
MYCOLOGICAL SOCIETY
OF AMERICA

Special Topics Award Winners

The Special Topics Awards support studies in the area of Applied Mycology. The awards are used to support investigations involving applications of fungi to pratical and innovative problems.

Jacob Hopkins
Postdoctoral Scholar
The Ohio State University



BIOGRAPHY

Jacob Hopkins is a USDA postdoctoral fellow advised by Alison Bennett (The Ohio State University). Prior to his postdoc, Jacob earned his PhD in the lab of Benjamin A. Sikes (University of Kansas), and his BS from Indiana University Bloomington. In July 2021 he will start his postdoctoral fellowship at OSU, where he will use the intermediate disturbance hypothesis framework to study how soil microbial responses to tillage and environmental stresses influence soil health and crop production. Applying the intermediate disturbance framework to agricultural systems is a promising avenue for maximizing microbial contributions to agricultural sustainability and food security.

Linking Fungal Community Composition and Function in a Frequently Disturbed Ecosystem

SYNOPSIS

Receiving an MSA Special Topics award was a boon for my PhD research, as it allowed me to develop my fledgling research program. I applied for these funds as a third year PhD student with a strong interest in disturbance-microbial interactions and their implications for ecosystems. With the help of my colleague Tatiana Semenova-Nelsen and advisor Benjamin A. Sikes, I designed a project that tested the effect of prescribed fire and mowing on fungal communities and fungal saprotrophic enzyme production in tallgrass prairies. I have previously worked in other disturbance mediated ecosystems (e.g. Longleaf pine savannas - fire), and this award was instrumental in expanding my work into a new system where I could explore how land management influences fungal communities and enzyme production. While it comes as no surprise that fungi are critical components of terrestrial ecosystems due to their important functional capabilities, linking community structure to function can be difficult. With the assistance of this award, I was able to link fungal community and functional responses to land management, and show that soil fungi not only have the ability to quickly react to changes in nutrient availability, but also are functionally resilient in the long term to management disturbances. By including microbial roles in disturbance ecology, we can improve our understanding of the forces that structure and maintain ecosystems while opening up the “black box” of soil ecology.

Carlos J. Pardo De la Hoz
Ph.D. Candidate
Duke University



BIOGRAPHY

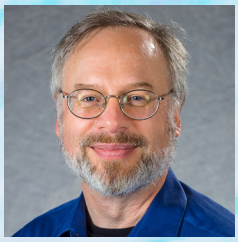
Carlos is a Ph.D. Candidate in the Biology Department at Duke University, where he is advised by Dr. François Lutzoni. He is originally from Santa Marta, Colombia, and obtained his BSc. in Microbiology from Universidad de Los Andes in Bogotá. Carlos has always been interested in the ecology and evolution of interactions between fungi and photoautotrophic organisms. As an undergraduate, he studied host specificity of *Colletotrichum* species towards important crop species in Colombia under the supervision of Dr. Silvia Restrepo. His current research focuses on the spatiotemporal factors that shape the interactions between lichen-forming fungi and their cyanobacterial partners.

Do Lichen-Forming *Peltigera* Species Select *Nostoc* Photobionts According to Their Capacity to Fix Nitrogen?

SYNOPSIS

One of the main questions that I am interested in is how symbiotic organisms "choose" their partners. I address this question using the symbiosis between species from the lichen-forming genus *Peltigera* and its *Nostoc* cyanobacterial partners. In this lichen symbiosis, fungi tend to be "choosy" with regard to their cyanobacterial partners. Since the *Nostoc* that associate with *Peltigera* are able fix nitrogen (N), it is possible that their N-fixing capabilities play role in partner selection. The N-fixing process can be mediated by three enzyme complexes that are dependent on different metals: molybdenum (Mo), vanadium (V), or iron (I). Although the Mo-dependent complex is the most efficient, recent evidence suggests that the V-dependent (*vnf*-encoded) complex might be the most prevalent in boreal ecosystems. Our preliminary observations raised the hypothesis that *Peltigera* species in the boreal biome preferentially associate with Nostoc strains with two copies of *vnf*. The funds from the MSA Special Topics Award were incredibly helpful for setting up a workflow for large-scale sequencing of molecular markers from *Peltigera* and *Nostoc* symbionts from hundreds of lichen thalli sampled in the boreal biome in Alberta, Canada. This allowed us to characterize their interactions and we are now screening the *Nostoc* partners to determine the number of *vnf* copies and address whether the *Peltigera* species prefer *Nostoc* that have two *vnf* copies. The results of this study will advance our understanding on the role of N-fixation in structuring symbiotic communities in the boreal biome.

Chris Schardl
Professor
University of Kentucky



BIOGRAPHY

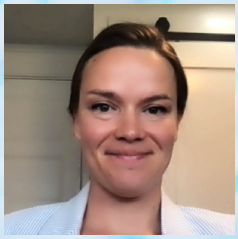
Chris Schardl is Chair of Plant Pathology and Harry E. Wheeler Professor of Plant Mycology at the University of Kentucky. He received his PhD in Biochemistry at the University of California, Davis (1983) with plant bacteriologist C.I. Kado, and did a postdoc at the Plant Breeding Institute in Cambridge, England with plant molecular biologist David Lonsdale. In 1985 he started his new assistant professorship at the University of Kentucky with a new interest: fungi. He has built an eclectic program on fungal secondary metabolism, genetics, genomics, evolution and ecology, all with special attention to the seed-transmitted endophytes of genus *Epichloë* and relatives. His group discovered fungal genes for ergot alkaloids, loline alkaloids and indolizidine alkaloids. Meanwhile, moving from ITS-based to multilocus phylogenies of *Epichloë*, they discovered that many protective mutualists are diploid or even triploid interspecific hybrids, and that their genome structures facilitate massive chemotypic diversification. Chris Schardl is a fellow of the Mycological Society of America and the American Phytopathological Society, and was the Scientific Program Director of the 11th International Mycological Congress in 2018. He has mentored 21 graduate students, 24 postdocs, and more than 80 others, and has published 144 peer-reviewed and 47 invited papers. His latest obsession is the society journal *Mycologia*, for which he has served as Associate, Executive, Reviews and, currently, Managing Editor.

Detoxifying a Fungal Endophyte Using CRISPR?

SYNOPSIS

An important reason that tall fescue is the most widely planted forage and conservation grass in the United States is its seed-transmitted endophyte, *Epichloë coenophiala*, which enhances stand longevity, stress tolerance and biomass production. Unfortunately, the common *E. coenophiala* strains also produce ergot alkaloids that can be toxic to livestock and wildlife. A possible resolution of this dilemma is suggested by a notable feature of the tall fescue-*E. coenophiala* symbiosis; namely, that it is only ever transmitted via seeds from mother to daughter plants. Therefore, if the ergot alkaloid genes can be eliminated the resulting mutant strain can be put back into the grass to generate ergot alkaloid-free cultivars of tall fescue. However, major obstacles to this approach are that *E. coenophiala* is a complex interspecific hybrid with two copies of the ergot alkaloid gene cluster, transgenic approaches to mutation are very tedious in this slow-growing fungus, and any new DNA in its genome raises regulatory and public concerns. Our Special Topics Award funded a CRISPR-based experiment to use single-guide RNAs and the Cas9 protein to remove ergot alkaloid genes. The approach was highly successful. Not only could individual genes be deleted, but entire 11-gene clusters up to 196 kb in length also could be deleted, and we even obtained mutants that had both ergot-alkaloid gene clusters cleanly removed. These mutant endophytes will directly benefit livestock producers when used in pastures, and wildlife when used in reclaimed strip mines, roadsides and lawns.

Jessie Uehling
Professor
Oregon State University



BIOGRAPHY

Dr. Uehling is an Assistant Professor of Fungal Biology and OSC Fungal Herbarium Curator in the Department of Botany and Plant Pathology at Oregon State University. Her labs' research offers insight into how fungi function in symbioses with bacteria, plants, and humans and how fungal genomes evolve as a consequence. They are currently using evolutionary genomics to study bacterial fungal interactions. Their goal is to understand mechanisms of fungal endosymbiont interactions and the consequences for genomic architecture as populations of fungi and endosymbionts evolve together. To answer these questions they use computational genomics, comparative functional genomics, microfluidics, microscopy, and phylogenomics.

Before her time at OSU, Dr. Uehling completed postdoctoral research together with Drs. John Taylor, Anita Sil, Bridget Barker, and Rachel Brem at the University of California Berkeley and U.C. San Francisco studying population genomics of Valley Fever (caused by *Coccidioides*, *Onygenales*, *Ascomycota*). This research involved sequencing and analyzing the genomes of >100 clinical *Coccidioides* isolates, an extraordinarily large computational endeavor. The goal was to identify novel therapeutic targets by correlating genetic diversity with novel virulence phenotypes in a clinical population using genome wide association studies or GWAS. The MSA Special Topics Award made her fungal GWAS research possible, jumpstarting a new phase of evolutionary genomics driven advances in clinical Valley Fever research.

Computational Infrastructure for *Coccidioides* Population Genomics

SYNOPSIS

I am grateful and honored to receive the MSA Special Topics as a postdoctoral researcher on my way into a faculty position. These funds allowed me to rapidly conduct cutting edge genomics based research. Further, they enabled me to hone my bioinformatics expertise, a skill set I am now passing on to my trainees in a new course at OSU titled "Population Genomics" in which students get hands on experience manipulating *Coccidioides* sequence data in real time. With MSA funds, I was able to purchase a custom designed computer with remote log in access, over 500TB of storage capacity and lightning-fast analytical capacity. Population analyses including hundreds of fungal genomes require unique computational resources, and therefore the Special Topics Award enabled research that wouldn't otherwise have been possible. One of my long term goals is to establish a diverse set of future Mycologists who are capable bioinformaticians answering impactful questions about fungal biology. With the help of the MSA Special Topics Award, I am making substantial progress toward that goal.