, soil and ecological sciences.

#13 --- **Anji reddy Konda, Ki Youl Park, Kan Liu, Lucas Busta, Chi Zhang, Bin Yu, Thomas E. Clemente and Edgar B. Cahoon | DEVELOPMENT OF SYNTHETIC BIOLOGY TOOLS FOR ENGINEERING OF MAIZE ROOT TRAITS** | The Center for Root & Rhizobiome Innovation's Aim 3 is focused on the development of synthetic biology tools and their application for improvement of root traits. This includes the control of exudate production, which influence soil-microbe interactions for use in Aim 2 and 4. Towards synthetic biology tool development efforts, a collection of maize candidate promoters for genes that confer root-enriched expression have been identified, and research is underway to identify promoters that confer conditional expression in response to nutrient-deprivation and specific soil microbes. To date, hairy roots have proven recalcitrant for rapid evaluation of synthetic biology tools in maize. As an alternative approach, we have developed a pipeline for candidate promoter evaluation using rice as a model system and can obtain transgenic plants in about 2.5 months. From this pipeline, we now have experimental evidence to support computational predictions for several maize root-enriched promoters. Complementing these efforts, GoldenBraid 2.0 has been adapted for modular-assembly of gene cassettes or "transcriptional units" based on the use of Type IIS restriction sites to link and reassemble multiple gene cassettes. The first assembly is a three gene construct that is designed to enhance root production of strigalactones. Efforts are also underway to use root-enriched promoters to drive synthetic RNAi to target genes involved in root exudates biogenesis or responses to the soil microbiome.

#14 --- **Camila Pereira Braga, Martha Lopez-Guerrero, Peng Wang, Guangchao Sun, Karin van Dijk, Daniel Schachtman, James C. Schnable, and Jiri Adamec | METABOLOMIC PROFILING OF ROOT AND EXUDATES SAMPLES** | Integrated analytical platform for untargeted metabolomics analysis was used to study the metabolism of plant roots and exudates. The platform consists of several steps including sample preparation, metabolite extraction and separation by various LC-MS techniques. To maximize coverage of metabolites for profiling analysis, liquid-liquid extraction by methanol/water/chloroform was used to separate polar (aqueous phase) and non-polar (organic phase) molecules. The non-polar metabolites were analyzed using an Agilent 1200 Series HPLC coupled to a high resolution FTICR mass spectrometer. The polar metabolites were analyzed using an UPLC M-Class System coupled to a Xevo G2-XS QTOF mass spectrometer. To identify major metabolic differences, selected genotypes and controls were compared using hierarchical clustering. To map the interaction between root and its environment, both common and unique metabolites in the exudates and roots were quantified and preliminarily identified.

#15 --- **Nick Iwata, Tu Doan, Truc Doan, Michael Kangas, Luke Schroeder, Grace Su, Kiley Taylor, Andrea Holmes, Erin Doyle and Tessa Durham Brooks | IMPROVED ACCURACY AND AUTOMATION OF A METHOD TO LOCALIZE FREE AMINES ON THE SURFACE OF MAIZE ROOTS** | Root exudates are important chemical signals and metabolic components that facilitate interactions with microbes, other plants, and soil particles in the rhizosphere, but much remains to be learned about their localization and composition. Previously, we developed a simple, inexpensive method that utilizes a novel colorimetric paper to detect free amines on the root surface of maize seedlings. Although we demonstrated the method was effective in localizing and estimating quantity of free amines in root exudates, opportunities exist to improve accuracy and automation of the method. The accuracy was improved by using a more uniform substrate, PES, and by depositing the sensor and standards with an industrial grade printer. Automatic calibration of the signal was improved by printing a grid of standards on the substrate. To reduce the stress on the plant, a lightweight roller was used to apply uniform pressure across the root surface. To eliminate toxicity from the sensor, the indicator was printed after rolling. Additional studies are underway to determine the optimal conditions to develop the signals. This improved method will allow us to perform larger studies on the variation of the exudate localization and can be adapted to study other exudate components.

#16 --- **Jade Prochaska, Erin Doyle | ISOLATION OF PHAGES ON HOST BACTERIA P. SYRINGAE** | Bacteriophage are viruses that infect and kill bacteria. Phage exhibit many different morphologies and infect a variety of different hosts, but individual phage are host specific. By isolating a phage, we can potentially use it in phage therapy.



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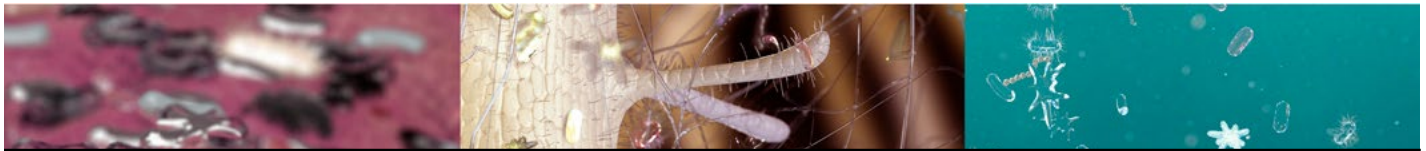
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#17 --- **Priscila Guzman, Andre J. van der Vlies, Niloy Barua, Thomas G. Platt, Ryan R. Hansen | HIGH-THROUGHPUT SCREENING OF MICROBE-MICROBE INTERACTIONS UTILIZING MICROWELL ARRAYS** | Microbial interactions are extremely important in shaping microbiome structure. These interactions are often hard to study. This work uses microwell arrays that allow for high-throughput screening of microbe-microbe interactions and retrieval of the bacteria within microwells of interest. This retrieval capability allows follow-up genetic and phenotypic characterization of the cells within targeted microwells. In this way, our approach can identify members of the microbiome that either promote or antagonize a focal organism. Using the plant pathogen *Agrobacterium tumefaciens*, we seed, grow, and retrieve live cells from small ($\approx 20 \mu\text{m}$ diameter) microwells. This approach uses a light-responsive, poly(ethylene glycol) hydrogel as a membrane that confines motile cells within microwells, permits continuous cell monitoring, and allows nutrient exchange and cell growth. This new technology enables us to simultaneously screen thousands of microbial interactions, open wells of interest with high precision, and retrieve cells from heterogeneous populations for isolation and further characterization.

#18 --- **Leslie Ronish, Kurt Piepenbrink | MOLECULAR MECHANISMS OF CLOSTRIDIUM DIFFICILE BIOFILM FORMATION** | Type IV pili (T4P) are extracellular protein fibers, composed of subunits called pilins, which have diverse functions, including twitching motility, cellular adhesion, horizontal gene transfer, and biofilm formation. T4P have been well characterized in gram-negative bacteria and found in many gram-positive bacteria, including *Clostridium difficile*. *C. difficile* is a spore-forming, rod-shaped obligate anaerobe that is the leading cause of nosocomial infections in the United States. Previous investigations have underscored the importance of T4P for biofilm formation by *C. difficile* and animal models have demonstrated a role in colonization. To understand the mechanism by which T4P promote biofilm in *C. difficile*, we have elucidated the three-dimensional structures of the primary subunit (PilA1) and a minor component (PilJ). Current studies are investigating potential of T4P to promote biofilm by interacting with component of the extracellular matrix. While the soluble portions of PilJ and PilW, minor pilins, have no sequence identity, they have both shown binding to recombinant plasmid in agarose mobility assays. Ongoing work aims to determine the DNA-binding interface of PilJ using our high-resolution structure and Hydrogen-Deuterium exchange mass-spectroscopy (HDX), as well as determining the PilW three-dimensional structure by crystallography and modeling the pilus.

#19 -- **Jessica Hotovy, Sarah Tjards, Reilly Cooper, Clayton Cressler | MANIPULATION OF GUT MICROBIOTA USING CROSS-GENERATIONAL ANTIBIOTIC EXPOSURE: A CASE STUDY USING DAPHNIA MAGNA** | Many gut microbiota studies concentrate on a single individual and the cost of manipulating the individual's microbiota. I aimed to study the cross-generational implications of manipulating the gut bacteria from a host organism, noting the effects on growth, survival, and fecundity. This experiment was designed to observe host fitness over five generations with varied antibiotic exposure to manipulate the gut microbiota. Some hosts were raised in constant antibiotic environments, some in constant antibiotic-free environments, and some in antibiotics followed by subsequent generations in antibiotic-free environments. Data analysis of all five generation's host fitness outcomes were completed in R. 16S metagenome data is currently being processed. Within this study, two key questions were asked: 1) How is host health impacted by antibiotic exposure across multiple generations, and 2) Does the gut microbiota recover once antibiotic exposure is removed? Results show that manipulating the gut microbiota through antibiotic treatments impacted host survival, temporarily affected reproduction, and had no influence on growth. Metagenomic data suggests that the microbiota recovers quickly when removed from antibiotics, partially explaining host fitness recovery. The insights gained through this study aid in further cross-generational microbiota investigations and host-microbiota relationships.

#20 --- **Sean Carr, Jennie L. Catlett, Megan D. Smith, Nicole Buan | CHARACTERIZATION OF MUTUALISTIC INTERACTIONS BETWEEN HUMAN GUT MICROBES** | The human gut is composed of a complex system of interactions between the host human tissue and the microbes which inhabit it. This system of independent microbial metabolisms combining to form a larger community nutrient exchange is hypothesized to be essential for proper human health, although the details of this proposed syntrophy are still being investigated. To better characterize this potentially widespread interaction, we have chosen to focus on two common potential gut symbionts: the gram-negative bacteria *Bacteroides thetaiotaomicron* and the methanogenic archaea *Methanobrevibacter smithii*. Both of the organisms we have chosen to study fill a vital niche within human gut health; *B. theta* assists the gut by fermenting dietary polysaccharides whereas *M. smithii* consumes end-stage fermentation products, mobilizing them into CO₂ and methane. Using metabolic modeling and media dropout studies our lab has characterized the shared growth requirements for these two organisms and we are now underway investigating the biochemical and physiological interactions between them. Using genetics, transcriptomics, metabolomics, and microbial growth studies we aim to tease out the details of this proposed syntrophic relationship.



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#21 --- **Saurav Sarma, Victoria J. Vieira-Potter, Tzu-Wen L. Cross, Kelly S. Swanson, Zhentian Lei, Lloyd W. Sumner, Cheryl S. Rosenfeld | CORRELATING SOY-INDUCED FECAL METABOLOME SHIFT WITH GUT MICROBIOME IN OVIECTOMIZED FEMALE RATS** | Soy based diet has been associated with alleviating many adverse health conditions including adiposity and post-menopausal symptoms which is attributed to the rich phytoestrogen contents in soy. s-(-)Equol is not indigenous to food but a bacterial metabolite of soy isoflavone diadzein, and identified as critical for positive health effects. The efficiency of converting diadzein to s-equol significantly varies among demographics, possibly due to diverse gut flora. Thus, identification of microbes that facilitate the s-equol production and identifying other potentially beneficial bacterial metabolite are critical for extracting maximum health benefit of soy diet. Accordingly, we have conducted a comprehensive profiling of the fecal metabolome in ovariectomized and intact female rats to correlated the most significantly different metabolites with the most significant microbiome strains upregulated in soy diet. This study reveals potentially new s-equol producers as well as significantly different metabolite profile that demands further investigation.

#22 --- **Reilly O. Cooper, Clayton E. Cressler | MICROBIOTA COMPOSITION AND FUNCTION IN A HOST PLANKTONIC CRUSTACEAN** | What functions do species within the microbiota provide for each other and for their host? We studied this in *Daphnia magna*, a planktonic host crustacean ideal for addressing these questions due to its fast, asexual reproductive cycle and its relatively simple microbiota. Shotgun sequencing of the *Daphnia* microbiota reveals differences in community composition between adult and juvenile hosts. Assembly and binning reveals between four and eight high-quality metagenome-assembled genomes of bacterial species. Many of these species are in the *Limnohabitans* genus, which was previously shown to increase *Daphnia* fecundity. In these *Limnohabitans* species, we show the presence of metabolic genes that may interact with host functions.

#23 --- **Joshua R. Herr | THE MUSHROOM MICROBIOME: BACTERIAL DIVERSITY ON AND WITHIN MUSHROOMS** | The role of the microbiome in host-environmental relationships has been a major research focus over the last decade. Many studies have recognized the role of microbes, such as bacteria and archaea, in association with fungi in many different ecosystems. Quite surprisingly, fungal sporocarps or fruiting structures have largely been ignored when observing the taxonomic and functional diversity of organismal microbiomes. Here, I present data on the diversity of microorganisms associated with fungal sporocarps and attempt to understand the role in fungal exudates in shaping their microbiome. From initial sequencing experiments, fungal sporocarps appear to be highly enriched in members of the Enterobacteriaceae and Burkholderiaceae relative to their environmental matrices. The role of associates may extra- or endo-hyphal in nature and may provide key metabolic processes helping fungi utilize nutrients derived from the environment.

#24 --- **Edward Hillman | Wayne Riekhof & Joshua Herr | IT TAKES A VILLAGE TO GROW A FUNGUS: AN ANALYSIS OF THE MORCHELLA MICROBIOME** | The Ascomycete genus *Morchella* is fascinating for a number of reasons. *Morchella* species are globally popular mushrooms collected for the table so they represent a curious recreational activity and a potential income source for mushroom growers. Despite this popularity and a concerted effort to understand their propagation, they have not been consistently cultivated on a large scale, partly because the life history of *Morchella* species remains poorly characterized. It has been hypothesized that they form tight bacterial associations with *Pseudomonas* spp., but these associations remain largely uncharacterized. Using a combination of cultural and metagenomic analyses, we aim to characterize unknown bacterial-fungal interactions. We have analyzed publicly available metagenomic datasets and extracted bacterial reads in order to define a baseline bacterial community. Samples have been taken from wild-harvested sporocarps to culture potential bacterial associates. The latter will be identified using 16s RNA sequencing and compared to publicly available metagenomic data.

#25 --- **Erin Carr, Wayne Riekhof, Joshua Herr, & Steven Harris | YOU'RE ONLY AS GOOD AS YOUR PARTNER: SURVIVABILITY VIA SYMBIOSIS** | Biological soil crusts (BSCs) are complex biofilms that can withstand a wide range of extreme conditions, including: heat, freezing, desiccation, osmolarity, UV, and heavy metals. Organisms that are most commonly found in BSCs are fungi, algae, bacteria, and lichens. Microbial species of interest to our research are mainly polyextremotolerant fungi from the order Chaetothyriales, *Methylobacterium* spp., and *Chlorella* spp. Unique features of these organisms make them intriguing to study alone, but may also provide insight into the evolution of fungal-algal and fungal-bacterial interactions. These microbes share similar features with that of lichen-forming microbes, therefore they enable the study of the lichen lifestyle without the challenges of directly working with lichens. We hypothesize that in a BSC polyextremotolerant fungi, algae, and bacteria interact in a mutualistic fashion and observing these interactions will reveal clues about the nature of the microbial communication that underlies the formation of BSCs. We have performed both culture based and non-culture based methods to describe microbial interactions in a BSC from a semi-arid sand dune ecosystem in B.C., Canada. Current efforts are focused on integrating phylogenetic, phenotypic, and microbiome data to understand the functional interactions that enable the formation and maintenance of BSCs.



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#26 --- **Samantha Reese, Steve Harris and Mark Marten | AN RNA-SEQ ANALYSIS OF HOW AN ECHINOCANDIN ANTIFUNGAL DRUG EFFECTS GENE EXPRESSION OVER TIME** | When the environment challenges filamentous fungi with a stressor, a specific response is transmitted through the signaling pathways. *Aspergillus* responds to cell wall damage by certain repair mechanisms that try to restore cell wall biogenesis through the Cell Wall Integrity Signaling (CWIS) Pathway. The damage could be caused by an antifungal such as micafungin. This echinocandin drug inhibits the production of beta-1,2-glucan which is essential for cell wall formation. Research in *Saccharomyces cerevisiae*, has shown that mitogen-activated protein kinase (mpka) is an important enzyme in the CWIS pathway, but it has been found the CWIS pathway in this yeast is very different from the signaling pathway in *Aspergillus*. This poster's goal is to investigate the shift in gene expression through time in response to cell wall damage and repair.

#27 --- **Nicole A. Fiore, Sanjay Antony-Babu, Rebecca A. Daly, Kelly C. Wrighton, Rebecca Kiat, Donald Pan, Caitlin Lahey, Olivia Healy, Sophie Payne, Nicole Buan, Karrie A. Weber | CONVERSION OF CARBONATE MINERALS INTO ACETATE AND METHANE** | A majority of carbon on Earth (ca. 80%) is sequestered in the form of sedimentary carbonates. At acidic pH, these carbonates are highly soluble and will readily dissolve. At alkaline and neutral pH, they are considered insoluble and stable, though microorganisms can catalyze carbonate dissolution. Here we demonstrate the conversion of calcium carbonate into acetate and methane by an anaerobic enrichment (pH 8.3) initiated from alkaline saline wetland soil. Shotgun metagenomic sequencing and genome assembly of the enrichment identified an acetogen (*Clostridium* sp.), a methanogen (*Methanobacterium* sp.), and additionally *Pseudomonas* sp., *Desulfovibrio* sp., and *Tessaracoccus* sp. These genomic data suggest the possible conversion of carbonate into acetate coupled to the oxidation of H₂ by the *Clostridium* sp. Sequence data confirms the *Clostridium* sp. has genes for key enzymes in the Wood-Ljungdahl pathway, including carbon monoxide dehydrogenase (CODH) and acetyl-CoA synthase (ACS). The generation of acetate has the potential to create an acidic microenvironment at the mineral interface, increasing carbonate solubility. The inorganic carbon can then be used by the methanogen to generate CH₄ via hydrogenotrophic methanogenesis. These results indicate the metabolic potential for the conversion of solid inorganic carbonate minerals into methane and multi-carbon compounds at alkaline pH.

#28 --- **Jeffrey Westrop, Olivia Healy, Sanjay Antony Babu, Jason Nolan, Donald Pan, Rebecca Kiat, Karrie Weber | VARIATIONS IN MICROBIAL COMMUNITY STRUCTURE WITH LITHOLOGY AND GEOCHEMISTRY IN SUBSURFACE SOILS AND SEDIMENTS** | Deposition processes can generate lateral and vertical variations in physical and chemical sediment properties that support microbial communities. Variations in microbial community structure and abundance with lithology and geochemistry were investigated in lithologic faces from two ~50 meter subsurface cores collected through the vadose and saturated zones of an oxic alluvial aquifer in an agricultural region. The cores were divided into six lithofacies (soil zone, silty clay, Fe-stained silty clay, silty sand, poorly-sorted sand and gravel, and clay shale) based on physical characteristics. Bacterial, archaeal, and fungal taxa were identified using high-throughput amplicon (16S rRNA gene and ITS) sequencing. The majority of the 16S rRNA sequences were identified as bacteria with only 0.6% of sequences classified as archaea (*Crenarchaeota* and *Euryarchaeota*). The 16S rRNA OTUs were dominated by *Pseudomonas* spp in marine-clay shale and poorly-sorted sand and gravel whereas *Geobacter* spp. dominated the frequency of identified OTUs in a lithofacies classified as Fe-stained silty clay. Ascomycota was the most abundant fungal taxa at all depths; however, 2-30% of ITS sequences could not be classified below Kingdom. While variation in microbial community structure was observed with lithology and geochemistry, specific bacterial taxa predominated specific lithofacies.