

SYMPOSIUM SCHEDULE

8:00	Breakfast - Atrium
8:45	Opening Remarks Jeff Gralnick
9:00	Anne K. Dunn Associate Professor, University of Oklahoma
9:45	Ann Fallon Professor, University of Minnesota
10:15	Break - Atrium
10:45	Linda Thomashow Research Geneticist, Washington State University
11:30	Dan Knights Assistant Professor, University of Minnesota
12:00	Lunch - Atrium
1:00	Heidi Goodrich Blair Professor, University of Wisconsin-Madison
1:45	Ran Blekhman Assistant Professor, University of Minnesota
2:15	Break - Atrium
2:30	Manish Raizada Associate Professor, University of Guelph, Ontario
3:15	Peter Tiffin Associate Professor, University of Minnesota
3:45	Closing remarks Nathan Springer
4 - 5:00	Reception - Atrium



RAN BLEKHMAN
Assistant Professor
Department of Genetics, Cell Biology, and Development
University of Minnesota
“A role for host-bacteria interactions in shaping patterns of genetic variation across human populations”

The composition of bacteria in and on the human body varies widely across human individuals, and has been associated with multiple health conditions. While host genetic factors are expected to control the human microbiome through the immune system and metabolic pathways, elucidation of the genetic influence on microbiome composition has proven to be a challenge. In my talk, I will present a genome-wide association study aimed at identifying human genetic variation associated with microbial diversity in multiple body sites. By mining the shotgun metagenomic data from the Human Microbiome Project for incidental host DNA reads, we gathered information on host genetic variation for individuals for whom bacterial abundance data are also available. We identified candidate human genes that are associated with microbiome composition in 15 host body sites. These genes are significantly enriched in immunity functional categories, and form an interaction network highly enriched with immunity-related functions. To investigate the evolutionary history of bacteria-associated host genes, we used available sequencing data from the 1000 Genomes Project, and find that these genes show a significant excess of highly differentiated allele frequencies among human populations. Combined, these results highlight the role of host immunity in determining bacteria levels across the body, and underline a possible role for the microbiome in driving the evolution of bacteria-associated host genes.



ANNE K. DUNN
Associate Professor
Department of Botany and Microbiology
University of Oklahoma
“Understanding the role of bacterial metabolism in the *Vibrio fischeri*-*Euprymna scolopes* symbiosis”

The symbiosis between the bioluminescent marine bacterium *Vibrio fischeri* and the Hawaiian bobtail squid *Euprymna scolopes* is an important model system for understanding the complex relationship between beneficial bacteria and their multicellular hosts. Our research goals are to use this model system in combination with molecular and genetic tools to understand how bacterial physiology influences the outcome of the bacterial-host interaction. Through our studies we have gained a better understanding of

the expression and function of different energy conservation pathways in *V. fischeri*, and how these pathways could contribute to growth and survival both in and outside of the host.



ANN FALLON
Professor
Department of Entomology
University of Minnesota
“Microbes and Mosquitoes: The *Wolbachia* Story”

Wolbachia are obligate intracellular bacteria that were first described in reproductive tissues of mosquitoes. Genome sequencing has shown that *Wolbachia* lack many of the metabolic capabilities of free-living bacteria, and PCR-based studies show that *Wolbachia* infect a high percentage of insect species. In many insects, *Wolbachia* cause cytoplasmic incompatibility, which favors reproduction of infected females that pass the *Wolbachia* to their offspring. In contrast, when uninfected females mate with infected males, the eggs fail to hatch. That *Wolbachia* provide a potential tool for controlling pest species was demonstrated in Burma (Myanmar) in the early 1970’s, where a filariasis vector was replaced with a related mosquito that does not transmit the disease. Our goal is to improve use of *Wolbachia* as a gene drive mechanism for insects in general. Our research focuses on identifying the molecular basis of cytoplasmic incompatibility, understanding the metabolic interactions between *Wolbachia* and its host cell, and exploiting these interactions to develop insect cell lines that will facilitate genetic manipulation and transformation of *Wolbachia*.



HEIDI GOODRICH-BLAIR
Professor
Department of Bacteriology
University of Wisconsin-Madison
“Causes and consequences of intestinal colonization explored in a nematode-bacterium symbiosis”

Although microbes influence the health and disease of all animals, we still understand little about mechanisms underlying microbial specificity for hosts and tissues or microbial contributions to host biology. My lab investigates a tripartite association in which nematodes of the genus *Steinernema* parasitize insects by virtue of their mutualistic association with *Xenorhabdus* bacteria. My talk will focus on the molecular basis of species specificity between the nematodes and bacteria. Understanding NilB function in *Xenorhabdus*-*Steinernema* mutualism will provide insights into NilB homolog function in human associated microbes.

**DAN KNIGHTS**

Assistant Professor
Department of Computer Science and Engineering
University of Minnesota

“Diet and microbiome: Which came first, the chicken nuggets or the Eggerthella?”

Although we have been co-evolving with our microbial symbionts for ages, we have only known of their existence for a few centuries, and we have only begun to understand their vast molecular diversity in the last few years. In addition to protecting us from infection by pathogens, and aiding in the education of our immune systems, they help us extract nutrients from our diets. Indeed, diet appears to be one of the main drivers of animal gut bacterial profile. In this talk I will discuss diet and gut microbiome variation in ancient humans, yogurt-eating mice, and Malawian children. We find that long and short-term dietary patterns are associated with taxonomy and metabolic capabilities of the microbiome, and that microbiome composition mediates the effectiveness of diet interventions. I will also present new results linking human genotype to shifts in the gut microbiota.

**MANISH RAIZADA**

Associate Professor
Department of Plant Agriculture
University of Guelph, Ontario, Canada

“Conservation and diversity of seed associated endophytes in Zea across boundaries of evolution, ethnography and ecology”

Endophytes are microbes that live inside plants without causing disease. We asked whether endophytes were conserved in Zea as it became domesticated from its wild ancestor (teosinte) to modern maize (corn) and moved from Mexico to Canada. One key finding was that seed endophyte community composition appeared to co-evolve with host plants. However, there was a core microbiome that was conserved in Zea seeds across boundaries of evolution, ethnography and ecology. Furthermore, the majority of seed endophytes in the wild ancestor persist today in domesticated maize. Cultured microbes were evaluated for multiple traits including their ability to grow on nitrogen-free media, solubilize phosphate, antagonize pathogens, reduce ethylene and produce auxin. GFP tracking confirmed that some seed endophytes could spread systemically. One seed isolate, *Enterobacter asburiae*, was able to exit the root and colonize the rhizosphere. Zea-microbe relationships will be discussed in the context of ecology, crop domestication, selection and migration.

**LINDA THOMASHOW**

Research Geneticist
Departments of Microbiology and Plant Pathology
Washington State University

“Control of cereal root diseases in dryland agroecosystems”

Indigenous and introduced strains of fluorescent *Pseudomonas* spp. that produce antibiotics in the rhizosphere of cereals can promote plant growth and suppress root diseases. Our work has focused on strains that produce phenazines and 2,4-diacetylphloroglucinol, compounds inhibitory to a wide range of soilborne plant pathogenic fungi. We have shown that indigenous populations of these bacteria are genetically diverse and that their distribution in soils of the Inland Pacific Northwest depends on levels of annual precipitation. Current studies are focused on genomic analyses of these bacteria and the identification of pathways that may help to explain the adaptation of phenazine-producing pseudomonads to arid conditions. We also are exploring the impact of water availability on the composition of the microbial community of the wheat rhizosphere.

**PETER TIFFIN**

Associate Professor
Department of Plant Biology
University of Minnesota

“Genomic variation and selection in mutualistic Sinorhizobia bacteria”

Sinorhizobia-Medicago is a model system for understanding the genetics of the legume-rhizobia mutualism, a mutualism that is an important contributor of plant available nitrogen to natural and managed ecosystems. I'll present results from work aimed at understanding the functional importance of structural variation within Sinorhizobia as well as relative strength of selection acting on horizontally transferred and duplicated genes. I'll also discuss the evolution of host genes that have been implicated as having a direct role in the mutualism. The work provides insight into the genetic basis of naturally occurring variation in this well-studied mutualism and highlights some of the challenges likely to be met when studying more complex and less-well understood microbe-host relationships.

Thank you for attending.

Please direct any comments or questions to mpgi@umn.edu

THE MICROBIAL & PLANT GENOMICS INSTITUTE

4th Annual Fall Symposium



Contributions of microbes to eukaryotic fitness

Thursday, August 29th, 2013

Hosted by Nathan Springer and Jeff Gralnick
Cargill Building for Microbial and Plant Genomics
Seminar Room 105

