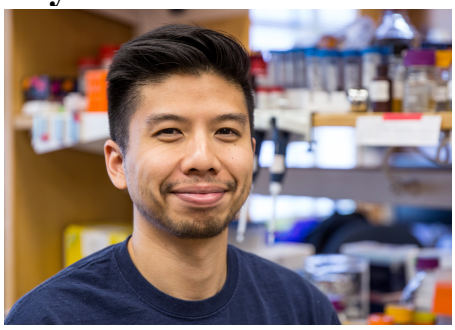
Luis Escobar

Bio:
Luis Escobar is Doctor of Veterinary Medicine, Master in wildlife management and veterinary sciences, and PhD in disease ecology. His work focuses on the application of ecology and biogeography to the study distribution and emergence of infectious diseases. His laboratory explores classic and new theoretical frameworks and methods for investigating the linkages between environmental change and disease dynamics. Escobar research includes multi-parasite, multi-host diseases systems for vector-borne diseases such as dengue and leishmaniasis, bat-borne diseases such as vampire-bat rabies, and water-borne diseases such as cholera. Due to the research niche of the Escobar's Lab, he is generally involved in additional studies of biodiversity conservation and climate change. His research has three focal themes, which in turn are the main lines of his academic program: [1] Diseases Biogeography, [2] Global Change, and [3] Ecoinformatics.

Title:
Macroecology of Zoonotic Diseases

Abstract:
Infectious diseases do not occur at random across time, host species, or geographic areas. Instead, infectious diseases have patterns that make them predictable. Many infectious diseases, especially zoonotic diseases, circulate in complex systems that may include diverse vector species and host reservoirs. Thus, classic epidemiological approaches may have limitations to capture important signals in complex zoonotic disease systems. Macroecology aims to understand major patterns on the distribution of biodiversity accounting for evolutionary and ecological signals from many taxa. This talk will provide a brief overview of the field of macroecology. Then, we will explore potential applications of macroecology to understand zoonotic diseases, including the effects of climate and landscape change on the emergence and expansion of infectious diseases. Finally, ongoing macroecological research at CeZAP will be presented to promote intellectual exchange and collaboration among researchers at CeZAP and beyond.

Bryan Hsu



Bio:
Bryan is an Assistant Professor in the Department of Biological Sciences at Virginia Tech. His current research interests include understanding how phages influence bacterial consortia, their implications for the microbial ecology within the gut, and ultimately how phages and their communities can be modulated for therapeutic purposes. He is also interested in developing biomaterials for improving delivery and diagnosis within the gastrointestinal tract. Prior to starting at VT in January 2020, Bryan was a Rosenbloom Postdoctoral Fellow at Harvard Medical School in the lab of Dr. Pamela Silver studying the effects of lytic phages on defined commensal bacterial communities in the gut in collaboration with Dr. Georg Gerber. He earned his PhD in Chemistry at MIT developing polymeric drug delivery formulations in the lab of Dr. Paula Hammond. Bryan also holds bachelors' degrees in Chemical Engineering and Materials Science from the University of California, Berkeley.

Title:
Characterizing and reprogramming the gut microbiome

Abstract:
Bacteriophages (phages) constitute an interesting yet understudied aspect of the gut microbiome. By preying upon bacterial species, these prokaryotic viruses have the potential to influence microbial communities with downstream host effects. In mouse models of the gut microbiota, we found that phage predation on a subset of species in a defined consortium can induce a broader remodeling of this microbiota leading to modification of the metabolome. Furthermore, we have engineered temperate phages--those phages capable of integrating into the bacterial chromosome--to repress the bacterial virulence factor Shigatoxin and show that when applied to a mouse model this antivirulence phage significantly reduces toxin production in vivo without relying on bacterial lysis. In continuation, we developed a more generalizable strategy that combines an engineered temperate phage expressing dCas9 with an aqueous-based encapsulation formulation to enable the programmable targeting of a specific bacterial gene in the mammalian gut by a single oral dose. Together, these strategies indicate a potential for the use of phages as specific modulators of the gut microbiota.

Sophie Wenzel

Bio:
Sophie Wenzel, MPH, DrPH is Associate Director for the Center for Public Health Practice and Research, and Assistant Professor of Practice in the Department of Population Health Sciences. She holds a DrPH in Public Health Leadership from the University of Illinois at Chicago, an MPH in International Health and Population Studies from Emory University, and a BS in Linguistics and Spanish from Georgetown University.
Dr. Wenzel started her career in public health when she joined the Peace Corps and was sent to rural Paraguay to promote maternal, child, and adolescent health. She was selected to join the Centers for Disease Control Public Health Prevention Service, with which she served one year at the CDC in Atlanta and two years in Alaska. She was awarded the Bales-Bradford Award for Excellence in Public Health Leadership at the end of her three years. She then took a position managing the State of Alaska's Adolescent Health Program.

In her current capacity, Dr. Wenzel promotes collaboration between faculty, students, and community partners to enhance public health in Southwest Virginia and beyond. She oversees multiple evaluation and research projects across the region and state. Dr. Wenzel's research and professional interests include maternal child and adolescent health, youth risk behaviors, international health, sexual and reproductive health, healthy eating/active living, community engaged research and participatory methods, and evaluation of public health programs.

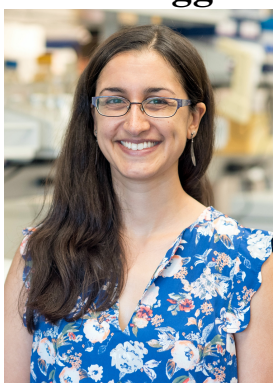
Her position is partially supported by the New River Health District of the Virginia Department of Health, through which Dr. Wenzel coordinates the New River Academic Health Department.

Title:
Meaningfully engaging communities in public health research and initiatives.

Abstract:

Through the Center for Public Health Practice and Research, Dr. Wenzel conducts community-engaged research throughout Southwest and Southside Virginia and beyond, with a focus on rural and health disparate populations. She uses qualitative and applied participatory research methods to engage community partners in her research. Her research addresses a wide range of public health topics including adolescent health, sexual and reproductive health, and substance use. In her seminar presentation, she will highlight several research projects that she has conducted through the Center for Public Health Practice and Research, with both Virginia Tech and community partners.

Nisha Duggal



Bio:
Nisha Duggal is an assistant professor in the Department of Biomedical Sciences and Pathobiology in the Virginia-Maryland College of Veterinary Medicine at Virginia Tech. She received her PhD in the laboratory of Dr. Michael Emerman at the Fred Hutchinson Cancer Research Center and the University of Washington in Seattle, where she studied the evolution of the intrinsic immune response to HIV-1 and other retroviruses in primates. She completed her postdoctoral training in the laboratory of Dr. Aaron Brault at the CDC in Fort Collins, CO where she studied West Nile virus, Zika virus, and other flaviviruses using animal models. Her current work investigates the co-evolution of emerging mosquito-borne viruses and their hosts. The lab studies Zika virus sexual transmission and Usutu virus pathogenesis using molecular virology and phylogenetics in order to identify mechanisms of viral emergence and disease.

Title:
Persistence of Zika virus in the male reproductive tract

Abstract:
Abstract: Zika virus (ZIKV) is an emerging arbovirus that caused a pandemic in the Americas in 2015-16 and is estimated to have caused 800,000 cases, including thousands of cases of congenital ZIKV syndrome in infants. ZIKV is also transmitted sexually and *in utero*, which leads to devastating birth defects in babies and is a unique feature amongst mosquito-borne viruses. During the ZIKV pandemic, we established a human cohort of 185 ZIKV-infected men to study the sexual transmission potential of ZIKV. We found that shedding of ZIKV in semen occurred in 50% of infected men and persisted for longer than 6 months in some men. Furthermore, in our mouse model of sexual transmission, which recapitulates the ZIKV replication kinetics in human semen, sexual transmission of ZIKV from infected males to females enhanced infection of the female reproductive tract and fetuses compared to subcutaneous exposure of females to ZIKV. Thus, we identified sexual transmission of ZIKV as a significant risk factor for ZIKV *in utero* transmission in pregnant women. In our current work, we are investigating the persistence of ZIKV in the male reproductive tract and the mechanisms of sexual transmission.

Joseph Hoyt

Bio:
Joseph Hoyt is an assistant professor in the department of Biological Sciences. He completed his PhD at the University of California, Santa Cruz in Ecology and Evolutionary Biology. Joseph has primarily worked on emerging infectious diseases of wildlife and his research interests lie at the intersection of disease ecology and conservation biology. Specifically, he has worked extensively on the emerging fungal disease of bats, white-nose syndrome. In this system, he has answered questions focused on exploring connections that lead to pathogen transmission within and among species and understanding the contribution of environmental pathogen reservoirs to infectious disease outbreaks. His lab focuses on understanding how free-living pathogen stages contribute to various aspects of disease dynamics including pathogen transmission and virulence.

Title:
Sit-and-wait pathogens: The role of environmental pathogen reservoirs in infectious disease dynamics

Abstract:
Infectious disease outbreaks can have severe effects on host population. The ability of pathogens to survive as a free-living stage has the potential to exacerbate impacts to hosts by preventing pathogen fade-out, maintaining high levels of exposure, influencing pathogen virulence and increasing the probability of host extirpation. While many studies have highlighted the importance of environmentally meditated transmission and the presence of environmental pathogen reservoirs, few studies have examined the contribution of this important pathogen attribute in infectious disease dynamics. In this talk we will explore how the inclusion of environmentally mediated transmission influences disease outbreaks, how the extent of the pathogen contamination in the environment influences disease severity and mortality in hosts, and finally explore future directions aimed at understanding how frequency, dose, and duration of exposure differ between host to host and environment to host contacts.

Clay Wright

Bio:

Current Position: Assistant Professor, Biological Systems Engineering, Translational Plant Science Program, Virginia Tech, Blacksburg VA USA.

Education: Postdoctoral Fellow, Departments of Biology and Electrical Engineering, University of Washington, 2014-2018; Ph.D., Chemical and Biomolecular Engineering, Johns Hopkins University, 2014; B.S., Chemical and Biomolecular Engineering, North Carolina State University, 2008

Non-scientific Interests: My 1.5 year old daughter, mountain biking, being outdoors, cooking, and fermenting.

Brief bio: Clay Wright's research aims to understand how signaling networks facilitate both plasticity and robustness in plant form and function and to harness this knowledge to engineer proteins, signaling networks, and biosynthetic pathways for applications in agriculture and biotechnology.

The Wright Plant Synthetic Biology lab integrates approaches from synthetic and computational biology, protein engineering, bioinformatics, molecular evolution, and genetics to quantify signaling dynamics, genetic interactions, and functional relationships in plant signaling. In the lab, we utilize synthetic biology and genetically tractable model bacteria, yeast, and plants to measure signaling dynamics by recapitulating small modules of complex signaling pathways in a bottom-up engineering approach. We also build tools, such as biosensors and bioinformatics tools, to facilitate quantitative top-down genetics approaches to understanding signaling.

Title:

Synthetic Biology: Quantifying the known unknowns and discovering the unknown unknowns

Abstract:

We now have the ability to precisely engineer plant genomes. However, in most cases we do not know which genetic changes will yield a desired trait. My group aims to fill in this knowledge gap by combining bottom-up approaches from engineering and

top-down approaches from biology to gain a quantitative understanding of plant signaling. Particularly, we use synthetic biology to measure the functional effects of natural and non-natural genetic variation in signaling networks and use this measure of functional variation to predict plant phenotype and identify “engineerable” nodes of signaling networks. In the past we have used this approach to identify a natural genetic variant in a growth hormone (auxin) receptor which predictably alters root architecture. We have also discovered and quantified epistatic interactions between auxin receptor gene family members. We are currently expanding this approach to explore pathogen and herbivore defense signaling (jasmonate)—a common target for pathogen interference with plant immunity. We aim to fast forward this evolutionary arms race between plants and pathogens by combining directed evolution with this synthetic recapitulation of jasmonate signaling and the pathogen effector genes that sabotage this defense signal.