# 2025 Annual Meeting Abstract Book

Fungal Futures:
Cultivating Mycology
and Mycologists

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## 93rd Annual Meeting of the Mycological Society of America

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# Table of Contents

# Table of Contents (Continued)

## SYMPOSIUM 1:
## Future Fungaria: Re-Envisioning the Roles and Curation of Biological Collections in an Age of Increasing Need and Decreasing Resources

*Todd Osmundson (Chair), Caitlin DeSilvey (Presenter), Barbara Thiers (Presenter), Andrew Wilson (Presenter), Timothy James (Presenter), Christian Schwarz (Presenter)*

**Overall Abstract** The recent decision by Duke University to close their herbarium/fungarium collections has caused widespread concern in the biological collections community, highlighting the fact that even large, renowned collections are vulnerable to threats such as resource and staffing shortages and changing administrative priorities. Simultaneously, an explosion in citizen scientist-led mushroom DNA barcoding projects is producing a number of voucher specimens that could easily overwhelm curatorial resources in existing fungaria. In “Curated Decay,” cultural geographer Prof. Caitlin DeSilvey takes the unorthodox position that the persistence of memory and meaning doesn’t always require preservation of cultural artifacts and sites in a pristine state. Extending DeSilvey’s philosophical framework to biological collections could provide a starting point for some necessary and challenging discussions about how to manage biological collections in an age of increasing collection potential but diminishing curatorial resources. This symposium and discussion will raise questions about the future of mycological collections, including how they can remain relevant and how new concepts about collections and their ownership could address future needs and threats.

### Curated Decay, or the Decay of Curation?

Caitlin DeSilvey, University of Exeter

The root of the word ‘curation’ is the Latin curare, ‘to tend’ or ‘to care.’ The sense in which it is used to refer to the act of arranging or assembling emerged only in the 19th century. In this presentation, I will explore a spectrum of different modes of care applied to objects in collections – from strict preservation through to pragmatic and palliative approaches. I’ll also consider how these modes of care relate to the broader contemporary context of “increasing collection potential but diminishing curatorial resources” noted in the symposium description. In Curated Decay: Heritage Beyond Saving (2017), I argued that objects valued for their cultural heritage significance could (in certain contexts) be released to allow for their ecocultural potential to emerge. In this presentation, I’ll consider how objects valued for their natural heritage significance relate to, and complicate, this argument. I’ll do so by sharing recent examples of experimentation in the Netherlands and in Denmark, in which collections curators have acknowledged or invited in agencies of decay and deterioration. I’ll consider what elements of this work might be productively applied in the curation of fungaria and other biological collections—but also flag the risk of using such ‘post-preservation’ thinking as a pretext for withdrawal of curatorial resources.

### Too Big to fail: New Directions and Old Specimens at the University of Michigan Fungarium

Timothy James, University of Michigan

The University of Michigan Fungarium (MICH) is one of the largest and taxonomically significant collections of fungi with over 280K specimens. Critically, the MICH collection has over 2,300 holotype specimens requiring permanent preservation and access for taxonomic stability. The collection was built through the hard work of many mycologists, such as Alexander Smith and Lewis Wehmeyer, at the university during the “golden age” of collections-based research and taxonomy. Since this golden age, the number of staff and the duties of the staff have largely shifted due to changes in scientific and academic pressures. This leaves us with the pressing question: how do we manage, maintain, and encourage use of such a large collection that isn’t getting any younger? In this talk, we will review some of the challenges of preserving and enhancing large collections while at the same time growing in new directions. Specifically, we will discuss collaborations with citizen scientists, our efforts to generate DNA barcodes for collections, and our expansion into cryopreserved specimen curation. New directions with old specimens provide an opportunity to cash in on the golden age.

### Data is Not the Destination: Culture and Community Science

Christian Schwarz, Norris Center for Natural History, University of California, Santa Cruz

In the past century, human impacts on the natural world have accelerated, despite a parallel increase in our awareness of these impacts. The practice of science as an engine for the production of knowledge has often been invoked as a counteracting force against. But community science operates differently than "normal science". What are the roles of aesthetics, spirituality, and community in this bottom-up mode of knowledge-making? How can we incorporate a broader range of motivations and goals into an expansive paradigm of community science? Where might this practice lead us beyond mere data?

### Evaluating the Future of Fungaria: What Are the Opportunities for Future Success?

Andrew Wilson, Denver Botanical Gardens

Like many natural history collections fungaria struggle to stay afloat due to the limited availability of resources. However, fungi, especially macrofungi (mushrooms and fungi with macroscopic reproductive structures), are going through a renaissance of public interest. Therefore, now is the perfect opportunity to evaluate and address shortcomings in the support of fungal collections. This presentation will examine several topics relating to future opportunities for supporting fungaria. The first topic reviews the responses to two 2024 surveys that explored the state of North American fungaria to understand their perspectives on various challenges and opportunities. Another topic explores fungaria as a resource for amateur mycologists. Through groups like the North American Mycological Association, there are increasing contributions from the amateur community to document fungal diversity emphasizes the potential for the public to support collections. Next is the role fungaria have in fungal conservation efforts. Natural heritage programs are increasingly enthusiastic in incorporating funga in addition to the fauna and flora their programs. In order for these programs to add fungal data to NatureServe and IUCN Red Lists, natural heritage programs rely on mycologists generating lists of rare taxa produced from fungarium records. Fungaria will be crucial for the development of the goals in the topics listed above. These collections will also be needed for training the next generation of fungal taxonomists and systematists that continue to pursue these goals. This presentation will examine these topics in an effort to inspire hope in the future of fungaria and the opportunities available to them.

### A Strategic Approach to Protecting Fungal Collections and Associated Data

Barbara Thiers, The New York Botanical Garden

The U.S. community of fungal biodiversity collections has significant strengths. Most collections have been digitized, with their data available online, and infrastructure exists to further enhance these resources by linking specimen vouchers to gene sequences, illustrations, images, notes, publications, and observations. A recent workshop organized by the Biodiversity Collections Network highlighted broad interest in integrating collections-derived data with a larger network of biological and environmental data. Under normal circumstances, the primary challenge facing mycological collections has been the lack of a critical mass of professional mycologists to lead outreach and funding efforts, train students to continue this work, and participate in broader collection community initiatives. However, in addition to these ongoing concerns, government funding cuts are now creating instability among institutions that house collections, increasing the risk of ill-considered decisions that could lead to permanent losses. To address these challenges, collections-focused organizations have formed a task force to assist institutions in making informed decisions that will preserve the long-term utility of their collections. Those managing fungal collections can take proactive steps by developing strategic plans aligned with their parent institutions and creating disaster preparedness plans that account for the specific needs of fungal collections, including options for short- and long-term offsite storage. The Mycological Society of America can also play a vital role by establishing an emergency fungarium fund modeled after the ASPT Herbarium Fund.

## SYMPOSIUM 2:
## Mobile Genetic Elements and Their Role in Fungal Diversity and Evolution

*Emile Gluck-Thaler (Chair), Alexandra Weisberg (Co-chair), Alex Zaccaron (Presenter), Michael Habig (Presenter), Nicolas Corradi (Presenter), Sanzhen Liu (Presenter), Aaron Vogan (Presenter), Samuel O'Donnell (Presenter)*

**Overall Abstract** Advances in sequencing technology and the ever broadening scope of genomics research have revealed new dimensions of diversity within fungal genomes. Just as fungi often colonize plants and animals, fungal genomes are themselves colonized by multitudes of diverse mobile genetic elements. These DNA-based entities replicate semi-independently of fungal genomes yet are fully nested within them. We now know that fungi harbor elements ranging in size from several hundred base pairs in length to massive genomic islands and entire accessory chromosomes, with new classes of elements being discovered at breathtaking speed. Once thought to be little more than junk or "selfish" DNA, mobile elements and repetitive elements in general are increasingly shown to have important consequences for fungal evolution and function. This session will explore how these elements shape fungal physiology, ecology, and evolution across the fungal tree of life by highlighting diverse perspectives and approaches ranging from the molecular to the computational.

### Mobile Genetic Elements in the Evolution of the Fungal Pathogen Sphaerulina Musiva

Alex Zaccaron, Department of Botany and Plant Pathology, Oregon State University

The objective of this study is to better understand genomic factors influencing the evolution of Sphaeria musiva, an important fungal pathogen causing Septoria leaf spot and stem canker disease of poplar trees. The genomes of 18 geographically diverse North American isolates of S. musiva were sequenced using Oxford Nanopore technology. The genomes were assembled using Canu and transposable elements were predicted using RepeatModeler and RepeatMasker. Presence of mobile starship elements was performed using the starfish package. Comparative analyses revealed substantial variation in transposable element (TE) content among isolates, ranging from 7% to 16% of their genomes. Notably, higher TE abundance was observed in isolates from Oregon, British Columbia, and Alberta, regions outside the native range of S. musiva. This was consistent with lineage-specific proliferation of TEs, that also largely accounted for differences in chromosome size among isolates. Additionally, we identified a 300 kb region exhibiting presence/absence variation among isolates. This region corresponded to a predicted mobile starship element carrying over 40 cargo genes. These cargo genes encode proteins with diverse functions, including predicted roles in toxic anion export and host-pathogen interactions. Surprisingly, this starship element was detected in only 7% of a large collection of 130 North American isolates, showing no evidence of fixation within S. musiva subpopulations. Interestingly, a genetically similar but partially conserved starship element is present in some isolates of the wheat pathogen Zymoseptoria tritici, a close relative of S. musiva. In Z. tritici, the element is integrated 3 2025 MSA Annual Meeting into dispensable chromosome 14, and represents nearly 45% of the chromosome's total size. These findings advance our understanding of genome plasticity in fungal pathogens, highlighting the role of mobile genetic elements in shaping chromosomal architecture and adaptive potential in the fungal pathogens S. musiva and Z. tritici.

### Horizontal Transfer of Accessory Chromosomes in Fungi – a Regulated Process for Exchange of Genetic material?

Michael Habig, Kiel University

Horizontal transfer of entire chromosomes has been observed in several fungal pathogens, often with a significant impact on the fitness of the recipient fungus. Notably, all recorded cases of horizontal chromosome transfer (HCT) have predominantly involved accessory chromosomes, while the transfer of core chromosomes is rare or absent. Despite these findings, the mechanisms driving HCT and the factors determining its specificity for accessory chromosomes remain poorly understood. Here, we show that an accessory chromosome was frequently horizontally transferred between strains of the asexual insect pathogen Metarhizium robertsii during co-infections of an insect host. The same chromosome was also transferred to the more distantly related M. guizhouense, representing an instance of HCT between species. No other genetic material was co-transferred, highlighting the specificity of horizontal transfer for this accessory chromosome. Moreover, this mobile accessory chromosome contains genes that could affect chromosome segregation and chromatin conformation, potentially playing a role in its preferential horizontal transmission. Intriguingly, we find similar functions encoded on horizontally transferred accessory chromosomes in other fungi. This raises the possibility that horizontally transmitted chromosomes could carry the machinery for their own transfer, suggesting that such a transfer might be a regulated process.

### Diversity, Evolution Regulation of Transposable Elements in Glomeromycotina

Nicolas Corradi, University of Ottawa

We hypothesize the genome of all AMF lineages separate into two A/B compartments with distinct gene and TE densities. The A stable compartment carries conserved genes, while the B compartment is more rich in TE and candidate secreted proteins. To test this hypothesis, we investigate TEs diversity and density in all available AMF genome assemblies. We uncovered multiple, family-specific bursts of insertions in different species, indicating variable past and ongoing transposable element activity contributing to the diversification of arbuscular mycorrhizal fungi lineages. We also found that transposable elements are preferentially located within and around candidate effectors/secreted proteins, as well as in proximity to promoters. Altogether, these findings support the role of transposable elements in promoting the diversity in proteins involved in molecular dialogs with hosts and, more generally, in driving gene regulation. The mechanisms of transposable element evolution we observed in these prominent plant symbionts bear striking similarities to those of many filamentous plant pathogens.

### Dispensable Mini-Chromosomes in Blast Pathogens

Sanzhen Liu, Kansas State University

The genomes of Magnaporthe oryzae (synonym Pyricularia oryzae), the fungal pathogen that causes blast disease on diverse grass species, have seven core-chromosomes and may contain additional mini-chromosomes. Here, we seek to understand the evolution of mini-chromosomes and the potential driving forces. We have explored mini-chromosomes using long-read genome sequencing and assembly, chromosomal karyotyping, and computational approaches. Our data and other reports indicate that mini-chromosomes are prevalent in M. oryzae isolates. The number and composition of mini-chromosomes vary significantly among isolates from different host-adapted pathotypes and among isolates from the same pathotype. Such mini-chromosomal variation can be even observed in different cells of an isolate. Analysis of wheat blast strains (Triticum pathotype) collected from different years between 1986 and 2020 revealed the presence of mini-chromosomes in all recent wheat strains but their absence in most of the strains collected before 1991, suggesting the preferential selection for strains carrying mini-chromosomes in recent years. Although mini-chromosomes in wheat blast pathogens are enriched with transposable elements, most also carry various effector genes, such as PWL2 and BAS1. Evidence indicates that the variation of effector genes on mini-chromosomes might play important roles in pathogen adaptation and the maintenance of high-level virulence. This talk will discuss the evolution of mini-chromosomes in wheat blast pathogens.

### Giant Transposons as a Crucible of Evolution

Aaron Vogan, Uppsala University

Horizontal gene transfer (HGT) disseminates genetic information between species and is a powerful mechanism of adaptation. Yet, we know little about its underlying drivers in eukaryotes. Giant Starship transposons have been implicated as agents of fungal HGT, providing an unprecedented opportunity to reveal the evolutionary parameters behind this process. These elements are unique in that they not only incorporate the genetic machinery for their own movement, but also mobilize a vast diversity of fungal genes. Through a combination of comparative genomic and molecular biology approaches, we have demonstrated that Starships are mobile within and between fungal genomes. We observe the recurrent transfer of Starships with adaptive cargo, such as genes for heavy metal resistance, between species including those in distinct taxonomic orders, showing how these elements frequently mediate rapid adaptation. Furthermore, we now have experimental validation that Starships can transfer between species under laboratory conditions. Our results demonstrate the key role Starships play in mediating HGT in fungi, elevating the importance of this process in eukaryotic biology.

### New Computational Toolkits for Exploring Starship Biology

Samuel O'Donnell, Department of Plant Pathology, University of Wisconsin, Madison

Giant cargo-carrying transposable elements, called Starships, are a recently described feature found in the genomes of filamentous fungi throughout the Pezizomycotina. These elements are characterised by a single conserved feature required for transposition: a tyrosine recombinase referred to as the captain that is located at one edge of the element. The remainder of the element, spanning 20-700kb, typically harbors genes that are unrelated to transposition but may confer beneficial traits to their host. However, the detection and analysis of these elements, particularly the automation of these processes, remains challenging. The only available toolkit for Starship annotation, starfish, offers several functions that aid in detection, but its approach is conservative and moderately reliant on contiguous genome assemblies. Here, we present additional tools and pipelines for a more comprehensive analysis of both Starships and Starship-like regions, including methods for identifying evidence of Starship-mediated Horizontal Gene Transfer (HGT) using public datasets. Additionally, using the Basidiomycota (which to date lack evidence for full-length Starships), we describe a new captain-agnostic approach for identifying undescribed giant cargo-carrying elements.  These tools can provide a more comprehensive description of Starship genome compartment and will help us better understand both Starship biology and their hosts.

## SYMPOSIUM 3:
## Fungal Bacterial Frenemies: Interaction Biology, Evolution, and Applications

*Jessie Karen Uehling (Chair), Daniel Farthing (Presenter), Daniyal Gohar (Presenter), Erin Nuccio (Presenter), Ben Haefner (Presenter), Giovana Slanzon (Presenter), Louis Berrios (Presenter), Nhu Nguyen (Co-chair), Nancy Keller (Co-chair)*

**Overall Abstract** Fungi and bacteria co-occur in nearly all habitats, underpinning the recent emergence of fungal bacterial interactions (FBI) as a fast-growing field. Appreciation of the ubiquity and diversity of FBIs has rapidly increased with DNA sequencing, metagenomic 1 2025 MSA Annual Meeting computational tools, and high-resolution imaging. Technological advances have enabled insights into the roles FBIs play in fungi pathogenicity, in structuring environmental and clinical microbial communities, and in understanding fundamental fungal biology. Emerging patterns in FBIs include their impact on each other's primary and secondary metabolism, nutrient acquisition and carbon cycling, applied disease development and management. The fundamental ways fungi and bacteria impact each other have implications for agriculture, biocontrol, drug development, ecological community modeling, remediation, biotechnology, and food production. The broad implications of these interactions have created strong interest in this nascent field, but research remains in its infancy. Deeper insights require coordination and development of new transdisciplinary research. This symposium will bring together speakers and topics to stimulate discussion and collaborations to drive this exciting area of fungal biology forward.

### Understanding Basidiobolus-Bacterial Interactions Using a Stabilized Microbiome Model

Daniel Farthing, Department of Botany and Plant Pathology, Oregon State University

Basidiobolus is a fungus that is adapted to different ecological niches. One stage of its life cycle occurs in the gut microbiome of species of amphibians and reptiles. In this environment, Basidiobolus is abundant, prevalent, and co-structured with the bacterial community. The Basidiobolus genome is enriched in genes annotated to encode for non-ribosomal peptide synthetases and other specialized metabolites. While many of these compounds are predicted to be involved in interactions with bacteria, their impact on the structure, function, and general ecology of the gut environment is not yet understood. We hypothesize that specialized metabolites produced by Basidiobolus decrease compositional and functional diversity of the bacterial community, shifting the relative abundance of specific taxa in a predictable direction.

To test this, a fecal sample from a lab-reared wood frog (Lithobates sylvaticus), raised in the absence of Basidiobolus, was cultured in multiple media conditions and serially transferred into fresh media every 48 hours. After the seventh passage of cells, composition of the cultures was assumed to be stable, and two additional transfers were conducted and treated with Basidiobolus crude extract or control. The 16S rRNA amplicon sequencing results from this stabilized microbiome model show that bacterial community composition is diverse, stable by the third passage at the family-level, and that Basidiobolus crude extract has a significant nonrandom effect. We will also present metagenome-assembled genomes (MAGs) data to examine functional shifts in the bacterial community and LC-MS2 results from the crude extract to characterize metabolites that may function in bacterial-fungal interactions. The stabilized microbiome approach employed in this study illuminates how Basidiobolus may influence the gut microbiome of herptiles. Additionally, the use of similar experimental methods should be considered an important tool for studying bacterial-fungal interactions. The stabilized microbiome approach employed in this study illuminates how Basidiobolus may influence the gut microbiome of herptiles. Additionally, the use of similar experimental methods should be considered an important tool for studying bacterial-fungal interactions.

### Evaluating the Role of Bacterial Endosymbionts in Evolution and Diversity of Plant-Associated Mucoromycota Fungal Communities

Daniyal Gohar, Oregon State University

Mucoromycota fungi are ecologically and economically significant, and yet they are amont the least understood fungal groups. As one of the earliest-diverging lineages, they engage in mutualistic relationships with plants while also functioning as decomposers. Environmental Mucoromycota fungi regularly harbor ancient and highly coevolved endosymbiotic bacteria (EB). The presence of endosymbiotic bacteria significantly impacts fungal biology, including metabolism, gene expression, and sexual reproduction. Despite their importance, knowledge of how EB impact Mucoromycota diversity and consequently plant-associated fungal community structure remains limited. We hypothesize that fungal endosymbiont interactions can alter fungal symbioses with other organisms, including plants, soil microbes, and fungi, producing testable predictions for fungal and plant community structures. To investigate the role of endosymbionts in ecological community assembly and the diversification of Mucoromycota, we collected soil samples from over 300 sites across California (USA) and South Africa. Leveraging the chitinolytic capabilities of Mucoromycota, we used crabshell baiting to culture and isolate DNA from these fungi. We have generated and are currently analyzing >700 novel genomes from this culturing and sequencing effort. In this presentation, we will discuss the distribution patterns of host fungi with and without EB across geospatial scales and host plants, as well as the genomic heterogeneity of these isolates, to understand how EB may influence fungal genome evolution and diversification. Additionally, we will discuss how selection pressures influence bacterial genomes and drive their evolutionary trajectories, drawing from genome-scale phylogenetic and comparative analyses of Burkholderia-related EB and their free-living relatives. This work will ultimately provide insight into how EB influence functional dynamics and contribute to structuring microbial communities, shedding light on their broader ecological significance.

### Evaluating the Role of Bacterial Endosymbionts in Evolution and Diversity of Plant-Associated Mucoromycota Fungal Communities

Erin Nuccio, Lawrence Livermore National Lab

The hyphosphere, the interface between fungal hyphae and soil microbial communities, is hypothesized to play a critical role in nutrient acquisition from organic matter in arbuscular mycorrhizal fungi (AMF). Hyphosphere interactions occur in the microns surrounding hyphae, making it methodologically difficult to study these microbial communities and their activities. Stable isotopes provide a means to target the microbial populations that exchange nutrient currencies (e.g., 13C, 15N, 18O) with AMF hyphae in complex soil communities. In multiple experiments, we used 13CO2 fixation by plants to trace the flow of carbon from the plant to its underground fungal partners. Hyphosphere SIP-metagenomes offer valuable insights into potential trophic interactions between mycorrhizal fungi and bacteria—such as predation, organic matter decomposition, and ammonia oxidation—which are derived from combining taxon-specific isotope enrichment with the content of bacterial genomes. However, 13C uptake does not define the entire hyphosphere—we observed taxa that increased in abundance using amplicon sequencing, but did not incorporate 13C. This suggests that AMF may have stimulated these organisms by alternate mechanisms that did not involve 13C consumption, such as by changing local edaphic or nutrient conditions (e.g. increasing or decreasing pH, N, P), or by non-assimilative C processes. These findings highlight the complexity of hyphosphere interactions, suggesting that AMF influence microbial communities through multiple mechanisms beyond direct carbon transfer, shaping nutrient dynamics and microbial activity in ways that extend beyond 13C assimilation.

### Fungal Lactone Interference of Bacterial Quorum Sensing: A Driving Force in Microbiome Community Dynamics?

Ben Haefner, University of Wisconsin, Madison

The soil microbiome is flooded by molecular dialogues that shape the composition of microbial communities. These complex interactions influence microbial behavior in ways that cannot be predicted from individual or pairwise interactions alone. Here, we explore the impact of the fungal lactone metabolite patulin on bacterial quorum sensing and community dynamics. To evaluate the potential for quorum sensing interference, we assessed the effects of purified patulin and extracts from a wild-type Penicillium expansum strain and a patulin-deficient mutant on phenotypes commonly associated with quorum sensing in Gram-negative bacteria. Specifically, we measured biofilm formation, swarming motility, and violacein production by a quorum-sensing biosensor strain. We used the well-characterized THOR (The Hitchhikers Of the Rhizosphere) microbiome to investigate the potential for broader ecological consequences of patulin-mediated interference. THOR is a model bacterial community originally isolated from the roots of soybean and alfalfa plants, consisting of Pseudomonas koreensis, Flavobacterium johnsoniae, and Bacillus cereus. We have found that patulin interferes with quorum sensing activities in diverse Gram-negative bacteria. Notably, patulin significantly decreased biofilm formation by Pseudomonas aeruginosa, Agrobacterium tumefaciens, and Chromobacterium subtsugae. Additionally, we found that patulin disrupts swarming motility in P. aeruginosa and Pseuodomonas koreensis, and the synthesis of violacein by the biosensor C. subtsugae, further indicating disruption of bacterial communication. In the THOR community, fungal extracts of wild-type but not a patulin-deficient P. expansum strain enhanced the fitness of F. johnsoniae, further suggesting that patulin plays a role in shaping bacterial community composition.

This work suggests that quorum sensing interference may be a driving force in microbial community composition. Understanding these interactions can provide insight into microbial competition, cooperation, and stability in natural and agricultural ecosystems.

### Quantitative Stable Isotope Probing (qSIP) and Cross-Domain Networks Reveal Fungal-Bacterial Interactions in the Hyphosphere

Giovana Slanzon, University of Hawai'i at Mānoa

Our understanding of microbial co-occurrence patterns on carbon (C) cycling is often limited, particularly in relation to bacterial-fungal interactions. In this study, we used 13C quantitative stable isotope probing (qSIP) to characterize associations among fungi and bacteria in the hyphosphere, the area of fungal influence surrounding hyphae. Our aim was to identify active and interacting taxa that drive C dynamics in a grassland soil. We used ingrowth bags filled with pure sand as a trap for fungi and the bacteria associated with these fungal hyphae. Bags were buried within a plot of Avena spp., which were labeled with 13CO2 as a tracer to identify organisms that consumed plant metabolites. DNA from each ingrowth bag was extracted and fractionated. Amplicon libraries targeting the 16S rRNA and the ITS rRNA gene were prepared and sequenced for each fraction. A cross-domain network of 13C-assimilating bacteria and fungi was built as a novel way to identify potentially interacting partners through C exchange. We found a total of 54 bacterial ASVs and 9 fungal OTUs that were significantly 13C-enriched. These were saprotrophic and biotrophic fungi, and motile, sometimes predatory bacteria. Among these, 70% of all 13C-enriched bacteria identified were motile. Notably, we detected fungal-bacterial network links between a fungal OTU of the genus Alternaria and several bacterial ASVs of the genera Bacteriovorax, Mucilaginibacter, and Flavobacterium, providing empirical evidence of their direct interactions through C exchange. We observed a strong positive co-occurrence pattern between predatory bacteria of the phylum Bdellovibrionota and fungal OTUs, suggesting the transfer of C across the soil food web. To date, our ability to associate microbial co-occurrence network patterns with biological interactions is limited, but the incorporation of qSIP allowed us to more precisely detect interacting partners by narrowing in on the taxa that were actively incorporating plant-fixed, fungal-transported labeled substrates.

### The Fate of Bacteria-Fungi-Plant Symbioses in a Changing world: Why It Matters and What We Can Do about It

Louis Berrios, Stanford University

Previous studies have shown that bacteria in the genus Burkholderia function as positive predictors of ectomycorrhizal fungi abundance and plant health in nature. It is unclear, however, whether these bacteria support fungal and plant health. Given the multitude of independent confirmation suggesting that these organisms benefit one another in forests, I hypothesized that Burkholderia species would enhance ectomycorrhizal root colonization and host plant growth responses. A combinatorial plant growth experiment was used to test the individual and combined effect(s) of bacteria on ectomycorrhizal fungi (EcMF) and plant growth responses. Host plants were either inoculated with water, bacteria, EcMF, or bacteria and EcMF, grown in a growth chamber for six months, and harvested thereafter. Soils and roots were profiled for microbial activity, and shoots were chemically analyzed. The addition of Burkholderia enhanced EcMF colonization and plant biomass relative to single inoculations. Additive growth responses were mostly observed, but Burkholderia and EcMF exhibited a non-additive effect (i.e., higher order interaction) on shoot height. This study provides the first direct evidence that Burkholderia species function as mycorrhizal helper bacteria in Bishop pine forests. Recent reports have shown that climate-related stress is reducing the abundance and diversity of EcMF and subsequently the abundance and diversity of Burkholderia species. The findings in this study therefore contribute not only fundamental, causal knowledge of a multipartite symbiosis in nature, but they also highlight the need to incorporate symbiotic bacteria into fungal conservation and reforestation efforts.

## SYMPOSIUM 4:
## Underground Explorers: Supporting Mycorrhizal Researchers Working in the Most Underexplored Ecoregions around the World

*Adriana Corrales (Chair), Candice Y. Lumibao (Co-chair), Evelin Yulisa Reyes Mendez (Presenter), Jordan "Alex" Siggers (Presenter), Allie Hall (Presenter), Candice Y. Lumibao (Presenter), Corrales, Adriana (Presenter)*

**Overall Abstract** In the race to map underground fungi before they are gone, it is imperative that we enlist the best mycorrhizal researchers from everywhere in the world. SPUN (The Society for the Protection of Underground Networks) has created the Underground Explorers program which is a granting program designed to support mycorrhizal fungi researchers from around the world particularly those working on the Global South, and underfunded countries to work on undersampled ecosystems. The program started in 2022 and since then, we have launched four additional funding calls (2023, 2024 and 2025). We are really excited to currently have 92 grantees from 43 different countries. In this symposium we will talk about the impact that this granting program has have for mycorrhizal researches and how in a collective, decentralized and decolonial effort we are working toward filling the knowledge gaps in mycorrhizal fungal diversity. In addition, four current and former grantees from the program will present their amazing findings and share the way they are interacting with local communities to rise awareness about the importance of the study and conservation of mycorrhizal fungi.

### Underground Explorers: Supporting Mycorrhizal Researchers Working in the Most Underexplored Ecoregions around the World

Adriana Corrales, SPUN

Mycorrhizal fungi are essential for the survival and functioning of plant communities and ecosystems. Documenting mycorrhizal fungal communities is critical for understanding and preserving their biodiversity, however recent global biodiversity studies have highlighted major gaps around the globe where no sequencing-based studies of soil mycorrhizal fungi have been performed. In the race to map underground fungi before they are gone, it is imperative to mobilize as many mycorrhizal researchers from all parts of the world. SPUN (The Society for the Protection of Underground Networks) has created the Underground Explorers program which provides small grants to support mycorrhizal fungi researchers from around the world. The program is particularly suited for those working in the global south and underfunded countries to work on under sampled ecosystems. The main goal of the program is to fuel mycorrhizal research globally by working in a collective, decentralized and decolonial way to fill knowledge gaps of Earth's mycorrhizal fungal diversity. The program launched in 2022 and since then SPUN has funded 92 grantees from 43 different countries. So far, these projects have generated environmental sequencing data (ITS and SSU) from over 2,700 samples collected and sequenced in the most underexplored ecoregions for mycorrhizal fungi. The grants are mainly focused on producing mycorrhizal biodiversity information that could be used for advocating for the conservation of these fungi at the local and national level. As a result, the program prioritizes funding local experts working in their native country who are closely interacting with local communities to translate these data into local impact. The Underground Explorers program has proven effective at producing high quality data while 3 2025 MSA Annual Meeting increasing local capacities in underfunded countries and connecting mycorrhizal researchers from all over the world.

### Demystifying Underground Mycobiome in the Gulf Coast Prairie Dunes in Barrier Islands through Science and Educational Outreach

Candice Y. Lumibao, Texas A&M University, Corpus Christi

The gulf coast prairie dune ecosystems of barrier islands along the northern Gulf of Mexico represent an important yet under-studied ecoregion particularly in fungal ecology. These islands face increasing anthropogenic threats with important consequences to the coastal communities, including loss of biodiversity and the first line of defense against hurricanes. While the dynamics of on dune vegetations in response to environment have been well-characterized, knowledge on the underground mycobiome/mycorrhizal communities in these nutrient-poor environment remains limited. Even more limited is public awareness of and knowledge on fungi, including symbionts, and their potential importance for the management on prairie dune ecosystems. Here, we aim to increase knowledge and awareness on both fronts: contribute to fundamental mycobiome knowledge and public awareness and training. Through the Society for the Protection of Underground Network (SPUN) grant, we addressed this in two ways. First, we characterized soil mycobiome (focusing on arbuscular and ectomycorrhizae) diversity along four barrier islands in South Texas, spanning salinity gradient and land-use history. We used high-throughput amplicon sequencing of the internal transcribed spacer (ITS) and SSU regions to assess community diversity and composition. Second, we conducted basic fungal educational training and participation of local students within Corpus Christi - from fungal culture, mycorrhizal quantification and molecular work to field sample collection (used in the first aim above). Our results showed high fungal diversity and strong geographic patterns, which was influenced more by spatial distance rather than land-use, soil nutrients and other properties. We 7 2025 MSA Annual Meeting also observed distinct composition among the underground communities. Next, our educational outreach resulted in hands-on fungal culture activity by 4th graders, participation and training of two local high school students in fieldwork, and research experience for undergraduate students in mycorrhizal quantification and fungal molecular work. Taken together, our project highlights the importance of accounting for fungal diversity in these typically nutrient-poor soils of barrier islands and increasing awareness among local students, which will aid in successful future management and conservation of these natural resources.

### Exploring Fungal Diversity in Agricultural and Wild Landscapes: Implications for Ecosystem Health in Honduras

Evelin Yulisa Reyes Mendez, Louisiana State University

We hypothesized that land-use practices significantly influence fungal community diversity and composition, creating distinct fungal assemblages in Honduras fungal community. Also, ecological gradients across different geographical locations in Honduras significantly influence the diversity and composition of soil microbiome. It is hypothesized that altitude, temperature, precipitation, and soil type variations across these gradients lead to distinct fungal assemblages, reflecting fungi's adaptability to specific environmental conditions. We collected soil samples from natural areas, organic farms, and non-organic farms and generated data from 16S rRNA metabarcoding and ITS sequencing to characterize fungal diversity across tropical rainforests, mountain regions, grasslands, and urban environments. We found that natural and non-organic farm systems support more unique species, whereas Organic systems show lower species richness and OTU overlap. These differences suggest that land management practices significantly shape fungal biodiversity and ecosystem functions, reinforcing the need for sustainable strategies to preserve soil microbial diversity.

### Drought Drives Differential Legacy Effects of Altered Soil Fungal Communities across a Grassland Precipitation Gradient

Jordan “Alex” Siggers, Colorado State University

Precipitation regimes are intensifying globally as atmospheric temperatures rise, leading to more frequent and severe drought events. Grasslands are differentially sensitive to water limitation, thus displaying unique drought responses. Across the North American Great Plains, soil microbial communities have been shown to be drastically altered by extreme drought, but very little is known about post-drought recovery. Given soil fungi are major determinants of ecosystem functionality, it is imperative to investigate the long-term outcomes of shifting precipitation regimes. Our objectives were twofold: 1) to assess potential legacy effects of extreme drought on soil fungal communities and 2) assess general patterns of soil fungal diversity across the North American Great Plains. We anticipated that soil fungal communities that underwent drought would be partially recovered four-years and fully recovered six-years post-drought, compositionally mirroring ambient communities. To address our objective, we sampled bulk and dominant plant rhizosphere soils at four sites across a precipitation gradient (shortgrass steppe of northeastern Colorado to tallgrass prairie of eastern Kansas) four- and six-years following the cessation of an experimentally imposed extreme drought. We conducted amplicon sequencing of previously droughted and ambient fungal communities using general fungal and arbuscular mycorrhizal fungal (AMF)-specific primers. Throughout the study, undergraduate students and local collaborators were trained on field sampling techniques, sample processing, and data analysis. Overall, fungal communities differed between previously droughted and ambient plots at three of four sites four years post-drought, but only at the driest shortgrass steppe site six years 9 2025 MSA Annual Meeting post-drought. Differences were largely driven by the fungal orders Agaricales, Pleosporales, and Cantharellales. Generally, AMF richness was highest at the C3-dominated mixed-grass prairie of central Kansas, and AMF communities differed at each site, although a single Paraglomus sp. virtual taxon composed ~50% of total sequences. Our results suggest that drought may drive lingering impacts on grassland soil fungal communities, which differ in baseline composition. Baseline fungal community data are desperately needed to understand how global change may impact these keystone taxa.

### Do Local Arbuscular Mycorrhizal Fungi Benefit Endangered Nānū Trees?

Allie Hall, University of Hawaii at Manoa

Anthropogenic disturbances and climatic changes have altered the natural landscapes of Hawaiʻi, resulting in the decline of many culturally and ecologically important ecosystems and species such as endemic Hawaiian Gardenia species (Nānū). In particular, Gardenia brighamii is considered one of the most endangered trees on earth with less than a dozen individuals remaining in the wild. An important player in remediating the negative impacts on Nānū and other endangered plants, may be mutualistic arbuscular mycorrhizal fungi (AMF), shown to assist plant resilience to drought, nutrient limitation, and pathogens. Using locally sourced AMF communities, we aim to increase the restoration success of Nānū to conserve what remains of a quickly declining native Hawaiian species. We ask (1) whether the health status of the wild Nānū tree influences the AMF community composition, and (2) if the AMF communities associated with healthier trees provide greater benefits to Gardenia seedlings grown ex situ for restoration. We collected soil samples from Nānū located in various sites across the Hawaiian Archipelago to be used for trap cultures in which spores were isolated and used as inocula for sterile Gardenia seedlings. AMF colonization of seedlings was assessed through root microscopy, and its impact observed through various plant response metrics taken over eighteen months. DNA amplicon sequencing of the AMF communities from field soils, associated trap cultures, and isolated spore slurries (inocula), were used in conjunction with our multiple plant response metrics to assess changes in AMF communities and the effects of AMF inoculation on Gardenia health. We found that AMF communities associated with healthier trees from less disturbed, more intact ecosystems are more diverse and provide greater benefit to seedlings relative to those associated with more feeble trees within more invaded sites. Our broad sampling efforts across the Hawaiian Archipelago contribute to cataloging the current diversity of AMF in these rapidly changing and threatened ecosystems, and create a baseline for future research and restoration of native trees using locally sourced mycorrhizal fungi.

## SYMPOSIUM 5:
## Growing the Mycology Network through Education

*Alejandro Rojas (Chair), Geoffrey Zahn (Co-chair), Corrales, Adriana (Presenter), Xiomy Janiria Pinchi Davila (Presenter), Javier Tabima (Presenter), Danielle Sublett (Presenter), Nicole Reynolds (Presenter), Jessie Karen Uehling (Discussant)*

**Overall Abstract** A significant portion of the impact made by mycologists is achieved through mentoring and education. This is crucial at various levels, including reaching out to the general community and mentoring and training undergraduate students and graduate students. While fungi are gaining more attention in the general community due to increased media activity, it’s important to ensure that this trend continues by sharing our experiences on how to effectively accomplish this. We plan a 2-hour symposium and it will be moderated by one of the MSA Education Committee Members. The speakers will cover different groups that they serve, such as undergraduate students, the general public, amateur mycologists, and graduate students. Incorporating various viewpoints will equip the community with tools and knowledge, fostering engagement and promoting mycology across multiple levels.

### Teaching Mycology in Colombia and Making Fungi Transversal in Ecological Research
Adriana Corrales, SPUN

I was an assistant professor at The University of Rosario in Bogotá, Colombia for five years. During that time I had the opportunity to interact with students and also coffee cultivating communities. Mycology is a neglected discipline and Colombia is no exception. Most people don’t know much about fungi so I made it my mission to make sure they learn about this kingdom. I taught undergraduate and graduate level courses. Even though none of my courses were focused on mycology, mycology was transversal to all of them. Fungi play a crucial role in ecosystem processes and make great examples for almost all ecological topics, so they were always mentioned. Parallel to my courses, I created an undergraduate research group. This group was an excellent source of motivated students to develop research projects. I interacted with coffee growers in a plant conservation project that I developed focused on the Black Oak (Trigonobalanus excelsa). Black oaks form ectomycorrhizal forests. Therefore, protecting the ectomycorrhizal fungi associated with this plant is as important as protecting the plant itself. So, I set on a journey to teach local communities about this symbiosis and its importance for the conservation of this ecosystem. My years teaching and interacting with students and rural communities were filled with a lot of growth as I learned about the best way to communicate science. Spreading the word about the importance of fungi has become a big part of my job and therefore, I'm very grateful to have had those experiences.

### Mycological Education and Outreach Focused on Zygomycete Fungal Biology

Nicole Reynolds, California State Polytechnic University, Pomona

The dynamic field of academic mycology continues to evolve and expand with changes in taxonomic classification and relationships, discovery of new lineages, and findings of exciting new ecological and symbiotic niches for fungi. Most mycological research is classically focused on Dikarya, and thus mycological textbooks and laboratory course activities have not incorporated recent mycological discoveries from other branches in the Kingdom. In addition, course foci, in person vs. digital laboratory or classroom format, term length and resources vary by institution, resulting in the need for modern mycological laboratory activities that are scalable. A previous NSF supported research project called the Zygomycete Tree of Life (ZygoLife) generated large data sets and a body of published findings focused on the two Phyla Mucoromycota and Zoopagomycota, "zygomycetes". Together these fungi are an important group representing evolutionary origins of terrestrial fungi, diverse ecological processes in nature, and industrial/ medical applications. Publicly available outcomes of Zygolife included high resolution microscopy images, updated life cycles, phylogenies, and genomic and bioinformatic resources. In addition, the Zygolife working group created a manual of laboratory activities. It contains modern overviews of diversity, biology, physiology and teaching material resource availability together with instructions for lab-based lessons including materials lists and morphological images for teaching purposes. In this presentation we will discuss the ZyGoLabs manual, recent applications of its' lessons, and how adaptation to various course structures, age groups, and budgets will facilitate the advancement of teaching and research of zygomycetes and ultimately help establish new generations of researchers in mycology.

### Research, Education and Outreach at an R2 Liberal Arts University: Expanding Mycology to Different Scales of Education

Javier Tabima, Clark University

Primarily undergraduate and R2 institutions are often underrecognized in their capacity to advance research, education, and outreach in mycology. This talk explores how intentional, equity-centered approaches at smaller institutions can meaningfully expand access to mycological science and foster inclusive scientific communities. At Clark University, we have developed a multi-faceted framework to engage students and community members in fungal biology. This includes founding student-led initiatives such as Latinxs in STEM (now ASCEND in STEM) and the Clark Mycology Club; building partnerships with local entities like the City of Worcester for community-based research; producing bilingual educational materials for Worcester Public Schools; and designing inclusive, research-integrated coursework tailored to our student population. These efforts have contributed to increased student engagement in research, the development of leadership pathways for historically excluded students in STEM, and the expansion of mycological outreach to K–12 classrooms and community partners. We have observed greater retention and participation in mycology-related research among undergraduate students and improved connections between the university and the broader community. These efforts have contributed to increased student engagement in research, the development of leadership pathways for historically excluded students in STEM, and the expansion of mycological outreach to K–12 classrooms and community partners. We have observed greater retention and participation in mycology-related research among undergraduate students and improved connections between the university and the broader community.

### The Power of Expanding Fungal Networks through Mentorship and Outreach

Xiomy Janiria Pinchi Davila, University of Georgia

Mentorship and outreach are essential in expanding mycology networks and impacts. Throughout my grad school journey as MSA SPS President, a FFAR Fellow, and former teaching assistant in Mycology, I had the opportunity to engage with diverse audiences, from students and policymakers to the general public. In this talk, I will share my experiences, common misconceptions I have encountered over time, and strategies for leveraging social media to expand professional networks. I will also share opportunities for professional development to support the new generation of mycologists and tips for communicating our science more effectively. Additionally, I will discuss how mentorship can empower students, facilitate career opportunities, and make mycology more accessible to everyone.

### Integrating 4DEE and the Few Nexus into Mycology Education: Scalable Approaches for Teaching Soil Fungal Diversity in Conservation Science

Danielle Sublett, College of the Sequoias

The Four-Dimensional Ecology Education (4DEE) framework provides a comprehensive model for engaging students in fungal ecology by integrating core ecological concepts, ecological practices, human-environment interactions, and cross-cutting themes. Additionally, fungi play a critical role in the Food-Energy-Water (FEW) Nexus, influencing soil fertility, carbon cycling, and water retention. This adaptable learning activity introduces undergraduate students—both at community colleges and universities—to fungal diversity and mycorrhizal networks in grassland conservation through field-based soil sampling and fungal analysis. Students will investigate mycorrhizal networks, saprotrophic fungi, and fungal roles in soil stability, nutrient cycling, and ecosystem resilience by collecting soil cores from conservation and agricultural sites, conducting morphological fungal surveys, and examining soil health metrics. The activity emphasizes the role of fungi in sustainable food production, carbon storage, and soil water retention, directly tying into FEW-related conservation strategies. Due to limited sequencing capabilities at some institutions, the activity incorporates pre-sequenced fungal community datasets from a prior study, allowing students to practice data visualization, community composition analysis, and interpretation of fungal functional roles in ecosystems. The activity is currently being implemented in a community college setting, where pre- and post-activity surveys will assess student learning gains and changes in scientific identity. Expected outcomes include improved understanding of fungal contributions to ecosystem stability, the FEW Nexus, and the integration of conservation principles into mycology education. The structured integration of experiential learning and quantitative analysis aligns with efforts to enhance ecological education and broaden participation in mycology at the 9 2025 MSA Annual Meeting undergraduate level.

## SYMPOSIUM 6:

## Fungal Futures, Indeed: Climate Change and the Threats of Mycotoxigenic Fungi

*Joan Bennett (Chair), Neriman Yilmaz Visagie (Presenter), Guohua Yin (Presenter), Anne Hatmaker (Presenter), Joan Bennett (Presenter)*

**Overall Abstract** Mycotoxins have been a global problem for millennia. One, then, might wonder: How do they relate to fungal futures? Although some mycotoxigenic species are manageable, many continue to be major problems in global food supplies and could become even bigger problems as climate change influences their adaptation, prevalence and toxicity. The purpose of this symposium is to explore mycotoxin-producing fungi that could become increasingly intractable issues in food production as Earth’s climate experiences continued warming and unpredictable weather patterns. How can we best navigate a fungal future that includes mycotoxigenic fungi? We do so by preparing in the present through climate-related scientific research.

### Primary, Secondary, and Tertiary Metabolites

Joan Bennett, Rutgers, Department of Biochemistry and Molecular Biology

Primary” indicates a foundational or basic element; secondary” specifies something derived or built upon the primary; while “tertiary” implies a further level of complexity or combination. In the biological sciences, primary metabolites are essential for survival. Secondary metabolites are not required for viability but provide a competitive advantage to the producing organism and are usually produced by multienzyme biosynthetic pathways encoded in clusters of linked genes. Many review articles describe volatile organic compounds (VOCs) as “secondary metabolites” a term that may be accurate for terpenoids, but which does not accurately describe the fact that most fungal VOCs are small degradation products of fatty acids or biotransformation products of amino acids. VOCs function as” infochemicals’ (semiochemicals) that serve important eco-physiological functions. Fungi produce many different compounds. Higher temperatures lead to enhanced vaporization and release of small molecules from storage tissues. Thus, warmer climate is a physicochemical driver of increased biogenic VOC levels in the atmosphere. We suggest that VOCs are worthy of focused mycological study, and that they be termed ‘tertiary metabolites’ so as not to confuse them with the well-known categories of primary and secondary metabolites. We suggest that VOCs are worthy of focused mycological study, and that they be termed ‘tertiary metabolites’ so as not to confuse them with the well-known categories of primary and secondary metabolites.

### Unraveling the Mycotoxin Cocktail: Fusarium Diversity and Contamination in Eastern Cape Maize

Neriman Yilmaz Visagie, Department of Biochemistry, Genetics and Microbiology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa

Maize is a key staple in cobs. Fusarium isolates were identified through morphological analysis and DNA sequencing, while mycotoxins were analyzed using LC-MS/MS. In 2023, 196 samples were collected from five farms, yielding 245 Fusarium isolates. Predominant species included Fusarium temperatum and F. verticillioides. Mycotoxin analysis revealed FUMs, Deoxynivalenol (DON), Zearalenone (ZEA), Beauvericin (BEA), Fusaric acid, and Moniliformin (MON). The results showed the presence of mycotoxin cocktails, increasing potential health risks. In 2024, 302 samples were collected from seven farms. All OR Tambo farms had FUM-positive symptomatic samples, some exceeding safety limits. Emerging mycotoxins like DAS, MON, Fusaric acid (FA), Enniatins, and BEA were detected. Fusarium species diversity was higher in 2024, with new species from the Fusarium fujikuroi species complex.This study is the first extensive survey of Fusarium species and mycotoxin contamination in Eastern Cape maize. s It reveals a shift in Fusarium diversity, likely due to climate change, and an increased risk of mycotoxin cocktails. Future research should assess the economic impact of mycotoxins and support food security projections and mitigation strategiesSouth Africa, vulnerable to Fusarium ear rot (FER) and Gibberella ear rot (GER) caused by mycotoxin-producing Fusarium species. Fumonisin B1 (FUM) was first detected in the Eastern Cape in 1988, but recent surveys suggest a decrease in its prevalence. This study investigates Fusarium diversity and mycotoxin contamination in maize over two growing seasons (2023 and 2024). Maize samples were collected from smallholder farms, focusing on symptomatic maize with FER and GER, as well as healthy.

### Ecological and Evolutionary Dynamics Associated with Mycotoxin Variation in a Pathogenic Fungus

Anne Hatmaker, University of Minnesota

Mycotoxin contamination results in billion-dollar losses for the agricultural industry and detrimental effects on humans and animals. One of the most dangerous classes of mycotoxins, aflatoxins, are produced by plant pathogenic species within Aspergillus. Previously, mycotoxin production was thought to be a species-defining trait, but we now know many species exhibit population-specific diversity in chemotypes, as some strains within a species may produce different mycotoxins than others or be atoxigenic. This population-specific variation occurs in diverse species, including Aspergillus flavus. Our recent work linked mycotoxin prevalence and production in A. flavus to population structure and selection associated with abiotic factors such as precipitation and temperature. We also demonstrate that genomic differences underlie chemotypic differentiation and can shape ecological interactions. Aflatoxin production varies among populations and geographic regions. Ecological tradeoffs in lower or non-aflatoxigenic lineages are evident, with these populations producing more of other metabolites like kojic acid. Population differentiation is also evident among patient-derived clinical A. flavus strains that are more commonly part of a non-aflatoxigenic population, with strains often lacking the genes necessary to produce aflatoxins. Our results highlight the necessity of an integrated approach to studying fungi which infect both humans and plants. We highlight how environmental change could cause shifts in population-specific toxin profiles of geographically isolated groups. By exploring ecological drivers of mycotoxin variation, we provide insights into the future of mycotoxin contamination on a global scale.

### Climate Change-Induced Volatilome Alterations in Penicillium species: Implications for Mycotoxin Threats and Fungal Ecological Adaptation

Guohua Yin, Qilu Institute of Technology

Climate change is driving profound transformations in fungal ecological niches, with mycotoxigenic Penicillium species emerging as a critical concern. As a ubiquitous fungal genus, Penicillium includes numerous species capable of producing hazardous mycotoxins, posing significant risks to food safety, public health, and ecosystem stability. Volatilome alterations in Penicillium species play a crucial role in their ecological interactions and biotechnological applications. Environmental factors, such as temperature, humidity, and nutrient availability, can significantly impact the production of volatile organic compounds (VOCs). Moreover, genetic modifications and interspecies interactions also lead to changes in the volatilome. These alterations not only affect the mold's communication with other organisms but also have implications for food spoilage, biocontrol, and pharmaceutical production. Understanding the mechanisms behind volatilome changes is essential for harnessing the potential of Penicillium species. The ramifications of mycotoxigenic Penicillium expansion are multifaceted. In agro-food systems, these fungi contribute to postharvest spoilage, incurring substantial economic losses. More critically, their secondary metabolites—such as patulin—threaten human and animal health through acute and chronic toxicity, including hepatotoxicity, nephrotoxicity, immunosuppression, and carcinogenic potential, even at minimal exposure levels. Within natural ecosystems, certain pathogenic Penicillium strains can compromise plant health, potentially destabilizing plant communities, reducing biodiversity, and impairing ecosystem functions. Elucidating the intricate interplay between climate change and mycotoxigenic Penicillium is therefore paramount for formulating adaptive strategies to safeguard food security, mitigate health risks, and preserve ecological integrity in a warming world.

# PARALLEL SESSION 1-1:
## Fungi and Global Change

### Parallel Session 1-1: Fungi and Global Change
### Annual Grass Invasion is Associated with Differences in the Community Structure and Abundance of Biocrusts and Arbuscular Mycorrhizal Fungi

Rachel Berner, Washington State University
Geoff Zahn, Utah Valley University
Alexis Spencer, Washington State University
Bala Chaudhary, Dartmouth College
Tanya Cheeke, Washington State University

Interactions between biocrusts and arbuscular mycorrhizal (AM) fungi may increase plant resilience to environmental stress in native grasslands. When non-native plants invade, they may have cascading effects on soil biota and their interactions, destabilizing grassland ecosystems. In a field survey we assessed the percent cover and composition of biocrusts in plots varying in percent cover of the invasive annual grass, ItalicizedVentenanta dubiaItalicized (Native, Transition, Invaded plots). We used field-collected soil as inocula in a glasshouse experiment to test whether the abundance of viable AM fungal propagules differs under biocrusts compared to bare soil, or across invasion levels. We used 18S rRNA gene sequencing on field-collected soil to test whether the structure of the AM fungal community differs under biocrusts versus bare soil across invasion levels. Invasion by ItalicizedV. dubiaItalicized was associated with lower biocrust cover, distinct biocrust community structure, lower AM fungal abundance below biocrusts, and distinct AM fungal community structure with invasion. Our results support broader United Nations Sustainable Development Goals focused on the protection and restoration of terrestrial ecosystems. A better understanding of the interactions among plants, biocrusts, and AM fungi is important for mitigating the impacts of invasive species and informing grassland restorations.

### Parallel Session 1-1: Fungi and Global Change
### Ectomycorrhizal Fungal Communities Influencing Long-Term Tree Growth in the Alaskan Boreal

Ellie Fajer, Stanford University
Peter Pellitier, Stanford University
Jay Yeam, Stanford University
Zoë Rehnborg, Stanford University
Kabir Peay, Stanford University

Boreal forests are dominated by diverse ectomycorrhizal (ECM) fungi which simultaneously influence above and below ground carbon dynamics by facilitating plant growth and driving soil nutrient cycles. Despite their widespread distribution, the role of ECM community variation in influencing ecosystem carbon dynamics remains poorly studied. We studied soil and root-tip inhabiting fungal communities inhabiting mature Picea glauca trees across ~1500 km of interior Alaska. We identified the role of ectomycorrhizal fungal communities in above- and below-ground carbon storage by pairing molecular sequence data with measures of multi-decadal (~25 years) tree growth derived from individual trees. After partially disentangling tree growth and soil carbon stocks from climatic factors, we found that ECM fungal community variation modulates tradeoffs in above- and below-ground carbon storage. Strikingly, we find that dominant ECM taxa linked to lower soil carbon concentrations are also linked to greater multi-decadal tree growth – most notably taxa within the Cortinariaceae. Foliar isotopic evidence further suggests that variation in soil N acquisition strategies influences these ecosystem level C tradeoffs. Ultimately, this work presents field-based evidence consistent with the emerging understanding that ECM fungi influence ecosystem C stocks through enzymatic degradation of soil organic matter and uptake of organic forms of N, thereby stimulating tree-growth whilst reducing soil C accumulation.

### Parallel Session 1-1: Fungi and Global Change
### Glaciers as natural biobanks: Cultivable fungal diversity in Styx Glacier and their genomic insights

Ji Seon Kim, Seoul National University
Ok-Sun Kim, Korea Polar Research Institute
Yeongcheol Han, Korea Polar Research Institute
Young Woon Lim, Seoul National University

Glaciers are important natural archives of past biotic and abiotic materials that have been introduced through various pathways over time. Many researchers have tried to revive past biotic materials, and in the case of microorganisms, most of the work has been done on bacteria, with very few studies on fungi. To unveil the secrets of past fungi preserved in glaciers, we studied the ice core of the Styx Glacier, Antarctica, by culturing and characterizing strains from four depth sections (ranging in age from approximately 50 years to 1,500 years old). In total, about 400 fungal strains were resurrected, representing more than 100 taxa spanning diverse taxonomic classifications. The isolated glacial fungi showed a flexible growth ability under different culture conditions, indicating their ability to withstand the challenges encountered in glacial environments. They also had significant levels of enzyme activity, evidence of their usefulness in applications and ecology. To further elucidate their unknown characteristics, we performed whole-genome sequencing for four representative taxa. Our findings highlight glaciers as invaluable microbial biobanks, preserving biological resources for centuries. This study extends our understanding of the importance of glaciers beyond their role as ecosystem services.

**Parallel Session 1-1: Fungi and Global Change**

### Increasing prevalence of plant-fungal symbiosis across two centuries of environmental change

Joshua Fowler, University of Colorado, Boulder
Jacob Moutouama, Rice University
Tom Miller, Rice University

Species' distributions and abundances are shifting in response to climate change. Fungal symbionts may provide resilience to environmental change by protecting their hosts from increasing stress. However, environmental change may lead to declines in hosts or symbionts. Symbionts preserved within herbarium specimens offer a unique opportunity to quantify changes in fungal symbiosis across broad temporal and spatial scales. We asked how the prevalence of seed-transmitted fungal symbionts of grasses (Epichloë endophytes), which can protect hosts from abiotic stress, have changed over time in response to climate change, and how these changes vary across host species' ranges. Specifically, we analyzed 2,346 herbarium specimens of three grass host species collected over the last two centuries (1824 – 2019) for the presence/absence of endophytes, and evaluated spatial and temporal trends in prevalence. We found that increasing prevalence over the last two centuries from ca. 25% prevalence to 75% prevalence, on average, across three host species. We also found changes in prevalence associated with observed changes in seasonal climate drivers; notably increasing precipitation corresponding to each host species' peak growing season. Our analysis performed favorably in an out-of-sample predictive test with contemporary data, however we identified greater local-scale variability in endophyte prevalence in contemporary compared to historic data, suggesting model fusion as an important step moving forward. Our results provide novel evidence for a cryptic biological response to climate change that may contribute to the resilience of plant-fungal symbiosis through context-dependent benefits that confer a fitness advantage to symbiotic hosts under environmental change.

**Parallel Session 1-1: Fungi and Global Change**

### Invasive Golden Oyster Mushrooms Are Disrupting Native Fungal Communities and Expanding Their North American Range

Aishwarya Veerabahu, University of Wisconsin, Madison
Mark Banik, USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI
Daniel Lindner, USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI
Anne Pringle, University of Wisconsin, Madison
Michelle Jusino, USDA Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI

The Golden Oyster Mushroom (GOM; Pleurotus citrinopileatus) is an invasive, edible wood decay fungus rapidly spreading throughout North America. Native to east Asia, GOM was introduced multiple times in the United States via commercial mushroom growing kits sold for home cultivation. Invasive wood decay fungi spreading in a new habitat may become competitively dominant- displacing native fungi and affecting decay processes and associated habitats. Our objective is to document how GOM affects the ecology in its invaded range and where else GOM may invade. To test whether GOM is associated with negative changes to native fungal communities, we collected drilled wood samples from pairs of dead trees with and without GOM from Dane County, Wisconsin, USA and sequenced the fungal communities using metabarcoding. GOM-colonized

trees show significantly lower fungal species richness and significantly different community composition compared to uncolonized trees. Using FUNGuild, we found fungal communities with GOM have similar guild composition, but most guilds have fewer species and rare guilds are at risk of disappearing, compared to communities without GOM. To contextualize GOM's impacts, we documented its spread in North America using community science databases iNaturalist and MushroomObserver. GOM is now found in at least 23 U.S. states and 1 Canadian province. Using species distribution modeling, we show there is currently uninvaded, suitable habitat for GOM in the West, Appalachia, Alaska, and parts of Mexico and Canada. With this evidence, we demonstrate that invasive GOM is endangering native wood-dwelling fungal communities and expanding its range.

### Parallel Session 1-1: Fungi and Global Change
### Warming and Reduced Rainfall Alter Fungal Necromass Decomposition Rates and Associated Microbial Community Composition and Functioning at a Temperate-Boreal Forest Ecotone

Anahi Cantoran, University of Minnesota
François Maillard, Lund University
Raimundo Bermudez, University of Minnesota
Artur Stefanski, University of Minnesota
Peter B. Reich, University of Michigan
Peter G. Kennedy, University of Minnesota

Changes in temperature and rainfall regimes will have significant yet potentially contrasting impacts on rates of soil organic matter (SOM) decomposition. To assess how a combined stress treatment of warming and drought impacts the decomposition of fungal necromass—a fast-cycling soil organic matter (SOM) pool—we incubated Hyaloscypha bicolor necromass under both ambient and altered conditions (air and soil warming +3.3°C and ~40% reduced rainfall) at the B4Warmed experiment in Minnesota, USA. We conducted two multi-week incubations, one assessing mass loss and microbial community composition on decaying necromass after 1, 2, 7, and 14 weeks and the second characterizing the substrate utilization capacities of necromass-associated microbial communities after weeks 1 and 7. Our results demonstrate that warming and reduced rainfall significantly accelerated the initial rate of necromass decay by ~20%, but that the overall mass loss was not different between treatments at the end of the 14-week incubation. The accelerated initial rate of decay paralleled shifts in microbial community composition and activity in the altered plots, demonstrating a higher metabolic capability to utilize C and N substrates early in decomposition but a lower capability later in decay. These findings highlight the dynamic, stage-dependent response of fungal necromass decomposition to altered climate regimes, underscoring the importance of considering both temporal dynamics and the functional capacity of microbial communities when assessing the impacts of climate change on soil carbon and nutrient cycling in forest ecosystems.

## PARALLEL SESSION 1-2:
## From Genes to Metabolites

### Parallel Session 1-2: From Genes to Metabolites
### A survey of fungal small secreted protein expression in the Aspen soil microbiome

Keaton Tremble, Duke University
Jake Nash, Duke University
Christopher Schadt, Oak Ridge National Lab
Melissa Cregger, Oak Ridge National Lab
Rytas Vilgalys, Duke University

The plant rhizosphere is a critical interface between plants and soil and serves as a diverse reservoir of complex fungal communities and intricate symbioses. In these systems the genetic mechanisms that mediate interactions between plants and fungi, and among fungi themselves, are poorly understood. Much work has shown that small secreted proteins (SSPs, a subset of effector proteins) are among the primary molecular tools used by both mutualistic and pathogenic fungi to colonize a host plant. Yet, these lessons come from just a few model organisms, usually in controlled axenic experiments. We understand little about the expression of fungal SSPs in natural communities, and how these patterns of expression change through time and space. Utilizing a substantial meta-transcriptomic dataset of Populus tremuloides rhizosphere root samples, collected across an elevational gradient throughout a growing season, we will present the ecological transcriptional landscape of both fungal and host SSPs in the aspen microbiome. Using a custom database of reference SSPs from 2,081 fungal genomes, we characterize the abundance and variability of SSP expression across different ecological groups and use a network approach to identify SSPs that are co-expressed among diverse taxa. We identified a set of SSPs that were constitutively expressed across diverse ecological guilds and ecological conditions, as well as a set of facultatively expressed SSPs. These findings provide insight into the context-dependency of molecular plant-fungal interactions.

## Parallel Session 1-2: From Genes to Metabolites
## Addition by subtraction: Genetic Dereplication of Penicillium expansum Reveals Production of a Cryptic Cyclopeptide

Justin Eagan, University of Wisconsin, Madison
Nancy Keller, University of Wisconsin, Madison
Mira Rawa, University of Wisconsin, Madison

Filamentous fungi produce bioactive secondary metabolites (SMs) with applications in medicine, agriculture, and food, however many biosynthetic gene clusters (BGCs) remain cryptic under laboratory conditions. Genetic dereplication simplifies metabolomic profiles by deleting major SM pathways and has been successful in activating cryptic BGCs. For instance, the dereplicated Aspergillus nidulans LO8030 strain led to the discovery of aspercryptin and is a chassis for heterologous expression of BGCs from other fungi. Building on this approach, we engineered a “flatline” Penicillium expansum strain by inactivating five major SM pathways for patulin, citrinin, roquefortine C, communesins, and andrastin C. This strain exhibited a cleaner metabolomic profile, and using the one-strain-many-compounds (OSMAC) approach, rice cultures induced unique SM profiles. We pursued isolation of a unique peptide signal, which revealed production of MBJ-0110 along with a novel derivative, which marks the first report of this compound from P. expansum. Based on the five-peptide structure, we hypothesized that a non-ribosomal peptide synthetase with five adenylation domains would be responsible for the biosynthesis. Ongoing efforts are elucidating the genetic underpinnings, as well as ecological role(s) this compound may play for P. expansum. This study highlights the utility of deleting major SMs combined with an OSMAC approach to reveal unique chemistry. There are other unique peaks in the flatline strain that remain uncharacterized, and future efforts may continue mining this strain for potentially novel compounds. More broadly, these strategies may be employed across fungal taxa to unlock cryptic chemical potential that we miss with standard methodologies.

## Parallel Session 1-2: From Genes to Metabolites
## Comparative metabolomics of Pseudogymnoascus

Abigail Ireland, University of Tennessee, Knoxville
Stephanie Kivlin, University of Tennessee, Knoxville

Pseudogymnoascus destructans (Pd) is a skin-degrading fungus and the causal agent of White-nose syndrome, first introduced to the United States from Europe in 2006. Since then, over 6.5 million bats have succumbed to this wildlife disease and the loss of their pest control services has had devastating ecosystem and economic consequences. Despite the overwhelming impact of Pd on native bat populations, little is known about the potential virulence of congenerics in the environment. Therefore, we performed comparative metabolomic analyses on over 100 Pseudogymnoascus cultures from North American bat hibernacula in an attempt to understand their ecological function. Phylogenetic analyses indicate these isolates are closely related species, many of which belong to clades associated with opportunistic dermatophytes, collectively recognized under the morphospecies name, P. pannorum. The aims of this study were to 1) investigate correlations in metabolomic profiles of putative saprotrophic and pathogenic strains of Pseudogymnoascus, and 2) evaluate the utility of comparative metabolomics in differentiating taxonomic clades. Given that unexplored taxa within the Pseudogymnoascus clade may be pathogenic to bats and/or humans, this project provides an ecological relevant testbed to apply metabolic fingerprinting to unknown environmental fungal isolates.

### Parallel Session 1-2: From Genes to Metabolites

### Environmental impacts on differential gene expression and metabolite production in the amphibian gut fungus Basidiobolus

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Basidiobolus is a genus of fungi with a complex life cycle of contrasting environmental niches and unique hyphal and spore morphotypes. It spends part of its life cycle as a free-living filamentous saprobe on plant detritus and exists in the anaerobic digestive systems of herptiles in a single-cell growth stage. Basidiobolus genomes exhibit a strong signal for biologically active specialized metabolites, which are predicted to provide an adaptive advantage. To elucidate functional variation and gain insight into the ecological relevance of this genus, we subjected phylogenetically pertinent strains of Basidiobolus to different pH levels and both aerobic and anaerobic conditions—abiotic factors that reflect the variation encountered in free-living environments and the herptile gut. In-vitro manipulation of oxygen and pH induced morphologies associated with these life stages, and fungal biomass was further assessed via RNA-seq and LC-MS/MS to evaluate gene expression and metabolite profiles. Preliminary data indicate that aerobic conditions resulted in greater variation of specialized metabolism within and between species than anaerobic conditions, suggesting anaerobic conditions may promote a more conserved metabolism within the gut environment. Additionally, the anaerobic low-pH condition showed an overrepresentation of upregulated chitin CAZymes and serine- and metalloproteases, supporting the hypothesis that Basidiobolus is metabolically active in the herptile gut microbiome. We will present data and analyses exploring metabolite production and differential gene expression in response to environmental variables relevant to the life history of Basidiobolus, providing insights into the functional diversity of this complex fungal genus.

### Parallel Session 1-2: From Genes to Metabolites

### Genetic and Evolutionary Mechanisms of Context-Dependency in an Ancient Plant-Fungal Symbiosis

Damian Hernandez, University of Miami
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Symbioses exist on a mutualism-to-parasitism continuum, with environmental conditions impacting the fitness benefits for each symbiotic partner through context-dependency. To predict how ecologically important symbioses will respond to changing environments, we need a generalizable framework of molecular mechanisms that underlie context-dependency. Using the ancient and ubiquitous symbiosis between plants and arbuscular mycorrhizal (AM) fungi, we identify gene family expansions as a key mechanism through which plants regulate their symbiosis context-dependently. Compared to the rest of the plant genome, we find that expanded gene families exhibit up to three times as much gene expression under environmental stress and twice as many SNPs associated with AM benefits to plant fitness. Through a gene duplication origin analysis, we identify tandem duplications as the main evolutionary mechanism that expands these AM-associated gene families, revealing the importance of continuous microevolution in plants' development of context-dependent symbiosis regulation. As a whole, our work reveals important molecular tools that hosts use to regulate their symbioses in response to environmental changes.

**Parallel Session 1-2: From Genes to Metabolites**

### Heavy metal tolerance in the ectomycorrhizal fungus Suillus tomentosus

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Tiffany Victor Lovelace, Brookhaven National Laboratory
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Ben Reimer, University of Florida
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Sara Branco, University of Colorado Denver

Heavy metal contamination in soils from human activity is an increasing issue and is detrimental to the growth and fitness of soil inhabiting organisms, further impacting whole ecosystems. Some organisms in the mycorrhizal genus Suillus, display metal tolerance and can alleviate metal toxicity in their plant partners, but it is unclear how common metal tolerance is and how it is achieved. We investigated cadmium (Cd), lead (Pb) and zinc (Zn) tolerance in Suillus tomentosus, a widespread ectomycorrhizal species that associates with pine trees. We used in vitro assays, pine bioassays, X-ray imaging and transcriptomic analysis to broaden our understanding of metal tolerance in S. tomentosus. We found out that intraspecific metal tolerance variation is decoupled from soil metal concentration and that Cd-tolerant isolates are also tolerant to Pb. Transcriptomic analysis of S. tomentosus Zn-sensitive and Zn-tolerant isolates highlighted the importance of metal transport and detoxification genes in Zn tolerance. In addition, S. tomentosus – P. contorta bioassays showed fungal inoculation can protect pines from metal toxicity. These results shed light on the scope and mechanisms of mycorrhizal fungal metal tolerance and pave the way for the development of approaches to mitigate the effects of ongoing soil metal contamination in forest ecosystems.

## PARALLEL SESSION 1-3:
## Latest Methodologies for Fungal Studies

**Parallel Session 1-3: Latest Methodologies for Fungal Studies**

### Dspikein Highlights the Bridging and Indirectly Stabilizing Role of Basidiobolus in Gut Microbiomes

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The host microbiome is integral to metabolic regulation, immune defense, and digestive performance. However, accurately correlating the host microbiome with its natural history requires moving beyond relative abundance (RA), which is susceptible to compositional. We employed a whole-cell spike-in protocol in conjunction with the DspikeIn R package (https://github.com/mghotbi/DspikeIn) to quantify absolute abundance (AA). This approach enables the transition from RA to AA quantification, enhancing benchmarking, and producing results that are comparable, and reliable across studies.

By leveraging AA, we effectively minimized false discovery rates and mapped the core gut myco- and microbiomes across reptiles and amphibians (herpetofauna) hosts and their natural histories. AA-based analyses revealed niche-dependent microbial patterns in herpetofauna: Lactococcus was associated with aquatic environments and carnivorous diets, while Cetobacterium was linked to semi-aquatic environments and insectivory. Basidiobolus, a filamentous fungus residing in the gastrointestinal tracts of herpetofauna, serves as a vital keystone taxon and a core member of the mycobiome. To elucidate its role in gut microbiome stability, we conducted a targeted knock-out through network analyses, selectively removing the Basidiobolus subnetwork. Eliminating Basidiobolus revealed its indirect role in maintaining gut homeostasis through cross-domain connectivity. With high betweenness, efficiency, and degree, Basidiobolus functioned as a critical bridge, linking isolated nodes and modules, aligning with Burt's structural hole theory and underscoring its role as an indirect stabilizing force in gut microbiome balance. DspikeIn enables precise quantification of absolute abundance while delivering unparalleled accuracy and comparability across diverse studies that can yield novel bacterial-fungal interactions in host microbiomes.

**Parallel Session 1-3: Latest Methodologies for Fungal Studies**

## MicroFisher: Fungal taxonomic classification for metatranscriptomic and metagenomic data using hypervariable markers

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Profiling the taxonomic and functional composition of microbes using metagenomic and metatranscriptomic sequencing is advancing our understanding of microbial functions. However, the sensitivity and accuracy of microbial classification using genome- or core protein-based approaches, especially for eukaryotic organisms, is limited by the availability of reference genomes and the resolution of sequence databases. To address this, we propose MicroFisher, a novel tool to filter out taxonomically useful reads from metagenomic or metatranscriptomic data, enabling taxonomic identification of community members based on multiple marker regions. MicroFisher pipeline compiled databases of hypervariable regions within fungal ITS and LSU sequences, including ITS1, ITS2, LSU D1, and LSU D2, covering 104,072 fungal taxa within 6,545 genera. By applying the hypervariable marker databases, MicroFisher can achieve higher resolution and accuracy, significantly reducing mismatches (false positives) and false negatives in fungal classification. To assess the performance of MicroFisher, we used it to profile the simulated mock fungal communities and found high sensitivity and accuracy in predicting fungal taxa and estimating their relative abundance. In addition, we also applied MicroFisher to real-world data, including metagenomic sequences from forest soils and metatranscriptomic sequences from root-associated eukaryotic microbes. Our results validated that MicroFisher provided more accurate profiling of environmental microbiomes compared to other classification tools. Overall, MicroFisher serves as a novel pipeline for the classification of fungal communities from metagenomes and metatranscriptomes.

**Parallel Session 1-3: Latest Methodologies for Fungal Studies**

## Synthetic Spike-In Metabarcoding for Plant Pathogen Diagnostics Results in Precise Quantification of Copy Number within the Genus Fusarium

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Rebecca Whetten, USDA-ARS Plant Science Research Unit
Imane Laraba, Agri-Food, Canada
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Synthetic spike-in metabarcoding (SSIM) assays generate quantitative next-generation sequencing (NGS) data, but are marred by inconsistency and have seen limited adoption. Previous efforts to develop synthetic spike-in metabarcoding (SSIM) assays have focused on the ITS and 16S rRNA genes. This study marks the first use of SSIM as a diagnostic assay to identify and quantify plant pathogens within the genus Fusarium and implements it using the single-copy TEF1 gene, which has relatively uniform G+C content and length. We identified variability between species in read quality score as a key source of bias that impacts SSIM to a lesser extent than other quantitative NGS approaches. SSIM was validated against another quantitative NGS assay that utilized qPCR (qMET) to calculate the total copy number. The comparison showed that SSIM was both precise (R2 > 0.93 for three Fusarium species) and proportional (slope ~1) in relation to qMET. Further, we applied SSIM to 24 wheat grain samples from Italy, uncovering a diverse array of Fusarium species and associated mycotoxins, with SSIM demonstrating superior predictive accuracy for most toxin concentrations compared to qPCR. Our results underscore the utility of SSIM for pathogen-agnostic diagnostics, offering important implications for food safety and management of mycotoxin contamination.

**Parallel Session 1-3: Latest Methodologies for Fungal Studies**

### Towards a Stable, Whole-Genome-Based Digital Taxonomy of Fungi Using Life Identification Numbers

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Lenwood S. Heath, Virginia Tech
Boris A. Vinatzer, Virginia Tech
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Jessie Uehling, Oregon State University

Fungal speciation is a fascinating topic given the biological, ecological roles, and genetic diversity of fungi. Species definitions have evolved over time and considered morphological, geographic, sexual compatibility, and phylogenetic data, and each method has strengths and limitations. Advancements in high-throughput sequencing have increased the availability of whole genome sequences (WGSs) providing a growing mycological resource; however, analysis of ever-increasing numbers of genomes in DNA databases represent a computational challenge. Additionally, only a fraction of the fungal kingdom has been described, and newly identified taxa often challenge current evolutionary frameworks and naming conventions. To meet these challenges, we propose adapting the life identification number (LIN) concept, a classification system designed for prokaryotes that assigns LIN labels to individual genomes reflecting genomic similarity, to fungi. The LIN workflow combines efficient k-mer and hashing algorithms for initial database-wide comparisons followed by average nucleotide identity computation which, in conjunction with the LIN concept, permits rapid, sensitive, and scalable WGS-based identification. This research utilizes LINs to understand how whole genome similarity relates to diversity across the fungal kingdom. Classifications generated via the LIN system will be evaluated against phylogenies derived from orthologous genes. We expect LIN-based classifications will enhance the understanding of fungal taxa, from the genus to within-species groups. This enables rapid strain level identification of isolates with no need for conventional Linnaean classification while also facilitating inference of phenotypes like virulence. This talk will discuss how LINs permit rapid identification, provide stability, complement Linnaean classification, and contribute to understanding fungal taxonomy.

**Parallel Session 1-3: Latest Methodologies for Fungal Studies**

### Using AI to Systematically Review Fungal Endophyte Literature: Do All Plants Really Host Fungi?

Beatrice Bock, Northern Arizona University
Nicholas McKay, Northern Arizona University
Nancy Johnson, Northern Arizona University
Catherine Gehring, Northern Arizona University

As Large Language Models and Artificial Intelligence rapidly advance, scientists must navigate both new challenges and new tools. Machine Learning (ML) is a powerful technology that can optimize tasks that would take humans much longer to complete, often with similar accuracy. While some may see this automation as a challenge, learning how to harness these tools allows us to tackle larger questions than ever before. In fungal endophyte research, a common claim is that all land plants host fungal endophytes. While this statement seems reasonable, it is often either uncited or incorrectly cited. One major barrier to verifying this claim is the sheer volume of literature—over 10,000 papers contain variations of the term “fungal endophytes.” Herein lies an opportunity: while manually reviewing all these papers would be impractical, our Natural Language Processing-based ML algorithm did it in less than five minutes with over 80% accuracy on a test dataset. In this talk, we discuss the strengths and weaknesses of using ML for systematic literature review, the role of automation in scientific synthesis, and what our results reveal about the true ubiquity of fungal endophytes in plants.

## PARALLEL SESSION 1-4:
## Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities

**Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities**

### From Disruption Comes Order: Plant-Mycorrhizal Fungal Networks Show Stability with Allelopathic Invasion

Sean O’Gorman, University of Tennessee Knoxville
James Fordyce, University of Tennessee Knoxville
Nick Smith, Texas Tech University
Jessie Mutz, University of Maryland
Evan Perkowski, Texas Tech University
Morgan Roche, United State’s Geological Survey
Susan Kalisz, University of Tennessee Knoxville
Stephanie Kivlin, University of Tennessee Knoxville

Invasive plant species are disrupting ecological communities worldwide. This disruption is important in belowground communities where invasive plants may sever connections among native plants and their mycorrhizal fungal symbionts. While the effects of aboveground invasion are evident, how belowground communities are affected by invasion remains unknown. The fate of plant-mycorrhizal fungal interactions in the context of global change, such as invasive plant introduction, can be predicted by the stability of the native plants and their associated microbial community. Network-based computational approaches, specifically bipartite networks, allow us to better visualize and quantify relationships and assess stability within communities. We assayed plant-mycorrhizal fungal networks in experimental plots with the allelopathic invader, Alliaria petiolata (garlic mustard). We compared plots where A. petiolata has been continuously removed since 2006 and those where A. petiolata was still present. We assayed the following network parameters indicative of network stability: Shannon diversity, web asymmetry, interaction evenness, and linkage density. We found that plant-fungal networks in invaded plots were unexpectedly more stable than weeded plots (Shannon diversity $p < 0.001$; web asymmetry $p < 0.001$; interaction evenness $p = 0.04$; linkage density $p=0.005$). Increased plant-AM fungal network robustness suggests that reversing the detrimental effects of A. petiolata invasion may prove challenging. Restoration efforts should focus on decreasing the generalist AM fungi in the network and strengthening specialist AM fungal relationships with plant species that have high mycorrhizal fungal dependency, providing a pathway for reversing the effects of plant invasion on the native plant communities.

**Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities**

### Novel Bayesian Network Models to Characterize Host-Microbe-Environment Interactions

Claudia Solis-Lemus, University of Wisconsin, Madison
Yunyi Shen, Massachussets Institute of Technology
Samuel Ozminkowski, Northwestern University

Microbial communities are among the main driving forces of biogeochemical processes. Understanding the composition of microbial communities and what environmental factors shape this composition is crucial to comprehend soil biological processes and to predict microbial responses to environmental changes. Unfortunately, advances in statistical theory for biochemical and biophysical processes have not kept pace with the growing complexity of soil data. Indeed, to identify the key drivers of soil biological processes, we need robust statistical tools that can simultaneously decode microbial responses to environmental cues, interactions among microbes, and the microbial drivers of biological phenotypes. Network analyses have served as a cornerstone in microbiome research for many years. Here, we introduce two novel network approaches to elucidate host-microbe-environment interactions. First, we propose a chain graph model with two sets of nodes (microbial abundances and environmental predictors) to generate a graph where edges denote conditional dependencies, representing both microbial interactions and environmental effects. Our model successfully uncovers key microbial contributors to soil community stability that current methods fail to detect. Second, we present a novel Bayesian Network Regression model that intrinsically accounts for the interactions among microbes and is able to identify influential edges (interactions) and influential nodes (microbes) that drive the phenotypic variability. We illustrate how our new methodologies outperform existing techniques by identifying key microbial drivers of biological phenotypes and accurately inferring both microbial correlation structures and environmental effects. Last, we will demonstrate our new open-source easy-to-use software which will benefit the broader scientific community.

**Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities**

**Rooted in Richness: Unraveling the Role of Neighborhood Effects on Mycorrhizal Fungal Communities in Eastern North American White Oaks (Section Quercus)**

Kathleen Thompson, University of Minnesota, Twin Cities
Alan Whittemore, Morton Arboretum
Andrew Hipp, Morton Arboretum
Jeannine Cavender-Bares, Harvard University
Paul Manos, Duke University
Ian Pearse, United States Geological Survey
Heather McCarthy, University of Oklahoma
Rebekah Mohn, Morton Arboretum
Peter Kennedy, University of Minnesota, Twin Cities

Oaks (Quercus sp.) are a foundational lineage central to the functioning of their associated ecosystems and considered to be the most important group of trees in North American forests. Therefore, to understand and protect North American forests, one must understand oaks and the factors that influence their success – including their associated mycorrhizal communities. Neighborhood effects have been shown to influence plant growth and distribution and, therefore, may be important in structuring oak-associated mycorrhizal communities. To test this, roots were collected from 10 white oak (Section Quercus) species at 30 sites spanning the U.S. range of Q. macrocarpa and submitted for sequencing. Roots were identified as Section Quercus using morphology and ITS sequencing to determine a final subset of 100 and 74 high-quality samples for EM and AM analysis, respectively. Identification and count were recorded for all trees within a 10 m radius ("neighborhood") of each focal Quercus tree. Across all oak species, EM richness was positively correlated with neighborhood richness and presence of Quercus neighbors. Similarly, EM richness in Q. macrocarpa, specifically, was positively correlated with neighborhood richness, but also with presence of EM-associated trees. Although AM richness across Quercus did not correlate with measured neighborhood variables, AM richness in Q. macrocarpa, specifically, was positively associated with presence of AM-associated neighbors and presence of Quercus neighbors. Overall, these results emphasize the importance of neighboring trees in shaping mycorrhizal communities in white oaks, including Q. macrocarpa, which may hold important implications for oak regeneration and afforestation management strategies.

**Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities**

**Shifting our focus to belowground phenology: High frequency community analysis of ectomycorrhizas associated with two temperate tree species**

Kelsey Patrick, University of Illinois, Chicago
Nicholas Medina, The Morton Arboretum
Peter Kennedy, University of Minnesota
Luke McCormack, The Morton Arboretum

Ectomycorrhizal fungi (EMF) are root-associated mutualists that play vital roles in forest health and nutrient cycles. The EMF guild is a taxonomically and functionally diverse group of fungi, and their community responses to seasonal abiotic and biotic factors are not yet understood. Previous studies on EMF phenology have focused on aboveground organs (e.g., sporocarps) or typically sample communities at few intra-annual timepoints, emphasizing the need for belowground studies with higher sampling frequencies. Fine roots associated with EMF were sampled from two mature, monodominant stands of functionally diverse temperate tree species (Picea abies and Carya ovata) at six timepoints between June and December. Fungal ITS2 regions were sequenced and assigned to taxonomic and functional groups using the UNITE and FungalTraits databases. The impacts of season, host species, and abiotic factors on EMF communities were tested using GAMs and PERMANOVA. EMF community composition and dominant genera varied seasonally and differed between host species, with some genera like Cenococcum and Hygrophorus showing distinct peaks in summer and fall. Additionally, preliminary results suggest that soil moisture was the most significant abiotic factor structuring EMF communities, but further research is needed to determine whether moisture directly or indirectly impacts EMF through its influence over fungal growth and mycorrhization, or fine-root growth, respectively. Expanding our focus to belowground EMF phenology provided insights on the environmental factors governing their community dynamics. Future studies can address how EMF community shifts will impact forest ecosystem functions like nutrient cycling and how intra-annual community dynamics respond to climate change.

### Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities

### Stochastic Vs. Deterministic- Ectomycorrhizal Fungal Diversity Tracks Goldilocks Effect Theory for Stochastic Variability in Soil Moisture.

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Jennifer A. Rudgers, University of New Mexico

Global weather has become more unpredictable, and theory predicts that such temporal environmental variability can have opposing effects on biodiversity, known as the Goldilocks Effect. On one hand, temporal environmental variability can cause local extinctions via the demographic costs of stochasticity, the unpredictable component of climate variance. On the other hand, temporal environmental variability can benefit biodiversity through the storage effect. Together, these mechanisms predict a peak in biodiversity at intermediate temporal variance. We manipulated temporal variance in soil moisture to test this Goldilocks Effect for ectomycorrhizal fungal (EMF) communities on roots of Pinus edulis (piñon pine). We separated variability into two components: extent (measured by the coefficient of variation (CV)) or type (deterministic or stochastic). Biodiversity should peak at intermediate CV, and stochastic variability should reduce diversity more than deterministic. Additionally, we compared two types of EMF communities: less diverse communities with a history of experimental field drought or more diverse communities lacking recent drought history. EMF richness on piñon roots increased linearly with CV in soil moisture consistently for both fungal communities and regardless of the type of variability. Under stochastic variability, more diverse EMF communities supported greater piñon survival than less diverse communities, but the gradient of deterministic variability did not affect piñon survival. We conclude that temporal variability in soil moisture promotes biodiversity in EMF communities and stochasticity can increase the sensitivity of piñon seedlings to past environmental conditions. Thus, negative ecological consequences of temporal environmental variability may be underestimated if stochastic variability is ignored.

### Parallel Session 1-4: Beyond species: Ecological Properties that Shape Mycorrhizal Fungal Communities

### The Impact of Trait Variation and Mycorrhizal Fungal Associations on Native Tree Performance in a Washington Old Growth Forest

Laura Nevins, Washington State University
Tanya E. Cheeke, Washington State University
James A. Lutz, Utah State University
Jenny Zambrano, Washington State University

Old growth temperate forests in the Northwestern United States are rare and fragmented but provide critical functions like carbon sequestration. The performance of these forests is supported by associations with mycorrhizal fungi, which enhance soil nutrient and water acquisition, positively influencing host tree growth and survival. The Wind River Forest Dynamics Plot (WFDP) in Washington State, an old growth forest undergoing long-term monitoring, is experiencing increasingly drier summers. While long-lived organisms like trees are slow to adjust their traits to environmental changes, fast-growing fungal symbionts can respond more rapidly. Thus, evaluating patterns of trait variation in tree hosts and fungal symbionts can reveal functional adjustments to rapid climate change that can be linked to tree demography. We sampled fungal communities in WFDP in summer 2023, and assigned functions related to water and nutrient acquisition. Tree leaves and roots were collected in summer 2024 to characterize host traits. Long-term demographic data from WFDP will be used to evaluate effects of trait and functional variation on tree performance. We hypothesized that: 1) drier summers result in an overlap of host trees and mycorrhizal fungi traits/functions towards more conservative strategies, and 2) tree host survival and growth variation is explained by convergence or divergence of their strategies with their fungal partners. We observed convergence of fungal symbiont functions and tree host traits,

supporting H1. The relationships between this trait variation and tree demography are currently being evaluated to test H2. Our results will help improve understanding of species responses to rapid climate change.

## PARALLEL SESSION 2-1:
## Fungal Evolutionary Processes

### Parallel Session 2-1: Fungal Evolutionary Processes
### Elucidating the Evolutionary History of Neocallimastigomycota

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Taylor Mills, Oklahoma State University
Julia Vinzelj, Oklahoma State University
Ty Young, Oklahoma State University
Paul Stone, University of Central Oklahoma
Donald Walker, Middle Tennessee State University
Alexander Rurik, Middle Tennessee State University
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Cameron Siler, University of Oklahoma
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Mostafa Elshahed, Oklahoma State University

Anaerobic gut fungi (AGF, phylum Neocallimastigomycota) are a clade of obligate anaerobic, zoospore-forming fungi inhabiting the digestive tract of herbivorous animals. Twenty of the 22 AGF genera were obtained from mammalian hosts. Culture-independent surveys, however, suggest a broader host range, and further indicate that at least 40 additional genera remain uncultured. Notably, the two most recently described genera, obtained from reptilian hosts (tortoises, family Testudinidae), represent the earliest-diverging AGF lineages, substantially pushing the origin of Neocallimastigomycota back to ~120 mya. We therefore theorized that other reptiles might harbor AGF as well, and that they might have served as AGF host before the evolution of mammals. To this end, we analyzed fecal samples from herbivorous and omnivorous reptiles using amplicon sequencing targeting the D2 region of the LSU. Preliminary results confirm the presence of AGF in both herbivorous and omnivorous reptiles and reveal putative novel phylum- and genus-level clades. Targeted isolation efforts yielded two novel genera, NY56 and NNM4, from tortoise feces. A more detailed characterization of both is currently underway, as are further efforts to obtain isolates from other reptilian fecal samples as well. With this study we hope to deepen our understanding of fungal phylogeny, the early event in the evolution of Neocallimastigomycota, and their role within diverse herbivorous hosts and ecological niches.

### Parallel Session 2-1: Fungal Evolutionary Processes
### Evolutionary Processes Driving Chemodiversity in Psilocybe

Matthew Meyer, The Ohio State University
Mine Gezgin, The Ohio State University
Darwin Munoz, The Ohio State University
Kou-San Ju, The Ohio State University
Jason Slot, The Ohio State University

Specialized metabolites mediate species interactions, defense, and environmental adaptation, yet the evolutionary mechanisms generating this chemical diversity remain underexplored in mushroom-forming Basidiomycetes. We investigate how speciation and hybridization generate metabolic diversity in Psilocybe, a globally distributed saprotrophic genus of over 160 species with significant diversification across continents. We hypothesize that interspecific hybrids combine parental metabolites (additive), create new compounds through enzyme promiscuity or pathway mixing (generative), and lose certain pathways (subtractive). These processes are likely driven by genomic changes such as transposons disrupting or relocating genes and the reorganization of biosynthetic gene clusters, both of which may merge ancestral pathways or deactivate them entirely. To test this, we integrate comparative genomics and metabolomics across three closely related African taxa: P. ochraceocentrata (recently distinguished from misidentified P. natalensis), true P. natalensis, and P. cubensis (including domesticated [Jack Frost] and wild-type [Blue Meanies] strains), alongside a stabilized hybrid (P. ochraceocentrata × cubensis – Yellow Umbo F6). We compare biosynthetic gene clusters and metabolite profiles of multiple fungal tissues using high-quality genomes (Illumina NovaSeq 6000, PE150, ~6 Gbp/genome) and metabolomics (HPLC-MS, solid-phase extraction). By contrasting ~2–5 million years of divergence with domestication and interspecific genetic exchange, we assess novel metabolite evolution and disentangle the roles of speciation, hybridization, and artificial selection in chemical diversification. This work addresses how biosynthetic gene cluster modularity, hybridization, and domestication impact chemodiversity that underpins chemical ecology in Agaricales.

### Parallel Session 2-1: Fungal Evolutionary Processes
### Pigment Loss and Melanin Mutations Are Associated with the Unintentional Domestication of a Cheese-Associated Penicillium

Nicolas Louw, Tufts
Justin Eagin, University of Wisconsin, Madison
Jackson Larley, Tufts University
Mateo Kehler, Jasper Hill Farm
Nancy Keller, University of Wisconsin-Madison
Benjamin Wolfe, Tufts University

Previous comparative and experimental evolution studies have suggested how fungi may rapidly adapt to new environments, but direct observation of in situ selection in fungal populations is rare due to challenges with tracking populations over human time scales. Here, we monitored a Penicillium population over eight years in a cheese cave and documented a phenotypic shift from predominantly green to white strains within this population. Diverse mutations in the alb1 gene, which encodes the first protein in the DHN-melanin biosynthesis pathway, explained the green to white shift. A similar phenotypic shift was recapitulated with an alb1 knockout and experimental evolution in laboratory populations. The most common genetic disruption of the alb1 genomic region was caused by putative transposable element insertions. White strains had substantial downregulation in global transcription, with genetically distinct white strains possessing divergent shifts in expression of different biological processes. White strains outcompeted green strains in co-culture, but this competitive advantage was only observed in the absence of light. Our results illustrate how fermented food production by humans provides opportunities for relaxed selection of key fungal traits over short time scales. Unintentional domestication of microbes by cheesemakers may provide opportunities to generate new strains for innovation in traditional cheese production.

### Parallel Session 2-1: Fungal Evolutionary Processes
### The Ecological Diversification of Lichen Symbioses

Matthew Nelsen, The Field Museum, Negaunee Integrative Research Center

Here we traced the underlying pathways by which symbiotic and phenotypic diversification occurred in one of the most iconic symbioses—lichens—while evaluating their ecological and macroevolutionary consequences. By inferring a time-scaled phylogeny of over 3300 species of lichen-forming fungi, we identified occasional instances of symbiotic instability that increased both the magnitude and diversity of lichen contributions to ecosystem processes from the Mesozoic through the Cenozoic. Symbiont switches broadly coincided with shifting environmental conditions, and the convergent evolution of phylogenetically or functionally similar associations in diverse lineages. We then inferred when lichens invaded arboreal habitats, and place them in a broader and more comparative framework by highlighting their paleoecological implications, and discussing them in the context of climate, vegetation, and the evolution of other epiphytic or arboreal lineages.

### Parallel Session 2-1: Fungal Evolutionary Processes
### The evolution of Thecaphora frezzii, causal agent of peanut smut, in response to host selection pressure

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Peanut smut is a significant disease of peanuts, thus far restricted to Argentina. The disease is caused by the smut fungus Thecaphora frezzii and the seeds of infected plants are replaced by a mass of dark teliospores, thereby reducing yield.

Because the smut only affects peanut seeds, which develop belowground, the pathogen was able to spread undetected to all peanut growing regions of Argentina. Previous work identified a single locus in the host that confers resistance to the pathogen and five peanut cultivars with this resistance locus have been widely released in Argentina since 2019. While significant progress has been made concerning the role of the host in disease progression, much less is known regarding the pathogen and how it is evolving in response to the broad deployment of resistant host material, which is expected to exert strong selection pressure on it. Following in vitro culture of the fungus in its haploid stage, we produced a chromosome level genome assembly of T. frezzii for the first time. At 39 Mb, T. frezzii has the largest smut genome sequenced to date with the highest repeat content and intron content relative to other sequenced smut fungi. We also obtained high-throughput short-read sequencing data for approximately 50 T. frezzii isolates collected from both susceptible and resistant peanut genotypes and performed association tests to identify genetic markers in T. frezzii that may contribute to overcoming host resistance. Herein, we will discuss the pathogen's evolution in response to the broad deployment of resistant host material.

### Parallel Session 2-1: Fungal Evolutionary Processes
### Tracing the Evolutionary History Behind the Emergence of Two Pandemic Plant Diseases: Wheat Blast and Gray Leaf Spot

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Pyricularia oryzae, syn. Magnaporthe oryzae, is recognized as the 'rice blast fungus' due to its global impact on rice crops but has more recently raised concerns as a potential threat to global wheat production. Wheat blast was first detected in 1985 in Paraná, Brazil, and by 1990, it was widespread throughout all wheat-growing regions and neighboring countries. In recent years, wheat blast outbreaks have been reported in Asia and Africa, making it an emerging concern for global agriculture. Another disease caused by P. oryzae, gray leaf spot (GLS), was first identified in 1971 in annual ryegrasses in Louisiana and Mississippi and later caused widespread outbreaks across the central U.S. by the mid-1990s. In this study, we reconstruct the evolutionary history of two recent populations of P. oryzae that are responsible for these two novel diseases (wheat blast and GLS). We provide evidence that wheat blast/GLS evolved through two distinct mating episodes: the first occurred around 60 years ago when an Eleusine-adapted fungal individual mated with a Urochloa-adapted individual. In the subsequent decade, a single progeny of this cross was mated with a small number of individuals from three additional host-specialized populations. As a result of these matings, non-functional alleles of two key host-specificity factors, whose recombination in a multi-hybrid swarm facilitated the host jump, were introduced into the population. We suspect this process has been initiated by the coincidental introduction of the Urochloa-adapted lineage, as Urochloa was first introduced to Brazil in 1952 as forage for the beef industry.

## PARALLEL SESSION 2-2:
## Systematics: Ascomycota

### Parallel Session 2-2: Systematics: Ascomycota
### Dramatic expansion of a cluster of extracellular phospholipase genes may ecologically define the genus Ceratocystis

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Comparative genomics of the Ceratocystis tree pathogen C. lukuohia (Rapid 'Ōhi'a Death) and C. fimbriata (sweet potato black rot) revealed a dense ~550kb cluster of ~70 heterogenous extracellular phosphatidylinositol-specific phospholipase-C genes (exPI-PLCs) in both species, potentially the largest conserved gene cluster known in fungi. These prokaryotic-type exPI-PLC genes, conserved across more than 50 Ceratocystis genomes, varied greatly in copy number (26 to 90+), and notably expanded in the Latin American Clade (LAC), the most aggressive clade of pathogens. Of its closest relatives, Berkeleyomyces basicola has an estimated 25 exPI-PLCs (which are not in a single cluster), whereas species of Chalaropsis each have only a single exPI-PLC gene. The presence and arrangement of the Ceratocystis cluster's flanking genes in Chalaropsis and Berkeleyomyces suggest the cluster's de novo origin in Ceratocystis, with expansion facilitated by gene duplication via uneven crossover events and/or transposable elements. Ceratocystis exPI-PLCs show unique amino acid substitutions at residues essential for PI-PLC function in other organisms (both bacterial and eukaryotic), pointing to potential novel function, perhaps involving destruction of plant membranes. Given the uniqueness of the cluster in Ceratocystis, the conservation of high copy number, the correlation between copy number and pathogenicity, and the inferred novel function, these exPI-PLC genes warrant further investigation. They may explain the unique mode of pathogenicity and unpredictable host ranges of this unique genus of canker and wilt pathogens.

**Parallel Session 2-2: Systematics: Ascomycota**

## New insights into molecular phylogeny of emerging foliar pathogenic fungi associated with anthracnose, brown blight, and gray blight of tea in Sri Lanka

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[Camellia sinensis (L.) O. Kuntze] is a commercially significant crop cultivated for the production of the renowned beverage, tea. While blister blight caused by Exobasidium vexans has received remarkable attention, the other foliar diseases such as anthracnose, brown blight, and gray blight caused by the species of Colletotrichum and Pestalotiopsis are largely overlooked. To address this knowledge gap, a fresh collection of fungi isolated from symptomatic tea leaves collected from 16 tea plantations covering the major tea-growing areas of Sri Lanka. From the anthracnose and brown blight symptoms, three Colletotrichum species belonging to C. gloeosporioides species complex were discovered by the combined phylogenetic analysis of internal transcribed spacer 1, 5.8S region and the internal transcribed spacer 2 of the ribosomal RNA gene cluster (ITS), β-tubulin (TUB2), and GAPDH (Glyceraldehyde 3-phosphate dehydrogenase). Based on the multi-locus phylogenetic analysis of ITS, TUB2 and translation elongation factor 1-α (TEF1-α) of the isolates obtained from gray blight infected tea leaves, multiple species of Pseudopestalotiopsis, Pestalotiopsis, and Neopestalotiopsis were revealed with few novel taxa. Further, this study unveiled the pathogenicity of some previously documented Neopestalotiopsis and Pestalotiopsis species on tea namely, N. hydeana, N. petila, N. saprophytica and P. adusta. Since many of these isolates were identified as potential pathogens of foliar diseases in tea, their rapid and accurate detection is crucial to minimizing widespread damage. Therefore, investigating the diversity, distribution, and pathogenicity of these causative agents is essential for developing effective disease management strategies to prevent pathogen spread and yield losses.

**Parallel Session 2-2: Systematics: Ascomycota**

## Sequencing of global Penicillium isolates recaptures speciation in Fleming's fungus and related species

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The penicillin-producing filamentous fungi Penicillium chrysogenum and Penicillum rubens have impacted human life in tremendous ways. These species were not always considered separate, however, as P. rubens was only defined in the early 2010s based on genetic divergence. Several cryptic species were also previously proposed from the P. chrysogenum complex, based on partial gene sequences. These proposed species lack genome assemblies. Therefore, we still do not understand speciation or species relationships within the complex. To explore the evolution of P. chrysogenum and P. rubens and identify cryptic species, we collected isolates from a diverse array of ecological niches, including both natural and built environments. We generated whole genome sequencing for >80 isolates and downloaded publicly available data for an additional 25 isolates. Some isolates identified as P. chrysogenum were instead found to be other species. We used single nucleotide polymorphisms to explore population structure in P. chrysogenum and P. rubens. In addition to the two species, which formed monophyletic clades in our phylogenies, we also discovered three additional clusters/clades possibly representing cryptic species, as well as identifying recombination within the P. chrysogenum clade. Based on single-gene markers, we have not been able to classify the putative cryptic species as those previously identified, possibly indicating additional cryptic species in the complex. Although further phenotyping is needed to characterize variation among P. chrysogenum and our so-called cryptic species, our work sheds light on the complexities within Penicillium, from which there is yet more to learn.

**Parallel Session 2-2: Systematics: Ascomycota**

### Sniffing for fungi: Use of a Conservation Dog Uncovers High Regional Truffle Diversity

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Hypogeous aromatic fungi ('truffles') contribute significantly to overall fungal diversity but are difficult to find using traditional survey methods because they fruit underground, leading to under-documentation and a lack of data on species distribution and ecology. Truffles evolved to emit strong aromatic compounds to attract wildlife mycophagists for spore dispersal, a trait that culinary truffle harvesters exploit using trained truffle dogs. We trained a conservation dog to recognize a broad range of truffle aromas across diverse fungal lineages to increase efficiency in finding these cryptic fungi. We present a case-study demonstrating the value of using a 'truffle diversity dog' through a survey of the floristically diverse Cascade-Siskiyou National Monument (CSNM), located on the southwestern Oregon and northwestern California border, U.S.A. The dog uncovered high biodiversity in this region, locating 103 truffle species in 34 genera across 23 families. The trained dog was particularly valuable for locating truffles that are visually difficult to distinguish from the substrate (e.g. the truffle genus Genea) and species that produce few fruiting bodies. Fewer than half of the unique taxa matched public sequence records, and many are likely new to science. We found high species turnover between oak and conifer habitats, suggesting high host specificity in truffles. The wide range of fungal taxonomic diversity found in this study by a conservation dog demonstrates the value of training dogs to generalize to all types of truffle aroma, providing a promising method to efficiently describe understudied fungal biodiversity.

**Parallel Session 2-2: Systematics: Ascomycota**

### The Biogeography and Systematics of Xylariaceous Fungi on Polynesian Islands

<u>Michael Malone, University of Wisconsin, La Crosse</u>

The xylariaceous fungi are an enigmatic group of macrofungi with scant knowledge of their biodiversity and evolutionary origins. The xylariaceous fungi are not only important wood decomposers, but they also live in plant leaves as endophytes. The responses of plant hosts to their endophytic fungi have not been fully determined. These fungi are especially understudied on Polynesian islands where they are rarely collected let alone sequenced. The lack of resolution in the phylogeny of these fungi can be attributed to the lack of sequence data from the Polynesian islands. Thirty-five specimens of xylariaceous fungi were obtained from Mo'orea. Xylariaceous fungi were also obtained from Kaua'i (n=25), Oahu (n=13), and Hawai'i (n=9) for phylogenetic comparison to the Mo'orea fungi. All specimens were morphologically identified to species when possible. DNA extractions were performed for all specimens and four genetic loci (ITS, RPB2, alpha-actin, and LSU) were PCR-amplified with Illumina-tagged primers. The final PCR products will be pooled into a DNA library that will be sequenced by the University of Wisconsin-Madison. After the sequences are read, they will be sent back for alignment and a phylogenetic tree will be constructed using the aligned sequences of each specimen. The phylogenetic tree will provide insight into the evolutionary relatedness of the Mo'orea fungi to xylariaceous fungi from other parts of the world through archived GenBank sequences. This study is the first to document the biodiversity and phylogenetic placement of xylariaceous fungi on Mo'orea.

### Parallel Session 2-2: Systematics: Ascomycota

### Where do we belong? Enigmatic phylogenomic placement of Laboulbeniomycetes within Pezizomycotina

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Laboulbeniomycetes is a class of poorly studied fungi that are obligately associated with arthropods, either as ectoparasites producing thalli on their hosts' exoskeletons (Herpomycetales, Laboulbeniales), or for dispersal purposes (Pyxidiophorales). Research into this class has been hindered due to multiple factors including difficulty of material preservation, extraction of high quality DNA, their diminutive nature, lack of morphological diversity, and the inability of most of them to grow in culture. Their placement within Pezizomycotina has been poorly resolved because only a few genetic markers have been available to date. Here, we present multiple genomes representing all three described orders and a phylogenomic reconstruction of Pezizomycotina and the most expansive phylogenomic tree of the Dothideomycetes to date. Our analyses give strong support to the placement of all Laboulbeniomycetes within a single lineage within the class Dothideomycetes.

## PARALLEL SESSION 2-3:
## Patterns and Mechanisms of Fungal Community Assembly

### Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly

### Common mycorrhizal networks mediate intraspecific and interspecific interactions of invasive Canada Thistle (Cirsium arvense) and native Pasture Thistle (Cirsium discolor)

Joanna Weremijewicz, North Central College

Common arbuscular mycorrhizal networks (CMNs) have the potential to interconnect and partition nutrients among about 72% of plant species in the world, including invasive plant species. Interspecific competition is one of the most important processes determining the likelihood of plant invasion; however, whether CMNs assist invasive plants in establishing new areas and how is not yet understood. We investigated the role of CMNs in mediating interactions between Canada Thistle (Cirsium arvense) and its native congener, Pasture Thistle (Cirsium discolor), in a fourteen-week target plant experiment using a suite of AM fungi. In pots, one species was the target plant, and the other was present as six equally spaced neighbors. CMNs were kept intact or severed, and in half the pots, we shaded Canada Thistle to reduce C provisioning to CMNs. Although CMN-mediated interspecific interactions were weak with little effect on target plant sizes, we found that when Canada Thistle neighbors had limited C provisioning ability, this benefited Pasture Thistle target plants nutritionally, causing CMNs to divert K and Cu to Pasture Thistle. When both species were in the neighbor position within pots, intact CMNs benefited the growth of both species, suggesting that CMNs mediated strong intraspecific interactions. Our findings suggest that Canada Thistle can disrupt mineral nutrient dynamics within CMNs interconnected to native plants, which may have more considerable consequences in the long term. The similar nutrient demands of conspecifics may make the role of CMNs in belowground plant competition more pronounced than when interconnecting heterospecifics.

### Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly

### Host Genetic Control Shapes Niche-Specific Arbuscular Mycorrhizal Fungal Assembly in Sorghum Field

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Plant-microbe interactions critically influence ecosystem function and agricultural sustainability, yet the mechanisms by which host genetics shape arbuscular mycorrhizal fungal (AMF) communities across root-associated niches remain unresolved. Using Illumina NextSeq sequencing of 18S rDNA, we investigated AMF assembly in roots, rhizosphere, and soil across 24 bioenergy sorghum (Sorghum bicolor) genotypes under field conditions with factorial N-P additions. Plant genotype exerted the strongest effect on AMF composition (PERMANOVA: root $R^2 = 0.123$, $p < 0.001$; rhizosphere $R^2 = 0.179$, $p < 0.001$; soil $R^2 = 0.193$, $p < 0.001$). Alpha diversity increased across niches (root < rhizosphere < soil; $p < 0.001$), with root communities exhibiting the lowest diversity (133 genotype-specific taxa), dominated by Glomus_OTU37 and Glomus_OTU115. Rhizosphere and soil communities shifted toward Claroideoglomus_OTU1 and Diversispora_OTU8, respectively. Genotypes with strong AMF filtering showed >50% Bray-Curtis dissimilarity between root and bulk niches. Fertilization effects were not significant ($p > 0.05$), consistent with minimal nutrient limitation observed in aboveground biomass. This suggests that host genetic control over AMF assembly superseded the influence of nutrient amendments, which were applied at agronomically relevant but non-saturating levels. Our results reveal niche-specific patterns of host-mediated filtering, with plant genetics exerting direct effects on microbial recruitment in the roots and indirect effects in the rhizosphere and surrounding soil. This study establishes niche-partitioned, genotype-driven AMF assembly as a critical factor in plant-microbe interactions. By prioritizing sorghum genetics, breeders can develop lines with enhanced microbial symbiosis tailored to field conditions, advancing sustainable crop management in systems with moderate nutrient inputs.

## Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly

### Mean Annual Precipitation Primarily Structures Leaf, Root, and Soil Fungal Communities in Remnant and Post-Agricultural Prairies along a Steep Midwest Precipitation Gradient

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Fungal communities provide critical ecosystem functions, including decomposition, plant nutrient acquisition, and soil aggregation. We are beginning to understand how shifts from human land use impact these fungi, but these responses often depend on climate elements that are also changing. Maintaining critical fungal functions to plant and soil health, for example, might differ between remnant prairie ecosystems and agricultural sites but also based on the amount of rainfall these sites receive. Our study explored the relative importance of land-use and precipitation history to plant-associated and soil-inhabiting fungi. We predicted that remnant prairies harbor more diverse communities than post-agricultural sites and that fungal diversity increases with mean annual precipitation. We also predicted that fungal communities are compositionally distinct in remnant prairies and post-agricultural sites because of agricultural use legacies and that they differ between arid and mesic environments. To test these hypotheses, we sampled leaves, roots, and soils in remnant prairies and post-agricultural sites across the steep precipitation gradient in Kansas, USA and analyzed fungal diversity and composition using ITS2 metabarcoded ASVs. Fungal diversity did not differ with precipitation or land-use histories and there was no apparent interaction. Fungal community composition strongly differed between arid and mesic environments in leaves, roots, and soils, and while root-associated fungi differed between remnant and post-agricultural prairies, leaf-associated and soil-inhabiting did not differ between land-uses and there was no apparent interaction. Understanding how environmental change and land-use legacies impact plant-associated and soil-inhabiting fungi will allow us to manage systems to maintain and optimize ecosystem functions.

**Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly**

### Symbiont-Mediated Mechanisms of Pinus Taeda and Its Root Mycobiome in Response to Soil Heavy Metal Contamination

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Fast economic and industrial development has significantly increased ecological and environmental concerns associated with soil pollution, including heavy metal (HM) contamination. Soils with high HM concentrations may pose considerable threats to biota, often resulting in decreased biodiversity and productivity. Mycorrhizal fungi play crucial roles in plant adaptation to HM stress, but their molecular interactions under such conditions remain less studied. To depict the impact of ectomycorrhizal fungi (EMF) on molecular interactions between root associated fungi and their host partner Pinus taeda under HM stress, we conducted a bioassay using P. taeda seedlings inoculated Suillus hirtellus and grown in HM-contaminated soils collected from a mine site. Metatranscriptomic analysis of root samples collected from the bioassay indicated that HM contamination significantly reduced both the richness and transcriptional activity of root-associated fungi in P. taeda seedlings. However, S. hirtellus inoculation effectively restored the fungal community and functionality. Predominant fungal taxa Rhizopogon and Suillus were actively involved in metal exclusion and detoxification. Furthermore, S. hirtellus inoculation restructured its relationship with P. taeda by mitigating metal toxicity and improving plant tolerant mechanisms, resulting in substantial reorganization of functional coordination between the fungal community and P. taeda, accompanied by shifts in fungal community composition. Our findings provide critical insights into how ectomycorrhizal fungi enhance plant fitness and plant-fungal molecular coordination under HM stress, shedding light on the mutualistic associations essential for plant resilience in stressed conditions.

**Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly**

### Testing the Stress Gradient Hypothesis with Plant-Microbial Interactions across a Temperate Elevation Gradient

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The stress-gradient hypothesis (SGH) posits that across a climatic gradient, two organisms are more likely to compete in mild climates and to cooperate in climates challenged with abiotic stress. Most research exploring the SGH has focused on interactions between plant species, and the degree to which either plant-microbial interactions or the role of microbes in facilitating intraspecific plant-plant interactions according to the SGH remain less explored. Here we examined the extent to which plant-microbial interactions fit the narrative of the SGH across a 1,000 meter elevation gradient present in temperate forests of the Pacific Northwest. The low elevation forests are considered mesic relative to the high elevation forests, with longer growing seasons, greater relative humidity, and less extreme temperature fluctuations. In line with the SGH, we predicted more pathogens and pathogenic interactions at low elevation sites and more mutualists and mutualistic interactions at high elevation sites. We tested this prediction through a combination of a field study and a large scale, controlled experiment. In the field study we characterized fungal functional guilds associated with soil and foliar tissue found across the gradient, and

in the greenhouse study we further explored plant-microbial interactions in these different climates through a reciprocal inoculation experiment using Douglas-fir seedlings, a conifer that ranges across the gradient. Our findings are congruent with the SGH, and more broadly indicate that plant-microbe interactions can function as an extended phenotype and the same plant species can evolve to associate with microbes differently in different environmental contexts.

**Parallel Session 2-3: Patterns and Mechanisms of Fungal Community Assembly**
**The Interplay of Drought Stress and Plant Age in Sorghum Root Mycobiome Assembly**

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Increasing environmental pressures like drought challenge crop productivity. In response, plants alter root exudation to facilitate the recruitment of beneficial stress-tolerant fungi. Bioinoculants made from these fungi are proposed as an alternative to increase plant tolerance to drought. However their efficacy depends on many factors including the root microbiome, host and environment. Most studies that test the effects of drought on plant biomass and root microbiome, overlook the confounding effects between the length of drought and host age, resulting in a major gap in our understanding of plant responses to drought. The goal of this study was to disentangle drought length, drought severity and host age to fully comprehend the climate-dependance of sorghum mycobiome assembly, its effects on plant biomass and root exudates. Using linear mixed models, I found that drought severity decreases plant biomass significantly, and that this effect is mainly driven by the length of drought and plant age. Analysis of the ITS2 region showed Shannon diversity increases with plant age but decreases with longer periods of drought. I also found that drought severity, length of drought, plant age and their interaction significantly affect the composition of fungal communities. Finally, the βNTI index showed that length of drought overrides the effects of plant age and drought severity, leading to more deterministic fungal communities. These results demonstrate that disentangling drought severity, length of drought and plant age is important to better predict plant responses to drought. Future work will analyze root exudates and their effects on root mycobiome assembly.

## PARALLEL SESSION 2-4:
### Fungi in Agroecosystems

**Parallel Session 2-4: Fungi in Agroecosystems**
**Field test of novel 3D-printed mycorrhizal reduction cores with Pseudotsuga menziesii seedlings in the Pacific Northwest**

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Mycorrhizal fungi are pivotal to the productivity of plants and health of ecosystems globally by increasing nutrient acquisition and resilience of their hosts. However, the difficulty of manipulating plant-mycorrhizal networks in field experiments limits our understanding of mycorrhizal ecology. Experimentally reducing or excluding mycorrhizal colonization from seedlings, while allowing for pathogens to infect plants in a field setting is challenging (e.g. fungicides can limit both). Based on designs from prior work, we designed, produced, and field-tested 3D-printed mycorrhizal reduction cores. They consist of a two-layer scaffold and a 35 µm mesh lining to allow pathogens and other microbes to move into the core while limiting external root competition. Rotation of the inner scaffold severs mycorrhizal hyphae and limits secondary colonization of root tips through mycelium. We tested the cores by transplanting 75 Pseudotsuga menziesii (Douglas fir) seedlings around 15 adult focal trees across three sites in a Pacific Northwest forest in fall 2024. Seedlings were transplanted into twice-autoclaved soil sourced from their respective focal tree. Treatments included no-core and no-rotation controls, one week and two week rotation schedules, and a thin walled core. After 19 weeks, we harvested 50 seedlings, leaving

25 to experience a longer timeframe. We present results of mycorrhizal colonization and ITS fungal metabarcoding of soil to demonstrate the efficacy of our design. We additionally discuss the practical considerations for the deployment of mycorrhizal reduction cores. These results inform future experiments that aim to investigate the ecology of plant-mycorrhizal networks in the field.

### Parallel Session 2-4: Fungi in Agroecosystems

### Friends in Low Places: Exploring the Impact of Rhizospheric Fungi on Disease Suppression in Winter Wheat

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Rhizosphere-associated bacteria and fungi are well-described in the development of disease-suppressive soils, acting through mechanisms such as direct antagonism, niche exclusion, and induced host resistance. Plant genotype is known to influence the assembly of microbial communities, suggesting the possibility of new breeding strategies for developing cultivated varieties (i.e., cultivars) that are enriched in antagonistic microbes, thereby bearing quantitative resistance to disease. The present work spurs from findings in winter wheat (Triticum aestivum), where significant variation was noted in the speed at which cultivars developed soils suppressive to the ascomycete pathogen Gaeumannomyces tritici (i.e., take-all). Rhizobacterial variation across in the initial study did not sufficiently explain variation, thus we expanded our work to investigate rhizospheric fungi alongside rhizobacteria. Using soil cycling to enrich the microbial signals, we developed soil suspensions from the rhizosphere of each of four wheat cultivars that differed in disease resistance to take-all in our initial work. We applied these suspensions to sterilized seeds of a common, disease-susceptible test cultivar and evaluated subsequent disease in greenhouse-grown seedlings. To explore the range of disease suppression, the seedling assays were run with another soilborne fungal disease of winter wheat common to the Pacific Northwest, Fusarium crown rot (Fusarium spp.). We identified significant differences in disease development between cultivars that aligned with our previous findings in the take-all pathosystem, suggesting that cultivars may exhibit microbiome-mediated disease resistance against multiple pathogens. Additional studies are in progress to determine whether rhizospheric fungi are interacting directly or indirectly in these dynamics.

### Parallel Session 2-4: Fungi in Agroecosystems

### Insights into the Diversity of the Bean Root Rot Complex

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The bean root rot complex is comprised of fungal pathogens belonging to clade 2 of the Fusarium solani species complex (FSSC), which contains up to 60 phylogenetically distinct species, most of which are cryptic. In recent years, three of the four causal species of bean root rot have been identified in Michigan, two of which were thought to be endemic to South America. There are significant gaps in the understanding of the diversity within FSSC. Novel species have been recently identified in South America, and with ongoing climate change, the distribution of these species could be more widespread than expected. The main objective of this study was to better understand the taxonomic diversity of FSSC present in dry bean hosts and farm soils in Michigan. Isolates from recent collections were identified using multilocus sequence typing, including loci sequences from translation elongation factor 1-α (TEF1), RNA polymerase II second largest subunit (RPB2) and β–tubulin (tubB). Using TEF1 and RPB2, a meta-barcoding approach was performed with soil samples to identify the FSSC species present. The analysis showed that the extent of Fusarium species causing bean root rot is greater than expected since it is not monitored extensively, and species endemic from South America could be present in the U.S. already. By identifying the causal species of bean root rot and their potential spread, these findings will help create better management practices, allowing for more targeted control measures and early detection in U.S. dry bean production.

**Parallel Session 2-4: Fungi in Agroecosystems**

## Pathogenic and Non-Pathogenic Fungi Associated with Cultivated and Wild Cacao in the Peruvian Amazon – the Revenge

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Cacao is the source of one of the most beloved commodities, chocolate. However, fungi associated with it are vastly understudied, especially in the heart of its center of diversity, the Peruvian Amazon. During the last four years, the Díaz-Valderrama lab has made a lot of progress in documenting the pathogenic and non-pathogenic fungi associated with cacao. We found in Amazonian remote areas, a common problem is the thread-blight disease caused by a new species of Marasmius, M. infestans, which we described. We also conducted a thorough population genetics analysis of Moniliophthora perniciosa, the causal agent of cacao witches' broom disease, finding high levels of genetic diversity, and revealing its invasive Amazonian routes. Moreover, we found the causal agents of cacao dieback, besides the globally common Lasiodiplodia theobromae, is L. iraniensis, for the first time reported for this crop. On the other hand, we have been successful in documenting epiphytic fungi associated with cacao. We have successfully isolated and identified more than one hundred and fifty yeast isolates from the surface of the leaves and fruits of cultivated and wild cacao. This study has resulted in the publication of the recently described new species Hannaella theobromatis, a common inhabitant of the cacao phyllosphere. All this is just a little taste because most likely there are many more fungi left to discover associated to cacao in the Peruvian Amazon. Due to visa issues, last year we couldn't present this talk, but now it has more published data, i.e., this is revenge.

**Parallel Session 2-4: Fungi in Agroecosystems**

## Rewilding of Palm Oil Plantations Leads to Soil Fungal Diversification

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The assembly of fungal communities following land-use change depends on multiple ecological processes, including dispersal, selection by environmental conditions, and stochastic events. However, key questions remain regarding the predictability of fungal reassembly during progressive restoration. The reversion of palm oil plantations to more ecologically complex systems presents an opportunity to investigate how soil fungal communities contribute to ecosystem recovery. As restoration progresses, fungal communities may shift from those adapted to high-intensity management toward more functionally diverse and resilient assemblages characteristic of natural forests. However, the speed and direction of these shifts, and their consequences for nutrient cycling, remain uncertain. By tracking soil fungal community composition over a five-year rewilding chronosequence, we investigate how fungal diversity, composition, and function respond to restoration efforts. Fungal community composition shifted over the five-year rewilding period, with notable changes in the relative abundances of major fungal phyla. After three years of rewilding, fungal communities had diversified, with an increase in Basidiomycota and minor contributions from Glomeromycota and Chytridiomycota. These shifts suggest a transition from fungal communities adapted to disturbed agricultural soils toward those associated with more natural, functionally diverse ecosystems. Fungal communities also became more stable and predictable as restoration progressed, possibly due to increasing organic matter accumulation and reduced disturbance. As palm oil yields decline due to land degradation agricultural interests are increasingly recognising the need to manage soil more efficiently. Our results provide insights into microbial contributions to soil recovery and can inform rewilding strategies in degraded tropical landscapes.

# PARALLEL SESSION 3-1:
## Mechanisms of Fungal-Bacterial Interactions

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions
### A Fungal Innate Immune Response in Neurospora Crassa Revealed upon Bacterial Co-Culture with Pseudomonas Syringae

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Recent comparative genomics and mechanistic analyses support the existence of a fungal immune system. Fungi encode genes with features similar to non-self recognition systems in plants, animals, and bacteria. However, limited functional or mechanistic evidence exists for the surveillance-system recognition of microbial ligands in fungi. We found that Neurospora species coexist with Pseudomonas in their natural environment. We leveraged two model organisms, Neurospora crassa and Pseudomonas syringae DC3000 (PstDC3000) to observe immediate fungal responses to bacteria. PstDC3000 preferentially surrounds N. crassa cells on a solid surface, causing environmental dependent growth responses, bacterial proliferation and varying fungal fitness. Specifically, the Type III secretion system (T3SS) ΔhrcC mutant of PstDC3000 colonized N. crassa hyphae less well. To dissect initial cellular signaling events within the population of germinated asexual spores (germlings), we performed transcriptomics on N. crassa after PstDC3000 inoculation. Upon contact with live bacteria, a subpopulation of fungal germlings initiate a response as early as ten minutes post-contact revealing transcriptional differentiation of Reactive Oxygen Species (ROS) mechanisms, trace metal warfare, cell wall remodeling dynamics, multidrug-efflux transporters, secondary metabolite synthesis, and excretion. We dissected mutants of plausible receptors, signaling pathways, and responses that N. crassa uses to detect and mount a defense against PstDC3000 and found seven genes that influence resistant and susceptibility phenotypes of N. crassa to bacterial colonization. In this study we provide a bacterial-fungal model system within Dikarya that allows us to begin to dissect signaling pathways of the putative fungal immune system.

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions
### Characterizing the Pathobiome of Fusarium oxysporum f. sp. vasinfectum Race 4: Effects of Microbial Interactions on Disease Severity

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Fungal pathogenesis can involve and depend on other microbes. Emerging evidence suggests that fungal infection dynamics are shaped by complex interkingdom interactions, particularly with microbes that colonize fungal hyphae. In this study, we investigated how Fusarium oxysporum f. sp. vasinfectum Race 4 (FOV4), a devastating cotton pathogen, interacts and forms pathobiome — a consortium of non-pathogenic microorganisms (pathobionts) that modulate fungal virulence and disease severity. We characterized microbial communities associated with the FOV4 hyphosphere, rhizosphere, and infected plant tissues to identify core pathobionts and examine their influence on FOV4 infection. Given FOV4's strategy of root penetration via hyphal growth, we hypothesized that pathobionts are actively recruited to hyphal tips within the rhizosphere, forming a cooperative microbial network that enhances pathogenic success. Comparative microbiome analyses of symptomatic plants with varying levels of disease tolerance revealed significant shifts in microbial composition correlated with disease severity. Furthermore, inoculation studies using field-derived microbiota associated with high and low disease severity showed that both inoculum density and microbial context influence FOV4 virulence. These findings support the hypothesis that FOV4 does not infect independently, but rather

in association with its hyphal network to structure a cooperative pathobiome that facilitates colonization and exacerbates wilt symptoms. This study highlights the hyphosphere as a critical interface in plant-fungus-microbiome that could provide insights into ecological factors shaping fungal pathogenesis.

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions

### Dissecting Rhizosphere Bacterial-Fungal Interactions Using Metabolic Phenotyping

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Bacterial-fungal interactions (BFIs) are essential to global biogeochemical cycling, soil fertility, and plant health. However, how BFIs influence these functions remains poorly understood. We hypothesize that substrate utilization plays a major role in shaping BFI phenotypes (e.g., antagonistic vs. neutral); competition or substrate cross-feeding has the potential to significantly govern the distribution of bacteria and fungi in soils and rhizospheres, influence their roles in biogeochemical cycling, as well as their ability to associate and colonize plant roots. Our work in the Bacterial-Fungal Interactions Science Focus Area focuses on bacteria and fungi isolated from the heat- and drought-tolerant grass, Bouteloua gracilis (blue grama) from arid grasslands in Southwestern United States. We have isolated phylogenetically diverse lineages of the bacterial and fungal members of the blue grama rhizosphere and have begun testing representative taxa for their potential to utilize a suite of 190 organic compounds using the Biolog Phenotype MicroArrays. Substrate utilization profiles document the potential for competition between our isolates indicating that they may have antagonistic interactions in situ (i.e., the blue grama rhizosphere). These data provide a foundation for generating new hypotheses for investigating and understanding the ecological roles and impacts of BFI. Using our isolate genomes, next steps will be to generate a predictive understanding of substrate preference and how genetic features can be leveraged to screen for and evaluate BFI in their natural environments, leading to new tools to improve BFI-mediated soil ecosystem serves (e.g., plant productivity, C sequestration).

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions

### Form, Function, or Family: What Drives Bacterial Community Assembly in Pezizales Ascomata?

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The Pezizales (Pezizomycetes, Ascomycota) produce some of the most widely recognized ascomata within the phylum, namely truffles and morels. Taxa within this order are ecologically and morphologically diverse, with nutritional modes ranging from saprotrophy to symbiosis and ascomata from cupulate to truffloid. Pezizales intimately interact with bacteria, including Morchella and Tuber spp. (morels and truffles). Bacterial partners can contribute to fungal-host biology by aiding in ectomycorrhizal synthesis, volatile production, modulating host metabolism, or even serving as a nutritional source. To investigate whether ascomata form, ecological function, or phylogeny plays a dominant role in microbiome assembly, we sampled hymenial tissue from ~700 healthy ascomata, across 12 Pezizales families for 16S rDNA bacterial sequencing. Additionally, we generated ~380 diverse Pezizales shotgun metagenomes, ~160 with paired amplicon data, to assess the functional potential of these host-associated bacteria. We processed 16S rDNA data using standard community analysis tools and assembled metagenomes via highly standardized metagenomics workflows (NMDC) that facilitate data reuse and integration. Metagenome-assembled genomes (MAGs) were assembled using contig-based binning and taxonomic and functional annotations were assigned using curated databases. We assembled 496 MAGs, 266 with >95% completeness, including bacterial taxa previously found to associate with Pezizales, including Acidovorax, Bradyrhizobium, Flavobacterium, Pedobacter, Rhizobium, and Variovorax. These metagenomic insights provide a first look at the identity and functional potential of these ascomata-associated bacterial communities. This study represents the most extensive investigation of fungal host-associated microbiomes to date, providing a comprehensive view of diversity, factors influencing assembly, and functional potential of Pezizales-associated bacterial communities.

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions

### Mortierellaceae transcriptomic and metabolic pathways involved in maintaining populations of endohyphal bacteria

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Mortierellaceae are an ecologically and economically important family of ubiquitous soil fungi that often host Burkholderia-related (BRE) and/or Mollicutes-related endohyphal bacteria (MRE). BRE and MRE exhibit reduced metabolic capacity, the extent of which varies by clade, and thus are nutritionally dependent on their hosts for survival. However, the functional relationships between Mortierellaceae and their endohyphal bacteria remain poorly understood. Thus, the goal of this study is to identify a core set of genes involved in maintaining endohyphal bacteria populations within Mortierellaceae, and to determine how these genes differ across host species and endobacterial clades. Benniella erionia, Podila humilis, and two Linnemannia elongata isolates were chosen that were host to Clade 2 MRE, Clade A BRE, a coinfection of Clade A BRE and Clade 1 MRE, and Clade 1 MRE, respectively. Isolates were cured of their endohyphal bacteria using antibiotics, and transcriptomes were generated for both wild-type and cured strains using RNA-seq. Preliminary differential gene analysis between wild-type and cured B. erionia show that host genes encoding glutathione synthetase, glutathione transferase, and γ-glutamylcysteine synthetase were upregulated in the presence of MRE, indicating host glutathione may play a role in maintaining endohyphal bacteria populations. Analysis between wild-type and cured P. humilis showed differential upregulation in genes encoding pyruvate carboxylase, phosphoenolpyruvate carboxykinase, and glutaryl-CoA dehydrogenase, suggesting the presence of BRE may induce glucose limitation in the host. By increasing our understanding of Mortierellaceae-BRE and MRE relationships, this study provides insight into the importance and function of these organisms in soil ecosystems.

### Parallel Session 3-1: Mechanisms of Fungal-Bacterial Interactions

### The fungal microbiome: Discovering and investigating novel endohyphal inhabitants

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Fungi are known to harbor complex microbiomes consisting of bacteria (including cyanobacteria), viruses, other fungi, and microalgae. However, the diversity of fungal microbiome constituents, their co-occurrence patterns, and the functional impacts on their hosts remain largely enigmatic. Previously undescribed associations are continuously being uncovered, and our group recently found new bacterial partners and discovered the presence of plant- and algal-derived plastids within fungal hyphae. We continue to investigate the fungal microbiome through sequence-based enrichment techniques and screens of publicly available fungal genomes and transcriptomes that allow for highly sensitive detections of associations. We have designed custom GOTTCHA2 databases that enable extremely accurate taxonomic read-based classifications. Lineage-specific sequences from these databases have also been used to design primers and probes from hundreds of taxa for qPCR and fluorescence in situ hybridization imaging to permit quantitative and visual characterizations of the fungal microbiome. Additionally, our team has developed bioinformatic pipelines to routinely screen fungal sequencing data for signatures of these microbiome inhabitants, and generate co-occurrence networks from bacterial-fungal data. These resources are available as a public resource (http://sfa-bfi.edgebioinformatics.org). Our goal is to develop and provide useful tools and resources that help expand knowledge on the diversity of the fungal microbiome and promote interest and research in this area. A greater understanding of the fungal microbiome is essential to understanding the ecological roles of fungi and how they interact with their environment and other organisms.

## PARALLEL SESSION 3-2:
### Genomic Variation in Fungi

**Parallel Session 3-2: Genomic Variation in Fungi Comparative Mitochondrial Genomics of endophytic, saprotrophic, and Pathogenic Xylarialean fungi: How Does Trophic Mode Influence Mitogenome evolution?**

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Mitochondria are essential for energy production in eukaryotic cells, although patterns of inheritance, gene content, repetitive elements, and genome structure and size can vary widely between and among plants, animals, and fungi. While mitochondrial genes are often used for molecular phylogenetic studies, comparative analyses of a growing number of fungal mitochondrial genomes have revealed substantial mitogenome diversity and dynamic evolution. However, the impact of fungal trophic and reproductive modes on mitogenome evolution remains an active area of research.
Here, we investigated the mitogenomes of 83 phylogenetically diverse Xylariales taxa, with a focus on ecologically diverse endophytic, saprotrophic, and pathogenic species in two sister clades, Hypoxylaceae and Xylariaceae s.l. Overall, we observed significant size variation among xylarialean mitogenomes, ranging from 27kb (Hypoxylon rubiginosum) to 340kb (Durotheca rogersii), both within the Hypoxylaceae. Compared to the consistently smaller nuclear genome sizes observed among Hypoxylaceae compared to Xylariaceae s.l. taxa, we detected no clear clade-level differences in mitogenome size or content. Instead, mitogenomes differed by ecological mode: plant pathogens had significantly larger mitogenomes (mean 257±50kb) compared to endophytic and saprotrophic taxa (means = 138±69kb and 156±78kb, respectively). Overall, increased mitogenome size could not be attributed to the duplication of 14 mitogenome core genes (atp6,8,9; cob; cox1-3; nad1-6,4L). Instead, larger mitogenomes contained higher numbers of homing endonucleases (GIY-YIG/LAGLIDADG), as well as other ORFs whose putative functions are not associated with oxidative phosphorylation. The presence/absence and functional annotations of non-core ORFs were highly variable among genomes, suggesting versatile mitogenome functions.

## Parallel Session 3-2: Genomic Variation in Fungi

## Defining Gene Networks Active during Fungal-Animal Mutualism

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Fungal farming insect symbioses include ambrosia beetles, tiny wood-boring weevils, and their fungal mutualistic partners. The fungus is the sole source of nutrition for larvae and adults, and ambrosia beetles have evolved symbiotic organs called mycangia to house, transport, and disperse/inoculate partner fungi. The Xyloborini represent a major tribe of ambrosia beetles, with Xyleborus affinis one species within this group. X. affinis can partner with several related fungi including Harringtonia lauricola which, while a food source for the beetle, is also a devastating plant pathogen, causing disease and death in host trees (laurel wilt). In X. affinis, fungal conidia are introduced during beetle feeding into paired pre-oral mycangia, where they undergo a dimorphic transition from filamentous extension to growth as budding yeast-like cells. Here, we report a transcriptomic analysis of mycangial colonization by H. lauricola across a dynamic timescale revealing genetic signatures of fungal adaptations to growth within this highly specialized and co-evolved environment. Distinct classes of fungal genes, including effectors, transporters, and biosynthesis genes showing differential regulation within the mycangia as compared to free-living cells and during plant infection were noted. Intriguingly, genes implicated in plant infection and more broadly fungal pathogenesis were upregulated during symbiotic colonization of beetle hosts, questioning previously held notions of "pathogenesis genes" and their roles in host interactions. Unique metabolic adaptations suggest nutrient and signaling flow/communication between the host and the fungus. These data expand our understanding of animal-fungal symbioses and pave the way for targeted genetic dissections of mycangial symbiosis.

## Parallel Session 3-2: Genomic Variation in Fungi

## Genome-wide analyses to delimit the Smittium culicis complex, a globally distributed group of insect gut fungi

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Biodiversity remains underexplored, with many microorganisms, including fungi, yet to be fully identified. Fungi represent one of the most diverse kingdoms of life, however, their species boundaries and evolutionary relationships are often obscured by cryptic speciation and convergent evolution. While molecular phylogenetics has advanced our ability to detect such phenomena, a unified approach to resolving species complexes remains elusive. Over the past decade, the use of multi-locus data has revolutionized species delineation, suggesting that large-scale data (e.g., genomics) may hold the key to addressing unresolved species boundaries. Here, we present a comprehensive approach to resolve species complexes, using Smittium culicis as an example. Previous studies based on a five-gene phylogeny revealed that S. culicis is not monophyletic, with its members clustering with S. culicisoides, S. simulatum, and S. fecundum. However, the limited resolution of these loci precluded further investigation. To address this, we employed genome-wide analyses, including phylogenomics, genetic distance metrics, and population structure inference, to gather additional evidence for species delimitation. Our results are congruent across methods, revealing two distinct clades within the S. culicis complex that exhibit divergent genetic patterns. These findings suggest ongoing cryptic speciation without accompanying morphological divergence. Furthermore, S. culicisoides, S. simulatum, and S. fecundum likely belong to the S. culicis complex, despite their current status as distinct species based on morphology and isozyme patterns. This study highlights the power of genome-scale data for fungal species delimitation and contributes to a deeper understanding of fungal diversity.

## Parallel Session 3-2: Genomic Variation in Fungi
## Genomic insights into secondary metabolism and assembly improvement in nineteen Basidiobolus isolates

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Basidiobolus spp. are gastrointestinal (GI) tract symbionts of amphibians and reptiles (herptiles) and can act as vertebrate pathogens. Basidiobolus genomes contain numerous secondary metabolism (SM) biosynthetic gene clusters (BGCs), in contrast to closely related Mucoromycota and Zoopagomycota lineages. SM BGCs are hypothesized to enable Basidiobolus to colonize herptile GI tracts and may contribute to their pathogenicity. However, the distribution and diversity of SM across Basidiobolus are unclear, and further study has been hindered by the limited number of available genomes. Here, we present nineteen annotated genomes from Basidiobolus isolates that vary geographically and in their herptile hosts. Genomes were sequenced using Illumina NovaSeq 2X150 reads, assembled, and annotated for SM. SM BGCs are present in all genomes, supporting the hypothesis that SM is a conserved trait of Basidiobolus. However, genome BUSCO scores ranged from 59.9% to 96%, indicating that assemblies may not adequately capture the genic content of each isolate. To address this challenge, we present a pipeline for generating accurate and contiguous hybrid Basidiobolus genomes. Hybrid genome assemblies are expected to have improved BUSCO scores, thus better capturing SM BGCs. We will generate hybrid genomes for all Basidiobolus type specimens. This will facilitate improved phylogenomic reconstruction of relationships within the genus and enable a broader study of SM. Understanding the diversity, distribution, and evolution of Basidiobolus SM is essential for uncovering how these species interact as herptile symbionts and pathogens, and for exploring the potential medical, agricultural, and industrial applications of their SM.

## Parallel Session 3-2: Genomic Variation in Fungi
## Genomic Variation and Accessory Gene Dynamics in Aspergillus Fumigatus

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The pangenome framework attempts to capture the full genetic diversity within a species, distinguishing between core genes, which are conserved across most individuals, and accessory genes, which exhibit presence–absence variation and are often associated with environmental adaptation. In Aspergillus fumigatus, intraspecific variation has been well-documented, and its genome is considered open, indicating ongoing genetic diversification. Accessory genes, which contribute to this variability, are frequently located in subtelomeric regions, where they undergo increased structural variation and recombination. This dynamic genome structure underscores the need for further characterization of A. fumigatus genetic diversity to better understand its evolutionary and adaptive potential. Here, we analyzed 260 A. fumigatus genomes, identifying 8,866 core genes, 4,334 accessory genes, and 2,109 singletons. Among accessory genes, 1,274 (29.39%) are shared by only two strains, while 3,139 (72.42%) are absent from the reference genome (Af293). Previous pangenome analyses relied on reference-based SNP calling, missing variation in non-reference genes. To address this, we incorporated de novo SNP detection in accessory genes absent from the reference genome, recovering overlooked variation and providing a more complete view of accessory region diversity. To characterize the evolutionary properties of accessory genes, we have assessed SNP diversity, synonymous versus nonsynonymous substitutions, and clade-specific variation. Additionally, we investigated the genomic locations, particularly their enrichment in subtelomeric regions, to examine the role of ploidy in shaping accessory gene variation. By linking gene presence–absence variation with mutation rates and structural features, we aim to better understand the role of accessory genes in A. fumigatus evolution and pathogenicity.

### Parallel Session 3-2: Genomic Variation in Fungi

## Phylo- and pan-genomics of the Laccaria bicolor species complex reveal surprising conservation of the mycorrhizal toolkit

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Laccaria bicolor (Maire) Orton is the preeminent model system for understanding the genetic underpinnings of the ectomycorrhizal-host mutualism, and comprises several phylogenetic lineages that are widely distributed across the Northern Hemisphere. Despite this geographic and phylogenetic diversity, most experimental studies of ectomycorrhizal colonization within L.bicolor have utilized a single isolate (S238N). It is unknown whether the genetic pathways necessary for host colonization within S238N are strainlineage specific, or are widely distributed across Laccaria. In this work, we generated 112 new genomes within the genus Laccaria, including 40 genomes within the L.bicolor species complex, to (i) resolve species boundaries within this diverse clade, (ii) characterize patterns of effector protein evolution, and (iii) identify whether previously characterized mycorrhizal pathways are part of the core or accessory L.bicolor pan-genome. Using these genomes we constructed a completely supported phylogeny and found that L. bicolor is composed of numerous cryptic species. Importantly, we found that proteins essential for host colonization by S238N are evolving dynamically. Pan-genomics revealed exceptional genetic diversity within the group, yet surprising conservation of the mycorrhizal toolkit. Over 63% of all genes upregulated by S238N in ectomycorrhiza are found within all genomes across the genus, and these loci are more conserved than the genome average. Furthermore, the composition of mycorrhizal genes across Laccaria is structured by phylogeny and not host identity, suggesting that host identity is not a strong driver of speciation in the group. Altogether, this work provides insight into the evolution of the ectomycorrhizal symbiosis on a global scale.

### Parallel Session 3-2: Genomic Variation in Fungi

## Unraveling the Basidiobolus genome: Cryptic Genome Organization and Horizontal Gene Transfer

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Basidiobolus is a zygomycete fungus best known for being associated with the gut microbiome of amphibians and reptiles. Previous reports of two Basidiobolus species suggest relatively large genomes of ~100 MB and unusual genome architecture with hundreds of chromosomes. Genomes also possess a higher gene count related to secondary metabolism than other zygomycetes. Many of these genes are hypothesized to be acquired by horizontal gene transfer (HGT) from bacteria, enabling adaptation to the gut environment. Here, we present a comparative genomics analysis of eight Basidiobolus reference genomes isolated from different species of amphibians and reptiles. Genome size varied from 58 MB to 143 MB, with hundreds of scaffolds characterized by canonical telomeric sequences. Kmer analyses revealed ploidy levels greater than haploid. Nucleotide composition analyses resulted in an average GC content of 39.7% with 23.2% of the genome being characterized as duplicated. An orthology analysis revealed that 47% of orthologous groups are part of the core genome. Basidiobolus isolates closely related to the species B. ranarum presented the higher number of gene models and the greatest number of specialized metabolite gene clusters, carbohydrate-active enzymes, and peptidases. Consistent with previous studies, evolutionary relationships of non-ribosomal peptide synthases (NRPS) indicated that Basidiobolus species are enriched in NRPS from bacterial clades, cyclosporin-like, surfactin-like, and siderophore clades. The most likely bacterial HGT donors included Betaproteobacteria, Cyanobacteria, and Gammaproteobacteria. Our work focuses on establishing the baseline knowledge of Basidiobolus, highlighting the cryptic genome organization and the impact of HGT from co-occurring gut bacteria.

## PARALLEL SESSION 3-3:
## Fungi in the Phylloshere

### Parallel Session 3-3: Fungi in the Phylloshere
### Foliar Microbial Community Trends Reveal Potential Symbionts, Competitors, and Opportunists in the Beech Leaf Disease Pathosystem

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Emma Borys, State University of New York College of Environmental Science and Forestry
Margaret Carroll, State University of New York College of Environmental Science and Forestry
Olivia Matz, State University of New York College of Environmental Science and Forestry
Shannon Lynch, University of California, Davis

Beech leaf disease (BLD) is rapidly spreading across eastern North American forests, threatening beech tree survival. Managing its causal agent, the invasive nematode Litylenchus crenatae mccannii (LCM), is challenging due to the limited understanding of foliar nematodes in trees. While previous studies showed differences in foliar microbial communities between BLD symptomatic and asymptomatic leaves, key questions remain about community patterns during critical BLD symptom stages (e.g., LCM overwintering in leaf buds). Further, it is uncertain whether microbes detected in symptomatic leaves are introduced by LCM or are opportunistic colonizers. My objective is to examine microbial community seasonal changes in symptomatic and asymptomatic Fagus grandifolia trees across tissue types, regions, and symptom severity. Asymptomatic, mild, and severely symptomatic leaves and buds were sampled from trees in 10 plots across sites in New York during winter and spring. Cultured microbes from these tissues and extracted LCMs were analyzed using multiple correspondence analyses to assess community trends. Preliminary results reveal consistent patterns across seasons, with Cytophaga-flavobacterium strongly associated with mild symptoms and LCM, suggesting a symbiotic relationship, whereas Diaporthe was linked to asymptomatic buds, indicating competition with LCM. Finally, Colletotrichum was strongly associated with severely infected leaves, suggesting an opportunistic infection. Understanding these patterns provides insight into BLD development and reveals potential biocontrols.

### Parallel Session 3-3: Fungi in the Phylloshere
### Fungal Endophyte Communities in Galled Oak Leaves: Stability in Leaves, Divergence in Galls

Christopher Bivins, University of California, Merced

Gall-inducing Cynipid wasps create unique structures on oak leaves, raising questions about their impact on fungal endophyte communities. This study employs a metabarcoding approach to investigate how these communities vary among ungalled blue oak (Quercus douglasii) leaves, leaves galled by two Cynipid wasp species, and the galls themselves. Our findings reveal that galled and ungalled leaves host similar fungal communities, but gall tissues harbor distinct, species-specific fungal assemblages. Notably, Urchin galls (Cynipis quercusechinus) exhibited fungal communities that diverged more strongly from those in the surrounding leaf tissue compared to the fungal communities in saucer galls (Feron gigas), which showed greater overlap with leaf-associated fungi. These results suggest that galls act as microhabitats shaping unique fungal assemblages, and fungal communities within galls are strongly influenced by the inducing wasp species. These species-specific interactions between Cynipid wasps and fungal endophytes may influence both the nutritional ecology of gall-inducing insects and the broader microbial dynamics within forest ecosystems.

### Parallel Session 3-3: Fungi in the Phylloshere

### Hemp Microbiome Composition and Function under Developing Pest Management Solutions

Allison Rietman, University of Louisville
Lucía Amani, Indiana University
Connor Morozumi, University of Louisville
Nicole Gauthier, University of Kentucky
Natalie Christian, University of Louisville

Fungicides are used in conventional agriculture to reduce or prevent damage by fungal pathogens but may have non-target effects on other organisms. For example, fungicide application could negatively affect fungal endophytes—non-pathogenic plant symbionts that can potentially confer benefits to their host, including reducFtion of disease severity. We performed an in-field trial to test how fungicide application altered communities of both fungal pathogens and non-target endophytic leaf fungi in hemp (Cannabis sativa L.). We found that fungicides effectively reduced pathogen abundance and disease severity. However, they also decreased endophytic fungal diversity while increasing heterogeneity, resulting in a bottleneck effect for endophyte communities. During our field trial, we identified Ophiocordyceps sp. as a common endophyte associated with hemp hosts. Ophiocordyceps is a common genus of entomopathogenic fungi, so we then tested its potential as a biological control agent against Helicoverpa zea (corn earworm), a common insect pest in hemp. While we expected H. zea to avoid food inoculated with this fungus, larvae in our in vitro study preferred the diet containing Ophiocordyceps, highlighting the many unknowns surrounding integration of microbes into biological control and sustainable agricultural approaches.

### Parallel Session 3-3: Fungi in the Phylloshere

### How fungal endophyte communities colonize and alter plant host chemistry in the wildflower white snakeroot

Noelle Visser, University of Louisville
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Natalie Christian, University of Louisville

Throughout a plant's growing season, leaves are colonized by diverse communities of endophytic fungi. Fungal communities can have broad benefits for plants, including increased resistance against herbivores and pathogens. It remains unclear how endophyte communities assemble in host plants, and if microbial community interactions within their host affect plant chemistry. Using culture-based methods, we describe foliar endophytic fungal communities from white snakeroot's (Ageratina altissima) growing season, a Kentucky wildflower known for its toxicity to macro-herbivores. Endophyte communities changed through its growing season. Dominant fungal endophyte genera throughout the growing season included Colletotrichum, Arthrinium, Daldinia, and Neopestalotiopsis. Rarer genera included Diaporthe and Leptostroma. We then tested how endophyte inoculation alters host secondary chemistry.
We inoculated endophyte-free white snakeroot seedlings with one of four treatments: 1) a dominant endophyte, 2) a plant microbiome transplant 3) a heat-killed dominant endophyte, and 4) sterile water as a control. We extracted phenolics from leaf tissue and performed liquid chromatography-mass spectrometry. Preliminary results comparing phenolic profiles across the treatments revealed microbial colonizers altered the production of secondary metabolites in plants. Plants inoculated with endophytes had a significantly larger breadth of chemical compounds in their tissues compared to uninoculated seedlings. Abundance of individual phenolic compounds also varied between treatments. Additionally, we plated dominant fungal endophytes on malt extract agar and white snakeroot infused malt extract agar, observing more growth on the malt extract plates. Together, our results highlight how a plant's fungal microbiome changes during the plant's life and how this may subsequently alter plant host chemistry.

### Parallel Session 3-3: Fungi in the Phylloshere

### Quantifying the 'hyperdiversity' of Foliar Fungal Endophytes in the Tropics

Ryoko Oono, University of California, Santa Barbara
Austen Apigo, University of California, Irvine

The tropics harbor an astonishing diversity of foliar fungal endophytes, yet the magnitude of this hyperdiversity has not been systematically quantified across multiple latitudinal zones and biomes. To address this gap, we tested for latitudinal diversity gradients and their underlying drivers by sampling endophyte communities across 20 forested sites spanning a 55-degree latitudinal gradient in Central and North America. To capture the full range of endophyte diversity per plant at each site, we sampled one individual of every co-occurring plant species within a 50 m² plot, across five replicate plots per site (100 plots total). We characterized fungal communities from 1,539 plant individuals representing 401 vascular plant genera using high-throughput sequencing of the ITS1 region. Our results reveal striking latitudinal patterns: endophyte richness per plant host in tropical forests is more than twice as high as in any other biome sampled—including the temperate rainforests of the Pacific Northwest (British Columbia and Oregon), which receive comparable precipitation, and the next warmest biome in our dataset, located in southern Mexico. Contrary to the long-standing hypothesis that species interactions become more specialized toward the tropics, we found the opposite: endophyte–plant associations became more specialized toward temperate latitudes. This pattern held even after subsampling interaction networks to equal sizes and accounting for covariates such as endophyte richness, plant richness, and plant phylogenetic diversity. These findings demonstrate that tropical endophyte hyperdiversity is accompanied by more generalized interaction networks and is shaped by a combination of biotic and abiotic factors.

### Parallel Session 3-3: Fungi in the Phylloshere
### Using Knockouts to Test the Role of Leaf Waxes in Fungal Establishment of Leaf Surfaces

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Teia Chou, Department of Botany and Plant Pathology, Oregon State University
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Posy Busby, Department of Botany and Plant Pathology, Oregon State University

Leaf waxes are physical barriers that can limit microbial colonization. In Populus trichocarpa, alkenes are major components of leaf waxes. The synthesis of alkenes is mediated by a 3-ketoacyl-CoA synthase (PotriKCS1) gene cluster, and its downregulation lowers alkene production. However, it is unclear how alkene synthesis influences microbial communities on leaf surfaces. Here, we used CRISPR knockouts of PotriKCS1 to investigate how alkenes influence fungal and bacterial communities on leaf surfaces in P. trichocarpa. We used both culture-based and culture independent approaches to sample microbes from the leaf surfaces of 20 independent knockout events (alkene minus plants) and 7 control events (alkene plus plants; each replicated 5x) growing in a common garden in Corvallis, Oregon. Our culture-based analysis indicates that yeast abundance is lower in alkene minus plants compared to controls; our culture-free analysis is ongoing. Leaf surfaces were washed to detach microbial cells and filtered to collect microbial cells in a membrane filter. DNA was extracted from the filter using the Qiagen PowerSoil DNA Isolation kit. Libraries are currently being amplified using the ITS4 and ITS3-KYO1 fungal primers and the 515F and 806R bacterial primers. Resulting libraries will be used to characterize the influence of the PotriKCS1 gene cluster on fungal and bacterial communities of Populus trichocarpa.

## PARALLEL SESSION 3-4:
## Fungi in the Phylloshere

### Parallel Session 3-4: Mechanism and Consequences of Fungal Sex
### Can Sex Maintain an Addictive Virus in Yeast Populations?

Primrose Boynton, Wheaton College

Viruses are cryptic and mysterious in fungal systems: they are often inherited only vertically and have little or no apparent impacts on hosts. I am using the Saccharomyces killer virus system to better understand how these viruses are maintained in fungal populations. This system includes a dsRNA totivirus and its dsRNA satellite; in the presence of the totivirus, the satellite produces a secreted toxin and the antidote to the toxin. I explore the hypothesis that toxin production maintains viruses through postsegregational killing (i.e., it is an "addiction module"). In postsegregational killing systems, a selfish genetic element kills the products of cell division that do not inherit it. Postsegregational killing can benefit selfish genetic elements, such as cytoplasmic viruses, with a fitness cost to the host. In systems with strong predominant vertical transmission, however, host and symbiont fitness are coupled. This coupling can be overcome through sexual transmission of the virus, but natural Saccharomyces have infrequent outcrossing. I use a population simulation to demonstrate Saccharomyces do not outcross frequently enough to maintain addictive viruses in the absence of other viral fitness benefits.

### Parallel Session 3-4: Mechanism and Consequences of Fungal Sex

## Fitness Consequences of Loss of Heterozygosity in Saccharomyces Cerevisiae

Yi-Hong Ke, University of Michigan
Michelle Orozco-Quime, University of Michigan
Joshua Bauman, University of Michigan
Anuj Kumar, University of Michigan
Timothy James, University of Michigan

Loss of heterozygosity (LOH) resulting from the repair of DNA double-strand breaks (DSBs) is a substantial source of genetic variation in diploid organisms. The resulting phenotypic variation has been shown to facilitate adaptive evolution in diploid fungal species such as Saccharomyces cerevisiae. To explore both the beneficial and detrimental fitness effects of LOH events, we genetically engineered S. cerevisiae to generate a library of strains containing random LOH events. With unique barcodes in each strain, we applied a bar-seq approach to measure the relative fitness among strains in 6 growth conditions. Among 134 strains analyzed, LOH events typically led to negative fitness consequences. In most conditions, fitness declined as the number or size of LOH events increased, and the average fitness among the LOH strains was less than 1. However, we found that LOH events indeed occasionally enhanced fitness, with 3% to 53% of strains exhibiting positive fitness effects depending on the growth condition. The best-performing strains in the 3 stressed media showed 9% to 21% higher fitness than strains without LOH. Nevertheless, performance trade-offs across different environments were common. No strain achieved universally positive fitness effects in all media types. Moreover, the extent of these trade-offs increased as the length of the LOH event increased. Our experiment demonstrates that LOH events and point mutation have a similar distribution of fitness effects in shape and could both provide fuel for adaptation. However, constraints due to antagonistic pleiotropy of LOH may raise complicated trajectories of evolution in real fluctuating environments.

### Parallel Session 3-4: Mechanism and Consequences of Fungal Sex

## Non-Coding Sequence Conservation Negatively Correlates to the Rates of Gene Expression Evolution and Sheds Light on the Evolution of Sordariomycetes

Yen-Wen Wang, Yale School of Public Health
Jefferey Townsend, Yale School of Public Health

Gene regulation and expression, typically studied with RNA-seq and CHIP-seq, directly and indirectly shape the phenotypic diversity in different lineages. However, to enable meaningful comparisons among species, environmental and developmental variables need to be controlled in different fungal species, but it is often difficult to achieve. Since much of regulation and expression is controlled by regulatory elements in non-coding sequences, investigating the evolutionary history of such regions could provide us an alternative path to understanding the evolution of gene regulation and expression. Here, we quantified conservation of non-coding sequences in Neurospora crassa as a model and 256 other members of the Sordariomycetes. We found a positive correlation between conservation in cis-regulatory regions and conservation of gene expression. High conservation was specifically indicated in accessible transcription binding domains. These observations highlight the relevance of conserved non-coding sequences. Our further findings of elevated conservation in the cis-regulatory regions of RNA polymerase genes in Neurospora suggest a potential requirement of strong regulation of gene transcription in this genus.

### Parallel Session 3-4: Mechanism and Consequences of Fungal Sex

## Population Genetic structure, Mating and Admixture in Rhizoctonia solani AG1-1B

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Rhizoctonia solani is a globally distributed fungal plant pathogen. This study investigates the genetic structure, gene flow and putative mating type loci in populations of R. solani anastomosis group IB (AG1-IB), causal agent of brown patch disease of cool-season grasses. Using double-digest restriction-site associated DNA sequencing, we analyzed over 10,000 single nucleotide polymorphisms for 55 isolates of R. solani AG1-IB sampled from tall fescue (Festuca arundinacea) across six field plots in North Carolina. Population genetic analyses revealed the presence of five putative AG1-IB populations; two populations were predominantly clonal and three were recombining with evidence of admixture. The two clonal populations exhibited low genetic diversity and were localized to specific field plots, whereas the other three populations displayed greater genetic diversity and were widely distributed. Comparative genome analyses showed conservation of homeodomain loci between isolates of R. solani AG1-IB, with a close relative R. solani AG1-IA, and Coprinopsis cinerea, a model fungus in the Basidiomycota with a well-characterized mating system. Based on sequence and synteny analyses, R. solani AG1-IB has two to four putative homeobox domains. Preliminary analysis indicates that isolates sampled for clonal populations possess mating incompatible homeobox genes and may be self-sterile. Isolates sampled from recombining populations have mating compatible homeobox genes and are potentially undergoing sexual reproduction. Further characterization of homeobox protein function and influence on population gene flow and structure will inform our research to better refine disease risk assessment models and develop improved and targeted strategies for managing Rhizoctonia diseases.

## Parallel Session 3-4: Mechanism and Consequences of Fungal Sex

### Sex Differences during Spore-Mediated Infections in a Mouse Model of Cryptococcosis

Sehrish Afsheen, University of Wisconsin, Madison
Nicolas Pereira, University of Wisconsin, Madison
Christina M. Hull, University of Wisconsin, Madison
Christina M. Hull, Medical Microbiology and Immunology

Cryptococcus neoformans is an opportunistic pathogen that causes fatal human infections. Spores are thought to be infectious agents responsible for cryptococcal meningitis in immunocompromised people. Although extensive research has been conducted on the virulence and pathogenic mechanisms of Cryptococcus, the effects of sex differences on infection outcomes remain unexplored for both the spore and yeast forms. This study aims to identify differences between spore- and yeast-mediated cryptococcal disease in male and female mice. We used a mouse inhalation model of cryptococcosis to determine outcomes in spore and yeast infections, including days of survival after infection and organ fungal burdens in both sexes. Our preliminary findings indicate that male (n=10) and female (n=10) C57/Bl6 mice exhibited different survival rates in response to Cryptococcus spores. Males showed increased susceptibility to spore-mediated infections relative to females with significant decrease in time-to-disease ($p = 0.0359$). In contrast, yeast-infected mice did not show any significant differences in disease susceptibility between sexes by the endpoint (n=10/sex). Fungal burden in the brain, lung, kidney, and spleen did not show a significant difference in fungal colony counts between both sexes infected with spores at end point. We hypothesize that dissemination to organs outside the lung occurs earlier in males, measure by colony forming units in organs over the course of CNS disease. Additionally, the roles of sex hormones in modulating immune responses likely influences sex-based differences in time-to-disease. Future studies will determine the timeline of dissemination in males vs. females with differences in immune cell functions during infections.

### Parallel Session 3-4: Mechanism and Consequences of Fungal Sex

### The (mis)use of Sex Categories in Fungi

Soleil Young, University of Wisconsin, Madison
Caitlin McDonough-Goldstein, University of Wisconsin, Madison
Anne Pringle, University of Wisconsin, Madison

The exclusion of fungi and other understudied eukaryotes from evolutionary thinking has perpetuated an inaccurate, animal-centric understanding of the evolution of sexual reproduction. To integrate fungi into sexual selection theory, scientists studying sex in fungi imported animal sex categories into mycology, using female and male to label fungal individuals and parts. The delineation of fungi sexual categories corresponds to three broad definitions related to either anisogamy, sex roles, or body parts. We reject these attempts to “sex” fungi based on structures or behaviors as biologically inaccurate, biased, non-explanatory, and in some cases mutually exclusive. We explain how sexed language can be replaced with more accurate, descriptive and neutral terminology. The incoherence of sex categories in fungi illustrates a larger problem: importing terminology and definitions developed for one (smaller) group of taxa smooths biological variability, distorting evolutionary theory and obscuring useful comparisons across diverse taxa.

## PARALLEL SESSION 4-1:
## MycoFlash: Advances in Fungal-Animal Associations

### Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

### A Novel Protocol for Screening Environmental Fungi as Possible Human Pathogens

Gregory Biddle, West Virginia University
Aisha Ford, Natural Resources and the Environment, West Virginia University
Matt Kasson, Natural Resources and the Environment, West Virginia University

Increased international trade and rising global temperatures have contributed to an expansion of devastating fungal diseases impacting diverse animals worldwide. From Candida auris to Batrachochytrium dendrobatidis, fungal pathogens have become an ever-pressing concern to the health of ecosystems and communities. Historically, antifungal drugs have minimized the potential impacts of thermotolerant human fungal pathogens, but resistance is on the rise. Agricultural practices such as the long term use of azole-based fungicides have been shown to transfer antifungal resistance from the environment to clinical settings, making invasive fungal infections harder to control. Using a One Health approach, we have developed a novel protocol to survey environmental fungi using thermotolerance, antifungal resistance, and pathogenicity assays. We collected preliminary soil samples from fruit tree orchards to isolate fungi that have been exposed to high fungicide pressure for many years. Fungi were screened for growth at 37C (human body temperature), and in the presence of tebuconazole—a commonly used clinical antifungal medication. Candidate fungi in the genera Aspergillus, Trichoderma, Talaromyces, and Metarhizium were among those that passed initial screenings. Further studies are ongoing to test the growth of these fungi against other azole-based antifungal compounds. Additionally, pathogenicity assays using Galleria mellonella as an infection model will be conducted to gain insights into the ability of these fungi to circumvent the innate immune system. Altogether, fungi that clear these screening tests should be considered possible candidates for future disease-causing organisms in humans.

### Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

### Anaerobic Gut Fungal Communities in Ostriches (Struthio camelus)

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Kathryn Nash, Oklahoma State University
Adrienne L. Jones, Oklahoma State University
R. Ty Young, Oklahoma State University
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Noha H. Youssef, Oklahoma State University

Anaerobic gut fungi (AGF; Neocallimastigomycota) are essential for plant biomass degradation in herbivores. While extensively studied in mammals, information regarding their occurrence, diversity, and community structure in non-mammalian hosts remain sparse. Here, we report on the AGF community in ostriches (Struthio camelus). Ostriches are herbivorous, flightless, hindgut fermenting members of the class Aves (birds). Culture-independent diversity surveys of fecal samples targeting the D2 region of the large ribosomal subunit (28S rRNA) revealed a uniform community with low level of alpha diversity. The community was mostly comprised of sequences potentially representing two novel species in the genus Piromyces, and a novel genus in the Neocallimastigomycota. Sequences affiliated with these novel taxa were absent or exhibited extremely rare relative abundance in datasets derived from mammalian and tortoise samples, indicating a strong pattern of AGF-host association. One Piromyces strain (strain Ost1) was successfully obtained in pure culture. Transcriptomics-enabled molecular dating analysis suggested a divergence time of ≈ 30 Mya, a time frame in-line with current estimates for ostrich evolution. Comparative gene content analysis between strain Ost1 and other Piromyces species from mammalian sources revealed a high degree of similarity. Our findings expand the range of AGF animal hosts to include members of the birds (class Aves), highlight a unique AGF community adapted to the ostrich alimentary tract, and demonstrate that – similar to mammals– coevolutionary phylosymbiosis (i.e. concurrent evolution of AGF and their animal hosts) plays a central role in explaining current AGF distribution patterns in Aves.

**Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations**

### Assessment of Sea Turtle Egg Fusariosis (STEF) in Olive Ridley (Lepidochelys olivacea) Nests at Abacoa Beach, Arecibo, Puerto Rico

Yahir Cuevas Soto, University of Puerto Rico
Gualberto Rosado Rodríguez, University of Puerto Rico

Lepidochelys olivacea (Olive Ridley) is the most abundant sea turtle species in the world and one of four that nests along the coasts of Puerto Rico. Despite its global abundance, nest occurrences in Puerto Rico are sparse, limiting the availability of local data. The Olive Ridley is currently listed as endangered due to threats such as climate change, habitat contamination, and predation. In addition, infections caused by bacteria, protozoa, and fungi have been linked to reduced hatching success in other sea turtle species. This study aims to identify the mycelial fungal diversity associated with Lepidochelys olivacea nests and unhatched eggs, with a particular focus on detecting Sea Turtle Egg Fusariosis (STEF), caused by the Fusarium species complex. The findings not only enhance the understanding of sea turtle nest ecology but also provide a foundation for future conservation research on Puerto Rico's north coast. By elucidating the relationship between fungal infections and embryonic development, this research can help develop more effective conservation strategies to ensure the long-term viability of the Lepidochelys olivacea population.

**Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations**

### Characterization of the Reptile and Amphibian Gut Bacteriome and Mycobiome; Discovery of Undescribed Basidiobolus Diversity

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Donald M. Walker, Department of Biology, Middle Tennessee State University

Herpetofauna (reptiles and amphibians) are among the most threatened vertebrate groups with approximately 21% of evaluated reptiles and 41% of amphibians threatened by extinction. The gut microbiome is a crucial element of herpetofauna conservation approaches, as dysbiosis in the microbiome may cause adverse health effects for the host. Understanding the diversity and dynamics of fungal-bacterial interactions in the gut microbiome can help to establish a baseline of knowledge to inform conservation strategies, however, relatively little work has been done to characterize the gut microbiomes of herpetofauna. Previous research has determined that filamentous fungi from the genus Basidiobolus are dominant members of the herpetofauna microbiome and its diversity shapes the bacterial community. By examining the bacterial and fungal assemblages in the herpetofauna gut across geographic space, host phylogeny, and natural history, we aim to advance our understanding of the unique role that ubiquitous members like Basidiobolus play in the herpetofauna gut. We fill a knowledge gap by documenting and characterizing bacterial and fungal gut assemblages in the most phylogenetically diverse group of herpetofauna to date (170 species from 770 individuals), using high-throughput amplicon sequencing of 16S rRNA and ITS1 rDNA gene region. Preliminary results suggest a strong signal of host phylogeny in predicting community structure of the bacteriome, but not mycobiome. Extensive undescribed diversity was documented within the genus Basidiobolus, with 136 unique OTUs identified compared to the 10 currently described species in this genus, accompanied by corresponding living isolates available for formal taxonomic description.

### Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

### Fungal Furry Friends: Understanding the Usage of Detection Dogs in Mycological Research

Claire Yager, Cornell University

Dogs have a long history in mycology as truffle dogs, but what utility do they have in modern mycology? Detection dogs have a wide usage in a variety of conservation fields, from simple presence assays to complex, long-range, long-term detection projects, including in the fungal field. Dogs' diagnostic skills far outstrip the highest sensitivity mechanical diagnostics in several metrics, and up to 45% of US households have dogs, yet they see limited deployment in fungal detection. Dogs are highly specific, highly accurate, fast, and outstrip humans in most assays when it comes to evaluating of searching for mycological samples. With all of this in mind, why do they not have a higher prevalence as a tool of research?  I have extensive experience in dog training and specifically civilian detection dog competitions with multiple dogs and in multiple venues. In this talk I will discuss the use cases for dogs in research, address the current state of research of detection dogs in Mycology, and discuss how and if a lab can use a dog in their research.

### Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

### Investigating Fly Behavioral Manipulation by Entomophthora Muscae through Proteomics

Julius Tabin, Harvard University
Carolyn Elya, Harvard University

Parasites frequently alter the behavior of their hosts in profound and targeted ways, yet the molecular signalling underlying their manipulation remains a mystery. The fungus Entomophthora muscae is such a pathogen, driving robust summiting behavior (elevation prior to death) in flies after invading the brain. Given that secreted proteins are strongly implicated in other systems where parasites impact host physiology, we leveraged the ease of cultivating and infecting Drosophila melanogaster (fruit flies) in the lab to determine the proteomic profile of fly heads across infection progression. We collected and analyzed fly heads at four distinct stages of infection: uninfected, infected (but not going to die that day), pre-summiting (infected and will be manipulated and die later that day), and actively summiting. The infection stages were reliably determined using real-time machine-learning analysis of behavior, as well as fungal morphology. The resulting data set provides a rare look into fungal infection dynamics, as well as host responses to fungal infection. We identified nine E. muscae proteins, including four proteins predicted to be secreted, that are significantly and uniquely enriched during summiting. Using the unparalleled genetic tools available in the D. melanogaster system, we will express these candidate proteins in fly neurons in the absence of infection to determine which fungal proteins are responsible for eliciting summiting behavior. This work will provide novel insights into the molecular mechanisms by which E. muscae manipulates host neurophysiology and behavior, revealing a new dimension of inter-kingdom communication.

## Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

## Microbiome of North American Ash for Biocontrol of Emerald Ash Borer

Claire Yager, Cornell University
Kathryn Bushley, USDA ARSEF
Judith Mogououng, Cornell University

Ash (Fraxinus) are economically and culturally important trees in North America, and host to numerous native wood boring beetles and their parasitoids. The Emerald Ash Borer (EAB; Agrilus planipennis), an invasive beetle from Asia, now threatens all native North American and some European ash species. However, little is known about the microbiota of both tree and insect and, more specifically, entomopathogenic fungi which may control or moderate EAB populations. We hypothesized that both Ash trees and EAB may harbor entomopathogenic fungi, and that these fungi may be more effective than commercial isolates in a bioassay setting. To investigate these questions, we collected tree tissue, insect frass, and insects in two regions of New York for culturing. Cultured fungal isolates included several potential entomopathogens from families Cordycipitaceae, Ophiocordycipitaceae, and Clavicipitaceae. These fungi were subjected to additional sequencing for identification, including multilocus sequencing and whole genome sequencing, and then employed in bioassays of EAB eggs, where they outperformed a common commercial isolate and the control. We expect that these results will not only elucidate the broad range of entomopathogenic fungi present in the system, but also identify future pathways of biocontrol in the field. As EAB expands its invasive range to Europe, finding viable control options is more critical than ever to mitigating damage caused to industry, culture, and ecology associated with these trees.

## Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

## The Influence of Basidiobolus on the Gut Microbiome of an Amphibian in a Live Animal Inoculation Experiment

Jason Dallas, Middle Tennessee State University
Mitra Ghotbi, Middle Tennessee State University
Lluvia Vargas-Gastélum, Oregon State University
Kerry McPhail, University of Utah
Joseph Spatafora, Oregon State University
Jason Stajich, University of California Riverside
Donald Walker, Middle Tennessee State University

Experimental manipulation of the gut microbiome through model systems enables researchers to observe how particular microbial members can influence community structure. For example, the genus Basidiobolus, a filamentous fungus, is prevalent and abundant in the gut of wild amphibians and reptiles and acts as an essential mediator in bacterial-fungal interactions within this ecosystem. We expanded upon previous research using wood frogs (Lithobates sylvaticus) to identify how the addition of Basidiobolus affected the gut microbiome. Following metamorphosis, captive-reared wood frogs were fed fruit flies inoculated with one of six Basidiobolus isolates cultured from the feces of five wild amphibian species and one reptile. Based on previous results, wood frogs were inoculated every other week to ensure long-term Basidiobolus residence. All wood frog feces were collected over the following month and pooled every week. The pooled samples received an internal standard for absolute abundance estimations prior to DNA extraction and underwent amplicon sequencing of the 16S rRNA gene and ITS1 region. To minimize the impact of maternal effects observed in prior research, we used wood frogs from a single egg mass in our analyses where possible. We observed that bacterial richness was similar across all treatments. Additionally, there was a significant effect of Basidiobolus treatment on the bacterial community using Bray-Curtis dissimilarity. These results suggest that the gut bacteria does shift in response to different Basidiobolus isolates originating from diverse hosts when controlling for potential maternal effects. Fungal bioinformatics have not yet been completed by the submission date.

### Parallel Session 4-1: MycoFlash: Advances in Fungal-Animal Associations

### Uncovering Seed-Handling and Nest Benefits in an Eastern North American Ant-Plant Seed Dispersal Mutualism

Julian Marshall, Binghamton University
Rosebelle Ines, Binghamton University
Kirsten Prior, Binghamton University

In eastern North American deciduous forests, Aphaenogaster ants and understory plants known as spring ephemerals are part of a widespread and prominent seed dispersal mutualism. In this mutualism, plants produce seeds with a fatty-acid-rich package (elaiosome) that attracts and provides ants with nutrition, and the plants experience several benefits, including lower competition. Aphaenogaster ants disperse seeds by first moving them from the parent plant into the soil-based ant nest where the ants remove the elaiosome and putatively feed it to their growing brood. Seeds without elaiosomes are then discarded, sometimes in the nest, and sometimes outside of the nest (redispersal). Previous work has found decreased seed-borne pathogen diversity on ant-handled seeds but less is known about how these changes in pathogens influence germination and establishment. Conditions of seed deposition locations may also provide currently unknown benefits to germination and establishment, even between ant species. We found that between two common Aphaenogaster species, A. rudis handles more seeds and processes them faster than A. picea, but further benefits remain unknown. We also found increased germination rates of seeds that were grown in ant nests. To understand what caused the differences in germination rates, I am now examining the abiotic soil conditions and the soil microbiomes in both the mesocosm experiment and natural Aphaenogaster ant nests from campus. Soil samples are being tested for percent moisture, organic matter, carbon, and nitrogen content. Microbiomes are being tested with 16s and ITS2 primers for variation in community and functional group composition.

## PARALLEL SESSION 4-2:
## MycoFlash: Advances in Fungal Community Ecology

### Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Arbuscular Mycorrhizal Fungal Nitrogen Patch Use Choice

Xin Lin, The Ohio State University
Alison Bennett, The Ohio State University

AM fungi are independent foragers who make foraging decisions, and exploring AM fungal nutrient foraging will improve our understanding of nutrient cycling, plant community assembly, and ecosystem functioning. However, we know little about how AM fungi make decisions when they encounter a nutrient patches. Here we identify AM fungal foraging behaviors in patches with different nitrogen availabilities (concentrations and forms). To address gaps in AM fungal foraging knowledge we set up three in vitro experiments using carrot (Daucus carota L.) hairy roots inoculated with Rhizophagus irregularis in bi-plates with different nitrogen availabilities. We imaged plates, and measured the length of branched absorbing structures (BAS) (responsible for nutrient uptake) and runner hyphae (RH) (responsible for soil exploration), then analyzed BAS length/RH length to evaluate AM fungal foraging behaviors. We tested (1) how nitrogen availability affects foraging behaviors, (2) how foraging behaviors change before, during and after encountering a patch, and (3) how encountering a new patch affects the foraging behavior in an old patch. BAS/RH increased with nitrogen concentration until reaching 5 mM after which it declined. Then BAS/RH didn't change before, and after encountering a nitrogen patch, but it increased when foraging in a patch. Also, when encountering a patch with higher relative ammonium (a preferred nitrogen form) concentration, foraging (as measured by BAS/RH) in the old patch increased. Here we show, for the first time, that AM fungal foraging behavior shifts with nitrogen availability, and we demonstrate that we can track these shifts and correlate them with environmental variability.

## Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Differences in Ectomycorrhizal Community Guilds between Co-Occurring Pinus and Quercus Species in Sierra Nevada Foothills.

Kanchan Gautam, California State Univeresity, Fresno
Elizabeth Melendez, California State University, Fresno
Michael Martinez, California State University, Fresno
Danielle Sublett, California State University, Fresno
Alija Mujic, California State University Fresno

Oak woodlands are a vital part of California's grassland and shrubland ecosystems housing numerous endemic Oak species. Blue oak (Quercus douglasii) and Interior live oak (Quercus wislizeni) are endemic oaks that co-occur in the Sierra Nevada foothills along with foothill pine (Pinus sabiniana). Blue oak and Interior live oak face increased pressure from the heavy use of woodlands for cattle grazing, agriculture land conversion, and climate change. Ectomycorrhizal (ECM) fungal communities of Q. douglasii, Q. wislizenii, and P. sabiniana are critical for establishment and survival of these trees, but these communities are understudied and very little is known about their endemic ECM guilds. It is becoming increasingly important to understand and catalog fungal communities of these Oaks and Pines for conservation efforts in the foothills. This study addresses this gap by beginning to identify what ECM fungal guilds are present. Using previously collected soil samples (eDNA) from the San Joaquin Experimental Range (SJER), DNA metabarcoding is used to identify the Operational Taxonomic Units (OTU, a putative species) present for all three tree species. Functional traits, and relative abundance of OTUs are compared using multivariate methods to determine community composition and overlap. We found  a higher overlap in ECM fungal guilds and OTUs between Q. wislizenii and Q. douglasii due to their phylogenetic relatedness, and some community overlap between Q. wislizenii and P. sabiniana due to their evergreen nature. We observed only a few shared OTUs in the ECM guild shared by Q. douglasii and P. sabiniana.

## Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Effect of Prescribed Fire on Post-Wildfire Diversity of Soil Fungi

Kathryn Anderson, California State University, Chico
Kristen Kaczynski, California State University, Chico
Gerald Cobián, California State University, Chico

Fire is a natural, recurrent process that many fire-adapted ecosystems depend on. However, today's fire regimes are extreme compared to those of the pre-colonization period. In at least the last 40 years, the frequency, intensity, size, and severity of wildfires in Northern California have dramatically increased due to anthropogenic factors. For time immemorial, people have used fire as a tool to meet cultural and ecological objectives including wildfire mitigation. While species-specific reactions to fire are mixed, observed consequences of these mega-fires on wildlife include habitat fragmentation, shifts in species range, and even species endangerment. Soil microbes, which hold vital roles in ecosystems including nutrient cycling and species-dependent interactions, are no different in that their survivorship and recovery depends on the fire characteristics and underlying soil properties. With increasing risk of high-intensity wildfire and reintroduction of prescribed fire in mitigation efforts, it is important to understand how the soil fungal community is affected by these compound events. This study will compare plots burned with prescribed fire to those left untreated, and subsequently all sample locations were burned in the 2024 Park Fire. The difference in post-wildfire fungal diversity between previously prescribed burned and untreated soil will be calculated in R studio after eDNA extraction, amplification with ITS primers, and Illumina high-throughput sequencing.

## Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Fungal Communities within Ammophila Breviligulata Respond to Epichloë Inoculation and Nitrogen Fertilization

Connor Morozumi, University of Louisville
Kylea Garces, Northeastern University
Shannon Walker, University of Louisville
Sarah Emery, Bowling Green State University
Natalie Christian, University of Louisville

Fungal endophytes in the genus Epichloë often confer mutualistic benefits to their host via changes to

plant chemistry and morphology but less is known about how these partnerships alter the rest of the plant mycobiome. Additionally, the composition of the mycobiome is shaped by abiotic factors such as nitrogen (N) availability, and the extent to which Epichloë alters the host environment is likely dependent on N supplementation. To date few studies have directly tested how Epichloë might synergistically shape microbiomes within different resource contexts. Here, we planted American beachgrass (Ammophila breviligulata) in a dune system of Lake Michigan, USA and factorially crossed Epichloë inoculation status with three levels of N amendment. We used metabarcoding to assess fungal richness, diversity, and composition in the aboveground and below ground mycobiome. Preliminary findings indicate that fungal richness increased with additional N amendment but only when Epichloë was absent, not when the mutualist was present within leaves, but did not differ significantly across treatments in roots. In contrast, we found that fungal composition was not statistically different across levels of N or Epichloë nor their interaction within leaf samples but did differ across the N amendments within roots. Our findings indicate that the role of Epichloë in shaping plant microbiomes depends in part on nitrogen availability which may have large consequences as N deposition increases in a changing world.

**Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology**

### Identifying the symbiotic fungi of the endangered ram's-head lady slipper orchid in Nova Scotia, Canada

Katie King, Acadia University
Gavin Kernaghan, Mount Saint Vincent University
Allison Walker, Acadia University

Cypripedium arietinum is an endangered orchid found in Eastern North America. We are identifying the symbiotic fungi this plant requires for seed germination and nutrient transfer. Roots were collected in the Summer of 2024 from all known C. arietinum sites in Nova Scotia. Roots were examined for fungal peloton structures and dissected to isolate fungi onto selective media. DNA was extracted from 114 of the resulting isolates and 73 identified through ITS rDNA barcoding. Fungal DNA isolated directly from root tissue revealed 115 genera using PacBio amplicon sequencing. Seeds were collected in the late Summer of 2024 for ex situ seed baiting germination trials, to target fungi specifically involved in seed germination. Multiple known orchid symbionts have been identified thus far, most notably from the genus Tulasnella; however, none of the samples that we have identified to this genus have been formally described. Taxonomic placement and sequencing of additional loci are underway to formally describe these Tulasnella species. The results of the seed baiting trials are still pending, but will undergo similar microscopy, molecular, and data analysis procedures if orchid seed germination is successful. We aim to fill this crucial knowledge gap regarding C. arietinum and identify fungi that play essential roles in the germination and growth of this endangered plant, which has relevance for propagation and conservation.

**Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology**

### Inoculation with native mycorrhizal fungi improves native plant establishment and reduces non-native encroachment in a grassland restoration

Tanya Cheeke, Washington State University
Reb Bryant, University of Kansas
Liz Koziol, University of Kansas
James Bever, University of Kansas

Understanding the mechanisms that promote native seedling establishment in disturbed ecosystems is key to improving the biodiversity and function of landscape restorations. In a long-term field experiment over seven growing seasons, we examined the effects of site preparation technique, soil inoculations, and their interactions on native plant establishment in the restoration of an invaded grassland. Prior to restoration, plots were either solarized to eliminate non-native grass or mowed, and one of three microbial treatments was introduced into each plot using native prairie seedlings as 'nurse' plants. Seedlings were inoculated with (1) arbuscular mycorrhizal fungi isolated from old-growth prairie remnants, (2) remnant prairie soil, or (3) autoclaved inocula. We found that site preparation technique and microbial inoculation were strong drivers of native seedling survival and the development of seeded plant communities. By the seventh growing season, there was greater cover of late successional native plant species and increased floral quality index scores in solarized plots and inoculated plots compared to mowed and uninoculated plots. Plots that received native soil microbes had 13% lower non-native plant cover compared to uninoculated plots. Although seedling establishment was higher overall in the solarized plots, the benefits of soil microbial inoculation were greater in the mowed plots, in which native seedlings were in direct competition with invasive grasses. By considering belowground communities at the same time as revegetation efforts, this study demonstrates how microbial inoculations can be used with different site preparation techniques as a nature-based tool to accelerate the recovery of invaded grasslands.

### Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### On-Going Studies of the Ectomycorrhizal Fungi of Coastal Maine and Its Islands

Pete Avis, University of Maine

Islands are important systems to study questions about the assembly of fungal communities and change in fungal populations over time and space. The relationship between factors such as island size and isolation and fungal dispersal, persistence, and longevity have long intrigued mycologists but have yet to be completely studied. In 2021, we initiated what is expected to be a decades-long mycological study of islands off the coast of Maine that aims to address some of these questions. Specifically, we ask if and how island size and isolation are related to ectomycorrhizal fungal species richness, diversity and community composition. To date, we have sampled 16 coastal islands and 18 coastal mainland locations and use Illumina MiSeq sequencing of the ITS amplicons generated from root and soil samples collected in mature red spruce forests to characterize the ectomycorrhizal fungal community attributes on each island. Our most recent collections focus on an archipelago of islands in the same region but of varying island sizes; and an extensive sampling of a very remote island for comparisons to less isolated islands of similar size and to mainland. This presentation will provide an update on the results of this ongoing community ecology study and how these studies are informing a set of recently initiated studies of the population ecology and genomics of key species of Amanita and Russula found across these islands and this region of North America.

### Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Prevalence of Dual Mycorrhizal Associations in Temperate Hardwood Trees of a Midwestern Forest

Kathryn Maley, Department of Botany and Plant Pathology, Purdue University
Mary Catherine Aime, Department of Botany and Plant Pathology, Purdue University

Mycorrhizal fungi are important symbionts of plant roots, playing pivotal roles in the establishment and survival of tree seedlings in forests. Although there are several types of mycorrhizae, arbuscular mycorrhizal (AM) and ectomycorrhizal (ECM) associations are the two most common in temperate hardwood trees. Trees are typically categorized by mycorrhizal type using literature, but sources do not always agree on mycorrhizal diagnoses, making it difficult to apply universally across the same taxa. Moreover, recent evidence suggests that many species may form dual mycorrhizal associations, challenging the assumption of exclusive AM or ECM relationships. These findings highlight the need for more empirical studies to diagnose mycorrhizal type and to determine what influences dual mycorrhizal prevalence. In this study, we used metabarcoding of seedling root tips to identify 30 tree species and their associated mycorrhizal fungi in a 27-hectare hardwood forest along the Wabash River, Indiana. Additionally, we compared dual colonization of four tree genera (Quercus, Carya, Acer, Fraxinus) between AM- and ECM-dominated plots to determine if local mycorrhizal dominance influences the tendency of trees to form dual associations. Understanding dual mycorrhizal associations will enhance our knowledge of tree interactions and resource access, which are key to the success of young trees in forest ecosystems. It is vital to consider these factors when predicting forest population dynamics and selecting compatible species and sites for reforestation efforts.

### Parallel Session 4-2: MycoFlash: Advances in Fungal Community Ecology

### Recent Advances in Fungal diversity, distribution, and Adaptations in Antarctic Soils.

Alisha Quandt, The University of Colorado, Boulder
Mary Childress, The University of Colorado, Boulder
Nick Dragone, The University of Colorado, Boulder
Noah Fierer, The University of Colorado, Boulder

Fungi have increasingly been described from various habitats in coastal and mainland Antarctica. Most studies have focused on specific sites on the continent and have used either culture dependent or independent methods exclusively. In our work we used archived soils from a large portion of the continent to examine fungal biodiversity using both culture dependent and independent methods. Our amplicon-based sequencing of the ITS barcode suggests that variation in soil fungal communities in Antarctica is most influenced by Mean Annual Temperature. Our results also showed limited overlap between the culture dependent and independent methods, and full length ITS sequencing suggests most of the fungi we cultured are not related to currently described taxa. All isolates were cultured at 4 °C to ensure transient spores unable to grow in Antarctic conditions were excluded from our survey. Cultured fungi, which included 13 genera of filamentous and yeast forms in Ascomycota, Basidiomycota, and Mortierellomycotina, were subjected to whole genome sequencing and analyzed for cold-adaptive and xerophilic genes.

## PARALLEL SESSION 4-3:
## MycoFlash: Advances in Fungal Community Ecology

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### Structure of Mucoromycota Fungal Communities and Their Associated Endosymbiotic Bacteria across Two Different Biomes in the U.s. and Israel

Nicole Reynolds, California State Polytechnic University, Pomona

Despite the ecological importance of Mucoromycota fungi as mycorrhizal symbionts, opportunistic human and plant pathogens, and post-harvest spoilage agents, they remain understudied compared to Dikarya. Fundamental aspects such as geographical distribution, dispersal patterns, and community structure remain unclear. The endosymbiotic bacteria (EB) that many Mucoromycota species harbor have generated new questions regarding their effects on fungal host evolution. To investigate communities, we collected rhizosphere soils from four sites in California and two in Israel representing two biomes (Desert and Mediterranean scrub). Metabarcoding data were generated using bacterial (16S rDNA) and fungal (28S rDNA) primers and show several OTUs unique to each habitat. Both biotic filtering and dispersal filtering significantly affected fungal and bacterial communities; however, dispersal filtering was only significant over larger distances (km rather than m scale). Desert samples had a higher proportion of fungal OTUs assigned to opportunistic human pathogenic species not detected from the coast. These results suggest that desert environments are likely reservoirs for these pathogens.

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### Beyond the reference strain: a fresh look at Candida albicans adhesion

Liza Loza, University of Wisconsin, Madison
Siobhan Dietz, University of Wisconsin, Madison
Robert Fillinger, Van Andel Institute
Matthew Anderson, University of Wisconsin, Madison

Attachment of the human commensal yeast Candida albicans to human epithelial cells is mediated by cell surface proteins called adhesins. Certain adhesins have been well studied in the reference strain SC5314. However, C. albicans encodes many predicted adhesins whose specificity has not yet been characterized. Furthermore, different clinical isolates may rely on different subsets of adhesins to interact with the host. To investigate this idea, we inoculated human epithelial cells with SC5314 or the clinical isolate 529L and collected RNA at set intervals. Genes that were significantly upregulated in SC5314 relative to 529L include genes encoding adhesins that have been previously studied in SC5314. Interestingly, four genes that were upregulated in 529L relative to SC5314 encode predicted but uncharacterized adhesins. 529L is thus an exciting context in which to study these putative adhesins. Using complementary approaches, I plan to test whether these four candidates are adhesins and, if so, determine their interaction partners. First, I will express each candidate in Saccharomyces cerevisiae and test transformants' adherence to relevant extracellular

matrix proteins (ECMs) in vitro. In parallel, I will delete the gene encoding each candidate adhesin in 529L. I will then assess mutant adherence to ECMs and epithelial cells; their rate of internalization by epithelial cells; and finally, their persistence in a mouse model of oral colonization. Defining the adhesin profile of 529L will expand our understanding of basic Candida biology beyond the reference strain and provide insight into fungal-host interactions that may dictate colonization dynamics.

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### Fungal Culture versus Dna Metabarcoding in the Search for Fungal symbioses: What Should You do?

Sophie Shand, College of William and Mary
Rosie George-Ambrocio, College of William and Mary
Michelle Jusino, Center for Forest Mycology Research, Northern Research Station, USDA Forest Service
James Skelton, College of William and Mary

Mutualisms between insects and Fungi are among the most fascinating, ecologically relevant, and well-known symbioses. DNA metabarcoding is an increasingly used alternative to traditional culture-based studies to identify the symbiotic mutualists of insects. The potential benefits of metabarcoding over culturing include reduced time and effort, increased detection of fungal diversity, and applications to preserved (dead) materials. However, there is a lack of direct comparisons between culture-based and metabarcoding results, leaving uncertainty in the reliability of both methods. In this study of the symbionts of fungus-farming ambrosia beetles, we performed a direct sample-for-sample comparison of fungal diversity recovered from the mycangia of dispersing beetles. Each sample was analyzed using a combination of quantitative fungal culture (CFU's from dilution plating on standard media identified by Sanger sequencing) and DNA metabarcoding via two popular DNA markers – ITS2 and LSU (28S). We compare species detections, total diversity, and relative species abundances among sampling methods. Our samples included diverse genera of ambrosia beetles, ambrosia fungi in several orders spanning Ascomycota and Basidiomycota, and included previously unknown host/symbiont associations. Our study illustrates the advantages and limitations of each approach so that researchers can now make more informed study design decisions.

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### Non-Destructive Raman Spectroscopy Imaging of the Arbuscular Mycorrhizal Fungal-Plant Interaction

Alison Bennett, Department of Evolution, Ecology, and Organismal Biology
Renee Romano, Department of Chemistry and Biochemistry, Ohio State University
Taylor Payne, Department of Chemistry and Biochemistry, Ohio State University
Zac Schultz, Department of Chemistry and Biochemistry, Ohio State University

Arbuscular mycorrhizal (AM) fungi are ubiquitous soil organisms and key symbiotic partners of plants. To assess the direct interaction between AM fungi and plants currently requires destructive harvests and expensive or time consuming root staining analyses. Thus, it is challenging to examine changes in colonization over time or to assess colonization in the field. We have developed an imaging protocol using Raman spectroscopy that can determine AM fungal colonization based on variation in carotenoids and chlorophyll. We conducted multiple experiments growing tomato with and without AM fungal inocula, and we imaged leaves using Raman spectroscopy and validated root colonization using traditional root staining and microscopy. Across experiments and samples we normalized all spectra to the Raman peak associated with cellulose, and then we used half our data to conduct a machine learning analysis to determine in which peaks changes occurred between sterile and AM fungal treatments. We then used our machine learning model to predict which samples in the second half of our data belonged to each treatment. The model's predictions were accurate 70% of the time on the hold out data. The application of stress (drought, jasmonic or salicyclic acid) did not alter our predictive capability, but variation in daylength (regardless of supplemental lighting in the greenhouse) across the length of the experiment was a confounding factor. Thus, we added variation in daylength to our model. Overall, across multiple experiments, we are able to accurately predict the presence of AM fungi in plant root systems without destructive harvests.

**Parallel Session 4-3: MycoFlash: Advances in Fungal Biology**

### Predicting Wheat Grain Mycotoxin Contamination Using Mycobiome Colonization Patterns

Briana Whitaker, USDA-ARS
Martha Vaughan, USDA-ARS
Susan McCormick, USDA-ARS
Talon Becker, University of Illinois, Urbana-Champaign
Kristi MacCready, USDA-ARS

Fusarium head blight (FHB) is a devastating disease of wheat that causes mycotoxin contamination in grains. FHB has traditionally been managed with integrated control strategies, but this has led to a proliferation of fungicide-resistant pathogens and soil erosion. Microbial biocontrols are a possible alternative – however, translation of promising strains is hampered by our lack of understanding on the colonization of crop microbiota across plant development and tissue types. To tackle this dilemma, we planted three varieties of wheat in replicated field plots at two Illinois locations. The fungal microbiome was analyzed across five developmental timepoints in wheat leaves and heads, and in corn debris from the previous season. Fungal microbiome composition varied most strongly by tissue type, however site and developmental timepoint were the next most important contributors to community composition. Host variety only significantly explained fungal community variation in wheat heads and was less important than FHB disease on head microbiomes. In addition, we identified debris as a major source of fungal colonizers to leaves early in development, but not later – and found that leaves were not a large source to head microbiomes at either developmental stage tested. Taxa enriched under high FHB primarily belonged to the Ascomycota (Davidiella, Leptosphaerulina), while taxa enriched under low FHB primarily belonged to the Basidiomycota (Cryptococcus, Entyloma, and Sporidiobolus). Our research highlights the potential for applications of biocontrol strains targeted to specific tissue types and wheat developmental periods, with implications for pre-harvest control of mycotoxin contamination and food safety.

**Parallel Session 4-3: MycoFlash: Advances in Fungal Biology**

### Scaling DNA Barcoding of Historical Macrofungal Collections: From Michigan to California

Stephen Russell, Mycota Lab

In 2024, we began DNA barcoding approximately 6,000 California macrofungal specimens housed at the University of Michigan herbarium. As a part of this process, a novel nanopore-based barcoding protocol was developed and implemented for DNA barcoding older herbarium specimens at scale. Despite the median age of 80 years for the samples, we achieved a 70%+ success rate across the specimens. Historically, barcoding older herbarium specimens has been challenged by degraded, fragmented DNA and contamination from non-target fungi. Traditional Sanger sequencing methods are often insufficient for specimens with these issues. Nanopore sequencing addresses these challenges, while providing longer read lengths, relatively simple library prep, and lower cost than Illumina sequencing. Building on this previous success, we are starting a new project in 2025 to barcode 15,000 specimens at the Thiers Herbarium at San Francisco State University. Methodological and molecular enhancements planned for the SFSU collections, designed to further improve sequencing efficiency, accuracy, and yield, will be discussed.

**Parallel Session 4-3: MycoFlash: Advances in Fungal Biology**

### Shifts in Sphagnum fungal communities and metabolomes with senescence elucidate the impact of host chemistry on fungal-mediated decomposition

Megan Nickerson, Washington State University
Malak Tfaily, University of Arizona
Laura Meredith, University of Arizona
Jana U’Ren, Washington State University

Unlike vascular plants, where photosynthetic tissues typically detach after senescence, senescing tissues of nonvascular plants such as mosses remain physically connected to living tissues and decomposition occurs along a continuous gradient. Previous work on temperate mosses found that living tissues are dominated by Ascomycota, whereas Basidiomycota abundance increases with senescence; such taxonomic shifts coupled with increased CAZyme transcriptome abundance was consistent with fungi playing an active role in decomposition. Yet, in boreal and arctic ecosystems, Sphagnum mosses are slow to decompose, contributing significantly to carbon sequestration in these ecosystems. Low temperature, pH, and oxygen levels can slow decomposition rates, but Sphagnum may also produce metabolites that inhibit microbial growth (e.g., polyphenolics and organic acids). Here, we examined how metabolites influence fungal diversity and composition in living and senescing tissues of three Sphagnum spp. (25 total individuals) and their associated soils in two sites near Toolik Lake, Alaska. Using untargeted LC-MS/MS, we recovered 5,382 metabolite features. Despite Sphagnum's reported antimicrobial nature, Illumina ITS1 sequencing identified ~1,000 putative fungal species representing Ascomycota and Basidiomycota, as well as nine other phyla. Fungal diversity was highest in living tissues, suggesting that Sphagnum metabolites are not universally inhibitory to fungi. However, lower fungal diversity in senescent tissues and soils indicates metabolite breakdown may generate inhibitory by-products and/or result in metabolites recalcitrant to fungal enzymatic breakdown. Ongoing analyses will determine the impact of specific metabolite classes on fungal diversity and composition, further elucidating biotic constraints on Sphagnum decomposition.

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### The Dictyostelium Host-Pathogen Model Enables High-Throughput Screening of Virulence Traits in Pathogenic Mucorales

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Daniel Stark, University of Sheffield
Dora E. Corzo-León, University of Exeter
Jason King, University of Sheffield
Elizabeth R. Ballou, University of Exeter
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Mucormycosis is an emerging infectious disease frequently caused by Rhizopus species (Mucorales, Mucoromycota). Rhizopus often harbors Burkholderiaceae-related endobacteria (BRE) that produce secondary metabolites which may contribute to fungal virulence. However, not all clinical Rhizopus strains contain endosymbionts, so it is unclear to what degree endobacteria contribute to fungal pathogenicity. Our goal is to experimentally evaluate fungal and bacterial contributions to mucormycosis using Rhizopus microsporus and Dictyostelium, a phagocytic amoeba and model for microbe-phagocyte interactions. We hypothesize that Rhizopus virulence has arisen from the need to evade soil phagocytic amoebae. To test this hypothesis, we are utilizing Dictyostelium-based assays that measure the effect of fungal spore conditioned media on amoeba growth and bacterial killing efficiency. We plan to differentiate fungal and endobacterial contributions to virulence by evaluating BRE hosts and non-host fungal isolates, including isolates cleared of BRE- strains, with the Dictyostelium assays. In parallel we are using R. microsporus uridine auxotrophs for CRISPR gene editing to knock out known fungal virulence factors. Pairing knockouts with hosts and non-hosts with and without bacteria in the Dictyostelium assays will allow quantitative evaluation of how fungal and bacterial factors contribute to virulence. Preliminary results suggest that spore conditioned media from different strains produces distinct and variable effects on Dictyostelium growth. This system allows for relatively high throughput testing of virulence factors and is straightforward in its implementation. In this presentation I will discuss the methods we are using to address virulence in mucormycosis and share preliminary findings.

### Parallel Session 4-3: MycoFlash: Advances in Fungal Biology

### Zoosporic Fungi Contain Large DNA Viruses

Jillian Myers, University of Michigan
Frederik Schulz, DOE Joint Genome Institute
Saleh Rahimlou, University of Michigan
Vikas Yadav, Duke University
Kevin Amses, University of Pennsylvania Perelman School of Medicine
Rabern Simmons, Purdue University
Sheng Sun, Duke University
Michelle Orozco-Quime, University of Michigan
Joseph Heitman, Duke University
Jason Stajich, University of California Riverside
Timothy James, University of Michigan

The overwhelming majority of known mycoviruses have RNA genomes, and only a handful of DNA viruses are known from the entire Fungal kingdom. This apparent rarity of DNA viruses in fungi likely results from biases in searches, rather than a true biological phenomenon. We report both "viral fossils", or relicts embedded in fungal genomes, and active infection by large DNA viruses in fungi, particularly in the zoosporic phyla Blastocladiomycota and Chytridiomycota. The recovered viral genomes span up to 350 kb, encode over 300 genes, and form a monophyletic family-level clade within the Nucleocytoviricota related to orders Imitervirales and Algavirales, which we name Mycodnaviridae. We observed variation in infection status among the isolates including apparent active infection and

transcriptionally-suppressed states, suggesting that viral activation may be constrained to certain life stages of the host. Metagenomics indicates that fungal giant viruses have a global distribution, which begs inquiry into the implications of these infections for host traits, host genome evolution, and the function of ecosystems.

## PARALLEL SESSION 4-4:
## MycoFlash: Advances in Fungal Functional Genomics

### Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics
### Aneuploidy-Induced Defects in Ribosome Quality Control Disrupt Quiescence and Aging in Wild S. Cerevisiae

Leah Escalante, University of Wisconsin, Madison
James Hose, University of Wisconsin, Madison
Hollis Howe, University of Wisconsin, Madison
Norah Paulse, University of Wisconsin, Madison
Michael Place, University of Wisconsin, Madison
Audrey Gasch, University of Wisconsin, Madison

Down syndrome, caused by an extra copy of chromosome 21, causes lifelong problems. One of the most common phenotypes among people with Down syndrome is premature aging, including early tissue decline, neurodegeneration, and shortened lifespan. Yet the reasons for premature systemic aging are a mystery and difficult to study in humans. Here we show that chromosome amplification in wild yeast also produces premature aging and shortens lifespan. Chromosome duplication disrupts nutrient-induced cell-cycle arrest, entry into quiescence, and cellular health during chronological aging, across genetic background and independent of which chromosome is amplified. Using a genomic screen, we discovered that these defects are due in part to aneuploidy-induced dysfunction in Ribosome Quality Control (RQC). We show that aneuploids entering quiescence display aberrant ribosome profiles, accumulate RQC intermediates, and harbor an increased load of protein aggregates compared to euploid cells. Although they have sufficient proteasome capacity, aneuploids also show signs of ubiquitin dysregulation and sequestration. Remarkably, inducing ribosome stalling in euploids produces similar aging phenotypes, while up-regulating limiting RQC subunits or poly-ubiquitin alleviates many of the aneuploid defects. We propose a model in which the increased translational load caused by the extra chromosome accelerates a decline in translational fidelity, contributing to premature aging.

### Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics
### Characterization of Gene Expression Patterns in the Nematode-Trapping Mushroom Hohenbuehelia Mastrucata in the Presence of Different Nitrogen Sources.

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Characterization of gene expression patterns in the nematode-trapping mushroom Hohenbuehelia mastrucata in the presence of different nitrogen sources.

### Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics
### Discovering the Effect of Basidiobolus on Gene Functions and Abundance in the Lithobates Sylvaticus Gut Microbiome

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The gut microbiome is a complex ecosystem shaped by host factors, diet, and inter-microbial interactions. Among these, fungal-bacterial dynamics play a critical role in shaping microbial community structure and functional potential. This study investigates how the fungal genus Basidiobolus influences the taxonomic composition and functional traits of the Lithobates sylvaticus gut microbiome. Using metagenomic sequencing, we explore whether Basidiobolus presence modulates microbial diversity, gene abundance, and metabolic capacity. We hypothesize that fungal-microbial interactions with Basidiobolus drive significant shifts in community composition, gene richness, and enzymatic profiles. Gene richness and abundance are quantified through metagenomic assemblies and differential analysis using DESeq2. Functional profiling is performed using KEGG and CAZy annotations to identify shifts in metabolic and enzymatic pathways. Preliminary results from 50 fecal samples reveal significant differences between control and Basidiobolus-exposed groups. The LsFMGC95 gene catalog, containing 5 million non-redundant genes, forms the basis for functional analysis. Differential gene abundance and pathway enrichment analyses highlight shifts in metabolic functions, including carbohydrate metabolism and secondary metabolite biosynthesis. Variations in CAZy enzyme families, particularly glycoside hydrolases, suggest ecological adaptation driven by fungal presence. These findings reveal that Basidiobolus significantly alters both the taxonomic and functional landscapes of the L. sylvaticus gut microbiome. This study contributes to a deeper understanding of fungal-microbial interactions and their ecological consequences, offering insight into amphibian gut health and microbial community dynamics.

## Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics

### Function and Conservation of Fungal Inhibitor of Apoptosis Proteins

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Meareg Amare, University of Wisconsin, Madison
Grant Nickles, University of Wisconsin, Madison
Nancy Keller, University of Wisconsin, Madison
Mehdi Kabbage, University of Wisconsin, Madison

Inhibitor of Apoptosis Proteins, or IAPs, are one of the only regulatory elements from animal apoptosis with homologs in fungi; as such, they provide a unique window into the regulation of fungal programmed cell death. Fungal genomes have previously been assumed to contain exactly one IAP gene, which is essential in some species and not in others, but a broad assessment of IAP homologs across the fungal kingdom has not been published to date. Remarkably, our bioinformatic analysis revealed that many fungal genomes encode multiple IAPs, including examples with up to eleven unique genes, and showed that IAPs are nearly universal in fungi. We have previously interrogated the function of AnBIR1, the IAP of the model fungus A. nidulans, and found that it is essential for survival, inhibits caspase-like activity, and its precise regulation is required for functional sporulation, secondary metabolite composition, and cell wall integrity. We are now working to characterize the IAPs of two species of Letharia, a lichen- forming fungus, which showed ten and eleven distinct IAP homologs. We are interested in exploring the evolutionary history of this gene expansion and its impact on IAP functions in this unique organism. Overall, this work assesses the functional conservation and diversification of IAPs across the fungal kingdom and aims to refine our understanding of fungal programmed cell death.

## Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics

## Genome-wide association studies and transcriptome analysis reveal the genetic mechanisms contributing to thermotolerance in Neurospora discreta

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Donald Natvig, University of New Mexico
Julia Kelliher, Los Alamos National Laboratory
La Verne Gallegos-Graves, Los Alamos National Laboratory
John Taylor, University of California, Berkeley
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Neurospora discreta has been identified as a potential model for understanding how fungi adapt to environmental change due to the distribution of closely related, but genetically distinct populations in different environments across the western United States. Race tube experiments indicated that an N. discreta isolate obtained from a warmer climate in New Mexico had a much higher growth rate at 42C compared to an isolate obtained from a colder climate in Alaska. Differential gene expression analysis was conducted to identify differences in how the two isolates respond to heat stress. These analyses revealed substantial differences in how each isolate responds to heat stress and provides insights into how an isolate from a warmer climate may have adapted to its local environment. A sexual cross between the two isolates from different climates revealed that the thermotolerant trait was heritable and the appearance of progeny with reduced thermotolerant phenotypes suggest that multiple regions in the genome are involved in conferring thermotolerance. Whole genome sequences obtained from both thermotolerant and non-thermotolerant progeny have been used to identify genetic variants associated with the trait of thermotolerance. The integration of data from both this genome-wide association study and the differential gene expression analysis demonstrates that thermotolerance in N. discreta is the result of a mixture of genetic mutations and differences in gene regulation. Many of the genes identified in this study have unknown functions, and prioritizing the functional characterization of these genes is a crucial next step in understanding how fungi adapt to warmer climates.

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## Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics

## Insights into the Cryptic Mating Behaviour of Chaga (Inonotus obliquus)

Benjamin Bohemier, Lakehead University
Leonard Hutchison, Lakehead University

Inonotus obliquus (Ach. Ex Pers.) Pilàt is a parasitic white heart rot fungus of circumboreal distribution belonging to the family Hymenochaetaceae. It is primarily hosted on birch, but can occur on other hardwoods. Typically, this fungus is recognized by a charcoal-like sterile conk with a yellowish-brown interior that forms on the host tree. Colloquially, this is known as Chaga and is hailed for its potential health benefits. As the name suggests, the sterile conk does not produce any basidiospores. Once in an infection cycle of approximately 10 - 80 years, a spore-producing resupinate and poroid basidioma will form beneath the bark of a recently dead host. This sporadic occurrence makes them difficult to locate and study. Wild strains of I. obliquus were isolated from paper birch in northwestern Ontario and examined for in vitro growth and fruiting characteristics. A protocol was developed to form fertile fruit bodies reliably under laboratory conditions. The nuclei within basidiospores were examined using Hoechst 33342 and fluorescence microscopy throughout the maturation of basidiomata. It was discovered that the basidiospores of I. obliquus have highly variable nuclear characteristics, as they can contain between 1 and 6 nuclei in different ratios at different times. This character, and the presence of non-clamped multinucleate hyphae, indicate that I. obliquus has complex mating behaviour which requires further examination. As this fungus can reliably fruit in vitro, it may be utilized as a model organism to study mating in the Hymenochaetaceae, where sexuality is misunderstood and largely unknown.

## Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics

### Targeting Polarized Growth in Conidial Germination of Fungal species: A Comparative Genomics Approach to Antifungal Drug Discovery

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Zheng Wang, Yale University
Frances Trail, Michigan State University
Oded Yarden, Hebrew University of Jerusalem
Jeffrey P. Townsend, Yale University

Fungal pathogens cause diseases affecting 6.55 million people annually, killing over half of them. Rising fungal infection rates, driven by increases in people with medical vulnerabilities, highlight the need for the urgent development of novel antifungal drugs. Conidia germination is essential for fungal propagation, environment colonization, and host infection. Conidia germination toward the first branch of the hyphae is a unique process absent in mammalian hosts and involves the whole polarized growth mechanism. Therefore, understanding this mechanism is crucial in advancing our knowledge of fungal biology, from their initial response to the environment to the development of pathogenicity. We hypothesize that identifying genes associated with fungal conidia germination, specifically polarized growth, and their functional divergences across distinct fungal species will provide insights into asexual spore germination and reveal potential targets for novel antifungal drugs. We performed a comparative genomic analysis to identify conserved and species-specific mechanisms regulating polar growth in filamentous fungi. We examined gene expression during conidial germination extending from isotropic to polarized growth to the first hyphal branch, in several fungal species grown in a common medium representing saprobic and pathogenic lifestyles. Disrupting polar growth mechanisms can hinder fungal virulence, presenting novel therapeutic opportunities. High-throughput screenings of small-molecule or targeted protein-degrader libraries against fungal mutants defective in polar growth genes provide a systematic approach to antifungal discovery. By integrating comparative genomics, functional genetics, and high-throughput screening, we can advance our understanding of fungal development and inform strategies for antifungal drug development.

## Parallel Session 4-4: MycoFlash: Advances in Fungal Functional Genomics

### What Makes Bioluminescent Fungi glow?

Xianfa Xie, Virginia State University
Roel Rabara, Virginia State University

Bioluminescent fungi are a unique group of fungi widely found on different continents, though they are rare within the vast diversity of fungi. So far, bioluminescent fungi have been found mainly from four lineages of Agaricales, including the Armillaria, Mycenoid, Omphalotus lineages and Marasmiaceae. While the genetic basis for bioluminescence has been elucidated to some degree in some of these lineages, the genetic pathways and genomic regulation for bioluminescence remains to be better defined in most of the bioluminescent fungal species. Here we present an in-depth study of bioluminescence in two species, Armillaria mellea and Panellus stipticus, the latter of which includes strains either bioluminescent or nonbioluminescent from different geographic areas. We first tested the effects of growing conditions, including different media/substrates, on the bioluminescence level of these two species. Next, we sequenced the genomes of both species, including multiple bioluminescent and nonbioluminescent strains of P. stipticus based on the third-generation long-read sequencing technology, from which DNA methylation information was also obtained across the genomes. The comparison between the bioluminescent and nonbioluminescent strains of P. stipticus as well as with the bioluminescent A. mellea species revealed the genetic basis for bioluminescence in both species and the loss of it in some strains of P. stipticus, while the global methylation analysis revealed potential mechanisms for genomic regulations of fungal bioluminescence

# PARALLEL SESSION 5-1:
## Systematics: Basidiomycota

### Parallel Session 5-1: Systematics: Basidiomycota Global Population Genomics of Psilocybe Cubensis Reveal Cryptic Diversity and Insights into Its Geographic Origin.

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Keaton Tremble, Duke University
Colin Domnauer, University of Utah
Javier F. Tabima, Clark University
Bryn T.M. Dentinger, University of Utah

The globally distributed “magic mushroom” Psilocybe cubensis is cultivated worldwide for recreational and medicinal uses. Described in 1904 from specimens originating in Cuba, there has been substantial debate about its evolutionary origin and historical spread. The prevailing view has been that P. cubensis was introduced to the Americas alongside domesticated cattle from Africa and Europe (~1500 CE), but that its progenitor was endemic to Africa. Here, we challenge this hypothesis following the recent discovery of a close wild relative of P. cubensis from sub-Saharan Africa, Psilocybe ochraceocentrata, whose common ancestor with P. cubensis likely long predates thr domestication of cattle. We also present a globally representative population genomic survey of P. cubensis derived from 45 newly sequenced genomes, including the holotype specimen of Stropharia cubensis Earle. One surprising result is that P. cubensis originating in Oceania are consistent with incipient speciation after isolation rather than recent migration from a founder population. This work will discuss the possible wild origins of P. cubensis and shed light on the increasingly complex natural history of both the evolutionary and human-mediated spread of psychedelic mushrooms around the world.

### Parallel Session 5-1: Systematics: Basidiomycota Phylogenomic Insights to the Genus Letninus and Species Recognition Criteria in the Allopatric lineage, Lentinus Tigrinus.

Alexander Bradshaw,
Thomas Rohel, Clark University
Isaac A. Perkis, Clark University
Javier F. Tabima, Clark University
David S. Hibbett, Clark University

Lentinus tigrinus (Bull.) Fr., the tiger sawgill mushroom, is a commonly found saprotrophic fungus that makes its homes on the dead wood of hardwoods along riverbanks. L. tigrinus is a member of Polyporales that produces gills and presents a unique system for studying fungal morphological development. They are polymorphic in North America, including an “agaricoid” form with exposed gills and a “secotioid” form with enclosed spore-bearing structures. However, the genus Lentinus has long been a systematic quagmire with many cryptic relationships, hindering our ability to ask more profound questions about their evolution. One mystery is the range of L. tigrinus, which has an allopatric distribution across the Eastern and Central United States and a second across the temperate landscape of Europe. Transcontinental species distributions are not uncommon in Fungi. However, previous work has shown L. tigrinus to form a complex of four cryptic clades, which cannot be resolved with canonical DNA barcode sequencing. In this work, we sequenced 62 genomes from historical vouchers and fresh specimens representing all major sections across Lentinus and both geographic populations of L. tigrinus. We present a phylogenomic reconstruction of Lentinus that will help to redefine our understanding of its evolutionary history and the placement of both the North American and European lineages of L. tigrinus. Understanding the evolutionary context across the genus and within cryptic species will provide the framework for phylogenetic species recognition criteria within Lentinus and set the stage for more in-depth studies of comparative genomics and population structure within L. tigrinus.

### Parallel Session 5-1: Systematics: Basidiomycota
### Re-evaluation of Hemileia coffeicola, a pathogen of Coffea species

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Ana Perez Lopez, Universidad de los Andes
M. Catherine Aime, Purdue University

Hemileia vastatrix, Berkeley & Broome, (1869) and H. coffeicola, Maublane & Roger, (1934) are the only two species of Hemileia that affect coffee production. Hemileia coffeicola differs morphologically from H. vastatrix by the absence of a ridge of tightly clustered spines dividing the echinulate and smooth areas of the urediniospores. Recent efforts to generate sequencing data for H. coffeicola revealed 100% similarity with the LSU region of H. vastatrix. Additionally, suspected H. coffeicola specimens from our lab amplified with microsatellite primers specifically designed for H. vastatrix. The similarity in LSU sequence, amplification with H. vastatrix microsatellites, and overlap in plant hosts, coupled with the small morphological differences, suggest the possibility that H. coffeicola is a subpopulation of H. vastatrix rather than a separate species. Our objective is to clarify whether there is more than one species of coffee rust. To achieve this goal, we are evaluating H. coffeicola and H. vastratrix specimens preserved in the Arthur Fungarium at Purdue University. DNA will be extracted to sequence the nuclear ribosomal internal transcribed spacer (ITS), large subunit (LSU), and microsatellite markers for all specimens. Additionally, we will compare the urediniospores of both species. We expect to find no significant differences between ITS and LSU sequences for H. vastatrix and H. coffeicola. Furthermore, we expect to observe an overlapping phenotypic range in the spine clustering of the urediniospores of both species. This study will improve current taxonomic information available for the genus Hemileia and support the work of diagnosticians and coffee rust researchers.

### Parallel Session 5-1: Systematics: Basidiomycota
### The Big Enigma of Laccaria Laccata

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Edoardo Scali, Department of Environmental Science, Policy and Management, University of California
Clarissa Lopez Del Visco, Department of Environmental Science, Policy and Management, University of California
Gabriel Moreno, Department of Life Sciences (Botany), Biology Building, University of Alcalá, Spain
Bernardo Ernesto Lechner, Laboratorio de Hongos Agaricales, Departamento de Biodiversidad y Biología Experimental, Facultad de Ciencias Exactas y Naturales, Universidad de Buenos Aires, Argentina
Matteo Garbelotto, Department of Environmental Science, Policy and Management, University of California

Laccaria laccata serves as the type species of its genus and has long been regarded by mycologists as one of the most widespread species in the Northern Hemisphere. A Google search for the binomial Laccaria laccata yields 155,000 results; Google Scholar lists 7,120 citations, and Scopus contains 278 papers. These findings highlight significant interest in this species from both scientists and the general public. Contrary to the common belief that Laccaria laccata is one of the easiest species to identify, molecular analysis shows that sequences attributed to this species cluster into nearly 30 distinct terminal taxa or clades. To address this taxonomic ambiguity, a study was conducted in Femsjö, Sweden, where Fries collected his samples and where Singer designated the lectotype of Laccaria laccata. This investigation aimed to clarify the true taxonomic status of Laccaria laccata by examining the lectotype and comparing it to recent collections from locus classicus. Within this study, some of the varieties of Laccaria laccata described by Singer have also been considered.

### Parallel Session 5-1: Systematics: Basidiomycota
### What a Mushroom Leaves behind: The Biodiversity and Chemical Ecology of Native and Invasive Amanita Phalloides

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Jacob Golan, Department of Botany, University of Wisconsin, Madison
Nancy P. Keller, Department of Medical Microbiology and Immunology, University of Wisconsin, Madison
Shaneya Miriyagalla, Department of Botany, University of Wisconsin, Madison
Jillian M. Myers, Ecology and Evolutionary Biology, University of Michigan
Livia D.S. Oster, Department of Agronomy and Plant Genetics, University of Minnesota
Sung Chul Park, Department of Medical Microbiology and Immunology, University of Wisconsin, Madison
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The deadly Amanita phalloides is invading endemic forests in California. The death cap produces a diversity of specialized metabolites (SMs), and while SMs may have an essential role in protecting spores, their ecological functions remain mysterious. We hypothesize SMs play a role in fungal invasion biology, and the Californian A. phalloides' have an ecological advantage because they have escaped co-evolved natural enemies and their SMs are acting as a novel defense against naïve enemies lacking co-evolved resistance to the death cap's chemistry. Our hypothesis specifically targets mycophagous invertebrates and mycoparasites. We have begun to characterize the chemical profiles and communities of invertebrates found in the sporocarps of A. phalloides and related Amanita collected from the same sites in the native range. Moreover, we have described the viral and bacterial communities of A. phalloides from both ranges by mining transcriptomes. Our results show the death cap's mushrooms have significantly different invertebrate communities compared to other Amanita, suggesting a pattern of evolved specialization to species-specific SMs. In support of enemy release hypotheses, we have found a reduction in invertebrate and viral biodiversity described from invasive death cap mushrooms when compared to their native counterparts. We predict a similar signal will be found in bacterial communities. The difference in biodiversity between Amanita species and the death cap's ranges demonstrates the potential for mushroom SMs to drive ecological and evolutionary dynamics of non-pathogenic fungal invasions.

## PARALLEL SESSION 5-2:

### Fungi from the Deep:
### New Insights into Aquatic Fungi

**Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi**

### Coastal Forested Wetland Soils Are Microbially Primed for Shrub Growth

Aeran Coughlin, Duke University
Justin Wright, Duke University

Plants influence soil microbial communities in species-specific ways, resulting in plant-soil feedbacks (PSFs), which play a critical role in structuring plant communities. Coastal freshwater wetland salinization under saltwater intrusion and sea level rise (SWISLR) has been associated with tree decline and subsequent expansion of shrub-dominated vegetation. Plant-microbial interactions represent a critical missing component of our understanding of plant community transitions with wetland salinization. We assessed the role of PSFs in coastal vegetation transition under SWISLR. We sought to determine the direction and strength of PSFs of key tree and shrub species and whether microbial community patterns predict PSFs.We measured growth of dominant tree (Pinus taeda) and shrub species (Morella cerifera and Ilex glabra) of salt-impacted coastal wetlands of Eastern North America in soils with home, away (forest or shrubland), and sterile inoculum additions. We quantified symbiont colonization and collected soils to sequence fungal (ITS1) and bacterial (16S) community DNA. In comparison with tree P. taeda, dominant shrub M. cerifera experienced a significantly stronger positive growth effect in away soil, suggesting that forest soils are microbially primed for the growth of shrubs. Pathotroph abundance was significantly negatively correlated with plant growth, however, while symbiotrophs were more abundant in plant-home soil pairings, their abundance did not predict growth. These findings highlight the potential role of microbial interactions in vegetation shifts under global change and demonstrate that microbial community composition can be related to the direction and strength of PSFs for some functional groups, but not others.

## Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi

## Expanded Genetic and Functional Diversity of Oceanic Fungi

Xuefeng Peng, University of South Carolina
David Valentine, University of California, Santa Barbara

Fungi are enigmatic members of the marine microbiome, with little known about their functions and activities in the open ocean water column. Often considered as descendants from their terrestrial counterparts, marine fungi are known to harbor diverse carbohydrate-active enzymes (CAZyems), but the specific substrates of these CAZymes remain elusive. Additionally, few studies have investigated potential interactions between fungi and bacteria in the ocean water column. We report previously unrecognized diversity and activity of fungi in the eastern tropical North Pacific Ocean, the ocean's largest oxygen minimum zone and a hot spot for biogeochemical cycling. Phylogenetic analysis of fungal transcripts points to unappreciated evolutionarily distinctions between oceanic fungi and their terrestrial counterparts. Among expressed genes predicted to code for extracellular carbohydrate-active enzymes (CAZymes), fungal glycoside hydrolase family 7 (GH7) dominated, indicating an outsized role fungi play in particle degradation despite their low abundance. The strong correlation between the gene expression of GH7 and chitin deacetylase suggests a potential synergy between bacteria and fungi in the degradation of chitin, one of the most abundant polysaccharides in the ocean. The correlation between nitrogen cycling processes and fungal hydrolytic activities provides new evidence for fungi as key players in linking carbon and nitrogen cycles in oxygen minimum zones. In sum, the evidence points to fungi as pivotal contributors to marine carbon cycling and particle remineralization. Ultimately, incorporating fungal processes into models of marine ecosystems will likely improve our understanding of global carbon and nitrogen dynamics.

## Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi

## First Latitudinal Profiling of Pufa and Carotenoids in Stramenopile Organisms along the Chilean coast: Influence of temperature and pH gradients.

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Patricia Arancibia-Ávila, Universidad del Bío-Bío
Moisés Valladares, Pontificia Universidad Católica de Chile
Cristian Torres-Díaz, Universidad del Bío-Bío
Edgar Pastene, Universidad del Bío-Bío
Nicolás Reyes-Quinteros, Universidad del Bío-Bío

This study analyzes polyunsaturated fatty acids (PUFA): docosahexaenoic acid (DHA), eicosapentaenoic acid (EPA), arachidonic acid (ARA), and carotenoids in organisms from the Stramenopile group or clade. Samples were collected along a latitudinal gradient on the Chilean coasts, where there is a thermal gradient of water exceeding ten degrees Celsius. Phylogenetic analysis identified the Oblongichytrium and Schizochytrium clades, along with a lineage containing Thraustochytrium aggregatum. Oblongichytrium sp. produced 34 times more DHA in coastal areas with higher pH (8.64) and lower temperature (9°C) than in regions with lower pH (7.30) and higher temperature (13°C). In contrast, Schizochytrium sp. and Thraustochytrium aggregatum produced DHA only in specific locations, showing no distribution pattern along the latitudinal gradient. EPA and ARA fatty acids were detected in all collected strains, but no clear pattern related to environmental conditions was observed. Additionally, all strains produced astaxanthin but not canthaxanthin, while β-carotene was present in some strains without a defined production pattern. These findings highlight the influence of temperature and pH gradients on DHA biosynthesis in Oblongichytrium sp., suggesting a link between environmental conditions and the production of biotechnologically relevant compounds in Stramenopile organisms, having important implications for lipid-based industrial applications.

## Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi

### Functional Genomics of Seasonal Wet Meadow Restoration in Coastal California

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Itzel Lopez

Natural wetlands have faced widespread destruction, creating an urgent need for ecosystem restoration. Constructed wetlands are increasingly being developed for water filtration in industries such as agriculture, manufacturing, and wastewater treatment. However, there is still much to understand about how restored wetlands function compared to their natural counterparts. This study aims to compare bacterial and fungal communities in restored and natural wetlands using bioinformatics to establish a molecular benchmark for ecosystem functionality. A focus on genes involved in nitrogen cycling will provide insight into the ecological processes vital for a balanced system. By mapping nitrogen cycling genes across bacterial and fungal genomes, we aim to evaluate the restoration efficacy and determine whether restored wetlands can replicate the functional characteristics of long-standing natural wetlands. Wetlands are highly productive ecosystems that support diverse microbial, plant, and animal life while playing a crucial role in oxygen production, water filtration, and flood mitigation. However, limited knowledge of wetland biogeochemical cycling, particularly microbial roles in nitrogen fixation and denitrification, hinders restoration efforts. This project will assess microbial community structure and functions through metabarcoding and metagenomics. We will analyze seasonal variations in bacterial and fungal diversity and investigate the microbial pathways involved in nitrification and denitrification. By monitoring key nitrogen fixation genes, we aim to develop biomarkers that can be used to assess the functional similarity between restored and natural wetlands. These findings will contribute to improved restoration strategies, supporting ecosystem resilience in the face of global environmental changes.

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## Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi

### Fungal Diversity Across a Depth and Salinity Gradient in the Deep Subsurface Biosphere

Quinn Moon, University of Michigan
Elliott Barnhart, United States Geological Survey
Michelle Orozco-Quime, University of Michigan
Ivan Paciorka, University of Michigan
Thomas Desrosiers, University of Michigan
Elizabeth Tomaszewski, United States Geological Survey
Matthew Varonka, United States Geological Survey
Timothy James, University of Michigan

The Deep Earth Biosphere may be the largest and least explored fungal habitat on the planet and fungi are suspected to play an important role in the maintenance and elemental cycling of subsurface microbial systems. The fungal diversity distribution remains largely unknown, making it difficult to understand both how increased anthropogenic pressures in the subsurface impacts fungi and how to manage and conserve the suspected mass of taxonomic and phylogenetic diversity that may be contained in the subsurface. We collected and filtered deep subsurface water samples across the Antrim Shale and Methane Basin in northern Michigan to examine how both total and culturable fungal diversity changes with increasing depth from the surface, and whether those variations match existing paradigms for prokaryotic diversity. With over 240 fungal isolates generated, many of which exhibit poor matches to sequenced representatives, it is becoming increasingly evident that the subsurface biosphere harbors diverse, culturable, and previously uncharacterized fungal diversity. As an exclusively microbial ecosystem void of ongoing photosynthetic input, investigation of the Deep Subsurface Biosphere enables examination of the presumed innate qualities of kingdom Fungi.

### Parallel Session 5-2: Fungi from the Deep: New Insights into Aquatic Fungi

### Seasonal Dynamics and Genomic Insights into a Novel Planktonic Cryptomycota Species

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Jason Woodhouse, Department of Plankton and Microbial Ecology, Leibniz Institute of Freshwater Ecology and Inland Fisheries, Germany
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Thomas Richards, Department of Biology, University of Oxford, United Kingdom
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Mariana Kluge, Chair of Urban Water Systems Engineering, Technical University of Munich, Germany
Christian Wurzbacher, Chair of Urban Water Systems Engineering, Technical University of Munich, Germany

Cryptomycota, an evolutionary early diverging group of fungi, are characterized by the absence of chitinous cell walls and a zoosporic, parasitic life cycle. Despite their prevalence in various habitats, including freshwater systems, the diversity and evolution of these organisms remain unclear. Currently, only two genomes are available, resulting in a significant underrepresentation of Cryptomycota in genomic databases. Consequently, studying this fungal group may uncover significant unknown fungal diversity and elucidate fungal evolution and adaptation to aquatic habitats. In an eight-year metagenomic time series of a shallow German bog lake, we identified a member of Cryptomycota that consistently emerges during the cold season. By employing sequential filtration and fluorescence in situ hybridization microscopy, we determined the organismal size as 1-2 µm and propose a planktonic lifestyle. An additional quantitative assessment of the organism's abundance using qPCR correlated positively with increasing nitrate and ammonium, as well as organic carbon concentrations in lake surface water from late autumn to early spring. We then combined dissection microscopy with single-cell sequencing to generate an initial genome assembly in order to study the organism's functional potential. Preliminary results indicate the absence of flagella, which, in combination with the previous findings, place this organism within a novel undescribed clade of Cryptomycota. Ongoing analysis combined with metagenomic data will provide a more thorough understanding of the evolution and significance of these organisms in aquatic food webs, which will be important for the conservation of these ecosystems in the face of ongoing biodiversity loss.

## PARALLEL SESSION 5-3:
## Priority and Legacy of Fungal Community Succession

### Parallel Session 5-3: Priority and Legacy of Fungal Community Succession

### Legacy effects in soil fungal communities 30 years after foundational plant removal in semiarid ecosystems

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In the Chihuahuan desert, Larrea tridentata (creosote bush) encroachment into grasslands historically dominated by Bouteloua eriopoda (black grama) has led to community shifts toward shrubland. While some land managers remove creosote to slow its spread, removal does not always facilitate black grama recovery, indicating that creosote may change soil biotic or abiotic properties with lasting impacts on plant community dynamics. We utilized a long-term removal experiment at the Sevilleta LTER in Socorro County, New Mexico where either creosote or black grama were removed for 30 years in grassland, shrubland, and ecotone habitats to determine the long-term impacts of creosote encroachment on soil properties. We sampled soil from removal and control plots and analyzed it for soil chemistry and fungal community composition using amplicon sequencing. Soil chemical composition was different between the three habitats (P

## Parallel Session 5-3: Priority and Legacy of Fungal Community Succession

### Legacy of repeated cultivation differentially drives fungal and bacterial community development in a tropical Oxisol soil

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Agricultural practices and the crop being actively cultivated are some of the most important contributors to soil microbial community assembly processes in agroecosystems. However, it is not well-understood how the cultivation of diverse crop species can directionally shift complex soil microbial communities, especially under continuous monoculture systems. We conducted a field experiment to assess how three crop species (Lactuca sativa, Brassica juncea, and Zea mays) may shift soil fungal and bacteria/archaeal communities when planted in a monoculture and repeatedly grown for three cycles in a tropical Oxisol soil. We found that while plant species made limited contributions to microbial community differentiation, repeated cultivation was a strong driver of community development over time. The bacterial/archaeal communities exhibited a cyclical community development pattern, initially with strong differentiation that attenuated to a steady state at the end of the three cycles. In contrast, fungal communities generally developed more linearly and may have only started to stabilize after three cropping cycles. These developments may speak to the stronger legacy effects on fungal communities. Together, these results highlight the differences between how bacteria/archaea and fungal communities develop, especially in tropical, underdeveloped, intensively degraded, or marginal soils.

## Parallel Session 5-3: Priority and Legacy of Fungal Community Succession

### Management regime and shade trees shaped decomposer fungal communities and impacted litter decomposition in an experimental coffee agroecosystem

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Laura Aldrich-Wolfe, North Dakota State University

Coffee agroforestry provides an opportunity to study how nutrient inputs and microclimate influence fungal communities and decomposition in tropical ecosystems. We investigated whether organic versus conventional management and the nitrogen-fixation capacity of shade trees shape leaf litter fungal communities and impact decomposition rates at a long-term experimental coffee farm in Costa Rica. Using metabarcoding of the ITS2 ribosomal DNA region, we tracked fungal communities in autoclaved leaf litter over 27 weeks across plots subject to organic, moderate conventional, and intensive conventional management. Plots were shaded by single non-nitrogen-fixing, single nitrogen-fixing, or two nitrogen-fixing trees. We expected diverging successional fungal communities would drive different decomposition rates, with more even communities accelerating decomposition through niche complementarity. Management and shade tree type independently shaped successional fungal community composition and decomposition. Organic plots, fertilized with manure, developed the most even fungal communities, enriched with several genera with known coprophilous taxa, including *Zopfiella*, *Arachnion* and *Podospora*. Litter in organic plots decomposed more than moderate conventional plots but not intensive conventional plots, even though their fungal communities were distinct from both conventional regimes. Conventional regimes were never compositionally distinct from each other. Plots shaded by two nitrogen-fixing trees fostered distinct successional fungal assemblages compared to other shade types and exhibited more decomposition than non-fixer shade plots. Contrary to our expectations, distinct fungal communities achieved similar decomposition rates and similar fungal communities yielded different rates, suggesting decomposition may be modulated more by factors influencing decomposer activity than by the identity or diversity of the decomposers themselves.

## Parallel Session 5-3: Priority and Legacy of Fungal Community Succession

## Priority Effects of Foliar Fungal Endophytes in Leaf Litter Decomposition

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Gerald Cobián, California State University, Chico

Foliar endophytic fungi (FEF) live inside the leaves of plants and are invisible to the unaided eye. These fungi have been shown to play important roles in plants by providing defense against pathogens and aiding in water retention, particularly in hot, dry climates. However, the roles of some fungal endophytes remain unclear. The project's main goal is to investigate and determine which of these fungi are involved in the decomposition of leaf litter. Since FEF communities are already present in the leaves before they abscise, they have the advantage of being established. This advantage allows them to increase their population size, which can influence the establishment of other fungal decomposers. The interactions between early colonizers and later arrivals can range from facilitation to complete exclusion, affecting the rates at which leaves decompose and thereby influencing the carbon cycle. To investigate the roles of fungal endophytes in the decomposition of leaf litter and ultimately their influence on the carbon cycle, 1) determine how FEF influence the composition of leaf litter fungal communities through priority effects; 2) investigate the efficiency of FEF as leaf decomposers; and 3) determine how FEF communities and leaf decay communities change over time. By understanding the influence of FEF on leaf litter decomposition and the carbon cycle, the results could have important implications for understanding and managing ecosystem services.

## Parallel Session 5-3: Priority and Legacy of Fungal Community Succession

## Testing the Generality of Assembly Order 'rules' during the Decomposition of Fungal Necromass

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The assembly of ecological communities, which can impact key aspects of ecosystem functioning, can be strongly influenced by the order of species arrival. Specifically, it has been hypothesized that species arrival order is most important when (i) there is a high niche overlap between the early and late-arriving species, (ii) the early-arriving species has a high impact, (iii) the late-arriving species has a high requirement, and (iv) the environment is more benign. Here, we tested these four scenarios during the decomposition of fungal necromass (i.e., dead fungal mycelium), a major component of soil organic C in forest soils. Our multi-week laboratory microcosm experiment included fungal and bacterial decomposers and different necromass types that varied in cell wall melanin content. Microbial activity metrics included necromass loss, percent C and N, gravimetric water content, and pH. Microbial abundance was quantified through qPCR. We found that fungi, but not bacteria, generated strong arrival order effects, with fungi facilitating bacterial growth and bacteria reducing fungal growth. Further, we showed that a high-impact fungus caused arrival order effects by preempting the niche of later-colonizing species, while the late arrival of a high-requirement fungus did not differentially impact its colonization. Lastly, we determined that environmental harshness played a limited role in arrival order effects, although order effects in more benign environments were linked to niche modification. Collectively, our work indicates that species arrival order can influence microbial interactions during fungal necromass decomposition, but the predicted 'rules' of arrival order effects appear to be highly system-specific.

# PARALLEL SESSION 5-4:
## Translational Mycology

### Parallel Session 5-4: Translational Mycology Biomass-Fungi Composite Materials and the Future of Sustainable 3D Printing: Challenges and Opportunities

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Biomass-fungi composite materials are sustainable alternatives to conventional petroleum-derived plastic materials used in the construction, furniture, and packaging industries. The utilization of 3D printing technology with biomass-fungi composite materials offers the potential to manufacture customizable products with minimal material wastage. This approach utilizes agricultural waste materials, such as hemp hurd and sawdust, combined with fungal strains like Ganoderma sessile and Trametes versicolor, to create the final products. In biomass-fungi composite materials, biomass particles work as the substrate, and the fungal hyphae bind the biomass particles together. Some challenges, such as optimizing substrate formulations, ensuring consistent fungal growth, and achieving desired mechanical properties must be addressed to realize the potential of biomass-fungi composite materials. Ongoing research aims to overcome these obstacles, paving the way for innovative applications and contributing to a more sustainable future.

### Parallel Session 5-4: Translational Mycology Bioremediation Potential of Fungi in Heavy Metal-Contaminated Drylands

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Kaelin Gagnon, University of New Mexico
Geisianny Moreira, University of New Mexico
Jennifer Rudgers, University of New Mexico
Jose Cerrato, University of New Mexico

The legacy of uranium mining in the Southwest U.S. has left extensive environmental and human health hazards due to long-term heavy metal contamination. Our study aims to evaluate the bioremediation potential of Ascomycota fungi native to metal-contaminated environments. The fungi were isolated from soils, biocrusts, and grass roots at the historic Jackpile mine in the Pueblo of Laguna. A microplate absorbance assay was used to assess fungal growth and metal removal ability in the presence of 4 mg/L of arsenic and lead separately. Growth was monitored by measuring absorbance at 600 nm every 24 hours over an 8-day period, and remaining metal concentrations were quantified post-cultivation to evaluate removal efficiency. Our findings reveal that the Ascomycota fungi were tolerant to both arsenic and lead, with most showing no significant difference in growth compared to control conditions without metals. While arsenic removal was minimal, lead was efficiently removed, with some species achieving up to 95% removal from aqueous solution. This study underscores the potential of utilizing local fungal species for targeted bioremediation efforts in areas affected by heavy metal contamination, particularly in arid environments like the desert grasslands surrounding mine sites.

### Parallel Session 5-4: Translational Mycology Designing Communities of Ectomycorrhizal Fungi to Understand Phosphorus Nutrition in Loblolly Pine

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Ectomycorrhizal (ECM) fungi form a vital symbiosis with loblolly pines, improving their nutrient and water uptake in exchange for carbon. The fungal extraradical hyphae extend beyond the root system, allowing them to explore a larger soil volume and enhancing nutrient acquisition. Loblolly pine, a commercially important species, is widely planted in the southeastern U.S., where phosphorus (P)-deficient soils are prevalent. While some individual ECM species have been shown to enhance plant P uptake, it remains unclear how interactions within a complex community of ECM fungi, as found in natural environments, influence P acquisition by loblolly pine. To address this, we are designing model communities of native ECM fungi commonly associated with loblolly pine to evaluate their effect on plant P nutrition. Prior to creating the model community, 13 ECM species were assessed for mycelial growth and biomass production, as well as their respective ability to improve pine P uptake under both P-limiting and P-sufficient conditions. Our preliminary results indicate that some species exhibit positive effects on biomass under varying P conditions. These findings will help us in the selection of individual species composing our model ECM communities for further evaluation.

### Parallel Session 5-4: Translational Mycology

### Discovering the Untapped Fungal Mechanisms in Response to PFAS Chemicals to Tackle the “Forever Chemical” Issue

Charles Ayers, University of Minnesota
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Large-scale manufacturing and disposal of fluorinated chemicals have led to global pollution by per and poly-fluoroalkyl substances (PFAS), namely “forever chemicals” in nature, that will require novel remediation techniques and investigation for their environmental fates. Fungi are dominant carbon nutrient recyclers in ecosystems, while their roles in responding to and degrading these persistent fluorocarbons remain largely untapped. In our research, we systematically investigated the fungal species’ responses to PFCA chemicals and their capacities in breaking down these chemicals by using the ion-selective electrode for quantifying free fluoride anions, the 19F Nuclear Magnetic Resonance (NMR) for monitoring PFAS removals in fungal cultures, LC-MS for characterizing transformation products, RNA-seq for interrogating the potential biochem pathways in responding to PFAS. The results of cytotoxicity assays showed that taxa within a unique class of fungi that cause “white-rot” type of wood decay have developed an inherent defense mechanism for fluoride and fluorocarbon chemicals, and their cultures can remove about 60% PFAS in an aqueous solution. Despite no clear deF in legacy PFAS (e.g., PFOA and PFOS) was evidenced, our work identified the dehalogenated PFCA structures associated with an electron-attracting, alkenyl group that provokes C-F cleavage, which set off a basis for studying the C-F degradation pathways by RNA-seq and Mass Spectrum. Our research, therefore, set a foundation for further unraveling and untapping the fungal capacities to tackle with PFAS, and it also highlighted future research should give sufficient attention to resident fungal communities in impacted environments due to their potential to recycle fluorinated compounds.

### Parallel Session 5-4: Translational Mycology

### Fungi, bacteria, and biochars walk into a hydrogel bead: How biodegradable microbial-char hydrogels impact soil health and plant growth in common wheat

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Renee Davis, University of Washington
Rosemary Randall, University of Washington
Roger Chen, University of Washington
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One major reason there has been a global decline in crop yields is because agricultural soils are in dysbiosis due to decades of intensive management. In this state, community functionality is unbalanced, which can hamper healthy plant-soil feedback loops. Rhizosphere fungi and bacteria have both been studied through separate lenses regarding their potential for plant growth promotion and soil health. However, less is known about how their complex cross-kingdom interactions can be leveraged for holistic solutions. The goal of this project was to understand if bacterial-fungal hydrogel beads hold potential to be a multi-functional solution that addresses both plant and soil health. To test this, we encapsulated arbuscular mycorrhizal fungi with plant growth promoting bacteria and biochars in hydrogel beads, and applied them in a greenhouse study. Common wheat was the selected crop and soils were sourced locally. Results demonstrate that bacterial-fungal-char hydrogels can increase soil organic matter and crop yield compared to conventional fertilizers and commercial inoculum. We found that a mix of arbuscular mycorrhizal fungi paired with our bacterial consortium had significantly higher grain yield, while Rhizophagus intraradices paired with our bacterial consortium and a hardwood biochar had the highest soil organic matter accumulation. Overall, the incorporation of biochars promoted soil health and grain yield varied across combinations. Therefore, fungal-bacterial-char hydrogel beads hold potential as a soil dysbiosis treatment. Yet, there remains a lot to untangle regarding how microbial players interact with different types of biochar within the hydrogel construct, and the established soil communities that surround them.

**Parallel Session 5-4: Translational Mycology**
**Spectral Dynamics in Fungi: A Novel Biomarker for Fungal Electronics**
Michael Preston, University of California, San Diego

Decades of research have characterized the role of electrochemical signaling in neural computation and information processing in animals, yet emerging evidence suggests that fungi also rely on electrochemical signaling. The electrical activity of fungi was first reported by Slayman nearly 50 years ago, however, few advancements were made until recent interest in potential bioengineering applications reignited research in this area. Fungi exhibit electrical properties that have potential utility in the development of flexible electronics and next-generation computing systems, however, potential applications are currently limited by our understanding of how electrochemical signaling mediates information processing in fungi. Nearly all studies to date have focused on “spikes,” i.e. transient electrical impulses analogous to neural action potentials, yet these signals exhibit additional electrical dynamics that have been largely unexplored. Here, we propose a novel electrophysiological biomarker in fungi, the spectral exponent, which can advance our understanding of fungal signalling and drive innovation in bioengineering. We demonstrate for the first time that electrophysiological signals recorded from fungi exhibit power law scaling, similar to those from plants and animals. Moreover, we show that this spectral exponent is sensitive to environmental stimuli, a property that can be leveraged in the development of fungal sensors. These findings suggest that the spectral exponent may be a universal biomarker of network state across eukaryotic kingdoms and motivate further research into physiological mechanisms and potential applications.

## PARALLEL SESSION 6-1:
### Fungal Biogeography and the Spores that Make Them So

**Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So**
**A Story of Spores across Scales: How Airborne Fungi Shape Mushroom Forecasting across the United States**
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Bitty A. Roy, University of Oregon, Institute of Ecology and Evolution
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Jana M. U’Ren, Washington State University, Department of Plant Pathology
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The mushrooms produced by macrofungi are charismatic and heavily sought after by researchers and hobbyists alike. Predicting which mushroom may pop up where is an exciting prospect, yet the ecological factors controlling fungal distributions at various spatial and temporal scales remains relatively limited. Given the abundance of fungal spores in air and their ability to travel a range of distances, understanding fungal spore dispersal at multiple spatial and temporal scales is crucial. Further, the relationship between local fungal spore and mushroom presence also remains underexplored. In this study, we sampled airborne spores over two years using passive spore traps across eight ecoregions in the United States. Within each ecoregion, traps were placed in three habitats (grassland, conifer, oak), totaling 31 sites. Spores were identified using high-throughput Illumina sequencing of the ITS1 region. To explore links between spore and mushroom co-presence, mushrooms were collected at varying distances from spore traps, combining targeted surveys with iNaturalist data. We found that fungal spore communities exhibited high stochasticity across all scales, with 36.9% of macrofungal OTUs detected only once. At the continental scale, spore diversity and composition were shaped by precipitation and temperature, though site ecoregion was the strongest driver. Locally, fungal spore communities showed inconsistent associations with habitat type and burn history, with mushrooms within 20 km accounting for ~40% of fungal spores. Collectively, these findings indicate fungal spore distributions show strong continental-scale patterns and that spore presence can be linked to local mushroom production in a scale-dependent manner.

## Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So

### Does Spore Shape Predict Ecological Niches in Amanita?

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Identifying the ecological niches of fungal species presents a significant challenge. With fungal biodiversity estimated between 1.5 and 10 million species, traditional approaches to natural history are impractical. To address this, researchers infer taxonomy, biogeography, and ecological niche by analyzing phenotypes and traits. The reported correlation between spore morphology and ecological niche is specifically interesting, with hypotheses suggesting that spore features can predict dispersal dynamics and trophic modes. However, there have been limited empirical tests of these hypotheses using phylogenetically explicit frameworks. The genus Amanita presents an ideal system to test if spore features reflect dispersal dynamics or trophic modes. This globally distributed, monophyletic group includes both decomposer and ectomycorrhizal species, with a single evolutionary origin of symbiosis within it. Additionally, Amanita species exhibit diverse spore morphologies, ranging from nearly spherical to elongate shapes. In this study, we use morphometric and phylogenetic analyses to test whether spore shape correlates with ecological niche in Amanita. We hypothesize spore shape will be significantly correlated with both phylogenetic history and ecological niche. By examining over 200 species and leveraging modern phylogenetic models, we aim to identify whether spore shape variation is driven by ecological specialization or other evolutionary processes.

### Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So

### Exploring the Conservation of Asymmetric Adhesion in Colletotrichum: Implications for Spore Dispersal

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Timothy Martin, Texas A&M University Plant Pathology & Microbiology
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Fungal spore adhesion plays a crucial role in dispersal efficiency and pathogenicity, yet the conservation of adhesion mechanisms across species is poorly understood. In Colletotrichum graminicola, conidial adhesion is restricted to a single side, a trait that may enhance dispersal by ensuring that some spores do not immediately attach to their initial deposition site. To explore the evolutionary conservation of this trait, we analyzed adhesive distribution across multiple Colletotrichum species. Eight species exhibited a single-sided adhesive strip, while C. truncatum uniquely displayed bilateral adhesion. In C. graminicola, the adhesive colocalized with an actin array that formed only after detachment from the conidiogenous cell, indicating that adhesive secretion occurs at this developmental stage. These results suggest that asymmetric adhesion is an adaptive feature in Colletotrichum, with potential implications for spore dispersal efficiency, host specificity, and fungal pathogenicity.

### Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So

### Exploring the Stress Gradient Hypothesis through fungal biofilm genes across US soils

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The Stress Gradient Hypothesis establishes that positive interactions among organisms become more advantageous as environmental stress increases. In fungi, the ability to form biofilms to interact with other microbes may become an advantage under stressful conditions like warming by buffering temperatures and heat induced desiccation. If extreme heat indeed selects for biofilm formation, we expect that genes related to biofilm production will be more frequent, especially in hot and dry regions. We tested this hypothesis by analyzing organic soil metagenomes publicly available in NEON's Soil Microbe Metagenomic Sequences database. The metagenomes correspond to 20 sites present in different ecoclimatic regions across the US. We assembled the metagenomic reads into contigs and quantified the frequency of known genes related to biofilm formation in fungal models. We then tested for a positive and a negative relationship between the frequency of genes with soil temperatures and moisture, respectively. We detected biofilm genes at most sites, indicating that biofilm genes are not restricted to model fungi but are also present under field conditions. Specifically, we observed a high frequency of regulatory genes. Contrary to our hypothesis, we found a negative relationship between gene frequency and soil temperature, and no significant relationship with soil moisture. Our results preliminarily suggest that biofilm formation may not be a general fungal stress response to environmental stress, challenging the Stress Gradient Hypothesis for this particular trait. Instead, hot and dry environments might select fungal communities that rely on alternative stress response strategies other than biofilm formation.

### Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So

### Fungal Biogeography in Homes: A Global Survey of House Dust Communities

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Fungal communities in built environments significantly impact our daily lives, influencing both human health and the structural integrity of wooden buildings. While many indoor fungi are often associated with adverse health effects, they also contribute to a surprisingly diverse ecosystem, containing numerous species that can be neutral or beneficial. This study investigates the global diversity and distribution of fungi found in household dust across residential settings. By utilizing a large-scale citizen science initiative and high-throughput sequencing, our dataset includes fungal sequences from approximately 3,600 subsamples collected from 900 buildings in nearly 100 countries across all continents. Our analyses reveal key environmental factors and building characteristics that shape indoor fungal diversity and community composition. Additionally, we demonstrate how surrounding landscape features influence fungal diversity and community dynamics, as well as potential associations with residents' allergies. This extensive dataset provides new insights into the biogeography of indoor fungal communities, offering a deeper understanding of the ecological and environmental drivers shaping their distribution. Additionally, our findings offer predictions on how globalization and climate change may influence fungal communities in built environments.

### Parallel Session 6-1: Fungal Biogeography and the Spores that Make Them So

### Role and Regulation of Dispersal in an Opportunistic pathogen, Candida Albicans

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Candida albicans is a prevalent, generally commensal member of the human mycobiome carried by most people their entire lives. Simultaneously, C. albicans is a major opportunistic pathogen – in immunocompetent individuals this generally manifests in vulvovaginal (yeast infections) and cutaneous infections while in immunocompromised people, C. albicans can also cause superficial oral infections (thrush) or internal solid organ or bloodstream infections. C. albicans' pathogenesis is associated with a cycle of biofilm formation and dispersal, and its ability to invade a variety of host tissues while evading the immune system and treatment is in part due to its ability to switch between cellular states with distinct metabolic signatures, adhesins, and morphologies. Candida cell state transition has also been linked to host immune and metabolic regulation. Despite the importance of these transitions, dispersal– the process by which hyphal cells give rise to yeast-form cells is poorly understood. Contrary to previous results, we have found that dispersal from biofilms occurs as a discrete event within biofilm development coinciding with the cessation of biofilm expansion regulated by intercellular signaling. By identifying the specific mechanisms of this regulation, we hope to uncover potential targets for treatment to encourage commensalism over pathogenesis.

## PARALLEL SESSION 6-2:
## From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi

### Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi

### Changes in the Relative Abundance of Fungal Mutualists and Plant Pathogens after High Severity Wildfire Affect Seedling Growth and Coexistence in Coast Redwood Forests

<u>Caroline Daws, Outer Coast</u>
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Shifts in fire regimes are altering the composition of forests. Though there is strong evidence of shifts in microbial communities following differing fires of increasing intensity, there are gaps in our understanding of how shifts in these microbial communities may influence dynamics of plant coexistence or competition. Microbes are particularly relevant in seedling recruitment, and wildfire-induced changes in the presence of both root-associated fungal mutualists and pathogens may influence seedling growth and competitive ability in the post-fire environment. In this experiment, we studied the influence of soil microbes on seedling growth and competition to better understand possible long-term successional trajectories of forests experiencing a wildfire regime of increasing severity . Using inocula from field soils across a gradient of burn severity, we conducted a greenhouse experiment to ask how post-fire soil microbial communities impacted seedling competition dynamics between the co-dominant tree species, coast redwood (Sequoia sempervirens) and Douglas fir (Pseudotsuga menziesii). We found that high pathogen loads and reduced mycorrhizal abundance after high severity fire negatively impact seedling growth, and that these dynamics can be alleviated or exacerbated by the presence of plant neighbors. Using modern coexistence theory models of plant-soil interactions, we predict that wildfires could destabilize coexistence in coast redwood forests, favoring coast redwood after high severity fire, but favoring Douglas fir after moderate severity fire. Our study suggests that soil microbes, burn severity, and seedling neighbor dynamics are likely to interact to alter the outcome of seedling recruitment and competition.

## Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi
## Fuel Buildup Shapes Post-Fire Fungal Communities and Their Relative Importance to Subsequent Fuel Decomposition

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Forty percent of terrestrial ecosystems require recurrent fires engineered by feedbacks between fire and plant fuels. Fuel loads control fire intensity which directly alters fungi, the dominant decomposers, as well as the soil nutrients and plant communities which shape fungal communities. Changes to post-fire plant fuel production are well known to feed back to future fires, but post-fire decomposition of new fuels is poorly understood. In a longleaf pine savanna, both near and away from overstory pines, we manipulated pre-fire plot fuel loads to modify fire intensity. We then assessed how fuel load and fire intensity influenced post-fire fungal communities and their relative importance to post-fire decomposition of new fuels. Larger fuel loads, particularly beneath pines, increased heat release which reduced fungal diversity and community heterogeneity. These effects were stronger in litter than soil and strengthened with greater pre-fire fuel loads. Plant-associated pre-fire fungal taxa were replaced in dominance by fire and drought resistant fungi after fire. Greater pre-fire fuel loads slowed decomposition of new fuels during the eight months following fire, but fungal changes from fire played an inconsistent role. Fire intensity effects on soil nutrients had the most consistent effects with fungal shifts being important to post-fire decomposition at 4 and 6 months following fire. Fire effects on fungi were strong, but their importance to post-fire decomposition was temporally dynamic, illustrating the importance of considering fire-fungi-fuel feedbacks across time. These feedbacks, however, could be critical to predicting fuel buildup and it's availability for future fires.

## Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi
## Linking Microbial Resilience and Ecosystem Recovery: A Five-Year Study following a California Chaparral Wildfire

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Arik Joukhajian, University of California, Riverside
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High-severity wildfires, common in fire-adapted chaparral ecosystems, impact microbial resilience and function, shaping ecosystem recovery. Soil microbes are essential for nutrient cycling and vegetation regeneration, shaping post-fire ecosystem dynamics. To understand post-fire microbial resilience and the factors affecting their recovery, we conducted high-resolution temporal sampling of 19 time points, spanning 17 days to 5 years post-fire. We assessed impacts on microbial biomass with 16S and 18S qPCR and evaluated microbial richness and composition with Illumina MiSeq sequencing of 16S and ITS2 amplicons. Additionally, we measured vegetation regeneration and key soil variables, including pH, NO3-, NH4+, moisture content, and texture. We found that neither bacterial nor fungal communities fully recovered to pre-fire conditions. However, bacteria exhibited greater resilience than fungi, recovering richness within 4.5 years, influenced by factors such as time, vegetation richness, and soil NH4+. In contrast, fungal richness did not recover, displaying negative correlations with time, burn severity, and proximity to unburned areas, but positive associations with vegetation and soil moisture. Bacterial stability improved with higher richness and reduced dominance, while fungal stability persisted due to the dominance of resilient taxa like Pyronema, Aspergillus, and Penicillium. These results emphasize the importance of diverse bacterial communities and well-established fungi for ecosystem resilience. Moreover, both bacterial and fungal species richness positively impacted vegetation and negatively affected soil NH4+ concentrations, while NO3- levels

correlated with bacterial richness. These findings highlight the intricate connections between fire and the soil environment, emphasizing the vital roles of microbes in post-fire ecosystem recovery.

### Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi
### Litter Decomposition in Oregon Prairies Depends on fire, with Differential Responses of Saprotrophic and Pyrophilous Fungi and Unexpected Autoclave Effects

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Heather Dawson, University of Oregon
Bitty Roy, University of Oregon

Fungi contribute to ecosystem function through decomposition, aiding in nutrient cycling and soil structure. Grassland fire may suppress fire-sensitive fungi, but pyrophilous fungi can continue to provide these ecosystem functions. The relative roles of pyrophilous saprotrophs and general saprotrophic fungi in litter decomposition remains underexplored. We measured litter decomposition at 3 prairies, each with an unburned and burned section by removing litter from the site, autoclaving half, placing litter in mesh bags, and removing bags at 3 month intervals for one year for weighing. The ITS1 region of rDNA was sequenced from 3 month and 12 month litter bags. We hypothesized that 1) decomposition would be higher at the unburned sites than burned, 2) increased decomposition at unburned sites would be correlated with higher overall saprotroph diversity, with lower diversity in autoclaved samples, and 3) pyrophilous fungal diversity would be higher at burned sites, and overall higher in autoclaved samples. Saprotroph diversity was higher in unburned sites in support of our hypothesis, however, overall diversity did not affect decomposition as we expected. Across all treatments, litter decomposition was greater in burned sites. Autoclaving increased decomposition and decreased overall saprotroph diversity, but increased the diversity of pyrophilous taxa. In contrast with overall saprotroph diversity, increased diversity of pyrophilous taxa did contribute to increased decomposition. This study elucidates the effects of autoclaving litter as a control method, and the significant effects that controlled burns in grasslands can have on both litter decomposition and the fungi that contribute to it.

### Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi
### Soil Fungal Responses to Short Fire Return Intervals in Southern California's Chamise-Chaparral Ecosystems

Esbeiry Cordova-Ortiz, University of California, Riverside
Sydney Glassman, University of California, Riverside

Southern California's chaparral is a biodiversity hotspot adapted to fire-return intervals of 30–60 years. However, due to a combination of global change factors many chaparral shrublands are burning multiple times within their natural fire-return interval. Repeated burns may result in type conversion of chaparral into non-native grasslands or altered stable states with unclear consequences for soil fungal biomass, richness and community composition and the biogeochemical processes they drive. We investigate how short fire-return intervals affect microbial recovery and nutrient cycling in Riverside and Orange County's Cleveland National Forest, where three overlapping fires occurred in the past eight years. We compare fungal biomass, species richness, and community composition in single versus overlapping fire. Preliminary analyses show significantly lower fungal biomass (18S; $p < 0.04$) in overlapping burn plots compared to unburned controls, while single burn plots were not significantly different. Two years post-fire, NO3- + NO2- mg/NL levels were significantly higher ($p = 0.0048$) in single burn plots but not in overlapping areas, suggesting repeated disturbances disrupt fungal recovery and soil nutrient cycling. Using Illumina Miseq sequencing, we assess microbial biodiversity loss and hypothesize that species richness will be lower in overlapping burn areas, with distinct community composition shifts between single and multiple burns. This research contributes to understanding chaparral ecosystem resilience under increasing fire pressures. The results can inform targeted restoration strategies and wildfire management policies to mitigate ecosystem degradation, protect biodiversity, and preserve the ecological benefits of chaparral in the face of increasing wildfire risks.

### Parallel Session 6-2: From the Ashes: Post-Fire Dynamics of the Phoenicoid Fungi

### Unraveling the Traits that Enable Fungi to Thrive Post-Fire

Sydney Glassman, University of California, Riverside
Dylan Enright, University of California, Riverside
Maria Ordonez, University of California, Riverside
Ryan Quaal, University of California, Riverside
Ehsan Sari, University of California, Riverside

While severe wildfires can reduce fungal richness by up to 70%, several pyrophilous “fire-loving” fungi massively increase in abundance post-fire, but the traits enabling them to thrive post-fire are largely unknown. Over 5 years, we cultured >250 fungal isolates from burned soils and mushrooms from 7 California wildfires. We selected a subset of 20 species spanning 5 orders from Ascomycota (Eurotiales, Pleosporales, Sordariales, Coniochaetales, Pezizales) and 3 Basidiomycota (Agaricales, Holtermanniales, Geminibasidiales). We performed biophysical assays including maximum survivable temperature, hyphal extension rate and hyphal density on malt-yeast agar vs. pyrolyzed organic matter media, and nutrient cycling via greenhouse gas emissions and extracellular enzyme assays. Overall, Eurotiales favored stress-tolerant and nutrient acquisitive lifestyles possessing high thermotolerance (up to 50ºC), high hyphal density (up to 5.28mg/cm2), and strong nitrogen cycling via fungal denitrification (nitrous oxide production up to 13.23ppm N2O/day) but as a trade-off had slow hyphal extension rates (average less than 2.2mm/day). In contrast, Pezizales favored a fast-growth lifestyle with fast hyphal extension rates (up to an average of 24.8mm/day) at the expense of thermotolerance (highest 40ºC) or nutrient acquisitive traits. We also produced high quality, contiguous PacBio HiFi genomes for 18 fungi and found dramatic trade-offs between fast growth and genes involved in aromatic hydrocarbon breakdown, corroborating our findings from the biophysical assays. Further, we identified mechanisms of evolution including ancient gene duplication events, sexual recombination, and horizontal gene transfer from bacteria to fungi. Our matching genomic and biophysical assays data provides unprecented insight into pyrophilous traits across diverse fungi.

## PARALLEL SESSION 6-3:
## Frontiers in Genetics and Genomics of Fungi

### Parallel Session 6-3: Frontiers in Genetics and Genomics of Fungi

### Comparative Codon Optimization Patterns in Endophytic and Non-Endophytic Xylarialean Fungi

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Mario E.E. Franco, Sustainable Plant Protection Program, Institute of Agrifood Research and Technology
Jana M. U’Ren, Washington State University, Department of Plant Pathology

The ecologically diverse Xylariales (Sordariomycetes) occur as saprotrophs, pathogens, and endophytes in tropical, temperate, and boreal forests. Previous comparative genomic analyses identified few differences in gene content among endophytic and non-endophytic taxa, potentially due to widespread ecological generalism. However, ecological niche differentiation may also be the result of differential codon usage, which can affect translational efficiency, potentially altering phenotypes and fitness outcomes. Here, we examined patterns of codon optimization (i.e. how codon usage matches up with the genome tRNA complement) for different functional gene annotation categories across 96 endophytic (n=44) and non-endophytic (n=52) genomes using the normalized species specific tRNA adaptation index (estAI). We compared endophytes vs. non-endophytes using all 96 genomes, as well as 30 genomes representing 15 sister taxa pairs with contrasting ecological modes. The latter comparisons were performed to examine the effect of trophic mode on codon optimization while controlling for phylogeny. Across all genomes, genes involved in translation, energy production and conversion, and peptidase inhibition had the highest mean estAI values (estAI >0.70; range: 0.71-0.79; i.e., more optimized than 70% of genes in genome). Comparisons of sister taxa revealed numerous gene categories with higher mean estAI values for endophytes; however, there was considerable variation among sister pairs, and no functional categories appeared universally endophyte-optimized. GO enrichment analyses of genes with estAI ≥ 0.75 for all endophytes revealed significant enrichment in hydrolase (GO:0016787) genes compared to non-endophytes. Overall, our results suggest that codon optimization of multiple

unrelated gene families may underlie differences in xylarialean fungal ecological modes.

### Parallel Session 6-3: Frontiers in Genetics and Genomics of Fungi

### Comparative genomics and transcriptomics of the boxwood blight pathogens Calonectria henricotiae and C. pseudonaviculata reveals putative species-specific virulence genes

<u>John Dobbs, Colorado State University</u>
Nina Shishkoff, USDA, ARS, Foreign Disease-Weed Science Research Unit
Jo Anne Crouch, USDA, ARS, Foreign Disease-Weed Science Research Unit

Boxwood blight is a destructive plant disease that causes devastating losses of Buxus spp. in conducive environments within nurseries and landscapes. Two closely related fungal pathogens cause boxwood blight, Calonectria henricotiae (Che) and C. pseudonaviculata (Cps). Cps is widely distributed across Europe and Oceania and has been present in North America since 2011. Che is currently only found in Europe and the UK but could be devastating to boxwood cultivation and production if introduced into the U.S. Che is a more aggressive pathogen, with greater heat and fungicide tolerances, compared to Cps. Understanding the pathogen's biology allows for a deeper understanding of the pathogen-host interactions. We are therefore using multiple 'omics platforms to elucidate mechanisms used by each pathogen that explain the difference in virulence on its host that single technologies are unable to identify. This research project has three main objectives: 1) identify putative gene differences between Che and Cps to determine likely genes necessary for high virulence in boxwood plants; 2) identify if these virulence genes (e.g., secreted proteins, effectors, carbohydrate-active enzymes, secondary metabolite clusters, transporters, and transcription factors) are differentially expressed when inoculated in a susceptible host; and 3) determine if these differentially expressed genes are shared among the other described populations of Cps. Based on differential gene expression, we discovered species-specific secreted proteins and effectors that identified four population clusters based on putative virulence genes in Cps.

### Parallel Session 6-3: Frontiers in Genetics and Genomics of Fungi

### Determining the Individual Function and Effect of Structural Variation among the TLO Gene Family Members of Candida albicans

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Zinnat Shahina, University of Wisconsin, Madison, Center for Genomic Science Innovation
Anirudh Ventkataraman, University of Wisconsin, Madison, Center for Genomic Science Innovation
Shahed Shazib, Ohio State University, Department of Microbiology
Abigail Ali, Ohio State University, Department of Microbiology
Matthew Anderson, University of Wisconsin, Madison, Center for Genomic Science Innovation

The clinical relevance of Candida species coincides with the expansion of several gene families involved in pathogenesis, such as adhesins and aspartyl-proteases. Among the Candida species C. albicans is the most clinically important and has experienced an even greater expansion of another gene family, the telomere-associated (TLO) genes. TLOs are present as 14 paralogs broken into three architectural groups (α, β, and γ) in the genome reference strain and are functional homologs of the Med2 subunit of the yeast Mediator transcriptional regulatory complex. However, their individual molecular and biological roles in pathogenesis and adaptation remain unknown. To elucidate their individual roles, a complete TLO knockout was constructed in the genome reference strain using CRISPR-Cas9 mutagenesis. This tlo null mutant served as the platform to build a panel of single TLO addback strains. The tlo null strain showed radical changes in morphological state from wildtype in standard conditions that could be complemented by addition of any TLOα or TLOβ gene but not most TLOγ genes. Similarly, other simple phenotypes could be predicted by the architectural group of the TLO re-integrated into the genome. Interestingly, addition of a truncated TLOγ gene, TLOγ4, restored wildtype phenotypes, consistent with the TLOα and not TLOγ genes. We are currently performing transcriptional and phenotypic analysis of single TLO genes and their encoded domains to determine how individual paralog function evolved and if each gene can provide unique responses that can contribute to fitness.

## Parallel Session 6-3: Frontiers in Genetics and Genomics of Fungi

### Galactose growth in Saccharomycotina yeasts lacking the canonical GAL pathway

Emily Ubbelohde, University of Wisconsin - Madison
Marie-Claire Harrison, Vanderbilt University
Chris Todd Hittinger, University of Wisconsin, Madison
Antonis Rokas, Vanderbilt University

Galactose catabolism via the GAL (Leloir) pathway in Saccharomyces cerevisiae is a well-studied model of gene regulation, metabolic control, and evolutionary adaptation. Scientists widely recognize the GAL pathway as the only galactose catabolism pathway in S. cerevisiae and other yeasts within Saccharomycotina.  Using machine learning, we identified yeast species that metabolize galactose despite lacking GAL genes, as confirmed by functional assays. This discovery led us to ask several questions: What genes encode and regulate galactose metabolism in these species? How did this pathway evolve? Alternatively, did species possessing the GAL pathway lose this pathway? Identifying core genes involved in this pathway will lay the foundation to answer these evolutionary questions. Here, we explore the hypothesis that galactose catabolism proceeds via an oxidoreductive pathway. HPLC confirmed extracellular galactose depletion in nine species. In three species, enzymatic assays revealed NADPH-dependent activity in cells grown in galactose, with NADPH oxidation to NADP+ upon galactose addition. After performing transcriptomics, we identified a highly upregulated gene cluster in the presence of galactose, suggesting its role in an oxidoreductive pathway.  We are developing an engineering protocol for Candida duobushaemuli, a close relative of Candida auris, to elucidate the function of the discovered gene cluster. Identifying the gene cluster hypothesized to be responsible for galactose metabolism in these species lays the groundwork for functional and evolutionary analyses. Gaining insight into this newly discovered pathway provides a unique opportunity to explore potential candidates for metabolic engineering for rare sugar production and possible convergent evolution events previously undescribed.

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## Parallel Session 6-3: Frontiers in Genetics and Genomics of Fungi

### Rediscovery of the Tardigrade Pathogen Sorochytrium milnesiophthora, a Blastoclad Boasting the Longest Known rDNA Internal Transcribed Spacer

Alden Dirks, University of Michigan
Matteo Vecchi, University of Jyvaskyla
Michelle Orozco-Quime, University of Michigan
Sara Calhim, University of Jyvaskyla
Timothy James, University of Michigan

Sorochytrium milnesiophthora is a necrotrophic pathogen of tardigrades and a member of the poorly sampled zoosporic phylum Blastocladiomycota. We rediscovered S. milnesiophthora parasitizing tardigrades in cliff-side lichen samples from Finland, cultured the pathogen from infected tardigrades, sequenced its ribosomal DNA, and assembled a draft genome. Multi-locus and phylogenomic analyses placed Sorochytrium as sister to the rest of the Blastocladiales, an order that harbors the common soil fungus Allomyces and arthropod pathogens such as the mosquito-infecting Coelomomyces and ant-infecting Myrmicinosporidium. Sorochytrium milnesiophthora was found to have an extraordinarily large ribosomal internal transcribed spacer (ITS) of approximately 5500 base pairs—the largest documented for eukaryotes. We discuss the potential reasons and biological implications for such a large ITS in the context of Sorochytrium, as well as its ramifications for metabarcoding studies. Sorochytrium milnesiophthora and other zoosporic fungi confound established paradigms for what constitutes a fungus, which is largely based on study of the speciose but phylogenetically limited subkingdom Dikarya, and thus merit further exploration. Future investigations should clarify the species boundaries in Sorochytrium by comparing more strains, including from the Appalachian Mountains of North Carolina, USA, the type locale of S. milnesiophthora. Deposition of Sorochytrium milnesiophthora in the Collection of Zoosporic Eufungi at University of Michigan ensures its long-term viability and availability for future study.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World
### Developing a Strategy to Facilitate Having Fungi Included in global, regional, and National Policies and Conservation Plans and Actions

Gregory M. Mueller, Chicago Botanic Garden
Cátia Canteiro, Society for the Protection of Underground Networks

Fungi are rarely considered in global, regional, or national policies or in conservation plans and actions despite the growing recognition of their ecological and economic importance. As evidenced by the success of the Global Strategy for Plant Conservation, the potential benefit of having a unifying strategy to help guide fungal biodiversity and conservation initiatives is high. Developing a Global Strategy for Fungal Conservation that recommends actions that will facilitate including fungi in conservation policies and actions was agreed during a workshop at the International Mycological Congress (August 2024) and was presented during the Congress closing plenary session. This strategy will consist of two connected components (1) a set of recommended voluntary actions that countries, NGOs, etc., should consider implementing to benefit from including fungi in their policies and conservation actions, and (2) a suggested research agenda for the mycological and conservation communities that identifies questions and projects needed to generate the data and create the tools that countries and NGOs will need to implement the recommended actions. A draft of the Strategy has been developed by an international team of mycologists. It is now in the review/consultation stage. MSA members are encouraged to participate in this review stage – we need your input.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World
### Integrating Crowdsourced and Automated Species Identifications in a Traditional Taxonomy Activity to Teach the Scientific Method

Emily Cantonwine, Valdosta State University

While crowdsourced species identification (CSI) platforms like Mushroom Observer and iNaturalist, and automated species identification (ASI) tools like Seek by iNaturalist, have disrupted traditional dichotomous key activities—by giving novice students easy access to identifications, they also offer new opportunities to teach scientific reasoning. This poster describes an augmented activity where CSI and ASI suggestions are treated as informed hypotheses and tested using the scientific method. Students begin by using the Seek app and crowdsourced feedback to obtain preliminary taxonomic identifications for sporocarps collected in the field. In the lab, they use species descriptions to generate a set of morphological predictions that would be true if the hypothesized identifications are correct. Students then make observations, take photographs as evidence, and evaluate whether each observed trait supports or contradicts their prediction. In the final phase, regardless of whether the hypothesis was supported or not, students use their notes and photographs to work through a dichotomous key. The submitted assignment includes a table with predictions, observations, and conclusions, and the key steps selected, each annotated using student observations and photography. In 2024, all students completing the assignment in a Biodiversity of Macrofungi course exceeded the instructor's expectations. One important drawback to the full activity is it takes more time to process a single collection than the traditional approach. Links to activity instructions, templates, and examples of student work will be shared.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World

### Many hands make light work: An academic and community partnership for research, education, and outreach

Anita Davelos, University of Wisconsin, La Crosse
Adam C. Schneider, University of Wisconsin, La Crosse
Joshua Hein, Outdoor Recreation Alliance
Jacob A. S. Hansel, University of Wisconsin, La Crosse
Arthur C. Grupe, University of Wisconsin, La Crosse

Biology classrooms are natural learning environments where the next generation learns critical skillsets. Additionally, the ability to train students in field skills while contributing to long-term biological inventory projects represents a unique "double-dipping" opportunity. This allows students to learn practical skills, contribute to ongoing biological surveys, interface with local stakeholders and community organizations through community science platforms like iNaturalist.org projects, and function as peer-to-peer educators in active learning environments. The Outdoor Recreation Alliance (ORA) Community Trail Farm is a 277-acre area, located in the town of Shelby, WI, that is managed by ORA Trails, a local non-profit. The goals of this organization are to provide access to equitable and sustainable outdoor recreation with a focus on restoration and the appreciation of cultural and historical heritage. Faculty at University of Wisconsin – La Crosse (UWL) were invited to collaborate in research, educational, and outreach partnerships with ORA Trails. Three UWL Biology classes (Mycology, Plant Taxonomy, and Plant Ecology) visited the site multiple times to survey plant and fungal biodiversity. One of the results of this collaboration is a public iNaturalist project group dedicated to the plants and fungi observed at the site, which combines educational and outreach objectives. Faculty and student research has also been facilitated at ORA Trails. Long-term research areas to monitor changes in plant and fungal communities have been established, which will provide opportunities for independent and class projects, utilizing a variety of field and laboratory techniques including cutting-edge DNA techniques.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World

### Mechanics in Mycology: Cultivating Mycology-Minded Engineers

Debora Lyn Porter, University of California Merced
Alexander Bradshaw, Clark University

Fungi, one of the most biologically diverse sections of life, also exhibit an immense variability in the micro and macro morphological characteristics which define them. Such variability in morphology has led to functional characteristics that allowed Fungi to occupy nearly every biome on earth, including internal and external symbiosis with the flora and fauna found within them. The numerous morphological structures, and their subsequent unique properties, present a wealth of novel questions to pursue from an engineering perspective. Here I will discuss multiple projects that offer insight into how the study of biomechanics in Fungi can provide better understanding of the evolution of these characteristics, and how they can be harnessed for bioinspired design. One project examined the properties of filamentous fungi on multiple length scales and how we can create and test fungi-inspired network models. The second project characterized the protective role of the outer layer of melanization in rhizomorphs produced by Armillaria spp, and demonstrated improved mechanical, chemical, and structural protections compared to cultured rhizomorphs that lacked. These projects offer new insights into the many emerging applications and research avenues through the combination of mycology and engineering mechanics.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World

### Myco-Ed: Mycological Curriculum for Education and Discovery

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The fungal kingdom hosts an incredible amount of phenotypic and phylogenetic diversity, yet genomic representation for many taxa is still lacking. In a collaborative effort, mycologists from diverse institutions are developing the Mycological Curriculum for Education and Discovery (Myco-Ed) to train students in fungal biology and comparative genomics while simultaneously enriching genomic representation across the kingdom. Students in mycology classrooms across the United States isolate fungi, assay them under specific conditions and document phenotypic responses. Then, if isolates are from genera without genomic representation, students harvest tissue for sequencing. Harvested tissue is first passed to the Arizona Genomics Institute for DNA extraction and then to the Joint Genome Institute (JGI) for genome sequencing, assembly, and annotation. Using the data generated by the JGI, students conduct bioinformatic analyses to learn comparative genomic techniques. Through analysis of novel biosynthetic gene clusters, fungal mating types and more, students provide important contributions to our collective knowledge of fungal biology. Myco-Ed is designed to be modular, allowing instructors to incorporate any aspect of the curriculum that fits their teaching goals. Myco-Ed has been successfully piloted in fifteen classrooms, reaching over 300 students. As a result, students have isolated 50 fungal species for genome sequencing and the JGI has released 16 of these genomes via the JGI MycoCosm platform for the community to explore. The next step is to continue expanding the reach of Myco-Ed, covering a wider range of institutions and introducing a diverse student body to mycology and genome science.

### Parallel Session 6-4: Fungal Futures: Tools, Policy, and Education for a Changing World

### Resilience Solutions Incubators: A New Model for Community-Engaged, Transdisciplinary Learning Experiences

Abigail Granath, University of New Mexico
Jennifer Rudgers, University of New Mexico
Jose Cerrato, University of New Mexico

The Resilience Solutions Incubator (RSI) at the University of New Mexico (UNM) is a new, hands-on course model designed to engage undergraduate students in climate resilience research through transdisciplinary collaboration and community partnership. Our pilot course focused on the intersection of fungal biology and heavy metal remediation to empower early-stage students to address real-world challenges in pollution and ecosystem health. While working alongside local stakeholders, students gained practical research skills including microbiology techniques, data visualization, and effective science communication. The RSI model prioritizes ethical research practices, integrates Indigenous knowledge, and fosters “brain gain” by connecting students with meaningful regional problems to solve. Results show increased student engagement, confidence in STEM skills, and meaningful community impact. We present the structure, pedagogy, and successes of the RSI course, demonstrating how innovative education models can simultaneously cultivate climate resilience and enrich undergraduate learning experiences.

**University Lectureship**

## Modernizing Eurotiales Taxonomy: A Comprehensive Revision of Species Concepts and Reference Data

Cobus Visagie, Forestry and Agricultural Biotechnology Institute (FABI)

Eurotiales represents a diverse fungal order containing economically significant genera like Aspergillus, Penicillium, and Talaromyces. Despite recent advances in molecular-based identification methods, taxonomic inconsistencies persist, with newly described species often representing synonyms of existing taxa. Our research addresses these critical challenges through three key objectives: evaluating recent species descriptions, updating the accepted species list, and establishing a curated DNA sequence reference database. We demonstrate the necessity of transitioning to a phylogenetic species concept while retaining morphological descriptions when introducing new species. Based on our phylogenetic analyses, of the 169 species described since 2023, we accept 128 while reducing 41 to synonyms. Additionally, 17 pre-2023 species were reclassified as synonyms. The revised accepted species list now includes 1390 species across four families and 26 genera, with Aspergillus (463), Penicillium (598), and Talaromyces (236) representing the most species-rich genera. To facilitate sequence-based identifications, we present a comprehensive reference database containing 18,784 DNA sequences (ITS, BenA, CaM, and RPB2) from 5,310 strains, capturing infraspecies variation. This freely accessible database will receive continuous updates. Our work represents a significant advancement in Eurotiales taxonomy, providing researchers with reliable identification tools and a robust framework for future studies of this economically important fungal group.

# POSTER SESSION 1

**Poster Number: 1**

## A Taxonomy of Amatoxins

Heather Hallen-Adams, University of Nebraska, Lincoln
Emma Engstrom, University of Nebraska, Lincoln
Qinwen Zheng, University of Nebraska, Lincoln
Hong Luo, Kunming Institute of Botany

Amatoxins – responsible for an estimated 90% of fatal mushroom poisonings in humans worldwide – are small peptides produced by certain mushrooms in four unrelated genera: Amanita, Galerina, Lepiota, and Conocybe (Pholiotina). Over the past twenty years we have learned much about amatoxin biosynthesis: the centrality of a ribosomally-encoded proprotein precursor ("MSDIN" – named for the first five precursor amino acids in Amanita), a designated prolyl-oligopeptidase which clips the active region free from the precursor and cyclizes it, a flavin monooxygenase and cytochrome P450 that contribute to post-translational modification. In Galerina, MSDINs only produce α- (and γ-)amanitin, and are tightly clustered (within 105 kb) with the other known biosynthetic genes. Amatoxin-producing Lepiota isolates have MSDINs for α-amanitin and from one to five additional peptides, and the biosynthetic machinery is spread out over several Mb. Amatoxin-producing Amanita isolates can have 40 or more MSDINs, including those for α- and β-amanitin, phalloidin and phallacidin, and the biosynthetic genes may span 30 Mb. Evidence for horizontal gene transfer of amatoxin biosynthetic genes (as opposed by ancestral presence and multiple losses, or multiple de novo derivations) is strong. We have recently sequenced Conocybe filaris and C. apala, and are in the process of fitting them into the bigger picture of amatoxin evolution and distribution.

**Poster Number: 2**

## Multiple grasses adjacent to cornfields in Central Illinois serve as alternative hosts of Phyllachora maydis

Eric Johnson, USDA ARS
Patrick Dowd, USDA ARS

A recently published scientific paper described experiments that found that the largest group of the tar spot pathogen, Phyllachora maydis, in the Americas was detected in corn and other grasses. These results suggest that grasses close to cornfields could possibly host the tar spot pathogen and spread it to adjacent corn. In a two-year study, we collected grass leaves with black spots in early spring through late summer, both overwintered and green ones, that were laying on the ground or growing adjacent to corn fields in Central Illinois. Field observations and laboratory analyses indicated, for the first time, that reed canary grass, a common weed, was a frequent host for the strain of tar spot pathogen that usually infects corn in the U.S. prior to and throughout the growing season. The tar spot pathogen was also occasionally detected in other collected grasses, for the first time, including brome grass, tall fescue, and green bristle (green foxtail) grass. These findings expand the known host range of the tar spot pathogen in the U.S and indicate that crop management practices for tar spot disease should consider that tar spot infected weedy grasses close to cornfields may act as disease sources to corn and be the source of initial infections that then spread through the cornfield.

**Poster Number: 3**

## Characterization of the Rust Pathogen Affecting Canna indica in Sri Lanka

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Sharanya Wijayakulasooriya, Sri Lanka Institute of Information Technology
Helmi Gammanpila, Sri Lanka Institute of Information Technology
Dimuthu Manamgoda, University of Sri Jayewardenepura, Sri Lanka

Canna indica, a widely cultivated ornamental plant in Sri Lanka is currently under threat by a rust pathogen which is morphologically identified as a Puccinia sp. However, molecular characterization of this rust pathogen is not available from Sri Lankan collections previously, leading to the accurate identification of the pathogen being unresolved. Therefore, this study aimed to resolve the identity of the pathogen based on fresh collection, morphology, and molecular data. Leaf samples infected with rust were collected from 50 different localities, and fungal DNA was extracted from urediniospores using commercially available Plant Genomic DNA Extraction Kit. Pathogen detection was confirmed via PCR amplification that was performed targeting the 28S rRNA gene using the rust-specific primers Rust28SF and LR5 followed by Agarose gel electrophoresis, which confirmed the successful amplification of the fungus. Ongoing comparative analyses with existing sequences and related taxonomical data will clarify species-level classification, which will address the discrepancies between morphological and molecular identifications. This study emphasizes the importance of integrating molecular characterization along with morphological analysis to improve accuracy in the identification of plant pathogens facilitating disease management.

**Poster Number: 4**

### Coffee phylloplane mycobiomes present an opportunity to better understand establishment of Hemileia vastatrix

Samira Fatemi, Synergistic Hawaii Agriculture Council
Charles Mason, USDA
Melissa Johnson, USDA

The rust fungus Hemileia vastatrix (Berk. & Broome) is a devastating pathogen of coffee. Economic losses due to the spread of coffee leaf rust, the disease caused by H. vastatrix, are estimated to be $1 to 2 billion annually. Despite its agricultural importance, much remains unknown about the biology and ecology of H. vastatrix. Further, the impact of phylloplane communities on the establishment of H. vastatrix on coffee leaves is not known. In this work, we seek to understand the influence of phylloplane mycobiomes on H. vastatrix. We present both greenhouse and field sampling strategies to investigate the differences in H. vastatrix establishment between different cultivars. We also explore community shifts associated with infection by H. vastatrix. We expect to see similarities in community composition across cultivars, but observable differences associated with infection status. Due to the complexity of rust fungal lifecycles, understanding the impact of mycobiomes on the ability of H. vastatrix to establish on plants can help uncover new paths of study regarding its biology. The results from this work can also be leveraged to help combat fungal plant pathogens while minimizing inputs that are environmentally and economically costly. This is especially important, since about 95% of global coffee production originates from small, family-owned operations.

**Poster Number: 5**

### Genetically Distinct Populations of the Potato Black Dot pathogen, Colletotrichum coccodes, Are Resistant to Fungicides with Multiple Modes of Action

Riley Eisenbraun, Fungal Ecology Lab
Matt Maughan, CSS Farms
Peter Mullin, Department of Plant Pathology
Erin Sayer, Department of Biochemistry
Teddy Garcia-Aroca, Department of Plant Pathology

Colletotrichum coccodes is the pathogen responsible for Black Dot and Tuber Blemish on potato. While this pathogen has been known for a while, information concerning its within-species genetic diversity in the Midwestern United States is limited. We evaluated the genetic variation within C. coccodes collected in the region and compared fungicide resistance/sensitivity among genetically distinct groups. We collected potatoes exhibiting symptoms of Black Dot and Tuber Blemish and isolated pure cultures of Colletotrichum-like fungi. Isolates (n=40) were subjected to Sanger sequencing for the GAPDH gene and compared with publicly available sequences of type cultures in Maximum likelihood (ML) and bootstrap support (BS) phylogenetic analyses. We confirmed all our isolates were C. coccodes and identified four genetically distinct within-species groups, potentially representing different Vegetative Compatibility Groups (VCGs). Representative isolates of each group were tested in vitro against different concentrations of fungicides in amended media. One population was resistant to a multi-site fungicide containing prothioconazole, trifloxystrobin, and fluopyram and another showed increased resistance to a single-site fungicide containing flutriafol. These resistant populations appear more closely related compared to the other two populations, as indicated by the phylogenetic analyses. The different active ingredients and modes of action indicate that the underlying genetic diversity could have been influenced by selection pressures from these fungicides. This study represents the first attempt to document fungicide resistance among genetically distinct C. coccodes populations in the Midwest. Further research may reveal genetic differences responsible for fungicide resistance in these groups.

### Poster Number: 6

### Sensing, Germinating, and Disseminating: Determining the Triggers of Cryptococcus Spore-Mediated Infection

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Megan McKeon, University of Wisconsin, Madison
Christina Hull, University of Wisconsin, Madison

Cryptococcus is an environmental yeast capable of causing fatal meningitis in humans. Cryptococcus causes disease from inhalation and then disseminates from the lungs to the brain via poorly understood mechanisms. To cause disease Cryptococcus must germinate from a spore into a replicating yeast. In cryptococcal infections germination occurs early, but the kinetics of this process and their effect on dissemination and disease are unknown. We aim to understand how both spore characteristics and germination environment impact germination kinetics and dissemination in mammalian disease. To understand Cryptococcus germination in vitro we developed a high throughput, quantitative germination assay (QGA) that has facilitated the characterization of germination under diverse conditions. Previous work showed that spores germinate synchronously in response to glucose over ~12 hours in vitro. In vivo, little is known about how germination is triggered or what kinetics occur. To address germination in a lung environment, we are developing a germination medium for QGAs from mouse lung homogenates. Preliminary data show that spores germinate in lung homogenates, but with differing kinetics and frequency of replication compared to rich growth media. Simultaneously, we are using a mouse model of intranasal infection to determine germination timing in vivo and rate of dissemination. Both approaches will facilitate studies of the germination kinetics and early dissemination capacity of various Cryptococcus strains and mutants. Studying the characteristics of early infection in physiologically relevant environments promises to inform our understanding of early events in Cryptococcus infection and will provide insights into how spores mediate fatal cryptococcal disease.

### Poster Number: 7

### Habitat fragmentation alters the spatial distribution of Lycoperdon marginatum fruiting bodies

Eva Schwarz, University of Minnesota, Twin Cities
Thomas Smith, University of Wisconsin, Madison

Habitat loss and fragmentation are among the most pressing threats to global biodiversity today, with remaining species relegated to smaller patches of habitat that are increasingly more isolated and with high edge-area ratios. Yet, while plant and animal responses to habitat fragmentation are well documented, it is not well understood how such changes impact fungi. Most existing studies of fragmentation effects on fungi focus on pathogenic or mycorrhizal species, cases in which fragmentation effects on fungi are hard to separate from those on their hosts. To better understand how fragmentation affects fungal populations directly, we surveyed abundance of fruiting bodies of Lycoperdon marginatum, a free-living, saprotrophic fungus, in a landscape-scale habitat fragmentation experiment that independently tests for edge effects due to increased patch edge-area ratio and effects of increased patch isolation. We address the following questions: 1. At what scale, if at all, does L. marginatum fruiting body abundance respond to habitat edges? 2. Does habitat connectivity impact L. marginatum fruiting body abundance? We found that increased patch edge relative to patch area had a negative effect on fruiting body abundance, but distance from edge had no effect. Surprisingly, patch connectivity had a negative effect on fruiting body abundance, potentially through indirect effects of connectivity on biotic and abiotic conditions potentially influencing puffball success. These contrasting results suggest that free-living fungi populations can have unexpected responses to different fragmentation processes and may help explain how both fungi and associated plant and animal communities may respond under increasing habitat fragmentation.

### Poster Number: 8
### We Need More Shrooms! (collected)

Brian Deis, Kapiolani Community College
Riley Hermosura, Kapiolani Community College
Alexandra Mercado, Kapiolani Community College
Luke Amerine, Kapiolani Community College

Our knowledge of plants, animals, and natural history in Hawaii (and worldwide) by far surpasses our knowledge of fungal species. An example of this comes from our concept of Native and Exotic species in Hawai'i. While we are readily able to apply these terms to groups of plants and animals, there is still some discussion as to what constitutes a native fungal species. The reasons for this are multifaceted, include: lack of baseline data to compare with contemporary data, Hawai'i, geographic isolation leading to rare a specialized species, and the possible influx of fungal species due to human activity, particularly in the past 160 years. These factors lead to a blurring in distinction of what evolved here and what could have been introduced as early as the first Polynesian settlers. Despite these challenges, since Fall 2022, Students at KCC have been involved with collection and identifying mushrooms collected around Oahu, HI. As of now the "KCC fungi lab" has identified over ~130 different species of fungi. In this project we compare these ~130 species to the species that are in the Bishop Museum's (the main natural history museum for the Hawaiian Islands) Fungi collection in order to gain insights on the natural history of fungi here. Our goals are to better understand the history of our knowledge of fungi, to highlight areas of future research on Hawaiian fungal biodiversity, and provide educational opportunities for students and the community.

### Poster Number: 9
### A phylogenetic analysis of sporocarp longevity and alternate life history strategies in Polypore mushrooms

Gayathri Venkatraman, University of Michigan
Timothy James, University of Michigan

The use of polymorphic phenotypic traits in Agaricomycetes to understand the processes that maintain and generate diversity of macrofungal fruiting bodies has largely remained underexplored. Colour variation is one potential trait that could be used for this purpose since colour polymorphisms arise as discrete and distinct phenotypes within a population due to underlying genetic variation in a species. However, another driver of chromatic variation could be polyphenism, wherein colour morphs of a species arise due to environmental conditions rather than genetic variation (i.e., identical genotypes). Mushroom-forming fungi produce a diversity of colours across the known species but the functional, ecological and genetic basis of colouration is still unknown. The hardwood decay fungus, Trametes versicolor (aka "Turkey Tail"), which exhibits concentric coloured ring patterns on its fruiting body with a wide range of colours, is a suitable species for investigating the causes of fungal colouration and for the decoupling of colour polymorphism and polyphenism. Here, I ask whether colour in various morphs of T. versicolor is linked to the decaying wood substrate on which they grow? To address this, I have collected and cultured wild Turkey Tails of various colours and banding patterns and have grown these on common wood substrates (such as cherry and oak) in a common garden experiment.

### Poster Number: 10
### Additional Genome Sequencing and Population Analyses of Canadian Synchytrium endobioticum, the Causal Agent of Potato Wart Disease.

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Ekaterina Ponomareva, Agriculture and Agri-Food Canada
Jeremy Dettman, Agriculture and Agri-Food Canada
Jiacheng Chuan, Canadian Food Inspection Agency
Xiang Li, Canadian Food Inspection Agency
Melissa Antoun, Canadian Food Inspection Agency
Bart van de Vossenberg, Netherlands Institute for Vectors, Invasive plants and Plant health

Synchytrium endobioticum is an obligate chytrid responsible for potato wart disease and is considered an important quarantine pathogen in many countries. Building on our previous genome studies from almost 10 years ago, we present our current work focusing on improving the genome of S. endobioticum. Using Illumina, we sequenced, assembled, and annotated the genomes of 10 Canadian S. endobioticum strains (3 from Newfoundland and 7 from Prince Edward Island) of pathotypes 6 and 8. This time we employed a different filtering method to discard contaminating sequences via a curated database and a more sophisticated genome annotation method. Orthologous grouping of single-copy genes and alignment-free k-mer methodologies, as well as genome population analyses will be explored to detect the subtle genomic differences between Canadian strains, and assess whether those differences are meaningful for pathotype identity and detection. In addition, we are testing target enrichment and Illumina sequencing of S. endobioticum DNA from single cells to improve our understanding of the pathogen's population structure. Our genomic work might contribute to more precise pathotype identification and better-informed disease management strategies.

**Poster Number: 11**

### Rising Threat of Candida Auris Incidence and Multi-Drug Resistance at the University of Maryland Medical System

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Nicole Putnam, University of Maryland, Baltimore
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Mary Ann Jabra-Rizk, University of Maryland, Baltimore

Candida auris is a fungal pathogen associated with life-threatening invasive disease with mortality rates of up to 60%. C. auris has been rapidly emerging to become a global risk and was declared an urgent health threat by the CDC due to its high level of transmissibility and multi-drug resistance. In this study, we aimed to identify current trends of incidences of C. auris infections and antifungal resistance within the University of Maryland Medical System over the course of a five-year surveillance period (2019-2024). A total of 26 isolates from 21 patients were recovered and phenotypically evaluated for their ability to aggregate and form biofilms, two important virulence factors, and antifungal susceptibility testing was performed. Amplification of the ITS and RHA1 genes identified 21 of the 22 isolates as belonging to clade 1 and 1 isolate to clade 3. Phenotypic analysis demonstrated wide intra-clade variation among the isolates in ability to aggregate and form biofilms, and antifungal susceptibility testing demonstrated high level of drug resistance. One clinical case was prospectively sampled over a one year period and multiple isolates recovered during the course of antifungal therapy. Where the first isolate recovered from the patient was susceptible to antifungals, the last isolate was resistant to all 3 classes of antifungals suggesting evolution of drug resistance development during therapy. Results from this study indicate a rising threat of C. auris warranting accurate monitoring for establishing effective protocols for controlling this serious pathogen.

**Poster Number: 12**

### Mojave Desert Tortoise (Gopherus agassizii) and associated soil microbiomes in California

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Brian Henen, U.S. Marine Corps Air Ground Task Force Training Command

Gopherus agassizii (Mojave Desert Tortoise) populations are challenged by habitat modification, human disturbance, and microbial pathogenesis. Yet, we do not understand the diversity and composition of microbes living on desert tortoises, or within their digestive tract. We sampled wild and captive G. agassizzi to characterize their gut and surface microbial diversity and composition, and how these factors relate to individual animal health. We extracted DNA from desert tortoise feces, soil samples, and swabs collected from tortoise oral cavities, plastrons, and forelimbs. We opportunistically collected fecal samples, and nearby soil samples, from tortoises that defecated during health assessments. We sequenced amplicons of the 16S rRNA gene and fungal ITS2 region and compared host microbiomes to soil communities within their' landscapes. We characterized microbial groups in host-associated and environmental microbiomes and found that they differed between sites or environmental sources, and were ostensibly influenced by diet. The composition of gut mycobiomes in wild animals were more similar to paired soil samples collected nearby than they were to the fungal gut mycobiomes in captive animals; however, this pattern was not detected in bacterial communities from these same animals. There was a small core microbiome shared across all tortoises, which was distinct from fungal consortia in nearby cryptogamic crust and soil communities. Findings from this study will help provide valuable information about tortoise microbiomes and the ecological resilience of these tortoise populations.

## Poster Number: 13

## Exploring the Impact of Climatic Stress on Ectomycorrhizal Colonization of Pseudotsuga Menziesii

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Abigail Neat, Oregon State University
Andrew Jones, Oregon State University
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Conifer trees associate with ectomycorrhizal fungi, a symbiont that enhances water and nutrient uptake in exchange for carbon allocation. This relationship can be expensive for the plant hostand is known to be largely influenced by abiotic pressures. We hypothesize that as climatestress increases, so will ectomycorrhizal colonization rates of Douglas fir seedlings. We believe this is because plants are more likely to invest in mutual symbioses in resource limited environments, consistent with the stress gradient feedback hypothesis. To address this hypothesis, Douglas fir seeds were collected from six sites spanning a 3000ft elevation gradient located in the Western Oregon Cascades Mountain Range. Over 1,100 of the seedlings were germinated under identical greenhouse conditions. Seedlings from each elevation source were then inoculated with either high or low elevation soil microbes. After one year, the seedlings were harvested, and microscopy was used to visually score and quantify root colonization rates.Each seedling has paired physiological data, including stomatal conductance, budburst timing and dry weight. This research aims to test the hypothesis that mycorrhizal recruitment increases with the level of abiotic stress in the environment where seedling populations originated.Commented [PB1]: author listCommented [PB2R1]: Andy too?

## Poster Number: 14

## A Proposed Evolutionary Origin of Pigmentation in Trichocoma paradoxa

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Fungi in the order Eurotiales are recognized for their ability to produce a wide variety of secondary metabolites. The genes that encode for a secondary metabolite are typically organized physically adjacent to one another as a biosynthetic gene cluster (BGC). BGCs encode for a number of products, such as antibiotics (e.g., penicillin), toxins (e.g., ergot alkaloids), and a diversity of pigments (e.g., melanin and azaphilone). The aim of this research is to identify the BGCs that encode for pigments in Trichocoma paradoxa and other members of the order Eurotiales. Whole genome assemblies of eleven related Eurotiales taxa, including T. paradoxa and species of Aspergillus, Byssochlamys, Elaphomyces, Monascus, Penicillium, and Talaromyces  were mined using antiSMASH and verified by identification of homologous proteins. Our results show that T. paradoxa has all of the required core pathway genes needed to produce the classical yellow, orange, and red Monascus azaphilone pigments (MonAzPs). We also show that there have been independent losses of the Monascus azaphilone BGC, or MonAzPs-type compounds, in the Eurotiales clade, but the ancestor to all Eurotiales taxa was likely able to produce azaphilone related pigments. Understanding the evolution and diversity of pigment encoding BGCs, and the species that produce them, will not only support future commercial applications, but will also enhance the broader understanding of Eurotialian taxa.

## Poster Number: 15

## Pathogenicity of Fusarium Spp. on Cereals Originating from Grape Vines in the Midwestern United States

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Grapevine trunk diseases can be caused by more than one organism or a complex of organisms. Prevalence of individual trunk diseases vary across geographic regions and with host plant age. Grapevine decline is a trunk disease caused by complexes of phytopathogenic fungi. It has been recently reported in young vines in Pacific states and is considered an emerging disease of mature vines in upper Midwest states. Casual organisms in the state of Iowa have been determined to belong to Fusarium spp. Origins of these fusaria and overlap of their populations with forage and cereal pathogens is unclear at this time. Here we describe the results of a pathogenicity screen of these isolates on cereal crops.

### Poster Number: 16

## A Cultivator-Inspired Approach Links Fungal Wood Rot-Types to Microbial Communities and Carbon Fates

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Collin Adams, University of Minnesota
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Fungi dominate decomposition of deadwood, with white rot-type species removing more lignin than brown rot-type species to gain access to carbohydrates. These fungi often compete to colonise the same substrate and a small shift in either rot type's success could have massive greenhouse gas implications. We need to know what controls white vs brown rot outcomes, starting with field studies that track fungi and the fate of wood lignin. Such experiments, however, have had skewed, white-rot-only outcomes and have lacked representation of bacteria that compete for wood sugars. To address this, we pre-inoculated small-diameter birch stem sections with a brown rot fungus, Fomitopsis betulina, and compared these to non-inoculated birch. We confirmed that our experimental design could reduce noise in field data and encourage binary brown vs white rot outcomes that were apparent in wood physiochemistry. We also observed a clear link between rot type and fungal dominance but found neither a parallel bacterial codominance nor co-occurrence patterns between fungi and bacteria. As expected, fungal richness was higher and Shannon index was lower in brown-rotted than in white-rotted wood, but surprisingly, we found a higher Shannon index for bacteria in brown-rotted wood. Bacterial beta diversity, too, was different between brown- and white-rotted wood. This fungal influence on bacterial diversity may be due to increased niche space for bacteria when brown rot fungi dominate. Collectively, these findings demonstrate that controlling fungal inoculum potential (and thus dominance) can illuminate connections between fungal rot-type, success of associated microbes, and the flow of carbon.

### Poster Number: 17

## Resolving Cystobasidiomycetes (Pucciniomycotina)

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Cystobasidiomycetes are dimorphic basidiomycetes, producing both a sexual filamentous morph and an asexual yeast-like morph. The filamentous morphs are mycoparasitic or mycophilic while the yeast morphs are considered saprobic and can be isolated from a wide variety of habitats and substrates. For example, the genus Cystobasidium parasitizes coprophilous ascomycetes in the filamentous phase, while the yeast-like morph exhibits adaptations to tolerate osmotic, cold, and heat stress, allowing colonization of environments ranging from marine to arctic to desert. The majority of Cystobasidiomycetes species are poorly characterized and known from only one morph. This is partly due to the ease of isolating and culturing the yeast morph, contrasted with the lack of an easily observed filamentous morph for most genera. Furthermore, misidentifications and misannotations of numerous publicly available sequences generated from this class can lead to erroneous taxonomic conclusions. To date, a robust phylogenetic hypothesis has not been achieved and many genera and families remain classified as incertae sedis. To construct a more robust phylogeny for Cystobasidiomycetes, we isolated and sequenced hundreds of strains, curated publicly available sequences, and included data from type strains for each of the 19 Cystobasidiomycetes genera. We then applied 7-loci analyses with our curated data to provide a robust phylogenetic hypothesis and revision of the class. Additionally, we compiled physiological data for all species from published and newly generated data. Finally, we provided comprehensive illustrations of both sexual and asexual morphs for all major genera, providing a foundation for future studies on Cystobasidiomycetes.

### Poster Number: 18

### Substrate-Dependent Degradation as an Outcome of Mycelial Interaction between Two Fungal Organisms with Distinctive Wood Decay Modes

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It is critical to understand fungal activities, such as lignocellulose degradation, when various fungal species coexist on the same natural woody substrate, both from an ecological perspective and for their potential applications in biomass conversion.
This study investigated the interactions between white-rot fungi (WRF) and brown-rot fungi (BRF) in controlled co-cultures, focusing on the effect of interspecies interaction on the decomposition of birch and cornstalk substrates. Twelve species pairings were assessed, and a model co-culture of Fomes fomentarius (WRF) and Fomitopsis betulina (BRF) was selected for in-depth analysis based on their balanced competitive abilities and their shared natural association with birchwood. Using solid-state culturing, the research quantified fungal degradation over five and ten-week periods by evaluating mass loss, solubilization rates, and compositional and structural changes. Results revealed that co-culturing significantly enhanced the degradation of cornstalks, with a 42% increase in mass loss and a 61% rise in solubilization compared to monocultures. However, the interaction on birch had an additive effect with no significant differences between co-cultures and monocultures regarding mass loss or solubilization. Compositional and structural analysis revealed significant modifications in lignocellulose composition, particularly for cornstalk, where fungal interactions led to increased degradation of lignin, glucan, and xylan and reduced cellulose crystallinity. Despite these improvements in degradation, saccharification efficiency did not show consistent gains, indicating the complexity of fungal pretreatment effects. These findings emphasize the substrate-dependent nature of fungal interactions and suggest that while fungal co-cultures can enhance biomass degradation, the impact on digestibility and saccharification is not always straightforward.

### Poster Number: 19

### Cryptococcus spores can germinate in the near absence of oxygen

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Christina Hull, University of Wisconsin, Madison

Cryptococcus spores must germinate into yeast to cause disease in mammalian hosts. Because Cryptococcus is a non-fermentative, obligate aerobe in its yeast growth state, we anticipated that hypoxic conditions would prevent oxidative phosphorylation and block germination. However, we discovered that it is possible for a subset of Cryptococcus spores to germinate in the near-absence of oxygen, revealing an apparent conflict between the need for ETC activity during germination and the lack of need for oxygen at the same time. To determine the role of the ETC in germination, we tested inhibitors of ETC complexes and conducted a transcriptomic analysis of spores germinating hypoxically. Our data suggest that a second electron transport pathway that uses part of the canonical ETC in conjunction with an alternative oxidase (AOX1) acts during hypoxic germination. Future experiments will determine the mechanisms of AOX1 function in the ETC of germinating Cryptococcus spores.

### Poster Number: 20

### Haplotype-Phased Genome of Hemileia vastatrix, the Causal Agent of Coffee Leaf Rust Epidemics

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Nicholas Greatens, SCINet Program and ARS AI Center of Excellence, Office of National Programs, Agricultural Research Service, United States Department of Agriculture
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Coffee is the most widely traded tropical product with production dominated by smallholder farms in developing countries. Despite increases in coffee consumption worldwide, its production is threatened by coffee leaf rust (CLR), its most important disease due to its severity and global distribution. CLR is caused by the rust fungus Hemileia vastatrix (Pucciniales). A complete genome of H. vastatrix is crucial for the development of resistant coffee varieties and targeted disease management, as it allows for the identification of virulence factors and better understanding of population dynamics. Our

work seeks to generate a haplotype-phased whole genome assembly and annotation of H. vastatrix using a Hawaiian isolate. The haplotypes are of similar size, at 690 and 684 Mb but are highly divergent. The genome will be analyzed alongside RADSeq data for contemporary and historical CLR isolates collected worldwide from coffee growing regions, including sampling from the Lake Victoria region, where CLR was first observed on wild coffee plants. A complete genome for this pathogen allows the development of sensitive molecular markers to trace the movement of individual CLR genotypes and understand how climatic and management variables select for individual rust races. Additionally, it will allow for the characterization of pathogenicity genes, eventually aiding in more effective disease management strategies, ultimately minimizing disease outbreaks and improving crop resilience.

**Poster Number: 21**

### Transcriptomic analysis of Xylaria necrophora infection in soybean and cotton

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Xylaria necrophora is an emerging fungal pathogen in the southern United States that causes taproot decline (TRD) of soybeans and is capable of infecting cotton roots. The pathogen gains access to the host through the rhizosphere and likely translocates cytotoxic secondary metabolites to the leaves, causing interveinal chlorosis and necrosis of leaf tissue. Characterizing molecular interactions between the host and pathogen and identifying the genes X. necrophora expresses during infection is critical for developing effective management strategies. This study employs transcriptomic analyses of naturally and experimentally infected plants to elucidate the infection mechanisms used by X. necrophora and the corresponding defense responses from the host. Field samples were collected from both infected and asymptomatic soybean roots and leaves. Soybean and cotton seedlings were also grown in the lab in soil containing varying concentrations of inoculum to simulate early infection. RNA sequencing was performed on root and leaf tissue collected from these experiments to identify fungal genes associated with infection and plant genes associated with defense. Differential expression analysis will be conducted to examine transcriptional changes in response to infection and functional enrichment analysis will be used to identify key biological pathways activated in roots and leaves. Tissue-specific expression analysis will explore the distinct responses in roots and leaves of infected plants, providing evidence for the translocation of secondary metabolites from roots to leaves. These analyses provide insights into the molecular interactions between X. necrophora and its hosts, advancing our understanding of the pathosystem.

**Poster Number: 22**

### Antifungal interactions of Basidiobolus: type specimens & isolates from recreational zones in Massachusetts

Lauren Parry, Clark University
Ava Orofino, Clark University
Javier Tabima, Clark University

The genus Basidiobolus, commonly recognized as an amphibian gastrointestinal commensal and environmental saprobe, can shift to pathogenic behavior in response to environmental or host changes. In humans, Basidiobolus infections are difficult to diagnose due to nonspecific symptoms. Management of infection is hindered by the reliance on nonspecific, conventional antifungals with varying efficacy. This project examines current response patterns of Basidiobolus to conventional antifungals using type specimens and isolates from a pond used for recreation in Worcester, MA. Three antifungals were tested, Amphotericin B, Itraconazole, and Fluconazole based on previous use in treatment of Basidiobolus infections. Each isolate was tested independently on antifungal amended PDA media while growth rate was measured over a 12 day period. Results indicate growth rate in Amphotericin B amended cultures is not significantly different from the control (PDA), including concentrations exceeded minimum inhibitory concentrations (MIC). Conversely, growth in both Itraconazole & Fluconazole was significantly slower than the control. As resistance to Amphotericin B is uncommon, ongoing transcriptional assays aim to determine mechanisms behind this pattern. Basidiobolus presents a new perspective on antifungal resistance and opens research into treatment strategies for emerging fungal pathogens.

**Poster Number: 23**

### A systematic study of coralloid Thelephora from North America reveals nine new species

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Thelephora is a species-rich and understudied genus of ectomycorrhizal basidiomycete fungi. Fruiting body morphology across the genus is strikingly diverse, with species that variously form corticioid, coralloid, rosette, and vase-shaped fruiting bodies. Despite these broad differences in macromorphology, Thelephora species possess limited micromorphological features which makes them difficult to distinguish based on morphology alone. There has been limited taxonomic work on North American species over the last century, and most described species lack representative sequence data. Seven coralloid Thelephora species have traditionally been recognized in North America: four described from the U.S. and three from Europe, each described over a century ago. Ecological studies estimate the true number of Thelephora species far exceeds what is named and suggest that many North American species are distinct from European species. We constructed a phylogeny containing 357 ITS sequences to determine how many coralloid Thelephora species occur in North America and whether those species are distributed beyond the continent. We also used morphological analysis of specimens to match clades to described species. Our phylogeny shows coralloid Thelephora are polyphyletic, comprising 16 species-level clades, nine of which represent novel taxa. At least one species forms both coralloid and corticioid morphologies. This work is a first step towards identifying the multitude of undescribed Thelephora species in North America.

**Poster Number: 24**

### Modeling the geographic distribution of Cantharellus formosus under various climate change scenarios

Travis Zalesky, University of Arizona

Maximum entropy, presence-only, species distribution modeling of the current and future distribution of Cantharellus formosus in North America is modeled under a range of climate change scenarios. C. formosus is a culturally and economically important ectomycorrhizal Basidiomycetes mushroom species which is highly prized by foragers for its gourmet flavor and texture. It is symbiotic with Pseudotsuga menziesii (Douglas Fir) and widespread along the US W. Coast, particularly in heavily forested areas of Washington and Oregon, west of the Cascades. C. formosus has been observed as far south as Berkeley, California, and as far north as S. Alaska, as well as in limited areas of the N. Rockies, near the Canada - Idaho border. Using 663 research-grade, crowed-sourced presence observations obtained from the Global Biodiversity Information Facility and 23 ecological variables, the ecological-niche and species distribution of C. formosus was modeled across N. America using a “maximum entropy”, machine learning algorithm. Further, the future distribution of C. formosus was forecast using a range of climate projections, out to the year 2100. Projections indicate that while highly suitable habitat is likely to decline between 7% to 93%, particularly in Oregon, and Washington, suitable habitat is projected to increase and generally exhibit a northerly migration. Importantly, due to the ecology and symbiotic nature of C. formosus, while loss of habitat may occur relatively quickly under changing climatic conditions, establishment and/or expansion into new habitat is likely to be much slower by comparison.

**Poster Number: 26**

### From Glomalin to Glomalose: Unraveling the Molecular Identity of the MAb32B11 Antigen

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Glomalin is a substance found in soil, produced by arbuscular mycorrhizal fungi. In recent decades, it has gained significant attention due to its well-documented benefits for plant and soil health, including water retention, soil aggregation, and long-term carbon sequestration. Traditionally, glomalin quantification has been conducted using the Enzyme-Linked Immunosorbent Assay (ELISA) method with a monoclonal antibody known as MAb32B11, which was developed against crushed spores of the fungus Rhizophagus irregularis. This antibody was previously published to target a Heat-Shock Protein 60 (RiHSP60). We reexamined the molecular nature of the antigen that MAb32B11 recognizes. Contrary to earlier reports, we found that MAb32B11 did not cross-react with the RiHSP60 polypeptide. Furthermore, spore and hyphal extracts of R. irregularis, when autoclaved, displayed strong and dose-dependent cross-reactivity with MAb32B11, even when protein levels were undetectable, raising questions about whether the antigen is proteinaceous. We determined that treating soil extracts with protease did not affect the ELISA signal. However, when we treated the extracts with periodate, which degrades polysaccharides, the signal was significantly reduced. Our findings indicate that MAb32B11 recognizes a carbohydrate that likely originates from the cell walls of arbuscular mycorrhizal fungi, rather than a protein. Additionally, an analysis of glomalin extracts from R. irregularis spores and hyphae using size exclusion chromatography and fractionation suggests that the epitope recognized by MAb32B11 is a complex carbohydrate in the size range of 511-600 kDa. Understanding the true nature of glomalin will enhance our ability to quantify it accurately and leverage its agricultural benefits.

**Poster Number: 28**

### Survey and Characterization of Heat-Resistant Fungi in the Cave Ecosystems of Puerto Rico

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Heat-resistant fungi, capable of surviving temperatures exceeding 70°C, are traditionally recognized as contaminants in food preservation. However, these fungi also produce thermostable enzymes with applications in industrial processes and bioremediation. These organisms have been documented in diverse environments, including karst caves, where elevated temperatures result from geomorphological features, metabolic heat from bat populations, and guano decomposition. This study aims to isolate and identify heat-resistant fungi with bioprospecting potential from three caves in Puerto Rico: Cueva Matos and Cueva Culebrones in Arecibo, and Cueva Tuna in Cabo Rojo. Ten random soil samples were collected from each cave using sterile protocols. For spore isolation, 10g of each sample was suspended in 90 mL of sterile distilled water, agitated at 200 rpm for 30 minutes, and subjected to thermal treatments at 25°C, 75°C, and 90°C. The processed samples were cultured on Czapek-Dox agar supplemented with gentamicin and chloramphenicol, and resulting colonies were characterized macroscopically and microscopically. This research represents the first systematic survey of heat-resistant fungi in Puerto Rican caves, contributing to our understanding of fungal diversity in these unique ecosystems.

**Poster Number: 29**

### Enhancing Biodiversity Research through Development of an Innovative DNA Sequencing Technique

Luke Amerine, University of Hawaii
Brian Deis, University of Hawaii
Nhu Nguyen, University of Hawaii

Preserved specimens are an invaluable tool to address the gap between what is described and what is unknown in fungal biodiversity studies. DNA barcoding is the standard for identifying specimens, but preserved specimens are often too degraded to produce useful data for species delineation. Traditional methods (Sanger sequencing) frequently fail in their analyses of these specimens due to their inability to amplify degraded DNA. Additionally, the cost of traditional sequencing is often prohibitive. I propose a technique that targets shorter DNA fragments within a gene, followed by modern bioinformatics to assemble the entire segment. This method will implement a PCR-based high-throughput sequencing approach that simultaneously targets and amplifies multiple, shorter fragments of the internal transcribed spacer (ITS) region, a crucial genetic marker for species identification in mycological studies. The project will have two phases: method development and implementation. I will begin by testing primer pairs across the entire ITS region, including but not limited to ITS1F, ITS2, ITS5.8fun, and ITS4. Using these primers in various combinations, the ITS region will be amplified from individual fungarium specimens collected across O‘ahu. Upon successful amplification, samples will undergo multiplex sequencing on the Illumina platform. The resulting data will be demultiplexed, assembled, and compared to Sanger sequence data to gauge efficacy. If successful, this method will greatly increase sequencing success and reduce costs by an order of magnitude.

**Poster Number: 30**

### Insights into symbiosis of a fast-growing ectomycorrhizal Amanita: Amanita persicina

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Maria Higuita-Aguirre, North Carolina State University
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Summi Dutta, North Carolina State University
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Amanita persicina (formerly Amanita muscaria var. persicina) is a native species of the southeastern U.S. Amanita is a prominent genus of fungi containing well documented, cosmopolitan ectomycorrhizal species. Despite their prevalence, research on Amanita is challenging in part due to slow culturing time. Understanding the relatively quick growth of A. persicina may give insight into the role of related species in the southeastern U.S. and beyond. Various experiments were conducted on a local A. persicina isolate in order to better understand its biology in symbiotic and axenic conditions. Media optimization for plate and liquid culture was done in order to determine if certain nutrient markers contributed to desired culturing traits. Standard Modified Melin-Norkrans medium produced ample biomass and hyphal radius, though no significant differences in growth were observed between media types or when altering the C:N ratio. Co-culture experiments with loblolly pine (Pinus taeda) and southern red oak (Quercus falcata) were done to confirm the ability of A. persicina to associate with local prevalent tree species. A. persicina colonized both species, though neither increased root or shoot biomass significantly. Alongside culturing experiments, samples of axenic A. persicina cultures were sent for sequencing to help elucidate symbiosis-associated genes.

**Poster Number: 31**

### Deeply Rooted Switchgrass Extends the Habitat of Arbuscular Mycorrhizal Fungi Deep into the Soil Profile

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Kyungjin Min, Seoul National University
Di Liang, Lawrence Livermore National Laboratory
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Megan Kan, Lawrence Livermore National Laboratory
Edith Lai, Lawrence Livermore National Laboratory
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Erin Nuccio, Lawrence Livermore National Laboratory

Arbuscular mycorrhizal (AM) fungi are ancient symbionts that form root associations with most plants. However, our understanding of AM fungal physiology and ecology is largely based on studies conducted in surface soils less than 20 cm deep. In a national-scale field study, we explored the vertical distribution of AM fungal communities by collecting rhizosphere and background soil samples from deep-rooted switchgrass (Panicum virgatum) and adjacent shallow-rooted annual crop plots. Replicate soil cores exceeding 2 meters in depth were obtained at eight sites in the eastern United States (TX, MS, NC, NY, MI, WI, IL, SD). Using WANDA/AML2 primers, we compared the impact of deep vs. shallow-rooted plants on AM fungal communities. Additionally, three mock communities with nine AM fungal taxa were characterized to optimize the annotation of AM fungi associated with switchgrass and annual crops. Our results demonstrate that AM fungal communities are impacted by the rooting depth of their host plant, with switchgrass fostering deeper AM fungal habitats along its roots compared to annual crops. We observed higher abundance and diversity of AM fungi on switchgrass than annual crops throughout the root zone. Notably, Glomerales were more abundant in deeper soil layers along the roots of switchgrass but not in annual crops. These findings suggest the role that plants may play in shaping the vertical distribution of AM fungal communities throughout the root zone. By facilitating the downward movement of AM fungi, deep root systems may extend the influence of these fungi to subsoil carbon cycling and weathering processes.

### Poster Number: 32

## Using fungal herbarium specimens to unlock historical records of genetic and ecological diversity of macrofungi in a biodiversity hotspot of southern Arizona, USA

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Neda Arad, University of Arizona
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Betsy Arnold, University of Arizona

Fungi shape every ecosystem, from wild forests and grasslands to the agricultural systems on which humans depend. From tiny molds to yeasts, bracket fungi, and mushrooms, fungi are ecologically diverse, together encompassing a wide range of pathogenic, symbiotic, and saprotrophic modes. Macrofungi (fungi with macroscopic fruiting bodies) encompass ectomycorrhizal, decomposer, and pathogenic life histories, influencing ecosystem services by impacting plant health and nutrient cycling. However, we know little about factors influencing the ecological distributions or biodiversity of macrofungi, including in biodiversity hotspots such as the southwestern USA. We used a combination of field inventories of macrofungi, historical records in the Gilbertson Mycological Herbarium, iNaturalist records, and DNA sequencing of fungi occurring cryptically as symbionts of fresh plant material to identify communities of fungi in the Santa Rita Mountains and Santa Rita Experimental Range. We place these fungi in a comparative framework to propose how fungal communities in this area have shifted in biodiversity and fruiting time over the past 125 years. Our results reveal strong patterns of phylogenetic diversity, highlight taxa not previously observed in the region, and indicate that some macrofungi occur cryptically in plant roots without forming mycorrhizal affiliations. Such syntheses of data streams are essential for the next steps in biodiversity informatics, key to understanding diversity of fungi and other organisms in our changing world. In turn, newly archived fungal collections expand the biodiversity resources that, through preservation in herbaria, serve future research needs in areas such as phenology, ecology, systematics, and taxonomy of fungi.

### Poster Number: 33

## Ectomycorrhizal fungal gene expression linked to nitrogen decomposition rates and reduced bacterial nitrification

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Hui-Ling Liao, University of Florida
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While soil microbes play central roles in nutrient cycling, it remains unclear how the activities of different fungal and bacterial functional groups, and associations between functional groups, are related to soil nutrient cycling rates. Ectomycorrhizal fungi (EMF), a dominant microbial group in temperate forests, may impact nitrogen (N) cycling through their enzymatic and N-uptake activity, as well as through competition for N with other microbes. We tested the hypothesis that microbial communities dominated by EMF will have higher nitrogen (N)-decomposition activity, with a corresponding increase in net ammonification rates, and decreases in bacterial nitrification activity and net nitrification rates. At six sites across Massachusetts, USA that varied in forest stand composition, we assessed fungal and bacterial community composition (via high-throughput sequencing of 16S and ITS2 rDNA amplicons) and gene expression (through sequencing both the poly(A) enriched and ribo-zero rRNA depleted metatranscriptome) and soil biogeochemical cycling rates. In support of our hypothesis, as EMF relative abundance and EMF N-cycling gene expression increased, net ammonification increased, while net nitrification and the relative abundance of copiotrophic bacteria, especially nitrifying bacteria, decreased. N-decomposition gene expression by copiotrophic bacteria also increased. These findings suggest competition between EMF and copiotrophic bacteria for ammonium, causing a metabolic shift away from nitrification, a reduction in soil nitrification rates, and an increase in soil ammonification rates.

### Poster Number: 34

### Local Variation in Endophytic and Epiphytic Fungi of Arctic Cryptogams

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Brooke Sykes, University of Arizona
Taylor Cavallaro, Stanford University
Jozef Geml, Eszterházy Károly Catholic University, Hungary
Jolanta Miadlikowska, Duke University
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A. Elizabeth Arnold, University of Arizona

Mosses and lichens are key components of Arctic tundra biota and form symbioses with diverse microorganisms, including many lineages of fungi. Compared to vascular plants, they host greater species richness and phylogenetic diversity of fungal endophytes, but the scope of variation in these communities is not well studied at local scales. We examined how endophytic and epiphytic fungi associated with representative mosses and lichens vary at a local scale with regard in soil structure and associated permafrost dynamics. Fresh collections of Cladonia sp. (lichen) and Racomitrium sp. (moss) were made in three locations near Iqaluit, Nunavut, Canada at the height of the growing season in 2023. We sampled both host taxa in nine plots overall, including three sites that each featured areas with silty soil, bedrock, and mixed soils. Endophyte detection was done via culturing and culture-free sequencing for all samples. Epiphytes were detected in culture and isolated by morphotype for a subset of samples. We found that fungi were highly diverse and varied markedly in diversity and composition between mosses and lichens. Trends showed that fungal communities differed in richness, composition, and taxonomy among soil types. We discuss this finding in the context of broader characterization of these fungal symbionts in rapidly changing northern ecosystems.

### Poster Number: 35

### Novel Amanita species from the Guiana Shield

Casey Ledford, Cal Poly Humboldt
Terry Henkel, Cal Poly Humboldt

While species of the ectomycorrhizal (ECM) genus Amanita (Amanitaceae, Agaricales) are well described from temperate and boreal latitudes, relatively few species of Amanita are currently known from the tropics. Collecting expeditions to South America's Guiana Shield have yielded > 30 distinct morphospecies of Amanita from forests dominated by ECM trees of the genus Dicymbe (Fabaceae subfam. Detarioideae). Eleven of these species have been previously described, and the remainder await formal description. Here we highlight four novel species of Amanita that are among the most frequently encountered in Guyana's Dicymbe forests. Morphological and habitat descriptions will be provided, along with a molecular phylogenetic analysis suggesting infra-generic placement of the new species.

### Poster Number: 36

### Survey of Fungal Symbionts between a Hosts' Native and Introduced Range Reveals Strong Environmental Influence on Host-Associated Fungal Communities Regardless of Provenance

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Grace Perdue, Oregon State University
Fletcher Halliday, Oregon State University

Human-induced changes in the climate, including rising temperatures, and increased movement of species beyond their native range impact plant health and productivity. Given fungal symbionts affect host health, predicting how plant health and productivity will respond to increasing temperatures and host range expansions might also require an understanding of how these factors affect fungal microbial communities. We surveyed disease symptoms, cultured fungal symbionts, and collected tissue from Dactylis glomerata along a 900 m elevation gradient in the Wallowa Mountains of Eastern Oregon where it was introduced in the 1800s and a 1100 m gradient in the Swiss Alps where D. glomerata is native. We hypothesized that fungal symbiont diversity and disease symptoms would be lower in the introduced range. Additionally, we hypothesized that environmental filtering along the elevation gradient would be weaker for fungal symbionts in the introduced range as symbionts that escape a large biogeographical dispersal filter or colonize a novel host would be ubiquitous. Consistent with our first hypothesis, we observed 81.3% lower disease severity (i.e. percent of leaf area infected) and 53.8% lower disease prevalence (proportion of individuals infected) on average in the introduced range. Similarly, we recovered 88.4% fewer fungal symbionts through culturing in Oregon compared to Switzerland. Increasing elevation also negatively affected both

disease severity (p value = 0.0307) and prevalence (p value = 8.33e-6) regardless of the host density or provenance. Future studies will investigate how host responses to environmental stresses influence symbiont colonization and within host interactions.

**Poster Number: 37**

### Genomic analysis of Dendrothele nivosa, a bark-inhabiting crust fungus with host-specificity and an enigmatic ecological role

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Michelle Jusino, USDA Forest Service, Northern Research Station, Center for Forest Mycology Research
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Basidiomycete fungi in the genus Dendrothele are known for their large basidia and their association with living trees. However, since the revelation in 2003 that the genus was polyphyletic the phylogenetic placement and ecological significance of many of its species remains poorly understood. Here, we used Illumina short-read technology to generate a high-quality genome assembly of the understudied species Dendrothele nivosa, whose taxonomic placement has shifted between orders and families since the 19th century and whose ecology is not well understood. Our D. nivosa genome is 71Mb with 130,076 contigs and an estimated BUSCO completeness of 97.5%. Using publicly-available genomes, we built phylogenies and undertook analyses targeting gene function and transposable element dynamics. The quantity of carbohydrate-active enzymes in our assembly suggests D. nivosa may function as a wood-decay fungus, despite its association with the bark of living Juniperus trees. In contrast to other related basidiomycetes, nearly half of the D. nivosa genome consists of transposable elements (TEs) due to a massive invasion of long terminal repeat (LTR) retrotransposons, suggesting that TEs have played an important role in shaping Dendrothele evolution. Our phylogenetic evidence suggests D. nivosa requires the creation of a new genus and potentially a new family in Russulales, as D. nivosa represents a distinct clade separate from the nearest two families, Stereaceae and Bondarzewiaceae. Overall, we have generated more robust genomic data and analyses for Dendrothele nivosa, clarified its position in the Russulales, and gained insight into its ecological niche.

**Poster Number: 38**

### Unveiling the biodiversity of Amanita in Wisconsin and the Upper Peninsula

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Corbin T. Bryan, University of Wisconsin, Madison
Anne Pringle, University of Wisconsin, Madison

As the Earth undergoes rapid global shifts both from a changing climate and an increasingly interconnected human transport system, biodiversity is shifting and being lost. Conservation efforts aim to mitigate these changes; however, many organisms have effectively been left out of conservation thought. Historic perceptions of the kingdom of fungi have contributed to their neglect in this field. Most of the kingdom of fungi is undiscovered, making it extraordinarily challenging to even begin to preserve them, and baseline biodiversity data are needed to inform fungal conservation efforts. My research aims to address this issue within the genus Amanita in Wisconsin and the Upper Peninsula (UP). Through extensive field collections, morphological descriptions, and genetic sequencing, I will elucidate the presence, distributions, and taxonomic organization of Amanita species in Wisconsin and the UP. Thus far, 40 specimens have been collected representing 5 of the 11 sections of the genus. Of these specimens, 4 are potential novel species and at least 23 are a part of species complexes, giving us the opportunity to bring much needed clarity to each complex. Future work will entail collecting from underrepresented sections, additional phylogenetic analysis, and creating species descriptions for our newly organized taxa. The collected data will be published, submitted to NCBI, and built into an online monograph useful to both mycologists and the public as a Wisconsin and UP Amanita field guide, bringing us one humble step closer to gaining a holistic understanding of fungal biodiversity and informing our conservation strategies.

**Poster Number: 39**

### The CA FunDiS Project: Exploring Fungal Diversity in the Golden State

Warren Cardimona, Fungal Diversity Survey
Christian Schwarz, Fungal Diversity Survey
Harte Singer, Fungal Diversity Survey
Laura Morgan, Fungal Diversity Survey

California's diverse ecosystems harbor immense fungal diversity, much of which has been greatly underexplored—until recently. The California Fungal Diversity Survey (CA FunDiS) is a robust community science initiative aiming to elucidate fungal diversity in the state through field documentation and taxonomic study, and to build an extensive repository of fungal DNA barcodes and preserved specimens. All collections and sequences are publicly databased, each with images and detailed field notes. Over the last two years CA FunDiS has procured, sequenced, and archived over ten thousand fungal collections across the state, generating invaluable biogeographic, ecological and taxonomic data. We have made a special effort to fill critical knowledge gaps, particularly in obscure and under-collected groups of fungi, and in historically understudied Californian habitats. Our findings include newly documented species, range extensions, and insights into fungal-plant associations. This poster highlights significant advancements and discoveries we've made, emphasizing the benefit of large-scale fungal surveys and community engagement.

**Poster Number: 40**

### Evaluating the Relationship between Ectomycorrhizal Fungal Diversity and Trophic Status in Two North American Pyroloids

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Taylor Bright, University of California, Davis
Andrew Wilson, Denver Botanic Gardens

Mycoheterotrophic plants rely on fungi for sustenance. Previous works have shown that mycoheterotrophic plants exhibit a gradient of reliance on mycorrhizal fungi - from autotrophy, to partial mycoheterotrophy, to full mycoheterotrophy. Within the Pyroleae subfamily, all plants engage in some form of mycoheterotrophy. Previous studies document high fungal diversity associated with partially mycoheterotrophic plants. What is less understood is how fungal diversity in mycoheterotrophic plants is impacted by trophic status, nutrient requirements during flowering and fruiting, or if these factors shape recruitment of mycorrhizal fungi. This proposal investigates the fungal communities of two Pyroloids (Ericaceae), Pyrola asarifolia and Chimaphila umbellata across a wide geographic range in North America. Both require fungi to germinate (=initially mycoheterotrophic). At maturity, P. asarifolia is partially mycoheterotrophic, while C. umbellata is autotrophic. Roots of both plants, along with soil, were sampled from plots established in California, Colorado, and Minnesota to determine fungal associates. Root and soil samples were collected multiple times during the growing season to examine variation in fungal diversity in relation to flowering and fruiting time. Soils were sampled to survey which fungi might have been available to the Pyroloids. Using a 2-step metabarcoding process, fungal nrITS2 data was sequenced from root and soil samples. A total of 4,233 fungal MOTUs were observed in the study. Additional results of this study, including variation in fungal guilds, taxonomic diversity and evaluations of beta diversity between plants and sites will shed light on the factors that influence fungal diversity in mycoheterotrophic plants.

**Poster Number: 41**

### Biomass Production from Cigarette Filter Degradation Mediated by Fungi and Bacteria

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Cigarette filters are a major source of solid waste, and although the cellulose acetate structure degrades in relatively short periods of time (i.e., 15 years), they retain harmful substances like pesticides, neonicotinoids, heavy metals, and other hazardous compounds, which are released into the ecosystems. While various methods have been tried to recycle cigarette filters, biological treatments hold promise for detoxifying them in a cost-effective way. In this study, cigarette filters were used as substrates for inoculating commercial fungi, with the goal of generating useful biomass. Filters were pretreated with sodium hydroxide to promote deacetylation and fungal growth and compared with untreated filters. At the same time, the leachate from the deacetylation process was tested as a liquid medium for fungi and bacteria to avoid toxic byproducts. Structural changes in the filters were analyzed using ATR-FTIR, while heavy metals were measured using ICP-OES. Mycelial expansion and biomass production were analyzed using ImageJ and mass changes. The results showed that microorganisms can grow on discarded cigarette filters, though at slower rates compared to regular substrates. Deacetylation concentrated metals and slowed fungal growth, but additional nutrients helped recovery. The leachate with added sugars showed microbial growth, serving as an effective culture medium for the consortium. The microorganisms removed nearly 55% of the chemical oxygen demand in the leachate, demonstrating that biological detoxification can overpass physicochemical methods. The cumulative results of these experiments shows that cigarette filters can be incorporated into substrates and be reused for biomaterials that won’t be in contact with food.

### Poster Number: 42

### Three Genus of Trichoderma, Penicillium, and Cladosporium Positively Affected Festuca Sinensis Keng by Changing Its Genes Expression of Hormone Signal transdution, photosynthesis, and Mapk Signaling Pathway

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The endophytic fungi of Trichoderma, Cladosporium and Penicillium are the most studied groups of root fungus in recent years because of their ability to promote plant growth. However, their function of different genera on the same plant growth and the molecular mechanisms are poorly understood.  In this study, integrative analyses of plant phenotype, soil enzyme activity, and metabolomics and transcriptomics were studied using treated forage with endophytic fungus fermentation broth of Trichoderma, Cladosporium, and Penicillium. Firstly, the three genera of endophytic fungal strains were respectively screened from 16 strains; their effects of growth promoting were Trichoderma of 121> Cladosporium of 78 > Penicillium of 167, these tendency were coincided with the evolutionary relationship of these strains. Secondly, the most abundant metabolic pathways in forage roots was Ta121 (29), followed by Pe167 (19), and Cp78 (14). Thirdly, there were differences in the number of regulated DEGs among the three strains following treatment, the trend was as follows: Ta121 (10752) > Cp78 (664) > Pe167 (400), and the pathway showing significant enrichment varied across the different strains. Finally, the combined analysis revealed that a total of 368 DEGs, 6 core metabolites, and 7 transcription factors (TFs) were associated with the regulation of Ta121; while there are only 36 and 28 DEGs for both Cp78 and Pe167 respectively, and both only had one core metabolite, and also no transcription factors were involved in the regulation. There are greatly different molecular mechanisms among three fungi of Trichoderma, Penicillium and Cladosporium to plant.

### Poster Number: 43

### Effect of Two Trichoderma Strains on Juglans Neotropica Germination and Growth.

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Juliana González-Tobón, Boyce Thompson Institute
Fermín Rada, Universidad de Los Andes
Pedro Jiménez, Universidad Militar Nueva Granada (previous affiliation)

Juglans neotropica Diels., the only walnut species in Colombia, Ecuador, Peru, and Venezuela, holds cultural and ecological significance. Despite its importance, research on its seed propagation in Colombia is limited, particularly regarding challenges such as dormancy and field adaptation. This study evaluates the effects of inoculating J. neotropica seeds and seedlings with Trichoderma koningiopsis Samuels, Carm. Suárez & H.C. Evans Th003 and T. harzianum Rifai OBTh55 under greenhouse conditions.  Height was measured once a month over five months, and the photosynthetic rate, fresh and dry weights were determined five months after inoculation. From the fourth month until the end of the experiment, seedlings inoculated with T. harzianum and T. koningiopsis were up to 3.5 cm taller than the control (p-value = 0.00057 and 0.000729). Seedlings inoculated with T. koningiopsis had leaf fresh weight 3.8 g higher than the control (p-value = 0.049), and seedlings inoculated with each Trichoderma strain or the consortium had between

50% and 80% higher total dry weight (p-value = 0.018). Inoculation with T. harzianum before sowing, T. koningiopsis after sowing, and the consortium before and after sowing increased photosynthetic rate up to 139% in seedlings compared with the control (p-value = 0.00132). These results suggest that T. koningiopsis and T. harzianum individually inoculated altered photosynthetic parameters and stem, leaf, and total fresh and dry weight. Our results are helpful for local propagators to enhance J. neotropica growth in nurseries and to strengthen efforts to recover populations of this species.

### Poster Number: 44

### The Mycological Society of America, Student and Postdoc Section Welcomes You to Msa 2025 in Madison, Wisconsin

Xiomy Pinchi Davila, University of Georgia
Diana Vargas-Hernandez, North Dakota State University
Nandin Ganjoloo, University of Minnesota
Quinn Moon, University of Michigan
Isabelle Stiver, Oregon State University
Prasanth Prakash Prabhu, Clark University
Christopher Bivins, University of California-Merced
Lindsey Becker, Oregon State University

We are a student and postdoc led group within MSA, that aims to (1) facilitate communication among students of all levels and postdocs of MSA, (2) provide opportunities for SPS to network with other individuals in their own research fields and beyond, and (3) connect SPS members with career mycologists. For this year's annual meeting in Madison, the SPS will organize "Mycologists & Musings," a series of informal coffee half-hour meetings with mycological role models. This informal setup will help students learn about the professional journey of their heroes! We will also organize a career luncheon. Finally, SPS members are welcome to join us at the annual MSA SPS meeting and at our annual MSA SPS social. Throughout the 2024-2025 year, we held the "Latinxs en Micologia", provided $1190 in scholarships to 25 students and 8 postdocs that covered their society membership fee, held a writing workshop, a women in science panel, an art contest and a photo contest. Our monthly newsletters serve as a way to communicate our events and important deadlines to all MSA students, including reminders for abstracts, award submissions, and student spotlights. The SPS is an open and inclusive group which welcomes all graduate students, postdoctoral researchers, and faculty participation. We hope you can join us at our future events!

### Poster Number: 45

### Unraveling the Microbial and Viral Associations in Phragmites Australis dieback: Insights from Root and Leaf Transcriptomics

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Casey Butler, Louisiana State University
Jonathan Richards, Louisiana State University
Madison Flasco, Louisiana State University
Vinson Doyle, Louisiana State University

The dieback phenomenon affecting Phragmites australis populations in the Mississippi River Delta has raised ecological and economic concerns. While environmental stressors such as salinity incursions and insect herbivory have been implicated, the role of microbial and viral communities in this decline remains unclear. This study integrates transcriptomic data from P. australis roots and leaves to investigate the plant's associated viral and fungal communities, assessing their potential contributions to dieback. Through a combination of RNA-sequencing and bioinformatics, we have identified viral and fungal sequences within P. australis transcriptomes, constructing a database of putative viral and fungal taxa. Preliminary analyses reveal a diverse virome, with Kinglevirus, Andihavirus, and Megavirus among the most abundant taxa. Additionally, our investigation of fungal communities highlights a high abundance of mycorrhizal fungi, such as Rhizophagus, alongside plant-associated genera like Fusarium and Penicillium. While viruses are not expected to be the primary drivers of dieback, their presence alongside known fungal pathogens suggests complex interactions that may influence plant health. We will follow-up with a functional characterization of the microbial community to understand their contribution or response to dieback. Our findings will provide new insights into the microbial ecology of P. australis and lay the groundwork for further studies on the role of biotic stressors in plant decline. This research will contribute to a broader understanding of plant-microbe-virus interactions and may inform future conservation and management strategies for P. australis in affected regions.

### Poster Number: 46

### Exploring the Hidden Diversity of Rust Species (Pucciniales) in Central America: Systematics of Crossopsora and Crossopsorella

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M. CATHERINE AIME, Purdue University

Rust fungi are a diverse and ecologically significant group of plant pathogens, yet their species richness in Central America, one of the world's biodiversity hotspots, remains poorly characterized. Species in the genus Crossopsora (Crossopsoraceae) produce hair-like telial columns and are distinguished from other genera that produce similar telia by the presence of subcuticular spermogonia that lack paraphyses and caeoma-type aecia. Crossopsora species have been reported from a wide variety of hosts. A recent study showed that Crossospsora byrosonimae, which infects Bryosonima species (Malphigiaceae) was not congeneric with Crossopsora and the new genus Crossopsorella (Raveneliaceae) was erected to accommodate this taxon. However, the other Crossopsora species infecting Malphigiaceae have not been evaluated. The current study seeks to monograph Crossopsora and Crossopsorella from Central America, with emphasis on Crossopsora species on Malphigiaceae. All available herbarium specimens will be examined and sequenced at three loci—the large ribosomal subunit (28S), small ribosomal subunit (18S), and cytochrome c oxidase III (CO3)—which have been previously shown to provide good resolution in Pucciniales. Results will contribute to a more robust understanding of rust fungal phylogeny and biodiversity in Central America.

### Poster Number: 47

### Designing Tools to Engineer Symbiosis Between Trees and Fungi

Anna Johnson, Stanford University

This study proposes genetic tools to harness the symbiotic relationship between trees and ectomycorrhizal (EcM) fungi. By engineering this symbiosis, we aim to enhance resource exchanges, develop bioremediation strategies, and provide a toolkit for researchers to further investigate the molecular mechanisms driving this relationship. Specifically, we focus on the integration of synthetic biology techniques to modify the roots of a hybrid poplar species (Populus tremula x Populus alba) and utilize genetic logic gates to control gene expression at the root-fungal interface with its EcM symbiont, Laccaria bicolor. Our protocol facilitates the study of molecular interactions in this EcM symbiosis, providing a genetic toolkit to address key questions in the field, such as which mechanisms are involved in nutrient exchange and how environmental changes affect this process. This research not only contributes to a deeper understanding of fundamental biological processes but also serves as a biotechnological framework for developing innovative, nature-based solutions to environmental challenges. By elucidating and influencing these symbiotic mechanisms, we aim to enhance resource exchange between trees and fungi and create scalable bioremediation tools. Ultimately, our work provides a novel genetic toolkit to understand better understand this complex symbiosis.

### Poster Number: 48

### Machine Learning vs. Linear Regression in Messy Datasets: Insights into Cottonwood Mycorrhizal Symbioses

Beatrice Bock, Northern Arizona University
Nicholas McKay, Northern Arizona University
Nancy Johnson, Northern Arizona University
Catherine Gehring, Northern Arizona University

Ecological datasets often contain many statistical hurdles—high amounts of noise, non-normal distributions, and nonindependent covariates. In addition, there is an ever-growing awareness of the issues that over-reliance on significant p-values has created in our field. Machine Learning (ML) offers an alternative approach to linear regression modeling, allowing us to analyze messy datasets without the strict assumptions that regression requires. In this study, we present results from a greenhouse experiment where we grew different cottonwood crosstypes alongside the invasive species Tamarix sp. and exposed the pairings to drought. We analyze the data using both linear regression and ML, using this experiment as a case study to explore how ML can reveal ecological patterns that traditional statistical methods may miss. By comparing these approaches, we highlight both the advantages and limitations of ML in ecological research and discuss when and where ML may serve as a useful complement to traditional statistical methods.

### Poster Number: 49

### FoTeRs: A Novel Family of Telomere-Integrated Transposons in Fusarium Oxysporum

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Mostafa Rahnama, Tennessee Tech University

Fusarium oxysporum is a diverse species complex infecting a wide range of crops. The stability of its telomeric and subtelomeric regions varies among species, shaping genomic plasticity and adaptation. Here, we investigate the dynamics of Fusarium oxysporum Telomeric Retrotransposons (FoTeRs), a novel family of non-LTR retrotransposons that integrate into telomeric repeats, across nine species. Comparative analysis reveals that F. oxysporum f. sp. cubense strain II5 harbors the longest FoTeRs, potentially contributing to genome stability and prolonged host interactions. In contrast, F. oxysporum f. sp. lycopersici race 3 exhibits the shortest FoTeRs, possibly promoting recombination and rapid adaptation. Strawberry-infecting isolates (F. oxysporum f. sp. fragariae, including strains MAFF727510, BRIP62122, GL1080, GL1315, and GL1381) display intermediate and more conserved FoTeR lengths, suggesting an optimized genomic architecture for stable host interactions. Genetic evidence indicates that FoTeRs drive telomere instability, positioning them as key regulators of chromosome dynamics. This study identifies a new family of telomere-targeted transposons in Fusarium species, offering insights into genome dynamics and evolutionary mechanisms.

### Poster Number: 51

### Symbiosis-driven diversification: bacterial endosymbiosis defines the evolution and life history traits of Gigasporaceae (Glomeromycotina)

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Among arbuscular mycorrhizal fungi (AMF), species of family Gigasporaceae uniquely harbor the obligate intracellular bacterium, Candidatus Glomeribacter gigasporarum (CaGg), a beneficial mutualist. We sought to explore the exclusivity of CaGg symbiosis and its impact on the evolutionary history of Gigasporaceae to determine whether CaGg symbiosis is tightly linked to diversification in the family, as seen in analogous insect symbionts. We also sought to examine whether CaGg symbiosis might be linked to morphological and life history traits in Gigasporaceae that are unique among AMF. Through a comprehensive 28S rDNA phylogenetic analysis encompassing 146 AMF species, we generated a time-calibrated phylogeny and evaluated diversification effects with RevBayes using BiSSE models.
Results show Gigasporaceae’s significantly higher diversification rates compared to other AMF, driven by decreased extinction and especially increased character transition rates. CaGg symbiosis appears to be a key innovation at the crown of Gigasporaceae, granting enhanced fitness and competitive advantage without ecological niche expansion, in contrast to similar insect symbionts. This points to a potential role of CaGg in fostering Gigasporaceae’s success in stable, competitive environments. CaGg symbiosis shows a strong correlation with unique Gigasporaceae morphological and life history traits and vice versa, suggesting bidirectional influence (i.e. co-diversification). These findings improve our understanding of AMF-endobacteria co-diversification and the broader evolutionary impact of microbial endosymbionts, offering a model for symbiosis-driven evolution in fungi.

### Poster Number: 52

### Evaluating bacterial fungal interactions and environmental factors contributing to extracellular polymeric substance production in co-culture and soil systems

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Extracellular polymeric substances (EPS), secreted by soil microbes, are increasingly recognized for their role in microbial resilience and soil function, particularly under drought stress. We investigated the ecological and environmental drivers of EPS production through two complementary studies. In the first, co-cultures of soil bacteria and fungi were used to assess how bacterial fungal interactions influence soluble EPS composition. Results showed that EPS production was primarily driven by bacteria but modulated by fungi, with certain pairings significantly enhancing protein and polysaccharide production. In the second study, a soil mesocosm experiment was conducted using four Hawaiʻi soils with distinct mineralogy, subject to drought and replete moisture regimes. Using mesh core systems to selectively exclude plant roots and arbuscular mycorrhizal fungi (AMF), we evaluated the effects of moisture, plant-AMF-microbe interactions, and soil biogeochemistry on EPS production. Surprisingly, we found that drought and exclusion treatments had limited influence; instead, EPS quantity and composition varied strongly across soils. These results suggest that legacy effects of soil biogeochemistry and long-term environmental fluctuation, rather than short-term drought, shape EPS production. We also highlight key limitations in the current soil EPS extraction method and argue the need for improved protocols that more comprehensively and consistently represent EPS across soils. Together, these results contribute to a broader understanding of bacterial fungal interactions and their potential in supporting agriculture in shifting climates.

**Poster Number: 53**

### Genomic and Ecological Diversity of Aspergillus Spoilage Molds in Artisan Cheese Production

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Filamentous fungi play important roles in the development of surface-ripened cheese microbial communities, shaping both aesthetics and flavors. There has been significant past research on the genomics and ecology of desirable cheese fungi, but the diversity and natural history of cheese spoilage molds is generally lacking. In the past five years, outbreaks of Aspergillus spoilage molds in Northeastern United States cheese production facilities have threatened artisan cheesemaking. In this work, we characterized the genomic diversity of Aspergillus species contaminating artisan cheeses and identified the abiotic environment that may constrain the growth of Aspergillus in cheese facilities. Comparative genomics revealed A. westerdijkiae and A. ochraceus as the primary spoilage species, with multiple genomic types of A. westerdijkiae found across different facilities. Measurements of the growth of A. westerdijkiae across a range of temperatures indicated that cheese cave temperatures below 11°C should limit the growth of this spoilage mold, while other beneficial Penicillium species can still grow. Transcriptomes of A. westerdijkiae on standard lab media (malt extract agar) versus cheese curd media identified a suite of pathways enriched in expression on cheese, including carbohydrate metabolism. Literature and global fungal databases suggest that A. westerdijkiae is not found in natural ecosystems of New England, and it may therefore be entering cheese production facilities via the built environment. Our work reveals the genomic and transcriptomic of emerging Aspergillus spoilage molds in American artisan cheeses and suggests that careful management of cheese aging temperatures could be effective in controlling the growth of these undesirable molds.

**Poster Number: 54**

### Are Spore and Cystidial Traits Adaptively or Functionally Linked with Biogeographical Traits in the Hyper-Diverse Genus Inocybe?

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Inocybe is a monophyletic group estimated to contain some 1500-1800 species worldwide. Several biogeographical trait associations have been observed among species of this hyper- diverse ectomycorrhizal genus. However, none of these have been evaluated with phylogenetic correlation tests. In the present study, correlations of different traits with their biogeographical habitats have been proposed including (i) the high prevalence of smooth- spored taxa in Mediterranean habitats of western North America, southern Europe, southwestern Australia, and southeastern Australia; (ii) the high prevalence of nodulose- spored taxa in tropical regions; and (iii) association between species with thick-walled hymenial cystida and occurrence on calcareous soils. In the latter case, it has been suggested that species with thicker walled cystidia cope more efficiently with excess calcium. Given these observations globally, we wish to know if the traits enumerated above are adaptively or functionally linked to biogeographical traits. If yes, then one should expect to see replicated co-distribution or replicated elevated rates of net diversification among species with the paired traits in a given phylogeny. We propose to examine these questions in the context of a 500-taxon tree of Inocybe reconstructed from a 6-locus supermatrix.

### Poster Number: 55

### An Aspergillus fumigatus homeobox transcription factor regulates multiple developmental responses to copper starvation

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Copper homeostasis is a fundamental property in all organisms, yet the developmental response to copper starvation remains poorly characterized in the opportunistic filamentous fungal pathogen Aspergillus fumigatus. Machine learning analysis of RNAseq datasets identified Afu4g04320, one of seven putative homeobox transcription factors in A. fumigatus, as a candidate transcription factor relevant to copper response pathways. Through deletion and overexpression of this transcription factor, we investigate its influence upon physiology and development under both standard and copper-depleted conditions. Phenotypic assessments revealed that Afu4g04320 modulates multiple developmental processes across both environmental contexts. Notably, overexpression of this transcription factor under copper starvation substantially enhanced biomass accumulation and germination efficiency, while its deletion impaired germination under identical conditions. There were also notable phenotypic differences present under copper replete conditions, including altered hyphal morphology and increased germination in the overexpression strain. These findings suggest Afu4g04320 to be important in A. fumigatus developmental transitions that are most pronounced under copper starvation.

### Poster Number: 56

### Tracking Fungal Community Composition in Alnus rhomifolia and Quercus lobata at CSU, Chico

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Fungi and plants have integral relationships that facilitate essential biogeochemical cycling. Foliar fungal endophytes have been shown to facilitate plant growth and vitality, but once leaves abscise, fungal endophyte communities are influenced by the colonization of environmental fungi as leaves are decomposed. Fungal decomposers, saprotrophs, break down plant material and recycle vital nutrients such as carbon, nitrogen, and phosphorus back into the soil for plants and other organisms to use. The influence of fungal endophytes on the fungal community's overall composition affects community assembly, the process of decomposition, and ultimately the carbon cycle. Understanding the shifts in fungal community composition, from endophytes to decomposers, can help strengthen the connection between fungal ecology and ecosystem services. This project aims to aid in our understanding of community assembly processes by utilizing culture-dependent techniques. This allowed us to access these communities and isolate pure fungal samples over eight weeks. I hypothesize that the two host species would have differing initial fungal communities due to differences in host physiology with composition becoming more similar as the community becomes dominated by decomposers. In addition to assessing community assembly, this project provides a culture collection that will aid in further projects to evaluate interactions among fungal isolates during the transition from endophytic to saprotrophic communities.

### Poster Number: 57

### Phenotyping of Rhodotorula and Exophiala for UV-C Tolerance

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Extremotolerant fungi can exist under harsh environmental pressures from low water, high temperatures, and radiation exposure including high UV-C. These fungi can be isolated from many environments but often from arid environments including deserts, rocks, and mountains. This tolerance is enabled by their robust DNA repair mechanisms and protection provided by natural sunscreens such as mycosporines, melanin, and carotenoids. Despite their UV-C tolerance, quantification of phenotypic variation in tolerances within populations has not been conducted and there is limited work to link genotypic and phenotypic variation. This can be attributed to several factors, including difficulty culturing these fungi which can take weeks to grow, and a lack of tools to phenotype. To reduce this bottleneck we will screen hundreds of strains of Rhodotorula and multiple species of Exophiala from collections using equipment from

UCR's new ExFAB biofoundry and phenotypic data such as growth rate will be recorded and quantified by imaging plate growth over time. Using the phenotypic data paired with whole genome sequencing data, we aim to (i) assess and identify genes important for tolerance to extreme conditions, (ii) discover novel chemicals that have the potential for broad applications in biotechnology, biomedical research, and bioremediation, and (iii) link genomic variation to phenotypic variation. To develop and test the workflow steps we will perform screening of strains on individual plates to examine variation in growth after exposure to multiple UV-C levels at low and high pH to explore the diversity of these resistance phenotypes.

**Poster Number: 58**

## Yielding to Fungi: How Belowground Fungal-Bacterial Networks Reveal the Impacts of Differing and Prolonged Managements on Crop Productivity

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In the USA, a movement towards a three-crop rotation involving corn (Zea mays), wheat (Triticum aestivum), and soybean (Glycine max) is part of a broader push towards sustainable agriculture practices, along with reducing chemical inputs and preserving the soil through reduced tillage. This study explores how different crop management strategies affect the belowground (soil and root) microbial assembly. Samples were collected from the Kellogg Biological Station Long-Term Ecological Research Site (KBS LTER) from soils, roots, leaves and stems from each crop in a corn-wheat-soybean rotation. Multiple plants from replicate plots were sampled throughout the growing season. Four years of bacterial (16S rDNA) and fungal (ITS) amplicon sequence data were obtained from these samples and analyzed. Long-term management practices are hypothesized to shape belowground microbial communities in ways that influence microbial interactions and crop productivity. We expected differences in microbial network structure across managements with potential variation in modularity and connectivity, especially in no-till where reduced soil disturbance may foster more stable microbial associations. Preliminary results revealed significant management effects on three out of the four years of analysis by Principal Coordinate Analysis and PERMANOVA. Network analyses indicate that no-till exhibited greater modularity, with more distinct microbial groups and fewer interactions, particularly fewer negative (competitive) edges. Random Forest modeling was used to clarify relationships between microbial taxa, network properties, and crop yield, identifying potential productivity indicators. These findings contribute to a broader understanding of how agricultural management impacts microbial communities and soil health, elucidating possible optimization for improving crop yield stability.

**Poster Number: 59**

## Taxonomic Study of Hydnoporia (Hymenochaetales, Hymenochaetaceae) in East Asia with Two New Species

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The genus Hydnoporia Murill. (Hymenochaetales, Hymenochaetaceae) was first described in 1907. Then, the Hydnoporia species were reclassified into the genera Hymenochaete, Hymenochaetopsis, and Pseudochaete due to the similar morphological features, which generated multiple synonyms. Recent multi-marker phylogenetic analyses have identified the diversity of Hydnoporia, but East Asian specimens were not sufficiently treated due to the limited data. Thus, we conducted morphological and phylogenetic

analysis of East Asian Hydnoporia specimens based on internal transcribed spacer (ITS) and translation elongation factor 1–α (tef1) regions. Six Hydnoporia species were identified from 42 specimens, including two new species, Hyd. orienticorrugata M.Cho, Y.Cho, Y.W.Lim & J.J.Kim, sp. nov. and Hyd. subtabacina M.Cho, Y.Cho, Y.W.Lim & J.J.Kim, sp. nov., and one unrecorded species, Hyd. rimosa (Lloyd) Spirin & Miettinen. Hydnoporia in Korea is characterized by dimitic hyphal system, thick-walled setae, and cylindrical to allantoid basidiospores, but has distinct macro-morphology among species. In addition, phylogenetic analyses propose the recombination of Hymenochaete intricata and Hymenochaetopsis rigidula as Hyd. intricata comb. nov. and Hyd. rigidula comb. nov., respectively. The detailed morphological characteristics and phylogenetic trees are provided to support East Asian Hydnoporia species. This study contributes to a deeper understanding of the global diversity and phylogeny of the genus Hydnoporia.

**Poster Number: 60**

### Colletotrichum species diversity in Italy: Apple Bitter Rot and Glomerella Leaf Spot as a case study

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Species of Colletotrichum are known as important plant pathogens on a wide range of plant hosts. Historically prevalent in tropical and subtropical regions, their distribution has expanded due to climate change, global trade and intensified agricultural practices. The genus has undergone recent taxonomic re-arrangements and uncertainties have been raised about past classifications and possible misassigned genomic sequences in public databases. The distribution and host association pattern of species such as C. aenigma, C. alienum, C. fructicola, C. perseae, C. plurivorum, C. siamense and C. theobromicola remain ambiguous underscoring the need for accurate identification of new records. Currently, multi-locus sequence typing (MLST) is the most reliable tool for unravelling species boundaries in Colletotrichum, with up to 13 different loci available for species delimitation. Additionally, the increasing adoption of whole-genome sequencing (WGS) is improving taxonomic resolution and investigation on host-pathogen interactions. In this context, Colletotrichum spp. causing Apple Bitter Rot (ABR) and Glomerella Leaf Spot (GLS) have recently emerged as significant threats to apple production in Northern Italy. Colletotrichum spp. reported in the surveyed area belong to the acutatum and gloeosporioides species complexes with their diversity assessed through robust multi-locus phylogenies based on eight loci, combined with morphological characterization. This study emphasizes the relevance of a polyphasic approach in investigating Colletotrichum spp. and the critical role of molecular tools in achieving accurate species-level identification, essential for developing targeted sustainable management strategies to mitigate the impact of Colletotrichum on apple and other crops.

**Poster Number: 61**

### Fungal and Bacterial Microbiomes of Michigan's Lake Superior Copper Contaminated Beaches

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Industrial copper (Cu) mining in the Keweenaw Peninsula of Michigan has created approximately 500 million tons of mine tailing material, that has led to ecological concerns. Along the shore of Lake Superior, an artificial beach of mine tailings (known as "stamp sands") formed as a result of Cu extraction and processing. We investigated how Cu contamination and ecotone transitions influence the fungal and bacterial diversity of these stamp sand and natural sandy beach environments. Two contaminated stamp sand beaches, and one natural sandy beach were sampled along three transects per site. The transects ran perpendicular to the shore, from the forest to the water, and samples were taken for metal and microbiome analysis at nine points corresponding to different ecotones; (1) deep forest, (2) forest, (3) forest edge, (4) near forest, (5) mid stamp sands, (6) backshore, (7) shoreline, (8) swash zone, and (9) surf zone. These samples were reacted with a citric acid extraction to mimic microbial interactions with stamp sands. The extract was analyzed for metal content using ICP-OES and ICP-MS, to determine Cu bioavailability. We hypothesize that the increase in Cu concentrations and decrease in organic material along the transects will decrease species diversity. Amplicon libraries targeting fungi (ITS1F rDNA) and bacteria (V4 16S rDNA) were generated from the sand samples, and sequenced to describe the microorganisms living in these beach environments. Alpha and beta diversity metrics provided insights into how copper concentration and ecotones influence microbial communities on stamp sand and natural sandy beaches.

### Poster Number: 62

### Functional Composition of Subsoil Microbial Communities Changes with Oak Mortality

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As widespread tree mortality transforms Californian oak savannas, the future of this ecosystem's soil fungal community hangs in the balance. How do soil microbial communities associated with oak roots change as oaks die -- especially in the subsoil, where deep tree roots provide otherwise-scarce carbon? To investigate how oak mortality affects subsoil microbial communities, we collected soil cores across a 45 cm depth gradient underneath both living and dead Quercus douglasii trees three years post-fire. We captured finely-resolved biological data from these soils, comparing living (RNA-based) to potentially historical (DNA-based) microbial communities and assessing microbial biomass with phospholipid fatty acid analysis. We took a particular interest in ectomycorrhizal fungi, their associated bacteria, and the impact these microbes might have on subsoil carbon storage. Tree mortality greatly reduced the abundance of ectomycorrhizal fungi, particularly in subsoils. Fungal niches were more variable at depth under dead trees than under living ones, and RNA-based profiling captured substantially different communities than DNA, especially under living trees. However, tree mortality three years prior to our study did not impact the overall quantity of carbon stored in the soil. Tree mortality can have profound effects on the interactions between tree roots, mycorrhizal fungi, and soil bacteria, which may shift soil carbon dynamics over long time scales. Understanding the mechanisms of these interactions, and their time scales, will improve our ability to predict and manage soil carbon in savanna landscapes as drought, heat, and fire events kill more oaks in arid climates.

### Poster Number: 63

### Cryptococcus Spore Germination Can Occur in the Absence of Detectable Oxygen

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Cryptococcus spores must germinate into yeast to cause disease in mammalian hosts. To identify novel germination inhibitors, we carried out a high-throughput screen of small, drug-like molecules and discovered a subset of germination inhibitors predicted to target complex II of the electron transport chain (ETC). Because Cryptococcus is a non-fermentative, obligate aerobe in its yeast growth state, we anticipated that these inhibitors would block germination by stopping the ETC, therefore preventing oxidative phosphorylation. However, we discovered that it is possible for Cryptococcus spores to germinate in the near-absence of oxygen, revealing an apparent conflict between the requirement for ETC activity but not oxygen. To determine the role of the ETC in germination, we tested inhibitors of ETC complexes and conducted a transcriptomic analysis of spores germinating hypoxically. Our data suggest the importance of a second electron transport pathway that uses part of the canonical ETC in conjunction with an alternative oxidase during hypoxic germination. Future experiments will continue to determine the molecular interactions and potentially targetable mechanisms of cellular respiration in germinating Cryptococcus spores.

### Poster Number: 64

### Mycomorph Network for the Promotion of Mycorrhizal 6th Layer in Miyawaki Landscaping

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Miyawaki landscaping has been widely adopted as a methodology for creating dense and diverse forests in a short period of time. The success rate of the Miyawaki Forest plan depends on various factors, including soil quality, microclimate, and plant species selection. This plan proposes the use of fungal languages and the creation of a mycomorph network to promote and interface with the mycorrhizal 6th layer of Miyawaki landscaping.

**Poster Number: 65**

### Taxonomy and Biogeography of Suillus in the UK

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Suillus is a genus of fungi that is of particular research interest and there are ample records and collections of the genus in the UK. This study acts as a general overview for the taxonomy, phylogenetics, and biogeography of records for this genus maintained by the Kew Fungarium and the British Mycological Society (BMS). Citations, taxonomic references, and type specimen records are gathered to create a centralized reference material for future research. In the process, multiple gaps in typification are revealed. Recent collections from the Kew Fungarium are genetically sequenced and compared to existing data via GenBank. The resulting phylogenetic trees reflect the relationships shown in other studies on Suillus, including unresolved species complexes. Occurrence data collected by the BMS is mapped in comparison to collection dates, showcasing a possible change in distribution overtime. While it is unclear what is causing the apparent northwards shift, climate change is speculated to be a contributing factor.

**Poster Number: 66**

### A Population Genomic Assessment of the Endemic Pine Pathogen Fusarium circinatum

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Pine pitch canker is a serious disease of Pinus spp. caused by the fungus Fusarium circinatum. Endemic in Central and North America and invasive elsewhere, F. circinatum is considered one of the greatest threats to pine forests globally. While the primarily clonal invasive populations in California, South Africa, and southern Europe are well-characterized, comparatively little is known about the relatedness and structure of populations across the species' broad endemic range, the occurrence of recent sexual reproduction, or the geographic origin of the species. To address these knowledge gaps, we are utilizing a collection of over 60 whole genomes, composed of 50 new F. circinatum isolates from symptomatic pines in the southeast United States as well as representatives from Central and South America, Japan, and Africa, leveraging genome-wide SNPs to infer patterns of relatedness, structure, and admixture among North American populations. Additionally, we are employing a phylogenomic analysis to assess relatedness among all isolates and identify patterns of historic migration and recent movement between North America and invasion centers. Preliminary results indicate multiple separate F. circinatum populations within the southeast US, and link invasive populations to common sources in the Western Gulf states and Mexico. While some US populations were found to be isolated and geographically distinct, others co-occur across large areas, suggesting similar patterns of long-distance dispersal among multiple populations. Assessments of admixture and historic migration are ongoing and will provide further insight into possible recent recombination, as well as where the center of diversity for this species may lie.

**Poster Number: 67**

### The effects of fire intensity on soil microbial communities and ectomycorrhizal fungi in blue oak woodlands

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Wildfires are becoming more frequent and destructive due to climate change-driven drought and rising temperatures, threatening ecosystem stability and function. Fire alters soil chemistry and microbial communities, which in turn influence plant-fungal interactions. While fire is a natural process in many California ecosystems, its impact on soil fungal communities and ectomycorrhizal symbiosis in fire-adapted habitats, such as blue oak woodlands, remains unclear. The 2024 Park Fire, the fourth-largest wildfire in California history, burned 429,603 acres across Butte and Tehama Counties, providing an opportunity to examine these effects. *Quercus douglasii* (blue oak) relies on mutualistic ectomycorrhizal fungi for nutrient and water uptake, as well as soil stability. Given the critical role of these fungi, this study aims to investigate how fire intensity influences soil fungal communities and the survivability of ectomycorrhizal fungi in recently burned blue oak woodlands at the Big Chico Creek Ecological Reserve, burned by the 2024 Park Fire. Soil cores will be collected beneath blue oak trees across high-, medium-, and low-intensity fire sites and an unburned site. Fungal communities will be characterized to investigate how fire intensity influences soil fungal communities. Additionally, soils will be used to set up a greenhouse experiment, using blue oak seedlings to bait ectomycorrhizal fungi from each fire intensity site, evaluating post-fire fungal recruitment. This research will provide valuable insights into the resilience of fungal symbionts in fire-affected blue oak woodlands, which will inform restoration strategies and ecosystem management across fire-prone landscapes.

**Poster Number: 68**

### Local Coffee Waste as a Mushroom Substrate in the Circular Economy

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Pleurotus ostreatus a saprophytic fungus and a gourmet commodity crop in a fast-growing global industry. The ability of Pleurotus to adapt to various substrates and decompose organic matter provides an opportunity to divert waste products from the landfill stream. The standard substrate used in industrial cultivation consists of 55% hardwood, usually oak, and 45% soy hull pellets. The ratio of carbon to nitrogen is one of the primary factors dictating growth rate and yield. Untreated hardwood serves as the main source of carbon, and soy provides nitrogen. Soy hull pellets and coffee grounds have a similar nitrogen content. While both coffee grounds and soy hull pellets are waste products, soy hulls have many other uses such as animal feed; whereas, coffee waste is diverted to landfill. This project evaluates the feasibility of replacing soy with hyper-local coffee waste in mushroom substrate. It consisted of four treatments of varying amounts of coffee grounds replacing soy hull pellets, alongside multiple controls of standard substrate. Overall yields of the control substrate were significantly higher compared to yields from the coffee treatments. The difference in yield despite similar nutrient profiles suggests the influence of other factors such as caffeine which may be further explored in future analysis. Despite lower yields, the cost of the substrate per pound of harvested mushrooms is relatively comparable between control and most coffee substrate treatments. This cost-benefit analysis concludes that coffee grounds may serve as a cost-effective, sustainable substrate for gourmet mushroom producers, if space is not a constraint.

**Poster Number: 69**

### Spatial Dynamics of Foliar Fungal Community Structure in the Pando Aspen Clone

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The Pando aspen grove, a vast clonal colony of Populus tremuloides in Utah, provides an unparalleled host system for investigating plant-fungal symbioses due to its consistent genotype across 106 acres. While the significance of symbiotic fungi in plant health is well-recognized, the foliar fungal communities of this globally renowned organism remain poorly understood. This study characterizes the diversity, structure, and spatial dynamics of endophytic and epiphytic fungal communities within Pando, testing how edge proximity affects community assembly in a massive genetically uniform host and illuminating their roles in this unique ecosystem. We found that epiphytic fungi exhibit significantly greater diversity than endophytes, with Dothideomycetes dominating epiphyte assemblages and Leotiomycetes prevalent among endophytes. Endophytic communities were largely nested within the corresponding epiphyte communities on a given leaf, suggesting host selection influences recruitment in community assembly. Spatial analyses revealed distinct patterns in endophyte turnover, with community variance increasing significantly 100 meters from the grove’s edge, explaining 24% of observed variance. Conversely, epiphytic communities exhibited hypervariable but spatially unstructured patterns, implying stochastic assembly processes independent of edge effects. These findings highlight contrasting mechanisms underlying fungal symbiosis in Pando: epiphytes reflect diverse but randomly assembled associations, while endophytes are shaped by spatially mediated selection. Leveraging Pando’s uniform genotype as a model system, this work underscores the importance of fungal symbioses in shaping plant resilience in a changing environment. These insights contribute to community assembly processes in forest ecosystems and conservation of P. tremuloides populations increasingly threatened by fungal pathogens and other environmental stressors.

**Poster Number: 70**

### Single-Cell Genomics of Fungal Phycoparasites

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Fungi are critical research systems as they impact global carbon cycling and have remarkable potential for sustainable biofuel production processes. Current estimates suggest that under 10% of total fungal species worldwide have been described, and the overwhelming majority of those fall within the Dikarya. The true extent of the phylogenetic diversity among the non-Dikarya lineages is poorly explored. Thus, “Dark Matter Fungi” (DMF) is used to describe this understudied fungal diversity. The difficulties inherent in exploring the genetics of “fungal dark matter”, a reflection of their absence from sequence databases, can be overcome using single-cell sequencing. Reconstructing the genomes of uncultivated organisms directly isolated from the environment allows for meaningful comparative analyses and lifestyle predictions. In this study, samples were collected from freshwater environments around Michigan, USA, which included fungi associated with algae, micro-invertebrates, and protists. Coupling phenotypic characterization through direct microscopy with single-cell sequencing produced nearly 100 genomes representing previously and newly described lineages within the Chytridiomycota, Blastocladiomycota, Aphelidomycota, and Rozellomycota. We observe genome sizes ranging from 2.2 to 37.9 Mb (median 14.3 Mb), with completeness estimates of 44.98% to 98.91% CEGMA (median 92.79%). Phylogenomic analyses of these unsampled lineages support placements previously established using rDNA sequences. Additionally we explored gene family patterns consistent with lifestyles of these biotrophic organisms. This work represents the first large scale genomic investigation of environmental fungi using single-cell and microscopy approaches. These genomes, which include new phylum level lineages, will help further refine the phylogeny and biological understanding of undescribed zoosporic fungi.

**Poster Number: 71**

### First Record of Aplanochytrium on the Chilean Coast: Expanding Labyrinthulomycetes Distribution and Revealing Its Biotechnological Potential.

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Moisés Valladares, Pontificia Universidad Católica de Chile
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This study reports the first record of the genus Aplanochytrium on the coast of Chile, belonging to the class Labyrinthulomycetes in the kingdom Stramenopila. These marine protists play an essential role in carbon and nitrogen cycles as decomposers in the marine ecosystem. Although they are ecologically significant, their global diversity and distribution remain poorly understood. The organisms were cultivated and identified through classical taxonomy methods and molecular analysis. Phylogenetic analysis based on the 18S rRNA sequence showed a 98% similarity with the genus Aplanochytrium, thereby extending its geographic distribution from Asia and the Northern Hemisphere to South America. This finding enhances our understanding of the diversity and distribution of Labyrinthulomycetes. Additionally, the fatty acid profile of Aplanochytrium revealed a high proportion of docosahexaenoic acid (DHA), accounting for 50% of the total fatty acids, along with the presence of palmitic acid. Astaxanthin, a valuable pigment for biotechnological applications, was also quantified. These results highlight the importance of Labyrinthulomycetes in marine ecosystems and their potential in biotechnology.

### Poster Number: 72

### Rooting for ROSES: Comparing nontoxic DNA extraction methods and presenting a new combined DNA extraction protocol for ectomycorrhizal root tips

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Ectomycorrhizal roots pose challenges for DNA extraction, especially with extensive root tip collecting projects. Commercial extraction kits can be cost prohibitive and the generally available DIY methods utilize toxic substances (i.e. Phenol Chloroform). Therefore, there is a need to develop an efficient, non-toxic, and cost-effective DNA extraction for use on multiple root tips, essential for community surveys and environmental monitoring. This study evaluates non-toxic DNA extraction methods, highlighting their pros and cons. To overcome the interplay of plant inhibitory compounds, cost prohibitive commercial kits, and working with highly toxic substances —we present a protocol that combines Rapid One Step Extraction and silica powder extraction(ROSES). This integrated method quickly and affordably extracts DNA from extensive collections of ectomycorrhizal root tips and lichens, producing DNA concentrations comparable to those from expensive kits, with improved PCR reliability for large root tip pools.

### Poster Number: 73

### Airborne Fungal Spores in Ecotourism caves: Monitoring and Targeted Detection of Histoplasma Capaulatum

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This study aims to provide the first quantitative and qualitative assessment of airborne fungal spores at Las Cabachuelas Natural Reserve in Morovis, Puerto Rico. Also, a cross-sectional study for targeted detection of Histoplasma capsulatum will be done. The reserve is a distinctive karst region comprising at least 60 cave ecosystems. It has gained prominence as a destination for ecotourism, offering guided tours, insights into cave art, and opportunities for observation of diverse flora and fauna. This project will be conducted through the Lit-Geo program, which aims to promote inclusivity and facilitate collaboration between scientists and local communities through the lens of geosciences.In this study, we will examine these caves for the presence of Histoplasma capsulatum, a fungus that causes pneumonia-like symptoms and is especially deadly in immunocompromised patients. We will obtain air and soil samples in each of the caves visited. Air samples will be obtained using the Environmental Express IAQ 15 air pump with Air-O-Cell® cartridges for microscopic analysis and Via-Cell® for DNA analysis. In addition, soil samples from inside the caves will be analyzed using Qiagen's PowerSoil® Pro Kit and specific qPCR assays for H. capsulatum. We expect if this fungus is present, it would be in a cave with a high density of organic material and guano. The data collected will be used by the community to create biosafety protocols to safeguard public health while inside these caves.

### Poster Number: 74

### Rugonectria Purpurescens (Hypocreales, Ascomycota), a New Species from Panama

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Rugonectria is a small genus currently comprising 6 species in the Nectriaceae. Most taxa in the genus are wood decomposers, with the exception of Rugonectria castaneicola and Rugonectria wingfieldii, which are plant pathogens causing cankers on trees. Morphologically, Rugonectria species are characterized by having small, orange to red, non-papillate and solitary to stromatic perithecia with rugose to warted walls that turn dark to brownish red when exposed to 5% KOH. During a fungal collection expedition in a mangrove forest at Estero Rico, Chiriquí, Panama, a specimen of wood-decaying Nectriaceae was collected and later identified as a new species in the genus Rugonectria, which is in the process of being formally described as Rugonectria purpurescens nom. prov. The species differs morphologically from all other species in the genus by turning deep purple when exposed to 5% KOH, whereas all other species turn red to brown. In addition this new species possesses the smallest ascospores in the genus. A draft genome sequence of the isolate was generated to produce a multilocus phylogeny. Our phylogenetic analysis revealed this new species to be most closely related to the newly described Rugonectria wingfieldii from New Zealand

and the Neotropical Rugonectria rugulosa. Many species in Nectria and the several genera recently segregated from it are difficult to distinguish from one another, and a thorough revision of previously collected specimens, as well as newly collected ones, will pave the way for the discovery of new taxa.

### Poster Number: 75

### Genetics Underlying Early Secotioid Evolution in the Dimorphic Mushroom Lentinus Tigrinus

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Evolution of developmental transitions is difficult to study in fungi. Because few fossilized mushrooms exist, transitions between morphological forms must be inferred from phylogenies. Based on these analyses, gasteromycete mushrooms are hypothesized to evolve from hymenomycete forms through a secotioid intermediate. However, this hypothesis is difficult to directly test because few polymorphic species are known. One of those species, Lentinus tigrinus, is widespread in North America and has two morphologies: an agaricoid form with exposed gills and a secotioid form with membrane-enclosed gills. Both the agaricoid and secotioid forms of L. tigrinus are widespread in North America and follow simple Mendelian inheritance, with the agaricoid morphology dominant to the secotioid morphology. Additionally, a bulked segregant analysis of an inbred line identified a 1.5 Mb region of the genome correlated to the agaricoid/secotioid phenotype. However, the region was spread across three scaffolds and contained 212 associated genes. We are working to refine this region and identify a single locus that correlates with the agaricoid/secotioid morphology by re-mapping old data onto improved genome assemblies and by using a population genomics approach to do identify genomic differences between agaricoid and secotioid specimens collected from the wild. We currently have low coverage Illumina sequencing for 50 Massachusetts specimens and 25 Illinois specimens and will conduct more sequencing this summer. Identifying the secotioid allele will give us the first genetic explanation for the emergence of a secotioid morphology.

### Poster Number: 76

### Decay Modes and Substrate Types Influence Bacterial Communities in Decaying Wood

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Wood rot fungi have two major decay modes, white rot and brown rot, that result in the creation of chemically distinct microenvironments in decaying wood. Previously, we showed that the bacterial community composition in birch samples dominated by Fomes fomentarius (white rot) was different from those dominated by Fomitopsis betulina (brown rot). However, it is unclear if bacterial community composition is influenced by fungal species or the decay modes (white rot and brown rot) irrespective of the fungal species. We selected five white and five brown rot fungi and collected wood shaving samples (n=15 each fungus) from either birch, aspen or spruce. Using internal transcribed spacer (ITS2) sequencing, we first confirmed the identities of our selected fungi in wood samples. We coupled this with the 16S rRNA gene amplicon sequencing and explored the bacterial community diversity and composition in wood samples having relative abundance of ≥50% of the target/host fungi. Our results showed that both decay mode and substrate type influenced bacterial community compositions in decaying wood. However, the proportion of variance explained by substrate type (R2=0.071; P

### Poster Number: 77

### Understanding the spatial relationships among the snake skin microbiome, Ophidiomyces ophidiicola, and the environment

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There are several threats to snake biodiversity including climate change, habitat degradation, and emerging infectious diseases. An emerging infectious disease currently affecting phylogenetically diverse free-ranging snake populations across the globe is Snake Fungal Disease (SFD; Ophidiomyces ophidiicola). In an effort to understand how this pathogen affects diverse host species, research on the snake skin microbiome and its interactions with O. ophidiicola is needed. In the Southeastern United States, extensive work has been done to explore relationships between host snake species, the skin microbiome, and the presence of O. ophidiicola. However, a study of snakes from Western North America, including an exploration of bacterial-fungal interactions across various environments, has not yet been completed. By using metabarcoding and high-throughput amplicon sequencing of bacterial 16S rRNA and fungal ITS rDNA markers for ~800 snake individuals, we will investigate potential co-occurrence patterns within the skin micro- and mycobiome across diverse hosts and environments. We will elucidate underlying patterns of distribution, abundance, and microbial interactions within a metacommunity framework to provide a mechanistic understanding of disease patterns across multiple scales.

### Poster Number: 78

### Teaching marine mycology: a class on the Ascomycota from sandy beaches

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Teaching is a bilateral process that consists of two parts - to teach and to learn. Effective teaching by the teacher results in a good learning experience for the student. The teaching-learning process includes the reception of knowledge, its comprehension, retention, and application. To lecture or give a class is simply to treat or transmit knowledge of a subject, whereas true teaching is much more complex, profound, and committed. The objective of this work is the development of a plan for a class to teach students about the marine fungi that inhabit the sand of beaches. The objectives of the class were determined clearly and precisely, the justification for the topic was provided, and activities were prepared for interaction and feedback by the students. These activities were completed in 50 minutes (introduction 10 min, theme presentation 30 min, comprehension 5 min, and review 5 min). In the introduction, the students were provided with a synthesis of the material to be covered and the objectives of the class. During the theme presentation, the definition of arenicolous fungus was provided, along with their diversity, biology, and ecological role. Finally, during the feedback session, all students were questioned to assess their understanding.

### Poster Number: 79

### Turning up the heat: How Warming Shapes Fungal Litter Mat Growth and Leaf Colonization Rates in a Wet Tropical Rainforest

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Wet tropical forests are experiencing rising temperatures and increased frequency and intensity of extreme climatic events, such as cyclones, which can increase rates of erosion and surface runoff. Fungal litter mats, formed by agaric decomposer fungi, play a crucial role in stabilizing slopes and aiding nutrient cycling; however, little is known about how warming affects litter mat growth and function. We investigated two litter mat-forming fungi, Gymnopus johnstonii and Marasmius crinis-equi, in warmed (+4°C above ambient) and control plots in the Luquillo Experimental Forest, Puerto Rico. Growth and time to leaf colonization were monitored over six weeks in spring (both species) and summer (G. johnstonii only). We hypothesized that warming would inhibit fungal mat growth and slow leaf colonization, particularly for G. johnstonii since it is drought sensitive. As expected, warming significantly reduced relative growth rates (RGR) in spring, though M. crinis-equi showed slightly higher RGR than G. johnstonii. Leaf colonization was also delayed by 22% in warmed plots, with M. crinis-equi colonizing leaves 4.3 times faster than G. johnstonii. There were significant seasonal differences in response to warming for G. johnstonii, with warming increasing RGR during the consistently wetter summer sampling period. Overall, warming led to significant inhibition of leaf colonization when conditions were dry, whereas there was a trend toward increased colonization in warm and wet conditions. Our findings suggest that warming, when combined with drier conditions, is likely to suppress drought-sensitive fungal mat growth, reducing their ability to prevent nutrient and soil loss via erosion.

### Poster Number: 80

### Genotypic survey of Oregon isolates of Calonectria pseudonaviculata with an assessment of phenotypic response to temperature

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Calonectria pseudonaviculata, the fungal pathogen causing boxwood blight disease in North America, threatens production of the most valuable broadleaf evergreen of the United States nursery industry. With 19% of the domestic boxwood supply, Oregon is the single largest U.S. producer. To evaluate the genetic diversity of Cps in Oregon, 123 isolates collected from ten locations across three counties were analyzed by sequencing eleven simple sequence repeat (SSR) loci. Nine multi-locus genotypes (SSR-MLGs) were identified with 13% of isolates falling into five newly identified SSR-MLGs. The SSR-MLG G1 occurred at a higher frequency (20%) among Oregon samples than previously reported for studied populations outside of Oregon. Controlled environmental experiments evaluated mycelial growth rate variation in response to temperature. Seventy-one isolates, representing each of the nine SSR-MLGs identified, were grown on malt extract agar at five different temperatures ranging from 10 to 30&deg;C. Optimal growth for most isolates examined occurred at 20&deg;C which is cooler than previously reported for isolates collected outside of Oregon. These findings expand our understanding of C. pseudonaviculata.

### Poster Number: 81

### The Snake Fungal Disease Pathogen Influences the Evolution of the Skin microbiome

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Identifying evolutionary and ecological influences on host-microbiome interactions and their role in host health may prove vital to determining effective means for targeted pathogen remediation and wildlife conservation. Exploring how bacterial-fungal interactions develop over time, within a host-microbiome-pathogen system, can be challenging given a lack of experimental control over environmental variation, host life history characteristics and time scale at which the microbes interact. By implementing a controlled experimental evolution design, we were able to characterize variation in bacterial fitness, colony morphology, and system relationships for two species of bacteria (Stenotrophomonas maltophilia and Chryseobacterium sp.) in response to metabolites produced by the Snake Fungal Disease pathogen (Ophidiomyces ophidiicola). Strains of S. maltophilia and Chryseobacterium sp. were evolved on either a 10,000 ppm keratin control or a fungal spent keratin media. Using a fully factorial design, we passaged each strain independently and in coculture for ~90 generations, observing divergence in growth rates between both bacteria and media types, and survival in cocultures of S. maltophilia and Chryseobacterium sp. Our results will discuss mutation and growth rate variation for both in response to a fungal pathogen over time, and elucidate mechanisms of pathogen induced dysbiosis on the evolution of the microbiome. A deeper understanding of these microbial interactions within the snake skin microbiome may prove critical for conservation efforts targeting populations threatened by Snake Fungal Disease.

**Poster Number: 82**

### Cultivation of Three Ganoderma species: Evaluation of Antioxidant activity, Phenols and β-Glucan Content.

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The genus Ganoderma includes species of basidiomycete fungi widely recognized for their medicinal properties, with a long history of use in traditional Asian medicine due to their immunomodulatory, antioxidant, and therapeutic potential. These fungi are wood-decaying organisms capable of growing on various lignocellulosic substrates, allowing their cultivation on locally available agro-industrial waste materials. In this study, the growth of Ganoderma lucidum (M9720), G. sessile (E47), and G. australe (CIEFAPcc 657) was evaluated on three substrates formulated from local resources: willow chips (Salix sp.), rosehip chips (Rosa rubiginosa), and sunflower husk (Helianthus annuus). Productivity was assessed by measuring biological efficiency (BE). Total phenolic content (using the Folin-Ciocalteu method) and β-glucan content were quantified. Additionally, antioxidant activity was evaluated using DPPH and ABTS assays. The results indicated that the highest BEs were obtained with G. sessile on willow chips (36.96%) and G. lucidum on sunflower husk (35.83%). Regarding G. australe, basidiome production was only successful on the rosehip substrate. No significant differences were detected in total phenolic content or antioxidant activity among the species and substrates tested. However, variations in β-glucan content were observed, with higher values found in G. lucidum cultivated on rosehip chips (28.72%). These results highlight the impact of the substrate on the productivity and bioactive composition of Ganoderma basidiomes, emphasizing the importance of optimizing cultivation conditions for the production of nutraceutical compounds. This study contributes to the development of more efficient and sustainable production systems, promoting the revalorization of lignocellulosic by-products as alternatives for medicinal mushrooms production.

**Poster Number: 83**

### Novel Species and Taxonomic Revisions in Hygrophoraceae (Agaricales, Basidiomycota) from Western North America & the Hawaiian Islands

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Fungi in the family Hygrophoraceae are widely known for their often vibrant coloration, diverse ecological roles, and conservation significance. Despite their showy nature, the extent of their global diversity has yet to be catalogued. Over the last 10 years, collaborative efforts between academic and community scientists have contributed extensive, high-quality vouchered collections and DNA sequences of this family. These contributions have extended known biogeographic ranges and elucidated phylogenetic relationships. This project highlights several species that are hypothesized to be new to science, particularly in Western North America. Additionally, we will recombine three species of Hawaiian Hygrocybe in segregate genera based on new morphological and molecular data. These three species are rare and endemic to the Hawaiian Islands with two listed as endangered by the IUCN. This work aims to provide critical data about these species, informing land management and conservation agencies while engaging local communities.

**Poster Number: 84**

### Deciphering Cortinarius alboviolaceus-like species: Phylogenetic and Morphological Insights from Southeastern North American Specimens

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Cortinarius (Agaricales, Cortinariaceae) species are notoriously difficult to distinguish. C. alboviolaceus, a silvery purple hardwood-associating mushroom in subgenus Telamonia, was described from Sweden but has been misapplied in eastern North America based on a distance tree in GenBank. I documented 12 C. alboviolaceus-like collections from Black Mountain NC, hypothesizing 10 taxa based on macro- and micromorphology. Characters analyzed include pileus size and color, context staining, stipe dimensions, veil attachment, spore ornamentation, length, width and L/W ratio. Using ITS nanopore sequences of

C. alboviolaceus-like collections, we identified 9 different species in the following: section Anomali (C. caeruleoanomalus, C. iodes, C. albomalus), and in subgenus Telemonia: sections, Athabasci (Cotinarius 'sp-IN08'), Firmiores (C. obliquus), Pseudotragani (C. subrimosus), Telemonia (C. odoritraganus), and Dijungendi (Cortinarius 'sp-MI10' and Cortinarius 'sp. IUMQ3767'). Three of which appear to have not yet been described. We did not find five eastern North American species we expected based on Liimatainen and collaborators (C. subpulchrifolius, C. compressus, C. kauffmanianus, C. pseudophlegma, and C. paralbocyaneus) but include them in our key to C. alboviolaceus-like species. We used Geneious Software to correct, trim and align sequences followed by manual correction, and phylogenetic analysis using Geneious v. R9, with posterior bootstrap probabilities. My aims are to understand evolutionary relationships and geographic distribution of C. alboviolaceous-like species and to create a key to help professional and amateur mycologists correctly identify collections of these confusing species in the Southeastern USA.

**Poster Number: 85**

### Building a Genetic Toolbox for Brown Rot fungi: The Flashlight

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Wood-decay fungi are the primary decomposers of lignocellulosic biomass. They have evolved two distinct strategies of biomass deconstruction, white and brown rot. Brown rot fungi have evolved from white rot fungi at multiple points in evolution and are distinguished by the shedding of the genes encoding for ligninolytic enzymes. Despite this genetic loss, brown rot fungi are faster wood decomposers by utilizing Fenton chemistry to produce oxidative radicals to open up the complex polymers to gain access to cellulose. This unique strategy of decomposition has potential for biotechnological applications. However, the intricacies of brown rot degradation mechanisms remain to be clarified. To address this challenge, gene editing tools need to be developed for brown rot fungi. In this study, we use a model brown rot species, Gloeophyllum trabeum, to demonstrate one specific tool: the flashlight. Through genetic transformation, we delivered two different gene cassettes built with fusion PCR. The first cassette uses a constitutive promoter to continually express the enhanced Green Fluorescent Protein (eGFP) which serves as a lightbulb. Tagging key degradative enzymes with eGFP would allow us to localize them within the cell. The second cassette contains a tunable promoter that functions as a switch to turn the expression of eGFP on and off depending on environmental cues. This molecular reporting system can be used to develop a screening method for discovering unknown genes with desired functions. With a well assembled gene editing toolbox, we can illuminate the pathways of brown rot degradation.

**Poster Number: 86**

### Determining the Role of Starships in Fungal Plant Pathogenesis

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Plant pathogenic fungi cause widespread losses of economically important crops every year. Starships are a newly discovered group of transposable elements in filamentous fungi. Starships are unique because of their massive size (~100kb on average) and their ability to mobilize dozens of cargo genes with putatively adaptive functions. Starships may carry genes that increase fungal fitness, play a role in plant host specificity, and are predicted to play a role in the virulence of plant pathogenic fungi. However, the precise role of Starships in fungal plant pathogenesis remains unknown. Our research aims to determine the role of Starships in fungal plant pathogens using Sclerotinia sclerotiorum and Macrophomina phaseolina as model systems. We used starfish, a Starship annotation pipeline, to annotate Starships in all publicly available S. sclerotiorum and M. phaseolina genomes. We then used new and previously generated transcriptomics data to compare the expression of cargo genes to examine if Starship cargo has higher expression in planta vs in vitro. Next, we will validate the role of cargo genes in plant infection by reverse genetics and infection assays. Ultimately, this research seeks to predict fungal population diversity and adaptation by exploring the role of Starship cargo in fungal plant pathogenesis. These predictions will then inform and improve strategies for managing agricultural fungal diseases more effectively.

**Poster Number: 87**

### Rhizophagus Irregularis Has Varying Colonization on Different Varieties of Dwarf Corn

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Approximately 15 billion bushels of Zea mays (corn) are grown in the U.S. annually for food and fuel. Per bushel, corn necessitates 1-1.25 lbs. of nitrogen (N) with 40-60% of the N applied lost to the environment. Arbuscular mycorrhizal fungi (AMF), obligate endosymbionts of >70% of land species including corn, increase the amount of soil-derived N in plant material compared to plants without AMF. In growth chambers, common corn varieties are not grown to the seed stage, where the plant's N needs change. However, dwarf corn (DC) varieties can be grown to this stage. Mutations in genes responsible for DELLA proteins and gibberellin signaling make DC less likely to pair with AMF. Because AMF colonization is inhibited by extremely high and low gibberellic acid (GA); we tested the hypothesis that AMF colonizes some DC varieties more than others. To test this, we selected three DC varieties from the USDA germplasm repository. We inoculated these varieties with the spores of the model AMF species Rhizophagus irregularis. Using established staining techniques, we compared DC mycorrhization levels with each other and that of B73 a common high-yielding variety. Two DC varieties showed no apparent mycorrhization, while "Sweet Baby Blue" (SBB) had significantly more mycorrhization than B73. This result could be due to SBB's GA regulation. We plan to sequence the genome to identify mutations responsible for SBB's Dwarf phenotype and compare R. irregularis growth impacts between SBB and B73. SBB is a strong candidate for experiments assessing AMF-N dynamics throughout corn's life cycle.

**Poster Number: 88**

### Fusarium diversity and cryptic species from diseased soybean roots in Nebraska

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The genus Fusarium comprises at least 23 species complexes, recognized by their genetic diversity and morphology, with the most abundant being the F. incarnatum-equiseti, F. oxysporum, F. graminearum, F. solani, and F. fujikuroi species complexes (SC). Despite their known presence in the soil and plant roots, the diversity and distribution of Fusarium species and their impact on soybeans is not well documented. In this study, we conducted a survey to document root-associated Fusarium species from diseased soybean plants in Nebraska. Fusarium-like isolates (n=89) were sequenced for the translation elongation factor 1-α (tef1) gene. These sequences were aligned with 248 type sequences from Fusarioid-ID database and NCBI GenBank using MAFFT. A maximum likelihood (ML) phylogenetic tree was constructed with 1000 bootstrap support replicates using RAxML. Our findings indicate that Fusarium isolates from Nebraska soybeans belong to five major species complexes, with the highest diversity found within the F. incarnatum-equiseti species complex (SC), which contained six distinct species. In the F. fujikuroi-SC, five species were identified, while the F. graminearum, F. oxysporum, and F. tricinctum species complexes each had distinct species (n=3). F. commune was the only species identified in the F. nisikadoi-SC. Notably, 39 isolates could not be assigned to a specific species, indicating the presence of cryptic or novel taxa. These findings highlight the unexpected, hidden diversity of Fusarium species in soybean fields and emphasize the importance of accurate detection and identification to improve our understanding of the complex fungal interactions in natural and managed ecosystems.

### Poster Number: 90

### Tracing Host Specificity through Genomic Evolution of the “Insect Destroyers”

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Entomophthorales, commonly known as “Insect Destroyers,” are an ecologically significant fungal order with immense potential as biocontrol agents. However, their study has been limited due to challenges in culturing these obligate pathogens, as well as having only six publicly available genomes among hundreds of known species. This is in part due to their genomes averaging ~1 Gb, approximately 20 times larger than the average fungus. This knowledge gap has hindered our understanding of their evolutionary history, host specificity, pathogenic mechanisms, and phylogenetic relationships. By leveraging seven newly sequenced genomes, more than doubling the number currently available, this study aims to construct a comprehensive phylogenomic tree of Entomophthorales and identify novel genes involved in host infection. Our findings aim to expand the current genetic framework and broaden the known infection-associated gene repertoire. This will provide a crucial genomic framework for understanding the evolutionary trajectory of Entomophthorales, shedding light on their adaptation as insect pathogens and the genetic basis of their host interactions. This research will not only inform the development of these fungi as biocontrol agents but also deepen our understanding of their diversification, pathogenic strategies, and broader ecological roles.

### Poster Number: 91

### Antibiosis Bioactivity of Antarctic Fungi from Fildes Peninsula against Plant-Pathogenic Fungi Botrytis Cinerea and Fusarium culmorum

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Antarctic fungi are known for their adaptations to extreme environments, leading to unique bioactive compounds with potential agricultural applications. In this study, fungi were isolated from various substrates on the Fildes Peninsula in Antarctica and screened for their antibiosis activity against two significant plant pathogenic fungi, Botrytis cinerea and Fusarium culmorum. Using a dual-culture assay, the antibiosis activity of the isolated Antarctic fungi was evaluated. Several strains from genera such as Penicillium, Cyathicula, and Pseudeurotium exhibited significant inhibition of the pathogens’ growth, with Penicillium pancosmium showing the highest inhibitory activity against B. cinerea. Similarly, strains from Aspergillus and Tolypocladium displayed strong antagonistic effects against F. culmorum. Phylogenetic analysis using multi-genetic markers revealed diverse fungal species, some of which are novel, underscoring the underexplored biodiversity of Antarctic fungi. The findings suggest that these fungi hold promise for the discovery of new antifungal agents that can be applied in agriculture to manage fungal pathogens. This study contributes to expanding the knowledge of Antarctic fungal diversity and highlights their potential in biotechnological applications.

### Poster Number: 92

### Rooting substrate drives fungal community composition, diversity, and mycorrhizal colonization in tropical lianas

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Lianas play a significant role in forest ecosystems, contributing to connectivity, dispersal, and habitat formation. However, their increasing dominance in neotropical forests can suppress tree growth, alter canopy structure, and reduce forest productivity. Root-associated fungi, such as arbuscular mycorrhizal fungi (AMF) and dark septate endophytes (DSE), aid in nutrient uptake and stress tolerance, potentially providing a competitive advantage. This study investigates how lianas utilize adventitious roots and their associated fungi, focusing on how substrate variation affects fungal colonization rates and community composition. We hypothesized that substrate influences fungal colonization and diversity through environmental filtering, predicting that soils would have the highest colonization rates and most diverse fungal communities. Roots from co-occurring lianas were collected from three substrates—air, water, and soil—across five rivers in central Panama. Microscopic analysis showed differential colonization by AMF (soil > air > water) and DSE (soil/air > water). Molecular identification of fungal communities (Illumina NGS) revealed significant differences in Shannon and Simpson diversity indices, with soil hosting the highest alpha-diversity. Bray-Curtis dissimilarity showed fungal community composition varied by substrate: soil was dominated by Glomerales and Agaricales; air by Glomerellales, Xylariales, Hypocreales, and Agaricales; and water by Amphisphaeriales, Hypocreales, and Pleosporales. These results support the hypothesis that substrate influences fungal colonization and community composition, with soil showing higher colonization and alpha-diversity. The findings suggest that environmental factors like substrate may have a stronger impact on fungal community assembly than phylogenetic or spatial influences, enhancing our understanding of fungal community assembly and ecology of neotropical lianas.

### Poster Number: 93

### Evaluation of Passive Aerial Spore Trapping Techniques

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Fungal dispersal is a cryptic phenomenon with important outcomes for ecosystems and human health. Ranging from symbionts to saprotrophs, fungi perform essential functions in all terrestrial biomes of the Earth. Yet, questions regarding the dispersal of most fungi persist due to challenges associated with capturing and characterizing the microscopic spores used for fungal propagation. Previous studies have utilized passive spore trapping devices to capture deposition of aerial fungal communities. However, a lack of consensus on spore trap designs and sampling intensity limits the utility of these devices. Systematic comparisons between different spore trap designs are needed to identify the best practices for collecting passive deposition of fungal air spora. This study sought to compare the performance of three widely used passive spore trapping techniques: adhesive, liquid, and filter-based spore trapping. Twenty replicates of each spore trap were deployed within North Carolina's Duke Forest to assess both inter-method variability and the environmental stochasticity of air spora, which contributes to variation between replicates. After one week of outdoor exposure, molecular methods of DNA extraction, PCR, and amplicon sequencing were used to characterize and compare fungal communities from spore trap samples. Species accumulation curves were also generated for each spore trapping technique to determine the level of replication needed to capture aerial fungal diversity. Altogether, this study provides novel insights into the methods used for capturing airborne fungal propagules, which will support future research to expand our narrow understanding of fungal dispersal.

### Poster Number: 94

### Elucidating the Diversity of Galerina in Oregon Using Phylogenomics, Chemotyping, and Ecological Insights.

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The genus Galerina (Hymenogasteraceae, Basidiomycota) is a ubiquitous wood decay fungus that is taxonomically and chemically diverse. Galerina spp. are common in the Pacific Northwest and are found on every continent including Antarctica where they play critical ecological roles in carbon cycling as primary and secondary decomposers. In addition, some species produce deadly amatoxins and when accidentally consumed can cause death. Galerina marginata, G. castaneipes and G. venenata and relatives are found in the Naucoriopsis clade and are thought to be abundant in the Pacific Northwest. Despite their ecological and toxicological significance, understanding of the evolutionary history, chemical profiles, and ecological distributions of Galerina spp. are in their infancy particularly in Oregon. This study integrates phylogenetic analyses, chemotyping, ecological observations, and population genomics to better characterize species boundaries and toxic species distribution within the PNW with a focus in Oregon. ITS gene sequencing and phylogenetic analyses indicates that all three of the toxic species G. marginata, G. castaneipes and G. venenata frequently occur in Oregon and display populations with substantial molecular diversity. We will present preliminary results from our phylogenomic and chemotyping analyses of regional fresh and herbarium collections, as well as insights into population structure in the Pacific Northwest. Additionally, we will discuss the ecological significance of Galerina within forest ecosystems and how citizen science tools, such as iNaturalist, contribute to species documentation and distribution mapping.

**Poster Number: 95**

### Chestnuts: blight resistance among back crossed cultivars grown in tissue culture, and comparison of mycelial and spore inoculations

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Chestnut blight (Cryphonectria parasitica) has historically devastated the American chestnut, resulting in substantial ecological and economic impacts. Recent advances in plant tissue culture (PTC) offer new strategies for addressing diseases like chestnut blight. This approach generates genetically identical clones, providing a controlled environment to study disease resistance and fungal symbiosis, compared to traditional seed propagation. Here, we assessed blight resistance of four backcross chestnut cultivars of the burgeoning American chestnut industry —Marsol, Maraval, Marigoule, and Précoce Migoule, by comparing both detached leaf and stem assays. These assays demonstrated a spectrum of resistance levels across the cultivars, highlighting the potential for selecting and advancing blight-resistant lines. The identification of cultivars with enhanced resistance is essential for sustainable chestnut production, potentially mitigating the devastating effects of chestnut blight and supporting the recovery of this valuable species and industry. The generation of chestnut plantlets also provides opportunities to of integrating resistant chestnuts into truffle agroforestry systems. There is growing interest in integrating chestnuts into truffle agroforestry, which could potentially enhance biodiversity and yield economic benefits. We inoculated blight-resistant chestnut plantlets with Tuber species using both spores and pure mycelium on potting soil substrates. While it was possible to grow mycelium on these substrates, the method proved challenging and rarely succeeded in our trials. These results demonstrate the promise of chestnut micropropagation in nut and truffle agricultural ecosystems.

**Poster Number: 96**

### Using Validated PacBio Sporocarp ITS Sequences to Test the Accuracy of UNITE and GenBank and Improve the Identification of Macrofungal Environmental Sequences

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To better identify environmental sequences of macrofungi we used validated sporocarp PacBio ITS sequence data to check and augment UNITE and GenBank database matches. We also examined ITS variation within specimens, which can affect taxonomic decisions but is rarely accounted for. We collected and sequenced sporocarps (PacBio) and soil samples (Illumina) from the HJ Andrews LTER in Western Oregon. The sporocarp sequences were identified using a combination of GenBank BLAST tools, UNITE, specimen morphology (photographs of all specimens were posted on iNaturalist), literature searches for phylogenies including the top matches, comparing with known Types, and by comparison with the Pacific Northwest Key Council Regional Database of sequences. UNITE correctly identified only about 1/3 of sporocarp OTUs to species and 1/3 had no taxonomy assigned. The top BLAST match in GenBank was also correct about 1/3 of the time. Our sequence-based sporocarp identifications thus tripled our ability to identify environmental DNA to species. PacBio sequencing reveals that although there are multiple ITS variants associated with most (±99%) individual sporocarps, they are almost always dominated by one or two variants that are >99.5% similar. Conclusions: 1. The UNITE database is biased towards European taxa and does a poor job of identifying sequences from the Western US. We recommend augmenting the UNITE database with your own validated sequences. 2. ITS sequence variation within individuals is usually small enough to not matter to identification. Rare exceptions may suggest recent hybridization, if sequence divergences are clustered.

### Poster Number: 97

### One Symbiont Doesn't Fit all: Intraspecific Variation within Plant-Am Fungal Mutualisms

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Variation between plant and AM fungal species leads to different outcomes for both plant and fungal fitness. However, little is known about how intraspecific variation in plant and AM fungal symbionts influences these mutualisms. Since many plant and AM fungal taxa have widespread distributions, it is likely that local adaptation to different symbionts and environments alters the symbiotic capabilities of different plant and AM fungal genotypes. We tested how intraspecific variation in two AM fungal taxa: Scutellospora pellucida (4 genotypes) and Funneliformis mosseae (4 genotypes) influenced symbiotic outcomes with Capsicum annuum (4 cultivars). For C. annuum cultivars we measured vegetative and fruit biomass, and for AM fungi we measured root colonization and external hyphal biomass. AM fungal effects on C. annuum biomass varied between and within AM fungal species. C. pellucida had neutral effects on vegetative biomass, whereas F. mosseae generally had negative effects on biomass, but this effect varied between cultivars. While interspecific variation in AM fungal effects on biomass were greater than intraspecific effects, strain level effects did vary, with some C. pellucida strains having positive effects and some F. mosseae having neutral effects on biomass. While genotype x genotype interactions were non-significant for vegetative biomass, they did influence fruit biomass. C. pellucida and F. mosseae promoted fruit biomass for earlier fruiting cultivars; however, some strains were less beneficial than others. AM fungal colonization and hyphal biomass are being assessed. This demonstrates how intraspecific variation in AM fungal mutualisms influences the benefit received by plant and fungal symbionts.

### Poster Number: 98

### Post-Fire Oak Mycorrhizal Associations Are Dominated by Russulaceae, Thelephoraceae, and Laccaria in the Southern Appalachian Mountains

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Following disturbances such as wildfires, oak seedlings must form a symbiotic association with mycorrhizal fungi to survive. Wildfires, however, reduce available mycorrhizal fungal propagules in the soil. Ectomycorrhizal (ECM) fungi on oak seedlings sampled in severely burned (7 sites), moderately burned (7 sites), and unburned areas (8 sites) in the Great Smoky Mountains National Park were evaluated 21 months after the 2016 Chimney Tops 2 Wildfire by sequencing the nrITS region. Sequences were aligned and grouped into Operational Taxonomic Units (OTUs) based on well-supported phylogenetic clades and 98-100% nrITS sequence homology with sequences in GenBank. 179 root-associated fungi comprising 124 OTUs were recovered after removing duplicates (the same fungus on two or more roots of the same plant). The ECM genus Russula was the most diverse genus (25 OTUs), followed by the Thelephora/Tomentella clade (18 OTUs), Lactifluus (8 OTUs), and Lactarius (4 OTUs). Laccaria aff. laccata (14/179 total root-associated fungi = 7.82%). Russula OTUs were identified more frequently on oak roots from burned areas and in burned soils, suggesting that some Russula taxa may have a selective advantage in burned areas. High alpha diversity occurred within each of the burn categories, but little overlap of taxa occurred between burn categories (high beta diversity). Approximately half of the recovered OTUs (100/179 total root-associated fungi = 55.9%) were found only once. As wildfires become more frequent, it becomes important to understand post-fire symbioses. This study is a first step in that direction

### Poster Number: 99

### Characterization of Orchil Dye-Yielding Lichens in the Driftless Area

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As consumers rethink their relationship to waste and allergens in the textile industry, there has been a renewed interest in natural dye practices. Some species of lichen produce secondary metabolites that are known sources of dye-yielding pigment, and lichens have been used in textile dyeing for thousands of years. The identities of lichen specimens collected in the Driftless Area of western Wisconsin were confirmed using a combination of morphological characters and Sanger sequencing of the ITS region of the rDNA. A chemical analysis of the specimens was performed using HPLC and the secondary metabolites known to create dye-yielding pigment were characterized. Dye extractions using the ammonia method were created and analyzed using HPLC. This poster provides insight into a historically significant use of lichens and elaborates on the chemistry of orchil lichen dyes.

### Poster Number: 100

### Effects of agricultural intensity on soil fungal and bacterial communities

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Arbuscular mycorrhizal fungi of the phylum Glomeromycota are inextricably linked to terrestrial plant life. The fungal partner provides the plant with access to soil nutrients in exchange for organic compounds from the plant. AM fungi harbor a microbiome distinct from the surrounding bulk soil in an area called the hyphosphere. The bacteria in this region provide AM fungi with nutrients for their host plant that stabilize the mycorrhizal symbiosis. AM fungi cannot acquire these nutrients on their own, and thus the hyphosphere microbiome has been called the “second genome” of AM fungi. This results in a tripartite plant-fungi-bacteria relationship which has evolved due to environmental limitations. High-input agricultural practices remove these limitations and uncouple the evolutionary feedback between the plant and its partners. By better understanding how various intensities of agricultural practices affect AM fungi and soil bacteria, farmers can make informed decisions about how to manage their soil microbiota. While existing research has explored plant-fungi-bacteria relationships in organic farm soils, these relationships have yet to be profiled in Native American farms practicing traditional agriculture, of which many of the organic farming practices are based on. This research will explore how converting land to various intensities of agricultural use affects the fungi and bacteria in the soil. Similarly to how knowledge of the mycorrhizal symbiosis has changed the concept of what it means to be an individual plant organism, the inclusion of the hyphosphere microbiome into mycorrhizal research could revolutionize mycorrhizal theory.

**Poster Number: 1**

### Changes in Soil Microbial Diversity and Community Composition across a Pine Invasion Gradient

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Soil microbes are crucial in the establishment of forest ecosystem services. However, non-native tree introductions can disrupt microbial-mediated ecosystem functions. While invasions between hemispheres of ectomycorrhizal fungi-pine associations have been studied, their effect on free-living microbiomes in forest soils. We collected bulk soil samples from Pinus radiata trees in its native USA forests, Australian P. radiata plantations, eucalyptus forest invasions, and eucalyptus trees without pine invasions. We profiled fungal and bacterial communities of these soils using amplicon sequencing. Bacterial richness was significantly greater in the plantation interior than in any other Australian forests. Comparisons of the beta diversity between forest types were significantly different as well, with the exception of comparisons between the plantation edge, invasion front, and eucalyptus forests. In contrast, we observed significant increases in fungal richness for pine invasion sites compared to native eucalyptus forests. However, there was no significant difference in richness for the remaining Australian forest types. All forest types expressed significantly different fungal communities. Having the ectomycorrhizal fungal (EMF) community extracted from our fungal dataset, we did not observe a significant difference in alpha-diversity in EMF communities within sampled AUS communities. Beta diversity was significantly different except between plantation interior and edge. We identified Inocybaceae as an EMF family whose relative abundance is significantly higher in pine invasions than adjacent forest types, and may have a previously unexplored role in pine invasions for these ecosystems. Our work will continue to analyze the relation between taxa of fungal and bacterial communities present in these ecosystems.

**Poster Number: 2**

### Phylogenetic Assessment of Trichoderma Strains from Usda-Ars Culture Collection and U.s. Quartermaster Collection

Kirk Broders, USDA-ARs

The ecological, genetic and enzymatic variation of Trichoderma, combined with advances in molecular taxonomy and industrial applications has created renewed interest in assessing global ecology and enzymatic capacity of this genus. The ARS Culture Collection (NRRL) received the U.S. Army Quartermaster (QM) biodegradation fungi collection in the 1970's. These strains were collected during World War II, mainly in the South Pacific, Panama and Florida where tents, clothes and other fabrics were degraded faster than could be manufactured. The goal of this study was to provide an accurate identification and phylogenetic assessment of the Trichoderma strains in the NRRL and QM collections. We used a multi-gene approach sequencing the ITS, tef and rpb2 genes of 200 Trichoderma strains from the NRRL and QM collections and combined this with sequence data from type strains or vouchered specimens accessed from www.trichokey.info. We identify 71 distinct species from across the genus. This included 20 putative novel species, including several closely related species to T. reesei (QM6a) collected from southern Pacific Ocean islands, multiple species from the lowland tropics of Panama, as well as several species associated with soil, corn and fungal perithecia in the United States. This work demonstrates both the importance of retaining legacy collections as well as updating the molecular taxonomy of these collections and making these resources available to the public.

**Poster Number: 3**

### Members of the TLO (telomere-Associated) Expanded Gene Family display interwoven transcriptional and phenotypic roles in Candida albicans

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Gene duplication is the most common mechanism of producing new genes across the tree of life. Cells containing duplicated genes are usually culled from the population due to fitness defects. Thus, retained paralogs may have implications to organismal fitness by increasing gene expression, encoding a specialized function, or acquiring novel function. Repeated duplication can lead to the formation of highly homologous gene family members. While the function of gene duplicates has been studied in detail, little work has explored how emergence of repeated paralogs may restrict novel function development and lead to widespread redundancy. Here, we constructed a panel of single deletion mutants for the Candida albicans telomere-associated (TLO) gene family to test for phenotypes caused by loss of just one of the 14 paralogs. Tlo proteins function as interchangeable subunits of the Mediator transcriptional regulatory complex and therefore have the potential to alter a wide range of phenotypes, including those linked to the balance between commensalism and pathogenesis. Transcriptional and phenotypic analysis suggests both redundant and non-redundant functions among paralogs. Loss of a TLO gene altered the phenotype under most conditions, such as cell wall perturbation and lactate utilization. Conversely, some mutants were indistinguishable from the wildtype for growth rate in nutrient-rich medium and azole resistance and tolerance. Construction of two double mutants produced specific synergistic phenotypes, suggesting that TLOs “talk” to each other. TLO retention appears to enable adaptation across diverse conditions, with each gene contributing to significant and widespread expression changes, irrespective of architectural group association.

**Poster Number: 4**

### A Broad-Spectrum Antimicrobial from the Gras Fungus Aspergillus oryzae to Combat Human Pathogens

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Antimicrobial resistance (AMR) represents a critical global health challenge, as multidrug-resistant bacterial and fungal pathogens render conventional treatments increasingly ineffective. To address this global threat, we have developed Natural Protectant (NP), an antimicrobial product derived from the Generally Recognized As Safe (GRAS) fungus Aspergillus oryzae. NP is produced via the fermentation of food substrates, showcasing broad-spectrum antimicrobial activity against both bacterial and fungal pathogens, including those identified as serious AMR threats by the CDC and WHO. In broth culture, NP effectively eradicated methicillin-resistant Staphylococcus aureus (MRSA) and enteropathogenic Escherichia coli O157:H7, achieving greater than 1,000-fold reductions within 24–48 hours. Additionally, NP demonstrated strong inhibitory effects against other ESKAPE pathogens, a group of antibiotic-resistant bacteria highly associated with healthcare-associated infections. Beyond its antibacterial properties, NP exhibited potent antifungal activity, effectively killing human pathogenic fungi Candida auris, Candida albicans, and Aspergillus fumigatus, including azole-resistant strains. Encouraged by these results, we aim to further develop NP as a therapeutic for bacterial and fungal infections. Preliminary toxicity testing has shown that NP was not toxic to human MCF-7 cells, suggesting its potential for clinical application. Future efforts will focus on isolating and identifying the specific antimicrobial molecules in NP to develop a novel, broad-spectrum antibiotic that could play an important role in combating AMR and improving public health.

**Poster Number: 5**

### A Fungal masquerade: A Neotropical Hygrocybe Clade Containing Species with Long Stipes and Reduced or absent Caps and Gills

D Jean Lodge, Georgia Museum of Natural HIstory Fungarium
Cathie Aime, Purdue University

Surveys of basidiomycete fungi in Guyana and a cloud forest on the highest peak in Belize (Doyle's Delight) revealed through ITS and LSU sequencing a phylogenetic clade of Hygrocybe that includes a dozen long-stiped species with reduced caps and species lacking caps and/or lamellae that mimic Clavulinopsis and Cyphellostereum. A Physalacria-like collection from cloud forest in Ecuador was also found to belong to this clade based on BLAST searches in GenBank. This includes H. cantharellus and H. caespitosa in subgenus Pseudohygrocybe, section Squamulosae with monomorphic basidia and spores but most of the species in this clade have dimorphic spores and basidia. The appearance of dimorphic basidia and spores is scattered through the clade but the selection pressures for this trait are unknown. The selection pressures that led to a predominance of reduced basidiomes lacking caps or lamellae and the frequent production of long stipes are also not apparent. The radiation of this clade of Hygrocybe in Guyana is likewise unexplained, though increasing evidence that species in this genus are root endophytes leads us to hypothesize that host-plant relationships may have contributed to speciation in this group.

**Poster Number: 6**

### Culturing fungi, cultivating skills: A Myco-Ed approach to hands-on mycology research in the undergraduate classroom

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Providing undergraduates with hands-on research opportunities in mycology can foster skill development, confidence, and engagement with the scientific process. In collaboration with Myco-Ed and the JGI, a course-based research project was developed to introduce students to core mycological techniques while contributing to the broader goal of increasing the number and diversity of sequenced fungal genomes. Students isolated foliar fungal endophytes from locally collected plants and documented their collections on iNaturalist. Pure cultures were established, DNA was extracted, and the fungal ITS region was PCR-amplified and sequenced. Each isolate and its ITS sequence were documented on iNaturalist and linked to the original iNaturalist observation, creating a publicly available record. To explore functional traits, students conducted abiotic stress assays examining fungal growth across temperature gradients (4, 20, and 37 °C) and zinc concentrations (0, 1, and 10 µM). Although stress assay data were variable due to logistical challenges the project provided meaningful, hands-on experience in fungal culturing, molecular methods, and data interpretation. Of the 42 isolates generated, 34 yielded quality ITS sequences and assay data. Six were selected by JGI for whole-genome sequencing, contributing to the larger Myco-Ed effort to document underrepresented fungal diversity. As a Hispanic-serving institution with a large population of non-traditional students balancing work and family obligations, this course-based research model created an accessible entry point for students who may not otherwise participate in independent research. This project highlights the feasibility and impact of integrating open-ended, mycological research into undergraduate curricula.

**Poster Number: 7**

### Understanding Basidiobolus-bacterial interactions using a stabilized microbiome model

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Basidiobolus is a fungus that is adapted to different ecological niches. One stage of its life cycle occurs in the gut microbiome of species of amphibians and reptiles. In this environment, Basidiobolus is abundant, prevalent, and co-structured with the bacterial community. The Basidiobolus genome is enriched in genes annotated to encode for non-ribosomal peptide synthetases and other specialized metabolites. While many of these compounds are predicted to be involved in interactions with bacteria, their impact on the structure, function, and general ecology of the gut environment is not yet understood. We hypothesize that specialized metabolites produced by Basidiobolus decrease compositional and functional diversity of the bacterial community, shifting the relative abundance of specific taxa in a predictable direction. To test this, a fecal sample from a lab-reared wood frog (Lithobates sylvaticus), raised in the absence of Basidiobolus, was cultured in multiple media conditions and serially transferred into fresh media every 48 hours. After the seventh passage of cells, composition of the cultures was assumed to be stable, and two additional transfers were conducted and treated with Basidiobolus crude extract or control. The 16S rRNA amplicon sequencing results from this stabilized microbiome model show that bacterial community composition is diverse, stable by the third passage at the family-level, and that Basidiobolus crude extract has a significant nonrandom effect. We will also present metagenome-assembled genomes (MAGs) to examine functional shifts in the bacterial community and LC-MS2 results from the crude extract to characterize metabolites that may function in bacterial-fungal interactions.

### Poster Number: 8

### Diversity of Massospora Spp. (Entomophthorales) on Infected Periodical Cicadas

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Members of the entomopathogenic fungal genus Massospora are obligate pathogens of cicadas (Hemiptera, Cicadoidea). These fungi hijack sexual and other behaviors of the host to increase transmission and infection. Periodical cicadas are exclusively found in North America, and depending upon the species, emerge synchronously every 13 or 17 years. As nymphs eclose into adults, resting spores of Massospora cicadina present in soil infect their hosts. However, little is known concerning Massospora diversity on infected periodical cicadas and any impacts of cicada species and sex on such diversity. Here, using amplification and sequencing of four gene loci, namely, 18S, Tef1-a, b-tubulin, and ITS, phylogenetic analyses of a cohort of Massospora samples collected from infected adult periodical cicadas were performed. Phylogenetic trees based on the 18S, Tef1-a, b-tubulin, and/or ITS showed clustering of isolates into 2-4 subclades, and when using the concatenated (18S, Tef1-a, b-tubulin) sequence. Conidial spores were observed on most cicadas examined suggesting robust horizontal infection transmission. Conidial spores were examined morphological via brightfield, phase contrast, and fluorescent microscopy, the latter following DAPI and phalloidin nuclear and actin staining, respectively. The fungal cells were highly granular, with conidia containing one to three nuclei. Cells showed punctate patterns of phalloidin-actin staining. Two sub-morphologies of conidia were apparent: (i) cells which were slightly oblong (length: 10-14 µm; width: 7-10 µm), and (ii) larger and more circular cells (diameter: 15-20 µm). These data highlight potential diversity within M. cicadina, with the possibility of sub-species present.

### Poster Number: 9

### Enhancing Germination and Assessing the Impact of Fungal Communities on Seed Viability in the Tropical Medicinal Tree Mitragyna speciosa

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The propagation biology of a tropical seed can be largely influenced by endophytic and epiphytic fungi. Kratom (Mitragyna speciosa korth.), a Southeast Asian tree species producing indole alkaloids of pharmaceutical interest, exhibits poor seed germination in part due to persistent fungal colonization. In light of this, kratom seed was subject to variable chemical sterilization concentration and sowing medium amendments then assessed for germination strength and velocity, embryo viability, physical condition, and endophyte community assembly. The seed lot used was found to contain 31% viable seed, but exhibited only 6-10% germinability without chemical treatment, whereas maximal germination was achieved following 5% (v/v) sodium hypochlorite sterilization. The supplementation of Rhizophagus irregularis inoculum enhanced germination at all chemical levels compared to sterile substrate, which was found to be consistent when tested in separate seed lots. Additional culture-based methods and amplicon sequencing revealed the presence of endophytic fungi hosted by kratom seed. This study is the first to provide direct evidence of fungal associations with kratom seed, offering valuable insights for developing effective propagation techniques and fungal management strategies in kratom cultivation.

### Poster Number: 10

### Root-Associated Trichoderma: Their Role on Plant Growth and Pathogen Control in Foundational American Grasses

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Rhizosphere fungi are known to exhibit beneficial effects on plants through a number of different mechanisms. Trichoderma, a soil and plant-associated fungus, is known to produce volatile signal molecules responsible for mediating plant and microbial growth. This research focuses on the potential roles of volatile organic molecules in foundational American grasses produced by root-associated Trichoderma isolates. Trichoderma isolates tested on grasses using indirect contact assays showed positive effects on plant growth with respect to the controls with Trichoderma gamsii showing the largest increase on shoot and root growth compared to the controls and other isolates. The largest effect on plant growth results were obtained when Trichoderma was grown on malt extract agar (MEA) and observations under the microscope showed a reduction in the germination of pathogenic spores of seed-borne fungi in grass seedlings. T. gamsii is capable of inhibiting the germination and hyphal growth of Alternaria when cultures were in close proximity but not in direct contact with Trichoderma colonies. In this study, Trichoderma showed important ecological functions including the control of seed-borne pathogens in grasses and improvement of plant growth likely by mediating plant pathogens present in seeds during early stages of germination. Our study brings new light to the roles of Trichoderma, a root and soil fungus, in American grasslands. Further, the characterization of Trichoderma VOCs could enhance current understanding indirect fungal-plant interactions on plant establishment via the control of plant pathogenic fungi. Keywords: Rhizosphere, T. gamsii, Trichoderma, volatiles.

### Poster Number: 11

### Can Fungi Fix Carbon?

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Fungi have been shown to react to carbon dioxide (CO2) as an environmental signal. Previous studies suggest that species of Ganoderma and other fungi possess carbonic anhydrases, enabling them to convert $CO_2$ into bicarbonate. This could be adaptive in high CO2 environments. This project aimed to assess whether Ganoderma is able to capture carbon into biomass under differing CO2 conditions. Fungi were incubated in a closed system for 10 days in 0-28% CO2 concentrations. Headspace gas was diluted and tested using flame ionization detector (FID) gas chromatography. The biomass for each experimental group did not change and stayed at an average of 15mg after 10 days of growth. Headspace measured within the experimental vials showed an increase in CO2 (_______ppm/day/biomass) consistent across the different starting CO2 concentrations. We did not find evidence that fungi fix CO2, but this experiment allowed us fungal CO2 respiration. These data allow us to estimate how much fungal CO2 is produced in the environment as well as anthropogenic sources including mushroom farms and myco-material factories. Methods developed in this study can be used to investigate fungal biogeochemistry.

### Poster Number: 12

### Utilizing presence only prediction to model Morchella diminutiva distribution

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The morel mushroom has long been known for its superior taste, and due to their elusiveness and ephemerality some are left understudied. Morchella diminutiva has been recently described in 2012 where some of their ecology was postulated, but little follow up research has been put forward to support the suggestions. GIS analyses can create a predictive species distribution model which we can use to shed light on habitat preferences and

guide future environmental research. MaxEnt is a geospatial analysis program that we can use to do this; it uses environmental data and presence points to create a distribution model as well as identify which environmental factor(s) best predicts Morchella diminutiva growth. Mean temperature in the coldest quarter, land cover type, and forest type provided the biggest contribution to the model and we yielded an AUC of .899, meaning that the model shows a relatively high performance. These results are also currently in the process of being verified through an independent dataset generated from an eDNA assay, and are anticipated to support the current findings.

### Poster Number: 13

### Species-specific detection tools for the identification of the three fungal pathogens responsible for invasive oak wilt diseases in Japan, Korea, and the USA

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There are three invasive insect-vectored fungal oak wilt pathogens, Bretziella fagacearum, Dryadomyces quercivorus, and D. quercus-mongolicae, that are limited geographically to North America (NOW), Japan (JOW), and Korea (KOW), respectively. The eastern U.S.A. and eastern Asia have similar temperate biomes conducive to the survival of the beetle vectors and the pathogens, raising concerns that introduction of either of the JOW or KOW pathogens to North America would be devastating to U.S. forests. However, the susceptibility of North American oak species to JOW and KOW is not known. Understanding the biology and pathogen-host interactions allow for the development of robust rapid detection tools that currently do not exist for these pathogens and are necessary for early detection and spread mitigation. This international research project has three main objectives: 1) determine if host range of oak wilt pathogens extends to ecologically and economically important North American red and white oak species; 2) improve genomic resources for the oak wilt pathogens using hybrid genome assemblies and full-length transcripts; and 3) develop and validate laboratory and field diagnostic assays to detect the three oak wilt pathogens using multiple platforms (e.g., metagenomics, metabarcoding [tef1a, rpb2, and the ribosomal RNA operon], real-time PCR, LAMP, and RPA primers including a lateral flow component) to meet the varied needs of different stakeholder groups.

### Poster Number: 14

### Exploring Truffle Fungi in the Upper Midwest of North America

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Truffle fungi are a cryptic yet charismatic group including genera with rich culinary and ecological histories. Because their sequestrate spore-forming bodies are often found below ground, their distribution ranges can be less well-documented than other macrofungi. While there is a strong record of truffle documentation in certain parts of North America, there is still a need to fill in sampling gaps. One such area that has been comparatively under-sampled for truffle fungi is the Upper Midwest region. We present here a summary of truffle fungal diversity data for this region. The genera *Elaphomyces*, *Genea*, *Geopora*, *Hymenogaster*, *Pachyphlodes*, *Rhizopogon*, and *Tuber* are included among others. Sources for this data include MycoPortal, GlobalFungi, Mushroom Observer, iNaturalist, and surveys with academic and community scientists. The results are presented here to convey the state of our knowledge and to dig deeper into any patterns that can be discerned in the data.

### Poster Number: 15

### Baseline fungicide sensitivities for US clonal lineages of Phytophthora infestans

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Late blight disease of tomato and potato is caused by Phytophthora infestans, a heterothallic oomycete that proliferates primarily via clonal reproduction in the United States and is seasonally spread by wind. In potato, late blight disease causes up to $10 billion globally from crop loss and control costs. In the USA, US-23, which emerged in 2009, is the current dominant lineage. Lineages have fluctuated over time throughout the US, with lineages US-8, US-11, and US-23 being the most common in recent decades. Control of late blight depends heavily on chemical methods, as well as breeding for genetic resistance in tomato and potato. Monitoring for fungicide resistance in P. infestans is important for informed disease control. This work is a baseline fungicide sensitivity assay using at least 10 clonal lineages of P. Infestans with geographically and temporally diverse isolates, and a range of commonly used and recommended fungicides. The trade name and active ingredients of the tested fungicides are: Ridomil (mefenoxam); Orondis (oxathiapiprolin); Intego Solo (ethaboxam); Revus (mandipropamid); Omega (fluazinam); and Ranman (cyazofamid). Results will give lineage-specific information about fungicide resistance that is useful to growers. These assays could also serve to inform a future exploration of the molecular basis for resistance to respective fungicides.

### Poster Number: 16

### The Volatilomes of Penicillium Crustosum G10 and Penicillium Solitum Sa

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Penicillium crustosum and Penicillium solitum are common molds, capable of growing at cool temperatures and low water activities, best known for their capacity to contaminate cheeses, pome fruits, and meats. Many strains of P. crustosum and P. solitum produce bioactive secondary metabolites, however very little is known about their volatile metabolism. In this study, a comprehensive identification and analysis of volatile organic compounds (VOCs) profiles emitted by P. crustosum strain G10 and P. solitum SA was conducted by using gas chromatography-mass spectrometry (GC-MS). When grown in laboratory media, altogether, 25 different VOCs were identified from P. crustosum G10, and 17 different VOCs were identified from P. solitum SA. The VOCs from G10 were categorized into six groups according to their functional groups: alcohols (four VOCs), nitriles (three VOCs), alkenes (four VOCs), ketones (two VOCs), esters (five VOCs), and alkanes (three VOCs). Interestingly, 2-tetradecanol and benzyl nitrile have been developed as environmentally safe control agents of pests; 5-eicosene, (E)- has showed anticancer function; and 4-acetylphenoxyacetic acid has promise for the inhibition of HIV; while 7-hexadecene, (Z)-, octadecanal and 2(3H)-furanone, 5-dodecyldihydro- are volatile pheromones in insects. The VOCs from P. solitum SA were categorized into four main groups: alcoholic compounds (two VOCs), aromatic compounds (four VOCs), esters (three VOCs), and alkene compounds (three VOCs). The potential application values of these VOCs are discussed which may provide new perspectives on their future utilization.

### Poster Number: 17

### Deciphering Plant Molecular Responses to Enzyme-Based Foliar Pesticides

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The control of foliar diseases is imperative to guarantee a stable global food supply. Currently crop production relies heavily on synthetic chemical pesticides that have severe negative consequences on human and environmental health, while also posing a constant financial burden on growers. Zymtronix Catalytic Systems Inc., has developed a novel enzyme-based broad-spectrum biopesticide for suppression of foliar diseases. The biopesticide has been shown to have antimicrobial activity and to activate the plant immune system. However, the specific molecular mechanisms through which this is achieved have not been fully elucidated. We evaluated the biopesticide for control of foliar diseases caused by both bacterial and fungal pathogens of beets (Pseudomonas syringae pv. aptata) and tomatoes (Pseudomonas syringae pv. tomato, Alternaria tomatophila, and Phytophthora infestans) under greenhouse conditions. Leaf tissue was gathered 9h and 24h after each treatment (preventative spray, curative spray, and pathogen inoculation) and the transcriptomic profiles of these samples are currently being generated. This data will provide us with important insights into the molecular mechanisms mediating control of foliar diseases, while also providing targets for the management of fungal and bacterial pathogens that may aid in the development of more sustainable products.

Poster Number: 18

## Ectomycorrhizal fungi associated with three co-occuring Pinus species on the Far North Coast of California

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Ectomycorrhizal (ECM) symbioses predominate in many higher latitude forests around the globe. Northern California has many ECM tree species, but the ecology of their associated ECM fungi is poorly known. In California's far north coast the co-occurence of three Pinus species, along with a disjunction between populations of Pinus muricata in Mendocino and Humboldt Counties, offer a unique opportunity to investigate the spatial and host effects on pine-associated ECM fungi. In Humboldt native Pinus muricata and Pinus contorta subsp. contorta co-occur at their northern and southern respective range limits, while introduced Pinus radiata has been widely planted. In the present study ECM fungal sporocarps and root tips were collected in monospecific stands of each respective Pinus species at multiple sites. Ectomycorrhizal sporocarps were identified morphologically and barcode-sequenced to provide an identification database for NextGen-sequenced ECM fungi from root tips of each pine species. Preliminary results indicated that dune-inhabiting Pinus contorta subsp. contorta had a high relative diversity of ECM fungi with Thelephorales and Atheliales as key mycobionts. Ectomycorrhizal fungal communities also varied between disjunct Pinus muricata populations. Community composition and diversity of ECM fungi associated with each Pinus species will also be discussed.

Poster Number: 19

## Assessing Red Oak Stumps as Courts of Infection for Bretziella fagacearum in Michigan

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Oak wilt, caused by the ascomycete pathogen Bretziella fagacearum, is a devastating disease of oaks in the United States. New epicenters can lead to rapid mortality and pocket expansion through the translocation of fungal propagules via root grafts. Vector beetles carry spores to open wounds in the canopy and on the bole of mature oaks. However, literature is absent on whether Bretziella fagacearum can successfully infiltrate a fresh-cut stump and infect young stump sprouts. Oak wilt management in thinning and oak regeneration operations should be informed by the risk of stump infiltration and disease pressure. This study compared real-time PCR detection rates of Bretziella fagacearum in artificially inoculated fresh-cut red oak stumps across several biologically relevant inoculum concentrations. Sapwood, root, and stump sprout petioles were sampled from 36 stumps across two sites in 2023 and 2024. Multi-stem and adjacent oaks within root grafting distance were monitored for symptom development. All tissue types returned positive real-time PCR results, indicating stumps can act as courts of infection. As inoculum concentration increases, so does the ratio of infected stumps (0%-75%). Logistic regression analysis revealed significant differences between inoculation groups, with the 500,000 spore inoculation being seven times more likely to return a positive than the negative control. Sapwood samples were most likely to result in a positive detection (27.7%). Our findings highlight the importance of treating, covering, or removing stumps in locations with oak wilt on the landscape. These results can inform land managers and complement vector trapping studies and risk models.

Poster Number: 20

## New or Unusual Oomycetes Collected from Turfgrass in New Jersey and North Carolina

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As part of the testing of a new oomycete specific primer set designed to amplify the cox1, spacer, cox2 region and sequenced using an Oxford Nanopore Technologies (ONT) device, environmental samples were taken from turfgrass sites in North Brunswick, NJ and Clayton, NC. Phylogenetic analysis determined the presence of two new Pythium species in the New Jersey samples and the presence of a species of the poorly understood genus Pythiogeton in the North Carolina sample. All three taxa were baited out of cores taken from turfgrass plantings and their colony

morphology characterized on corn meal agar, V-8 agar and potato-carrot agar. The Pythium species were grown on V-8 agar at 0, 5, 10, 15, 20, 25, 30 and 35 C to determine their optimal growth temperatures. All taxa were grown on autoclaved grass blades in sterile water and incubated at 5, 10, 15, 20 or 25 C and observed for sporangia, zoospore release, hyphal swellings, appressoria, oogonia, antheridia and mature oospores. The Pythiogeton matches the description of P. ramosum, possibly the first record of this organism in the U.S. The organism is probably acting as a saprophyte, although Pythiogeton can be a weak plant pathogen. One of the new pythiums (provisionally Pythium quipu) releases zoospores from undifferentiated hyphae and has frequent hyphal swellings and infrequent thick-walled oospores, while the other (provisionally P. japamala) produces swollen lobed sporangia and frequent mono- and diclinous oospores.

### Poster Number: 21

### Draft Genome Sequence and De Novo Assembly of Mycotoxin-Producing Fusarium Cerealis Isolate Associated with Ear Rot of Corn (Zea mays)

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Fusarium cerealis represents a significant phytopathogen within agricultural systems, particularly impacting cereal crop production. Notably, crops such as corn, wheat, and oats exhibit high susceptibility to the diseases and mycotoxins produced by F. cerealis. Among these mycotoxins is the type B trichothecene known as nivalenol (NIV), which is a toxic secondary metabolite that poses risks to both plant health and food safety. The isolate of F. cerealis used in this study was obtained from symptomatic ears (ear rot) of corn collected in 2023 from Portage County (Wisconsin, USA). Genomes of plant-pathogenic fungi are replete with an array of virulence genes that encode various secondary metabolites, which play critical roles in the incidence and severity of diseases. This paper presents the first comprehensive high-quality genome assembly of F. cerealis, achieved through the utilization of long-read sequencing (Oxford Nanopore Technologies, Oxford, UK). The final genome assembly (Flye) comprises 63 contigs, with an N50 value of 8.8 Mb, indicating a substantial degree of continuity and quality. The largest contig reached a length of 11.8 Mb, and the mean genome coverage was 224x. This newly generated draft genome represents a vital resource that will facilitate future research endeavors aimed at exploring the genomic characteristics of pathogenic F. cerealis species prevalent in the Midwest, with a focus on identifying novel secondary metabolites that may contribute to their virulence and adaptability in various agricultural environments.

### Poster Number: 22

### Pathogen Induced Dysbiosis Predictably Restructures the Snake Skin Microbiome in Community Enrichment Experiments

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Snake Fungal Disease (SFD, ophidiomycosis) is an emerging disease that has been linked to declines in North American snake populations. Ophidiomyces ophidiicola, the causal agent of SFD, is an epidermal pathogen that causes dysbiosis to the skin microbiome of snakes across broad spatial and phylogenetic scales. The microbiome is an important component of host health that provides disease resistance against wildlife pathogens. Dysbiosis is defined as disruption to the typical composition and function of a microbiome, potentially resulting in adverse effects to host health. Limited understanding of the interactions between pathogenic fungi and skin microbial communities presents challenges for the effective management of fungal pathogen outbreaks in wildlife and human populations. This study will characterize the influence of O. ophidiicola on the structure of skin microbial communities in a simple and manipulatable laboratory system, to contribute to a greater understanding of the mechanisms dictating skin microbiome assembly. We have optimized an in vitro microbial community assembly system to test direct interactions between O. ophidiicola and the snake skin micro/mycobiome in synthetic minimal media that mimics skin chemistry. Using this experimental setup, we will measure shifts in community structure over time in response to pathogen induced dysbiosis of the microbiome. Observations will be paired with results spanning multiple experimental scales to cross validate observed ecological trends and contribute to the establishment of fundamental rules governing disease ecology and microbial community assembly.

**Poster Number:23**

### Mutation Patterns in Diplontic and Haplontic Yeast Species Reveal How the Mutation Process Evolves

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The rate and spectrum of spontaneous mutations varies across the tree of life, but the evolutionary forces shaping this variation are not yet clear. Higher mutation rates might be favored by natural selection if beneficial mutations are sufficiently common. Alternatively, natural selection may be unable to limit the spread of weak mutator alleles—which have small, indirect effects on fitness—particularly in smaller populations where selection is less effective. In principle, this idea should apply not only to populations of varying size, but also to common versus rare events in DNA replication and repair. In the budding yeast Saccharomyces cerevisiae, which grows mainly as a diploid, we found a higher mutation rate in haploid cells than in diploid cells of the same genotype. In the fission yeast Schizosaccharomyces pombe, which grows mainly as a haploid, we found a higher mutation rate in diploid cells than in haploid cells of the same genotype. In both species, haploid and diploid cells also differed in the mutation spectrum. In S. cerevisiae, the observed mutation patterns indicated translesion synthesis DNA repair as a likely mechanistic source of ploidy differences. When found that knocking out this repair pathway eliminated the ploidy difference in mutation rate. Our findings indicate that selection generally favors reduced mutation rates but is unable to act effectively on against mutator alleles affecting rare cell types. The comparative genetics of mutation patterns across fungal species and cell types can reveal limits to natural selection.

**Poster Number: 24**

### Phylogenomic Analysis of Diverse Pezizomycete Fungi Provides New Insights into the Evolution of the Ectomycorrhizal Trophic Mode

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The fungal class Pezizomycetes includes an estimated 2000 fungal species in 23 families representing a broad array of trophic strategies and specialized niches from saprobic fungi such as Ascobolus and Morchella, pyrophilic fungi such as Pyronema and Geopyxis, and many ectomycorrhizal (ECM) fungi such as Tuber, Helvella, and Terfezia. The ECM trophic mode appears to have evolved several times among Pezizomycetes, but uncertainty about the phylogenetic relationships between different ECM lineages and their sister groups has limited our understanding of patterns of ECM trophism in Pezizomycete fungi. This issue is further complicated by taxonomic issues resulting from the application of older genera names such as Peziza to diverse taxa across the Pezizomycetes. Here, we present the first broadly sampled phylogenomic analysis of the Pezizomycete fungi. Draft genome assemblies of over 350 specimens were generated and assembled de novo using a custom genome assembly pipeline. Additional assemblies were obtained from JGI. Phylogenomic analysis was conducted with Maximum Likelihood and coalescent methods. A more fully resolved phylogenomic tree of Pezizomycete fungi provides new insights about the diversity of ECM fungi and the multiple origins of ECM trophism. Still, careful study of individual groups is required to validate ecological hypotheses and accurately characterize Pezizomycetes diversity in a taxonomic framework.

## Poster Number: 25

## Exploring the Genetic and Ecological Diversity of Potential Fungal Pathogens in Andean Woodlands

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Endemic to the Andean Mountain range, growing at altitudes as high as 5,000 meters, Polylepis trees form the highest elevation forests in the world. While Polylepis woodlands are threatened by local (overgrazing, logging) and global (climate change) disturbances, an emerging fungal pathogen, Paraleptosphaeria polylepidis (Leptosphaeriaceae, Pleosporales), is a new threat to these woodlands. P. polylepidis was named the probable cause of Polylepis decline in two National Parks of Bolivia and is undocumented elsewhere. This study is the first to report the presence of P. polylepidis in the Vilacota Maure Regional Conservation Area (VMRCA) of southern Peru, as well as two undescribed species of Paraleptosphaeria and one undescribed species of Plenodomus (Leptosphaeriaceae, Pleosporales) growing on Polylepis trees in Huascaran National Park (HNP) of northern Peru. The results of this study show that Leptosphaeriaceae fungal presence in both VMRCA and HNP is linked with north-facing slopes as well as lower elevations, where drought and temperatures are generally higher. Here, we also describe morphological, ecological, and genetic diversity of these undescribed suspected Peruvian fungal pathogens compared to the described Bolivian counterpart. Ultimately, this study will aid in better understanding the ecology, distribution, and impact of these fungi as well as which regions of the Andes may be most susceptible to this potential emerging disease.

## Poster Number: 27

## Effects of Fire Return Interval and Fire Severity on Fungal Community Composition in Boreal Forests

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The boreal forests of northwestern Canada are experiencing increases in fire frequency and fire severity in many regions. These shifts in fire regimes can have wide-ranging impacts, including changes in plant and microbial community composition. We have investigated how burn severity and changes in fire-free intervals affect soil fungal communities in this region, and present work here from two different studies. First, we investigated the effects of short-interval (SI) vs. long-interval (LI) reburns on soil fungal communities, using paired sites (n=22 pairs) with matching pre-fire characteristics, pre-fire tree species composition, and stand structure. We found that there was a small but statistically significant effect of SI vs. LI on fungal community composition. Several taxa that have previously been associated with post-fire environments, including Penicillium sp. and Calyptrozyma, were significantly enriched in SI sites. Second, we investigated how burn severity affected soil fungal community composition, one and five years post-fire, across a range of 31 burned and 9 control sites from the same region. We found that although the effect of burning on soil fungal community composition decreased five years post-fire, fungal communities failed to show resilience in community composition, possibly due to strong interactions with living overstory and understory vegetation as well as fire-killed plant matter. Assessing the multi-year response of individual taxa to fires underscored that neither genus-level taxonomy nor putative trophic assignment is sufficient to consistently explain post-fire response. Together, this work contributes to our expanding understanding of post-fire fungal communities and their interactions with changing fire regimes.

### Poster Number: 28

### Small but mighty: Genome Analysis of a Basidiomycetous Species in the Genus Meira Isolated from North American Catalpa Seed Pods

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Meira (Exobasidiomycetes, Ustilaginomycotina), is a basidiomycetous genus with less than a dozen species described to date. Species have been found associated with plants, living as endophytes or inhabiting the surface of leaves and fruits, or associated with dead mites and powdery mildew fungi. Some may have the potential to be used as biological control agents. In this study, a single strain (M1555) of an unknown Meira sp. was isolated from a seed pod of Catalpa (Bignoniaceae, Angiosperms) in Maryland (USA) in September 2018. Maximum likelihood analysis of the nuclear large subunit rDNA (LSU) of this isolate showed showed a close relationship to M. argovae, previously found on mites associated with Ricinus communis leaves. Illumina and Oxford Nanopore sequencing was performed, and preliminary analysis of data resulted in a draft genome assembly size of 16.9 Mb organized in 4 scaffolds and containing 7,056 predicted protein genes. Only two secondary metabolite clusters were identified, and local BLAST searches indicated the entire mitochondrial genome sequence was contained within a single contig, with a size of 23.4 kb. Initial BUSCO completeness indicated 96.5% of universal single-copy genes are present in the genome assembly. Genomic analyses of previously under sampled and rare lineages of basidomycetous fungi are necessary not only to explore species diversity and to increase phylogenetic resolution, but also for novel gene discovery to harness the potential pest-fighting abilities of these fungi.

### Poster Number: 29

### Constructing a Pucciniomycotina Backbone Phylogeny from Ultra-Conserved Elements

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Phylogenomics using ultra conserved elements (UCEs) has resolved ancient relationships in animals, saving the monetary and computational costs of sequencing and assembling entire genomes. While fungal genomes are generally smaller than those of animals, lineages with large (reaching 1+ Gb) genomes, such as Pucciniales, exist, and the presence and utility of UCEs for phylogenomics in fungi are untested. While Pucciniales are the best-known order in the Pucciniomycotina due to their commercial importance as plant-pathogenic rust fungi, ca. 24 other orders are currently classified in the subphylum, several of which are monotypic or known from few species. To better understand the systematics and species richness of non-rust Pucciniomycotina, a backbone tree is needed to place the ca. 33 (out of 134) incertae sedis genera and resolve higher-level relationships in the subphylum. To accomplish this, we used simulated short reads from one genome representing each of ten classes with available data to identify ca. 1217 UCEs shared between at least four genome assemblies.To test the phylogenomic utility of these loci, we incorporated 41 additional Pucciniomycotina genomes and constructed a phylogeny from ca. 147 UCEs that were present in at least 70% of the 51 total genomes. Preliminary results show a topology consistent with prior studies but with well-supported deep nodes. As a test of our method, we compare our results with trees constructed from orthologous genes instead of UCEs, and specifically test the sensitivity and/or tendency for either method to over– or underestimate conspecifics.

### Poster Number: 30

### Population Genomics of Cercospora Cf. flagellaris: Investigating Host Associations and Genetic Structure in the Southern United States

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Cercospora leaf blight (CLB) is one of the top diseases affecting soybean (Glycine max) production in the southern U. S. To investigate the demographics and selective forces shaping populations of the primary causal agent, Cercospora cf. flagellaris, we conducted large-scale hierarchical sampling across the southern U. S. Fieldwork was conducted to recover isolates from 101, 369, and 427 symptomatic soybean and Phytolacca americana plants from agricultural and non-agricultural habitats across Louisiana, South Carolina, and Alabama, respectively. All cercosporoid isolates were screened using PCR-RFLP to identify C. cf. flagellaris, yielding 101 isolates from Louisiana, 135 from South Carolina, and 176 from Alabama. Whole-genome sequencing was performed on 101, 105, and 103 isolates from Louisiana, South Carolina, and Alabama, respectively. Multilocus phylogenetic analysis (Actin, Calmodulin, Histone3, ITS, and tef-1α) confirmed species assignments, grouping 89 Louisiana, 81 South Carolina, and 92 Alabama isolates into the C. cf. flagellaris clade. The remaining sequenced isolates grouped with other Cercospora species were not included in further analyses. Genome-wide SNP data are being used to assess migration and differentiation, while genome-wide scans for selection seek to identify loci associated with host or habitat adaptation. Evidence of recombination will also be evaluated to determine the role of sexual reproduction in shaping genetic diversity. We aim to integrate ecological and genomic data to understand the evolutionary forces that have shaped C. cf. flagellaris populations with a particular focus on factors of epidemiological importance.

**Poster Number: 31**

### Understanding the role of insect vectors in oak wilt disease cycle and impacts on chestnut restoration

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Oak wilt is a vascular disease caused by the fungus Bretziella fagacearum that has been identified on multiple species in the Fagaceae family, which includes chestnuts, beeches, and oaks. The disease has been proven lethal to a variety of chestnut species through a series of inoculations, however these experiments remove the insect vector component, leaving questions about vector transmission unanswered. Oak wilt infection on chestnut species is a developing concern to many nut growers, as the American chestnut is considered functionally extinct due to the rapid spread of chestnut blight, a fungal pathogen unrelated to B. fagacearum.  The spread of another fungal pathogen infecting and killing blight-tolerant chestnut species could be especially damaging to the chestnut industry. To better understand the role of insect vectors in the oak wilt disease cycle, this research will determine what wound types are most vulnerable to vector inhabitation, and what fungal pathogens are being transported by these vectors. This will be accomplished by trapping beetles on a combination of intentional wounds and cankers caused by chestnut blight, and sampling them for any fungal spores. Understanding the interactions between oak wilt vectors on non-oak species will help organizations such as the NYSDEC implement successful mitigation strategies for future oak wilt outbreaks and will further aid restorative efforts for both chestnuts and oaks.

**Poster Number: 32**

### Exploring Phyllosphere Yeast-Bacterial Interactions and the Evolutionary Placement of a Novel Cystobasidiomycetes Yeast

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Microbial interactions play a crucial role in shaping community structure and function, yet plant-associated yeasts' contribution to these dynamics remains relatively understudied compared to bacteria. This study investigates yeast-bacterial interactions using an in-vitro plate assay, finding a spectrum of effects on bacterial growth, ranging from neutral to positive or negative. Contact-dependent and contact-independent interactions indicated that yeasts influence bacterial communities through direct contact, agar-diffusible compounds, and/or volatile compounds. In addition, a comparative genomics approach was employed to identify potential adaptive features at the genomic level among Cystobasidiomycetes. Phylogenetic analysis using multiple loci and whole-genome sequencing data was conducted to determine the placement of a novel Cystobasidiomycetes yeast, EMM_F5, isolated from Magnolia grandiflora leaf surface. Phylogenetics based on ITS, LSU, SSU, TEF1-α, RPB2, and CYTB loci suggests that this novel yeast belongs to the family Microsporomycetaceae, and comparison with available genomes suggest it is closely related to Millanazyma bloemofonteinensis, Millanazyma cladoniphila and Microsporomyces hainanensis in the basal lineages of Cystobasidiomycetes.  However, further comparative analyses are necessary to refine its taxonomic placement by identifying features shared with closely related species. This study highlights the need for functional genomics and metabolomic profiling of these yeasts to understand the evolutionary drivers of fungal adaptation. Additionally, it provides insights into yeast-bacterial interactions and their potential role in shaping microbial communities in the phyllosphere. Future studies are needed to elucidate the underlying molecular mechanisms driving these interactions and their ecological significance, particularly within phyllosphere microbiomes.

**Poster Number: 33**

### Exploring Rubiaceae Phyllosphere Fungi as Antagonists of Mycena Citricolor

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America leaf spot is a seasonal disease in coffee, caused by Mycena citricolor (Berk. & M.A. Curtis) Sacc. Chemical fungicides are currently the main method used to control this disease, however, they also reduce the diversity of non-target organisms, as well as presenting a risk to animals and human health. Biocontrol agents, such as fungal endophytes, may provide a safer and environmentally friendly alternative for the management of this plant disease. We evaluated 14 Rubiaceae phyllosphere fungal isolates against M. citricolor in dual-antagonistic tests on two media, coffee leaf agar (CLA) and acidified potato dextrose agar (APDA). Trichoderma rifaii, an established biocontrol of M. citricolor, was used as a positive control. For 12 of these fungal endophytes, we also tested their antagonism against M. citricolor in four-isolate groups on CLA media to examine the growth of M. citricolor within a simplified microbial community. A disc of M. citricolor was centrally surrounded by four discs of mycelium in two possible arrangements: a) four discs of the same isolate; and b) one disc per isolate, for a total of four endophytes on the plate. The antagonism of isolates against M. citricolor varied based on the media type and the presence of other isolates. On the four-isolate groups test, single-isolate arrangements reported higher inhibition of M. citricolor than their multi-isolate arrangements. However, the isolate Nigrospora sphaerica (Sacc.) E.W. Mason presented similar antagonism in single-isolate and multi-isolate arrangements, suggesting its potential ability to reduce M. citricolor growth on diverse microbial scenarios.

**Poster Number: 34**

### Environmental drivers of brown spot needle blight emergence in southeastern US pine plantations

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Brown spot needle blight (BSNB), caused by the fungus Lecanosticta acicola, is an emerging threat to pine forest ecosystems globally. High disease severity of BSNB has been observed in loblolly pine plantations across the Southeastern US, resulting in substantial declines in productivity. However, environmental drivers increasing disease outbreaks remain unclear. To investigate these factors, endophytic fungal communities in symptomatic and asymptomatic needles from 60 trees in six loblolly pine plantations in central Louisiana were examined. Soil samples were collected to assess differences in soil microbial communities with increasing disease severity. The Shannon diversity and beta-diversity of the needle fungal communities were significantly lower in symptomatic needles compared to asymptomatic needles. The asymptomatic fungal needle communities showed greater site-to-site variation than the symptomatic communities. Additionally, the year of planting interacted significantly with disease severity, further influencing needle fungal diversity. A higher relative abundance of L. acicola was observed in trees with greater disease severity, and L. acicola and five Rhytismataceae ASVs were indicator species of symptomatic communities. While soil bacterial communities showed no significant differences with disease severity, several ectomycorrhizal taxa were lost at the highest disease severity levels. Greater precipitation totals were associated with the greatest disease severity. Similarly, minimum VPD, temperature, and precipitation were associated with the symptomatic fungal diversity of needles. These findings highlight the role of environmental factors, particularly the effects of moisture and temperature on L. acicola and fungal communities, emphasizing the need for further research into how future climates may exacerbate fungal needle diseases.

### Poster Number: 35

### Comparative Genomic Analysis of Four Myco-Ed Genomes across Aspergillus and Penicillium

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Fungi are integral to biotechnology, agriculture, and medicine, yet genomic representation for many taxa is still limited. To address this, we sequenced four new species isolated as part of the Mycological Curriculum for Education and Discovery (Myco-Ed) program. Here, we conducted a comparative genomic analysis of these four fungi (Penicillium fagi, Penicillium ribium, Penicillium sp., and Aspergillus fumigatus) across 25 Aspergillus and 11 Penicillium species, and alongside 9 outgroups. All genomes were sequenced using PacBio technology, yielding highly contiguous assemblies. Phylogenetic analysis confirmed established taxonomic relationships and we used comparative genomic techniques to explore variation in carbohydrate-active enzymes (CAZymes) and secondary metabolite biosynthetic gene clusters (BGCs). Aspergillus and Penicillium species exhibited diverse CAZyme profiles, including glycoside hydrolases (GHs) and glycosyltransferases (GTs), as well as abundant BGCs for nonribosomal peptide synthetases (NRPS) and polyketide synthases (PKS). These findings highlight the functional diversity and evolutionary relationships of these fungi, providing insights into their ecological roles and biotechnological potential.

### Poster Number: 36

### Exploring the Infection mechanisms of Xylaria necrophora: Histological and genomic approaches

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Xylaria necrophora (Xn) is responsible for taproot decline (TRD) of soybean (Glycine max) and cotton (Gossypium spp.) in the southern United States. TRD primarily affects roots but also causes foliar symptoms. Despite its importance, knowledge about infection strategies is limited. We aim to study the infection biology of Xn on soybean and cotton using histological techniques and comparative genomics. We will analyze the host’s cellular response to infection by studying the effects of secondary metabolites on host cells. We will also monitor the infection process through direct inoculation. Several seedling inoculation trials were conducted in which plants were inoculated with differing concentrations of Xn-colonized millet. Roots were washed, scanned, and the root architecture was characterized with Rhizovision. Inoculation with Xn resulted in significant reductions in total root length for both soybean and cotton although no obvious foliar symptoms were observed. Roots from these trials as well as field-collected samples are being processed for sectioning and staining to determine the impact of Xn on cotton and soybean host cells. A comparative genomics approach will focus on identifying genetic markers associated with infection by comparing strains adapted to soybean and cotton with those from wild/non-agricultural populations. We have sequenced genomes from several subpopulations of Xn from cotton and soybean and will compare those to two genomes from disjunct non-agricultural habitats. This study will aid in identifying resistant germplasm for crops affected by TRD and enhance our understanding of fungal pathogenesis.

### Poster Number: 37

### Investigating the Evolutionary History and Distribution of Starship Elements within the Fusarium Oxysporum Species Complex

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Fusarium oxysporum is a species complex of mostly plant-associated fungi with diverse ecologies. Strains within this complex are grouped into formae speciales, which are polyphyletic groups of strains that cause disease on the same plant host species. While previous research has shown that accessory chromosomes contribute to forma specialis variation, we hypothesize that recently characterized giant transposable elements, known as Starships, also contribute to plant host specificity. Starships are class II transposable elements that carry and transfer up to 700kb of genetic content, including adaptive genes, between fungi. Here, we explore the distribution and evolutionary history of Starship elements within the F. oxysporum complex using a 721-genome dataset of various forma specialis strains. Most genomes annotated have 1 Starship present, with some having up to 4 unique Starship haplotypes. By using a co-phylogenetic approach, we are testing if the phylogeny of Starship elements cluster based on the phylogeny or forma specialis designation of their fungal "hosts." Additionally, we are annotating the genetic cargo of Starship elements to find genes that have canonical functions in plant host-specific pathogenicity, such as the Secreted in Xylem (SIX) effector family. This study will thus give insight into how F. oxysporum Starship elements have co-evolved with their fungal hosts over time and reveal the role of these newly described elements in fungal lifestyle variation.

### Poster Number: 38

### Identifying Oxalotrophic Bacteria and Calcium Oxalate Biomineralization in Chlorophyllum Molybdites Fungal Mats

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Fungi produce and release oxalate into the soil environment where it is often stabilized temporarily into crystalline forms by complexing with cations such as calcium, producing calcium oxalate. Bacteria co-occurring with oxalate-producing fungi can oxidize calcium oxalates into more stable calcium carbonates, allowing for sequestration of carbon in soil. However, our understanding of this system is nascent and the mechanism behind fungal biomineralization of calcium oxalate crystals and the composition of bacterial communities associated with these biomineralizing soil fungi remain unknown. Here, we present an initial survey of in-vitro calcium oxalate crystal biomineralization by Chlorophyllum molybdites and characterize oxalotrophic bacteria associated with mycelial mats over four years by sequencing the 16S rRNA and formyl-CoA transferase (frc) gene as a marker for oxalate oxidation using Illumina sequencing. We will discuss the community composition of bacteria within these mycelial mats from both a 16S and frc gene perspective. This work provides an initial understanding of fungal calcium oxalate biomineralization and the interactions between the communities of soil fungi and bacteria and their implied contributions to the global carbon cycle.

### Poster Number: 39

### Soil Microbiome Analysis of the American Chestnut and Potential Restoration Sites

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Reforestation hinges on the survival of vulnerable seedlings but is largely conducted without consideration of the symbiotic microbes that can be responsible for their success or failure. The American chestnut (Castanea dentata) was an ecologically and culturally important tree until the early 20th century when an invasive pathogen (Cryphonectria parasitica) rendered them functionally extinct. There is limited understanding of whether blight-resistant transgenic chestnut trees recruit distinct microbial communities

or if soil microbiota play a role in either promoting or hindering their success in restoration plantings. Our objectives are to 1) compare the below-ground microbiomes associated with red oaks, transgenic American chestnuts, and their full siblings in orchard and shelterwood conditions; 2) identify indicator species in the soil microbiome of potential restoration sites that could affect seedling establishment. Soil, root, and rhizosphere samples were collected from each tree type and from three potential restoration sites in New York State. Data from Phospholipid Fatty Acid analysis and metabarcoding will be analyzed to identify whether communities differ between transgenic American chestnut and non-transgenic trees. Microbial community similarities would indicate that blight-resistant transgenic American chestnut trees may successfully occupy the ecological niche once held by native American chestnuts. Indicator species analysis from data at potential planting sites will inform site suitability for strategic restoration projects using blight-tolerant trees.

**Poster Number: 40**

### Invasive amphibian species play key roles in introduction and transmission of chytridiomycosis in northwestern Washington state

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Batrachochytrium dendrobatidis causes chytridiomycosis – the infectious disease implicated in amphibian declines and extinctions worldwide. Anthropogenic activity is responsible for the global spread of chytridiomycosis by transporting infected amphibians between continents. Evidence shows that chytridiomycosis has recently been introduced to the west coast of North America. In Washington State, little is understood about the status of chytridiomycosis spread in the region, and the threat that this disease poses to the state's amphibian communities. Here we present the results of a recent field survey to assess the prevalence and infection intensity of chytridiomycosis in wild amphibians of northwestern Washington state. Our field sites ranged from protected old-growth forests in Olympic National Forest – home to most of the region's native amphibian species, to urban waterways near major population centers (Olympia and Seattle) – where invasive amphibian species are currently expanding their ranges. We collected non-invasive skin swabs from captured amphibians in our study sites for pathogen detection by real-time quantitative PCR. In our field surveys, we observe very low incidences of chytridiomycosis in native amphibian communities residing in protected/intact forest habitats, with the majority of these communities unaffected. Incidences of chytridiomycosis, however, increase in our study near major urban population centers, with disease prevalence and infection intensity peaking in invasive African clawed frog populations around the Seattle metro area. These results suggest that native northwest Washington amphibian communities are still relatively free of disease, but that infected invasive species may tip that balance if not thoughtfully managed by governmental agency partners.

**Poster Number: 41**

### Entoloma sensu stricto from Guyana: A first look at Entoloma "aldinophilum" ined., and a key to the known species

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Species of Entoloma sensu stricto (= Entoloma subgen. Entoloma; Entolomataceae, Agaricales) have tricholomatoid statures, angled isodiametric basidiospores, and are putatively ectomycorrhizal (ECM). In South America's central Guiana Shield region, in the Pakaraima Mountains of western Guyana, five species of Entoloma s.str. have been described to date from collections made in close proximity to ECM tree species in the genera Dicymbe (Fabaceae subfam. Detarioideae) and Aldina (Fabaceae subfam. Papilionoideae). Here we discuss these species and their contribution to the ECM macromycota of the region, introduce the recently discovered Entoloma "aldinophilum" ined., and provide a key to Guyanese species of Entoloma s.str.

### Poster Number: 42

## Communities of Arbuscular Mycorrhizal Fungi (Glomeromycota) in High Altitude Grasslands and Cloud forest: Associating Patterns and Processes

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High-altitude grasslands and cloud Forests are ecosystems with unique environmental characteristics, making them vulnerable to climate change. Communities of arbuscular mycorrhizal fungi (AMF) in these environments are poorly studied despite their importance in assisting plants to overcome biotic and abiotic stresses. We aimed to inventory AMF community composition in areas of high-altitude grasslands and cloud forests in southern Brazil, and to identify the ecological processes structuring these communities. Fifteen soil samples were collected in three areas of each grasslands (GRS), cloud forest (CLF), and riparian cloud forest (RCF) during four seasons. AMF spores were extracted, counted and identified to the species level. A total of 72 species in 19 genera were recovered, with 47% of all species in Acaulosporaceae, the richest and the most abundant family in all ecosystems. Species richness was 53, 50, and 38 for RCF, CLF, and GRS, respectively. The most frequent species were Ambispora reticulata, Glomus trufemii, Acaulospora mellea, A. fragilissima, A. koskei, A. morrowiae, A. sieverdingii, A. alpina, Acaulospora sp.2 and Acaulospora sp.3 and the most abundant were Dominikia aurea, A. mellea and Glomus trufemii. Twenty-five species were shared among areas. Processes that structure AMF communities varied according to the scale: niche-based processes condition the structure at the landscape scale and stochastic processes structure at the local scale. This study showed that high-altitude ecosystems harbor a high diversity of AMF whose communities are structured by several factors, and this group of fungi should be considered in actions aimed to the conservation of these ecosystems.

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### Poster Number: 43

## Characterizing Nutrient-Dependent Bacterial-Fungal Interaction Mechanisms

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Soil- and root-associated microbial communities are some of the most complex and diverse microbial systems, and play important roles in soil nutrient cycling and plant health. Two major constituents of these communities, fungi and bacteria, are often studied in isolation yet mounting evidence suggests that these interkingdom interactions can have outsized impacts on their functions. While the importance of these interactions is clear, the underlying mechanisms and how environmental variables impact these interactions are not well studied. To characterize fungal and bacterial interactions (BFI) and their environmental roles, we have isolated fungi and bacteria from the roots of the highly stress-tolerant grass, Bouteloua gracilis, from three field sites across New Mexico. We have identified several nutrient-dependent BFI phenotypes for two fungal species that dominate our field sites, a Fusarium sp. and Monosporascus sp. We found that a Pseudomonas sp. inhibits Fusarium on defined media containing ammonium phosphate as the nitrogen source, but not with ammonium sulfate. Fusarium displays a nutrient-dependent pink pigmentation phenotype that correlates with the bacterial inhibition. We have also identified a nutrient-dependent response where a Bacillus sp. strongly antagonizes growth of a Monosporascus isolate in a diffusion-dependent mechanism. We are using transcriptomics and metabolomics to understand how fungal growth and metabolism are altered under these nutrient conditions and in response to these interacting bacterial partners. A greater understanding of nutrient impacts on BFI will enable further investigations of how microbial communities compete and coexist in different environments, such as in the assembly of plant root communities.

### Poster Number: 44

### Turnover of Fine Roots Colonized by Different Species of Ectomycorrhizal Fungi

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Fine roots represent an estimated 22% of global productivity and transfer large amounts of carbon to the soil. Fine root turnover is controlled by several soil factors, including the formation of ectomycorrhizae (ECM), with variation among ECM formed by different fungi. To assess differences in ECM turnover, we established twelve minirhizotron stations across two mature, naturally regenerated eastern white pine forests in Nova Scotia. ECM were imaged monthly (April to November) for three years, and then seasonally for a fourth year, with a 1200 DPI narrow gauge root imager. We tracked the morphologically distinctive ECM of Cenococcum geophilum (black), Piloderma bicolor (yellow), Suillus spraguei (tuberculate), Tomentellopsis submollis (pink), and a species of Russula (white) on pine. ECM were also collected within a few cm of the rhizotron tubes, and their identity confirmed by ITS sequencing. Persistence varied among fungal species and was shortest for Russula sp. ECM at 11-19 months, and longest for the tuberculate ECM of Suillus spraguei at 19-32 months. ECM of Cenococcum geophilum were very slow to colonize new roots and did not form ECM until the spring of the fourth year, and then only on birch. Previous studies report that most ECM persist for 3 to 7 months, with the recalcitrant Cenococcum lasting closer to 30 months. However, ECM in our system persisted for 11-32 months, not including Cenococcum geophilum. These slow ECM turnover rates may represent relatively long C and N retention times in the fine roots of northern forests.

### Poster Number: 45

### A Story of Spores across Scales: How Airborne Fungi Shape Mushroom Forecasting across the United States

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The mushrooms produced by macrofungi are charismatic and heavily sought after by researchers and hobbyists alike. Predicting which mushroom may pop up where is an exciting prospect, yet the ecological factors controlling fungal distributions at local and continental scales as well as within and between years remains relatively limited. Given the abundance of fungal spores in air and their ability to travel a range of distances, understanding fungal spore dispersal at multiple spatial and temporal scales is crucial. Further, the relationship between local fungal spore and mushroom presence also remains underexplored. In this study, we sampled airborne spores over two years using passive spore traps across eight ecoregions in the United States. Within each ecoregion, traps were placed in three habitats (grassland, conifer, oak), totaling 31 sites. Spores were identified using high-throughput Illumina sequencing of the ITS1 region. To explore links between spore and mushroom co-presence, mushrooms were collected at varying distances from spore traps, combining targeted surveys with iNaturalist data. We found that fungal spore communities exhibited high stochasticity across all scales, with 36.9% of macrofungal OTUs detected only once. At the continental scale,

spore diversity and composition were shaped by precipitation and temperature, though site ecoregion was the strongest driver. Locally, fungal spore communities showed inconsistent associations with habitat type, with mushrooms within 20 km accounting for ~40% of fungal spores. Collectively, these findings indicate fungal spore distributions show strong continental-scale patterns and that spore presence can be linked to local mushroom production in a scale-dependent manner.

**Poster Number: 46**

### A Large-Scale Phylogenomic Analysis of Entomopathogenic Fungi Host Specificity via Automated Data Retrieval

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Entomopathogenic fungi (EPF) infect and kill a variety of insects, making them important models for host-pathogen interactions, as well as important organisms in biocontrol applications and natural product discovery. Some EPF species have broad host ranges, while others are highly specialized and only infect select insect taxa. In order to establish a genomic basis for the EPF lifestyle, as well EPF host specificity, it is essential to first generate phylogenomic trees to elucidate the evolutionary relationships among species. Studies on EPF host range often depend on smaller, curated datasets, which have EPF host data manually assigned; attempts at creating a larger dataset are often quickly hindered by scale and complexity of gathering and curating genomic data with corresponding host metadata. To overcome these limitations, we developed custom scripts to automate the retrieval, curation, and processing of publicly available fungal genomes as well as associated host metadata. This automated approach dramatically increased our dataset size and allowed for a more rigorous articulation of EPF phylogeny and known host range. Here we present a phylogenomic tree constructed from a collection of hundreds of genomes which met our quality thresholds and includes a wide variety of EPF species. This foundational tree provides a framework for exploring relationships among many different EPF species and opens the door to further efforts draw connections between pathogen genomes and phenotypes.

**Poster Number: 47**

### MycoEd: Undergraduate Research on the Comparative Genomics of Fungal Endophytes

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Fungal endophytes, symbiotic fungi residing within plant tissues, play critical roles in enhancing plant health, stress tolerance, and secondary metabolite production. However, the genomic diversity and ecological significance of these fungi remain poorly understood. To elucidate greater understanding of endophytes and other understudied fungi, Mycological Curriculum for Education and Discovery (Myco-Ed) was developed. Through Myco-Ed, students across fungal biology teaching labs isolate endophytes and generate genome sequences. Analysis of these genomes is presented here. These undergraduate research exercises focus on performing a comparative genomics analysis of fungal endophyte genomes to investigate their genetic variability and functional potential. Participants utilized bioinformatic tools to assemble, annotate, and compare the genomes of multiple fungal endophyte species isolated from a variety of plant hosts. By identifying conserved and unique genomic features, students explored gene families involved in ecological interactions, such as plant defense mechanisms and stress response pathways. The exercise provided students with hands-on experience in genomic data analysis, fostering skills in bioinformatics, data interpretation, and scientific communication. The findings of this study underscore the complex genetic landscape of fungal endophytes and offer insights into their ecological and agricultural potential.

**Poster Number: 48**

### Mapping Origins of DNA Replication in Cryptococcus

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Eukaryotic DNA replication is a vital and necessary step to transfer genetic information to progeny and thereby perpetuate the species. Eukaryotic DNA replication is tightly regulated temporally and spatially with DNA replication strictly occurring during the S-phase of the cell cycle and initiating at discrete genomic loci called origins of DNA replication, henceforth origins. Disrupting the distribution of origins in a genome can sensitize a cell to replication pathologies, copy number changes, and breaks in chromosomes. While much work has led to our understanding of origin licensing in model eukaryotic genomes ranging from the budding yeast Saccharomyces cerevisiae to humans, far less is known in other fungi, especially pathogenic fungi. Cryptococcus is a pathogenic budding yeast and model organism for spore-forming pathogenic fungi. Previous work suggests that Cryptococcus lacks several of the "conserved" and essential components that form the pre-replicative complex (pre-RC). This observation raises the question of how and where Cryptococcus forms origins in its genome. To determine where origins can form in Cryptococcus, we are using SortSeq. SortSeq uses flow cytometry-based sorting coupled with high-resolution next-generation sequencing (NGS) to compare copy number changes between S-phase and G1-phase populations. Inflections in copy number ratio (S:G1) reflect DNA replication initiation events and thus origins of replication. Importantly, we are using SortSeq to map origins in both Cryptococcus yeast and germinating spores to compare replication for these two cell types to better understand both genome organization and timing of gene expression during escape from dormancy.

### Poster Number: 49

### Effectivity of Secondary Metabolites from Clonostachys Rosea and Rhizophaga as Plant Growth Promoters and Biocontrol Agents

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Clonostachys rosea is a soil-borne root endophyte showing great potential for agricultural applications as a mycoparasitic biological control and biofertilizer. Clonostachys rhizophaga is a closely related, seldom researched fungal endophyte that shows similar promise. Hundreds of different secondary metabolites (SMs) have been reported from the genus, making it of special interest within ecological solutions research. C. rosea has been tested as a biological control against insects, bacteria, and other fungi. However, the potential bioactivity of secondary metabolites produced by these fungi remains unexplored. Here, we studied the biological activity of C. rosea and C. rhizophaga on different plants. Pure cultures of each were isolated from soybean roots and crude extracts were obtained by filtering through a Buchner funnel and a PES membrane. First, we investigated the effects of C. rosea and rhizophaga raw filtrates on plant root length and chlorophyll content of a variety of host plants, including soybean, chickpea, tomato, and black-eyed-pea. Plants were exposed to different concentrations of the filtrates (25-fold, 50-fold, and 100-fold dilutions). A significant increase in plant root length was observed in all plants treated with Clonostachys spp. secondary metabolites. No statistically significant impact on chlorophyll content of plant leaves was observed between control and Clonostachys treatments. These results suggest that SMs of C. rosea and C. rhizophaga promote plant growth in roots of many agricultural plants.

### Poster Number: 50

### Investigating the Life Cycle and Host Range of Cryptostroma corticale in the Pacific Northwest Using Environmental Sampling and Molecular Detection

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Cryptostroma corticale (Xylariales, Sordariomycetes) is the causal agent of Sooty Bark Disease (SBD) of Acer. SBD causes blistering of the bark, wilting, and dieback. In Europe, periods of drought and higher temperatures have led to increased disease incidence and mortality of Acer pseudoplatanus (Sycamore maple). Since 2017, C. corticale has become increasingly recognized as a putative pathogen of A. pseudoplatanus and other non-native maple species (A. palmatum, A. platanoides) in the Pacific Northwest (PNW). Recently, increasing dieback and mortality of bigleaf maple (A. macrophyllum) has been associated with signs of SBD. Here, we sought to better elucidate the life cycle and host range of C. corticale in the PNW. As C. corticale is closely related to xylarialean saprotrophs and pathogens with endophytic life stages, we hypothesized that in addition to being present in woody tissues, C. corticale is a foliar endophyte of Acer, as well as other co-occurring plants and lichens. We collected photosynthetic leaves/thalli, leaf litter, and wood/bark of 10 species in four SBD-positive sites in Wildwood Park, Puyallup, WA. Tissues were surface-sterilized and total DNA was extracted to perform a nested PCR with previously published C. corticale-selective ITS nrDNA primers. Overall, 66% of samples were PCR-positive for C. corticale (49 of 74) including asymptomatic Acer leaves, litter, and SBD symptomatic bark/wood. However, due to the recent detection of a closely related Biscogniauxia species that can cause false positives, ongoing research is needed to confirm these results with additional culture-based and culture-free molecular methods.

**Poster Number: 51**

### Mating-type frequencies of Passalora arachidicola and Nothopassalora personata in Georgia, USA peanut fields

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Two of the most devastating foliar diseases of peanut (Arachis hypogaea L.) are early leaf spot, caused by Passalora arachidicola, and late leaf spot, caused by Nothopassalora personata. The sexual cycles of these species involve the production of pseudothecia and spermatia. Although these structures were described in the 1930s from lesions collected in Georgia, USA, the current USA populations are hypothesized to be reproducing only asexually because pseudothecia have not been reported recently. To assess the potential for sexual reproduction, 40 isolates of each species from a field in Tifton, GA were cultivated to determine if both MAT1 mating-type idiomorphs (MAT1-1 and MAT1-2) were present. Using published genome sequences, both idiomorphs were characterized for N. personata, and MAT1-2 was characterized for P. arachidicola. A multiplex PCR protocol was used to genotype each isolate based on primers designed using these idiomorph sequences. All P. arachidicola isolates amplified for MAT1-2, while 37.5% N. personata amplified for MAT1-1 and 62.5% for MAT1-2. Because only one idiomorph was detected in the P. arachidicola population, the hypothesis is supported. For N. personata however, sexual reproduction may be occurring since both idiomorphs are present.

**Poster Number: 52**

### Mycelial kombat: Inter and Intra-Specific Combative Ability of Pleurotus Citrinopileatus and Native Wood Decay Fungi.

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Pleurotus citrinopileatus Singer or the golden oyster mushroom is an invasive wood-decaying saprotroph introduced to North America from East Asia. Previous studies indicated that the fungus is rapidly expanding its range in the Midwest. Data collected from community science databases, such as iNaturalist, indicate that the fungus has been expanding into New England. The rapid range expansion of the species may be attributed to its ability to outcompete native Pleurotus species and alter the fungal communities present in wood. However, mechanisms by which P. citrinopileatus interact with the native fungal communities are unclear. We explored the interaction between the invasive P. citrinopileatus and native fungal communities under different growth conditions. The data suggest that the P. citrinopileatus uses invasive fronts to outcompete the different wood decay fungi. However, the different species of Pleurotus and the fungi from the native range of the species can resist the attack and forming a zone of inhibition. These data will be used for functional experiments of gene expression patterns to understand the molecular bases of these fungal-fungal interactions. Furthermore, we also detected the presence of conidia-like structures on the aerial hyphae of the invasive Pleurotus citrinopileatus, suggesting a plausible mechanism of rapid propagation similar to invasive plants and animals.

**Poster Number: 53**

### Differential Expression Genes of Apiospora arundinis from Seaweed and Bamboo for the Response to the Salt Stress

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Apiospora Sacc. is a cosmopolitan fungal genus in diverse environments, ranging from marine to terrestrial ecosystems. Apiospora arundinis is widely distributed and frequently detected in both habitats. Apiospora species could produce stress-related compounds, including antioxidants, to adapt to and control harsh conditions. The response to environmental stress can vary depending on adaptive evolution. However, there is a lack of research on whether Apiospora species exhibit evolutionary adaptations specific to different habitats and, if so, in which biological processes these differences occur. Therefore, this study aimed to compare the gene expression patterns of two Apiospora arundinis strains adapted to different environments under salt stress conditions to identify their distinct adaptive responses. Transcriptome analysis was performed using the NovaSeq X platform, followed by differential gene expression analysis with DESeq2. Functional variations were then analyzed based on Gene Ontology annotation to assess major differences in gene expression. The results showed that the marine strain Ap. arundinis KUC21229 exhibited a significant differential gene expression related to "transmembrane transport" in the biological process and "oxidoreductase activity" in molecular function when exposed to sea salt. In contrast, the terrestrial strain Ap. arundinis KUC21601 showed significant differences in the expression of genes associated with "organic substance metabolic processes" in the biological process and "catalytic activity" in molecular function when exposed to sea salt. These findings suggest that even within the same species, gene expression patterns can differ depending on the habitat, providing valuable insights into the adaptive mechanisms of Ap. arundinis in response to environmental stress.

**Poster Number: 54**

## Exploring a New Method for Characterizing Host Specificity of Microbial Communities.

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Evaluating the host specificity of microbial communities is useful to investigate fundamental questions of host-symbiont evolutionary dynamics, such as the extent to which a host asserts control over its microbiome. However, there are limitations with the current methods of characterizing microbial community host specificity. Indicator Species Analysis (ISA) is a popular method used to examine the degree to which one taxon is associated with a particular host. However, the ISA is limited to exploring single, common taxa, and excludes taxa that are non-dominant but might be host specific. Other methods, such as effective specialization, have the capacity to evaluate the host specificity of entire microbial communities, but do not have standardized thresholds for rare taxa removal. The decision to either include all rare taxa in analyses or use arbitrary thresholds have both been demonstrated to influence results and thus biological inferences. Here we present a new method for examining community-level host specificity in which we integrate the Indicator Species Analysis with a Community Weighted Mean (CWM) analysis. We then apply this method to a dataset of host-associated soil and foliar fungal communities found across a temperate elevation gradient. The method assigns a specificity value to each taxon, establishes a threshold for removing rare taxa, and concludes with a community-level analysis using all taxa that meet the threshold. The resulting specificity indices characterize and compare the specificity of microbial communities associated with certain hosts or groups (i.e. treatments, environments) in the dataset.

## Poster Number: 55

## Functional Entrenchment and Directional Evolution in a Conserved Fungal Protein Family

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Functional innovation at the protein level is a key source of evolutionary novelties. The constraints on functional innovations are likely to be highly specific in different proteins, which are shaped by their unique histories and the extent of global epistasis that arises from their structures and biochemistries. These contextual nuances in the sequence–function relationship have implications both for a basic understanding of the evolutionary process and for engineering proteins with desirable properties. Here, we have investigated the molecular basis of novel function in a model member of an ancient, conserved, and biotechnologically relevant protein family. These Major Facilitator Superfamily sugar porters are a functionally diverse group of proteins that are thought to be highly plastic and evolvable. By dissecting a recent evolutionary innovation in an α-glucoside transporter from a non-traditional model yeast, we show that the ability to transport a novel substrate requires high-order interactions between many protein regions and numerous specific residues proximal to the transport channel. To reconcile the functional diversity of this family with the constrained evolution of this model protein, we generated new, state-of-the-art genome annotations for 332 Saccharomycotina yeast species spanning ~400 My of evolution. By integrating phylogenetic and phenotypic analyses across these species, we show that the model yeast α-glucoside transporters likely evolved from a multifunctional ancestor and became subfunctionalized. The gradual accumulation of additive and epistatic substitutions likely entrenched this subfunction, making a simultaneous acquisition of multiple interacting substitutions the only reasonably accessible path to novelty.

## Poster Number: 56

## Fungicide Performance in Controlling Coffee Leaf Rust and Plumeria Rust in Hawaii

Nina Pejovic, University of Hawaii at Manoa

Coffee leaf rust (Hemileia vastatrix) and plumeria rust (Coleosporium plumeriae) are obligate biotrophic fungal pathogens that threaten coffee production and ornamental landscapes in Hawaii. H. vastatrix primarily colonizes the abaxial leaf surface, where it produces urediniospores that serve as the main inoculum for disease spread. As the infection progresses, mature spores develop into characteristic orange pustules. Similarly, C. plumeriae causes characteristic orange pustules on plumeria leaves, leading to premature defoliation. Given the limited genetic resistance in commercially grown coffee (and plumeria), chemical control remains a crucial strategy. This study evaluates the efficacy of fungicides with diverse modes of action against H. vastatrix and C. plumeriae under controlled laboratory and greenhouse conditions. The treatments include inhibitors of amino acid biosynthesis (cyprodinil), sterol biosynthesis inhibitors (propiconazole, difenoconazole, cyproconazole), mitochondrial respiration inhibitors (trifloxystrobin, pyraclostrobin), and succinate dehydrogenase inhibitors (SDHIs) targeting fungal respiration and cellular metabolism (penthiopyrad, fluxapyroxad, benzovindiflupyr). Potential microbial-based biofungicides will also be assessed. Disease suppression will be quantified by measuring lesion development, urediniospore germination, and sporulation rates across different infection stages. Statistical analyses will determine treatment efficacy and potential differences in pathogen response.Findings from this study will provide critical insights into fungicide performance against rust pathogens, informing integrated disease management strategies. Additionally, understanding pathogen-fungicide interactions will contribute to resistance management efforts and improve long-term disease control approaches for sustainable agriculture and ornamental plant health in Hawaii. These results will serve as a foundation for further evaluation of fungicide efficacy under field conditions, helping in the development of practical, real-world application strategies.

**Poster Number: 57**

### Assessment of wood 'endophyte' trait in predicting deadwood decomposition by repeated measures

Yanmei Zhang, University of Minnesota

Predicting wood decomposition is challenging due to the complex dynamics among decomposers that colonize and defend wood territories. In this study, we used repeated measures to track the decomposition of paper birch (Betula papyrifera) and red pine (Pinus resinosa) over five years in a northern forest in Minnesota, USA. We assessed wood properties and microbial succession, comparing the fungi and bacteria present in healthy wood (endophytes) to those that arrived as external colonizers. We also employed different treatments (ground vs. aboveground contact; bark on vs. bark off) to vary accessibility for colonizers. Over the five-year period, accessibility treatments significantly affected decay rates and the succession of fungal communities. The lignin-deficient white rot-type woody residues prevailed in all treatments. However, the dominance of specific fungal species varied by treatment. Most of the dominant fungi could be traced back to operational taxonomic units (OTUs) that were present as endophytes in healthy wood. This suggests that the treatments influenced the competition among endophytes more than the success of external colonizers during these stages of decay, even in cases of ground contact. Although the diversity of fungal communities decreased as certain taxa became dominant, the bacterial communities showed convergence regardless of treatment, without significant co-occurrence with fungi and without losing diversity. Our results imply that saprotrophic fungi may gain a strategic advantage by colonizing trees as endophytes. Additionally, they support the idea of including fungal endophytes, along with predictors of their competitive success, as 'plant' traits to enhance predictive models of wood decomposition.

**Poster Number: 59**

### Scaffolding Inquiry-Based Learning in Ecology to Teach the Mutualism-Parasitism Continuum of the Mycorrhizal Symbiosis

Joanna Weremijewicz, North Central College

The role of symbiosis in the natural world is a common learning objective in ecology courses, but teaching about symbiosis in an engaging, inquiry-based manner can be challenging to develop. Inquiry-based learning (IBL) provides many benefits to student learning, such as improved scientific literacy. The IBL framework has flexibility and can be scaffolded in a classroom to make learning the scientific process more digestible for instructors and students. At a small liberal arts college, I developed, implemented, and assessed a four-week, guided-inquiry laboratory module on the mutualism-parasitism continuum of the mycorrhizal symbiosis for 200-level college students. Students derived their own hypotheses based on the scientific literature and created a scientific results section as the product of the exercise. Through this activity, students could communicate a testable, well-reasoned hypothesis and translate the statistical results into biological terms to describe the experiment's outcomes. I discuss how this IBL exercise can be modified from guided to moderate to open inquiry, depending on student experiences in and comfort with the nature of science. Additionally, I provide factors to consider that would improve the experience for both instructors and students, such as changing the plant species to a highly dependent native plant species, adding to the assessment of plant and fungal science to assess content learning, and improving the communication of expectations to match assessment rubrics.

**Poster Number: 60**

### Unraveling the Fungal Pathogens Associated with Circular Leaf Spot Disease of Rubber in Sri Lanka

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Hevea brasiliensis (Para rubber tree) is the primary source of commercial natural rubber production. In Sri Lanka, rubber is one of the main plantation crops grown for the supply of latex for the industry. However, the rubber industry is struggling to survive after the rapid decline of latex partly due to a newly emerged Circular Leaf Spot Disease (CLSD) emerged recently. A similar disease also has been reported from several other places of Asia including India and Taiwan. The objective of the current study is to accurately identify the potential causal agent(s) based on molecular and morphological characterization. Samples were collected from two heavily infected plantations viz. Pussellawa Plantations-Awissawella and Aitken spence plantations-Galle. Fungi were cultured using single spore and tissue isolation techniques. In total, 70 pure fungal isolates were obtained and morphological and molecular characterization revealed that most of the isolates belongs to the genera Pseudopestalotiopsis, Neopestalotiopsis, and Colletotrichum. The 'BLAST similarity search for Its barcode region and following species show close similarities to EL12F4- Pseudopestalotiopsis gilvanii, SL23F4 - Neopestalotiopsis dolichoconidiophora, SL17F2-Pseudopestalotiopsis curvatispora,SL10F1-Colletotrichum xishuangbannaense, (and SLN2F3-Colletotrichum guiyangense. Thus, the CLSD of rubber is caused by multiple species belongs to at least three genera of ascomycetes, making it a complex and economically significant disease affecting rubber plantations. This knowledge will be critical in developing targeted disease management strategies, including resistant rubber cultivars and effective fungicide applications.

### Poster Number: 61

### Unearthing Two New Ectomycorrhizal Pezizales Truffle Species from Nothofagaceae Forests in Southern South America

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Truffles are enclosed, hypogeous fruiting bodies that have evolved hundreds of times across different fungal groups. Truffles are particularly diverse within the Pezizomycetes and the majority of species are ectomycorrhizal symbionts of trees. Because of their cryptic fruiting habits, truffles remain understudied and many new taxa remain to be discovered. Many truffle groups exhibit notable biogeographical distribution patterns, show distinct host preferences, and are found in specific forested habitats. Here we present morphological and phylogenetic evidence for two new ectomycorrhizal truffle species associated with Nothofagaceae trees in southern South America, Paragalactinia patagonia nom. prov. (Pezizaceae) and Geomorium nahuelbutensis nom. prov. (Geomoriaceae). The closest described relatives of these new species form fruiting bodies that are epigeous apothecia or modified apothecia, suggesting that these newly described taxa represent independent evolutionary events leading to the truffle morphology. Paragalactinia patagonia is widespread in northern Patagonia and was documented by Fernandez et al. (2013) as one of the most abundant ectomycorrhizal fungi on the roots of Lophozonia alpina seedlings grown in the greenhouse (as "Peziza sp. 1"). In contrast, Geomorium nahuelbutensis has only been found in well-preserved coastal forest in Chile towards the northern extent of Nothofagaceae in South America, an area that has been heavily impacted by deforestation, fires, and other human activities. This species is known only from two modern collections from Parque Nacional Nahuelbuta and one preserved specimen collected by Roland Thaxter from Concepcion in 1906.

### Poster Number: 62

### Colonization of Plant Biomass Particles by Fungi is Dependent on Transcription Factors Controlling Polysaccharide Degradation

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Plant biomass degradation by fungi is a complex process involving extracellular enzyme production controlled by a set of transcriptional regulators. In industrial fermentation, biomass particle size is larger than those used in lab-based studies, requiring the fungus to colonize these particles before they can degrade them. This inspired our evaluation on the impact of individual transcriptional regulators on the colonization process of the fungus. A previous study in our group demonstrated that an Aspergillus niger deletion strain of xlnR, the main transcriptional activator for xylan and cellulose degradation, showed strongly reduced colonization of wheat bran. The main polysaccharides in the cell walls of wheat bran are cellulose and xylan, implying a direct correlation between regulator function and colonization ability.

To determine whether this approach could be used to identify the primary transcriptional regulator in A. niger for diverse biomasses, we analyzed colonization of the A. niger wild type and deletion mutants for six transcriptional regulators on ten different plant biomass substrates. The tested regulators are involved in xylan (XlnR, ClrB, AraR), cellulose (XlnR, ClrA, ClrB), pectin (GaaR, AraR, RhaR) and galactomannan (ClrB) degradation. Analysis was performed using light, stereo, and scanning electron microscopy and compared to transcriptome data from the wild type and mutants on these substrates.

**Poster Number: 63**

### Development of diagnostic assays using specific markers for the detection of Armillaria and Desarmillaria species in Europe by Real-Time PCR

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Armillaria root disease, caused by Armillaria and Desarmillaria (Basidiomycota) afflicts a range of agronomic crops and timber trees worldwide, while its occurrence as a secondary pathogen in European forest trees is on the rise. This study aimed to develop hydrolysis probe-based real-time PCR assays for the detection of the seven Armillaria/Desarmillaria species in Europe (A. mellea, A. ostoyae, A. gallica, A. borealis, A. cepistipes, D. ectypa and D. tabescens) using specific markers, and to develop an Armillaria/Desarmillaria genus-specific test. Housekeeping genes (Intergenic Spacer and Translation Elongation Factor 1 α) and four single-copy orthologous genes from fully sequenced Armillaria/Desarmillaria genomes were used in the marker design. Assay specificity was confirmed using DNA from 50 Armillaria/Desarmillaria isolates, and the tests were multiplexed into two groups without compromising the assay specificity or sensitivity. The Limits of Detection (LODs) approximated around 1 x 10-4 ng/µl for all the species except for A. gallica and A. cepistipes, whose LODs approximated at 1 x 10-3 ng/µl. The assay was tested on DNA from 75 naturally contaminated environmental samples (barks with mycelial fans and rhizomorphs) originating from different species of coniferous and woody trees with suspected Armillaria/Desarmillaria infections. While A. ostoyae (38%) and A. gallica (39%) were the most abundant, three A. mellea (4%) infected samples and no other species were detected. Co-infections were observed in four samples (6%). This assay can be used in routine diagnostics of European Armillaria/Desarmillaria species directly from the environmental samples with optimum species-specificity and sensitivity.

**Poster Number: 64**

### Evaluating a Saponin Biological Seed Treatment on Soybean Disease and Yield in Michigan and the Challenges in Biological Seed Treatment Efficacy

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Soybean sudden death syndrome (SDS; Fusarium virguliforme) and white mold (Sclerotinia sclerotiorum) are major threats to soybean production in Michigan and all major soybean producing regions of North America. White mold and SDS management strategies primarily rely on host resistance and synthetic fungicides: typically, demethylation inhibitors (DMI – FRAC 3), succinate dehydrogenase inhibitors (SDHI – FRAC 7), or quinone outside inhibitors (QoI - FRAC 11). Fungicide resistance in pathogen populations is a continual concern and there is interest among soybean stakeholders around integrating biologicals into disease management programs. This study investigated the efficacy of Chenopodium quinoa saponin seed treatment 'Heads Up' in managing SDS and white mold in soybeans, as well as its yield impacts across Michigan in 2022-2024, by applying two treatments: a standard commercial base seed treatment (base) and base + Heads Up (61.3% a.i.;

15 mL·cwt-1), to 7 commercial soybean cultivars across 20 site-years of randomized small plot trials. These treatments were also applied to 7 additional cultivars across 8 site-years of on-farm split plot trials. No significant differences in soybean yield (P = 0.9), SDS root (P = 0.7), SDS foliar (P = 0.3), or white mold (P = 0.5) disease indices were detected. These findings align with previous studies, highlighting the need for further research into soybean response to exogenous saponins, target pathogen detoxification mechanisms, and potential negative off-target effects. This work provides practical insights for soybean producers, emphasizing the need for comprehensive understanding of biological seed treatments and their impacts on rhizosphere microbiomes.

**Poster Number: 65**

### The use of fungal-derived volatile organic compounds to mediate plants stress response to microgravity

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To support humanity as it expands further into space it is nec essary to develop conditions that allow plants to thrive as well. Plants provide humans with oxygen and food that are essential for our survival but abiotic conditions in space induce a range of negative effects for plants including oxidative stress and disordered root growth. The beneficial filamentous fungus Trichoderma harzanium is known to improve plant vegetative growth and ameliorate stress. This effect has been found to positively benefit Arabidopsis when challenged with a gravitropic assay. Prior research growing plants in proximity but not contact with T. harzanium has shown that volatile organic compounds (VOCs) are responsible for the beneficial growth effects. We aim to determine which of the more than 30 known fungal VOCs emitted by T. harzanium provide these benefits. VOCs will be dissolved into solvent and screened for activity via calcium signaling using Arabidopsis thaliana expressing the calcium sensor GCaMP and fluorescence microscopy. An observed response in calcium signaling indicates the triggering of an important response network that could alter gene expression both locally and systemically. Active compounds will then be used to supplement ½ Linsmaier and Skoog media in Petri dishes to grow Arabidopsis under simulated microgravity conditions using a clinostat set to 3 rotations per minute. The identification of the beneficial compound(s) will allow for exogenous application to harness the advantageous effects of fungal symbiosis without the risks of opportunistic overgrowth during co-cultivation or fungal contamination of the space environment.

**Poster Number: 66**

### A new species in the Gnomoniaceae isolated from Hudsonia sp. roots from the New Jersey Pine Barrens

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Three isolates of a novel species within the Gnomoniaceae were isolated from Hudsonia sp. roots from the New Jersey Pine Barrens. The internal transcribed spacer (ITS) sequences share around 94% similarity with those of Apiognomonia errabunda, large subunit of the rRNA gene (28S) sequences share around 97-99% similarity with Cryptosporella hypodermia, and the translation elongation factor 1-alpha (TEF1) sequences share around 82-84% similarity with Cryptosporella pacifica. Phylogenetic analysis showed that these isolates formed a distinct clade in Gnomoniaceae. More specific phylogenetic placement is in progress, and will use both single-gene and concatenated multigene trees, also including the second largest subunit of RNA polymerase II (RPB2) sequences. Morphological characteristics also confirm its placement in the Gnomoniaceae, with cultures grown at room temperature on malt extract agar or Instant Potato Sucrose and Coconut Agar developing conidiomata after around 2 weeks. Conidiomata are coelomycetic, with semi-clear to opaque, off-white to gray slimy conidial mass drops emerging from dark brown to black pycnidia. Conidiophores produced oval to oblong, aseptate conidia by blastic conidogenesis. Plant-fungal interaction experiments with Arabidopsis thaliana seeds are ongoing. Characterization of this species adds to the enormous diversity of the ecologically and economically important class Sordariomycetes.

### Poster Number: 67

### Horizontal transfer of Starships between the Ascomycota and Basidiomycota

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Starships are large, mobile, cargo-carrying genetic elements that have been described across many species of the Pezizomycotina in the Ascomycota. Starships have been observed to move to different loci within genomes as well as horizontally transfer between distantly related species. The tyrosine recombinases that are responsible for the movement of Starships, termed captains, have been found in members of the Basidiomycota, though never associated with a full-length Starship element. It is thus unclear whether any of these captains in Basidiomycetes are the result of horizontal transfer with the Pezizomycotina as Starships. To answer this question, we've developed a method based off the existing BLAST-based "Alien Index" metric that can detect large regions of putative horizontal transfer. We demonstrate that this method is effective in detecting previously validated horizontal transfers of Starships within Pezizomycotina and use it to search for regions of horizontal transfer associated with 1,201 predicted captains across 431 publicly available genomes from 249 Basidiomycete species. We found multiple putative horizontal transfers of large Starship-like regions from the Pezizomycotina into multiple Basidiomycetes, suggesting the presence of captains in the Basidiomycota is in part explained by their horizontal transfer from Ascomycetes, potentially as Starships. This tool is an effective alternative to existing methods for identifying Starships and similar horizontally transferring elements and will aid future research to better understand how Starship-mediated horizontal gene transfer shapes fungal evolution.

### Poster Number: 68

### Are there too many muscarias? Revising the Taxonomy of North American Amanita muscaria.

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Amanita muscaria is a complex of closely related but evolutionarily distinct taxa, and its type was originally collected in Europe. Early phylogenetic studies showed that two North American varieties of A. muscaria (A. muscaria var. guessowii and A. muscaria var. flavivolvata) represent lineages polyphyletic with the European type (A. muscaria var. muscaria). However, previous work to resolve North American A. muscaria with concatenation and single locus phylogenies have proved inconclusive, perhaps because of the recency of their speciation, or because of introgression. We present a revised taxonomy of the three varieties of A. muscaria co-occuring in North America using a combination of geographical, morphological, ecological, and phylogenomic evidence. Our findings suggest that North American A. muscaria are composed of three distinct taxa. Accordingly, we retain A. muscaria for the previously autonymic variety and reinstate A. chrysoblema for A. muscaria var. guessowii. Additionally, we present a novel combination, A. flavivolvata, for Amanita muscaria var. flavivolvata.

### Poster Number: 69

### Friends or Foes? Investigating the Relationship of Rhizopogon Vinicolor and its Potential Parasites

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Rhizopogon vinicolor, a truffle-forming fungus, establishes ectomycorrhizal relationships with Pinaceae, playing a vital role in maintaining biodiversity and forest health. Multiple tissue cultures were isolated from Rhizopogon vinicolor fruiting bodies during the routine study that were inconsistent with R. vinicolor morphology, and were later identified as Pseudeurotium and Cadophora. Given that these isolates were obtained from an R. vinicolor fruiting body, there is a question of whether this relationship is parasitic. Four sets of co-culture experiments were set up pairing R. vinicolor against three Pseudeurotium cultures and one Cadophora culture. Co- cultures were assessed microscopically for parasitic structures and anatomical changes. The average number of structures formed at the site of interaction was compared to sites with no interaction to determine whether there was a significant increase at the site of interaction. Our results show that Cadophora and Pseudeurotium cultures produce a significant increase in potentially parasitic structures in the interaction zone with R. vinicolor indicating a possibly novel ecology between R. vinicolor and these two genera. This study highlights the use of microscopy as a baseline for studying interactions between different fungi to better understand their relationship. Further research is warranted to investigate if these structures facilitate a parasitic relationship.

**Poster Number: 70**

### Making a Model: Building Protocols for Studying the "Zombie" Fungus E. muscae

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Entomophthora muscae is a behavior-manipulating fungal pathogen of dipteran insects. Before killing its host, the fungus elicits a series of behaviors aimed at optimizing the dispersal of its spores, the most iconic of which is summit disease, in which the host insect climbs to an elevated position before its death. Making use of a strain of E. muscae that infects Drosophila melanogasterhas enabled our laboratory to leverage powerful genetic systems developed in Drosophila to better understand the nature of summit disease. Tools for E. muscae, however, are incredibly limited. Here, I report on the methods I am developing for culturing E. muscae in vitro, re-establishing in vivo infection from in vitro cultures, and genetically manipulating the fungus. Developing these techniques will enable us to interrogate both sides of this infection system to learn more about E. muscae pathogenesis and behavior manipulation.

**Poster Number: 71**

### Unraveling the Regulation and Horizontal Transfer of Fungal Starships

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Fungal genomes harbor massive mobile genetic elements called Starships, which carry cargo genes encoding adaptive traits like heavy metal tolerance or metabolic pathways. While beneficial, their mobility risks genome destabilization through repeat-induced mutations. The regulatory interplay between fungal hosts and Starships remains poorly understood, particularly how environmental cues influence transposition and cargo gene expression. We hypothesize that shared regulatory mechanisms create a trade-off between maintaining genome stability and harnessing Starship-derived adaptations. In the human pathogen Aspergillus fumigatus, Starship presence varies across strains and may drive phenotypic heterogeneity. Using the Lamia Starship as a model, we explore how mobility and cargo function are balanced. Lamia includes the fumigermin biosynthetic gene cluster (BGC), which inhibits Streptomyces spore germination during co-culture. We will correlate Lamia transposition rates with fumigermin production under environmental stressors (e.g., Streptomyces co-culture) to test if external cues modulate both processes. We have identified three putative regulators of Lamia that will be explored through genetic deletions and overexpressions to assess their roles in transposition efficiencies. Additionally, we examine horizontal gene transfer (HGT) drivers by co-culturing donor and recipient fungi, then selecting for Lamia transfer events using marker-tagged elements. This will reveal environmental conditions favoring HGT and its contribution to rapid adaptation. This work advances understanding of transposable element-host dynamics, the evolutionary role of cargo genes, and eukaryotic HGT mechanisms. By linking fungal adaptation to genomic stability, it provides insights into pathogen evolution, particularly how stress responses and interspecies interactions shape virulence traits.

**Poster Number: 72**

### Is a Psilocybin Cluster Still a Mobile Element in Panaeolus?

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Pietro Voto, Independent Mycologist
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Panaeolus is a diverse genus of mostly grassland mushrooms with a global distribution. Phylogenetic analysis of ribosomal DNA sequences reveals extensive genetic diversity, with species such as P. cyanescens, P. foenisecii, P. papillonaceus, and P. cinctulus exhibiting paraphyly and polyphyly, suggesting taxonomic complexity. Psilocybin production, a variable trait in Panaeolus, originated by horizontal transfer of the psilocybin gene cluster (PGC) from the Psilocybe section Cubensae. However, with only two publicly available Panaeolus genomes—one with the PGC and one without—reconstructing the evolutionary history of the PGC in this genus has been challenging. Here we present eight new

Panaeolus genomes from across the genus, including the recently described P. oligotrophus to investigate the evolutionary processes underlying the patchy distribution of psilocybin. Using reciprocal synteny analysis of multiple PGC-variable loci, combined with phylogenetic analysis of coding sequences, we test the hypothesis that the PGC may be part of a recently or currently mobile genetic element in Panaeolus. Our results provide insight into the molecular evolutionary processes shaping chemical diversity in Agaricales.

### Poster Number: 73

### Investigating the Impact of Wheat Cultivar and Soil Cycling on the Abundance and Diversity of Rhizosphere-Associated Fungi

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Genotypically-distinct crop varieties (i.e, cultivars) have been shown to influence the composition of rhizosphere-associated microbiota. These communities play a role in plant growth, but may also mediate pathogen interactions and reduce disease severity. Previous research found cultivar-specific variation in microbial communities associated with winter wheat (Triticum aestivum) roots. This work suggested that variable communities have an active role in reducing the effects of take-all disease (Gaeumannomyces tritici). To date, most research on rhizosphere microbiomes has focused on bacteria, such as Pseudomonas spp., and less on fungal constituents. To understand variation across, and within, the mycobiomes of various wheat cultivars, we developed a soil cycling method to enrich the cultivar-specific fungal signal and explored community composition through a plate-based experiment. Root wash suspensions were created from each of four cultivars, across three increasingly enriched soil cycles, and were plated to observe morphotype abundance and growth. We found that soil cycling had a significant effect on fungal colony abundance and species richness. Yeast-like fungal colonies contributed largely to the abundance variation, while filamentous fungi abundance remained relatively constant across three cycles. Sequencing of the ITS and LSU gene regions identified morphotypes to the genus level, with samples including Trichoderma, Penicillium, Fusarium, Apiotrichum, and Sporobolomyces, among others. Further experimentation is being performed to determine the effect of these fungal communities against varying pathogens, such as Fusarium spp. and Oculimacula yallundae.

### Poster Number: 74

### Evaluation of Sea Turtle Eggs Fusariosis (STEF) in Dermochelys coriacea at Playa Grande Beach, Arecibo, Puerto Rico

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Emerging fungal diseases represent a significant threat to wildlife populations. In recent decades, several fungal pathogens have been identified as contributing to declines in amphibian and reptile species. These include chytrids Batrachochytrium dendrobatidis and B. salamandrivorans affecting amphibians, Ophidiomyces ophidiicola in snakes, and the Fusarium solani species complex in sea turtle eggs. The latter was first reported in Puerto Rico in 2009, where it was associated with up to 100% egg loss in leatherback turtle nests on the beaches of Mayagüez and Añasco. Several volunteer groups working in sea turtle conservation have observed egg losses in recent years, with fungal involvement suspected. This study aims to assess fungal presence in leatherback turtle nests and evaluate changes in fungal composition after the incubation period. Nocturnal monitoring was conducted at Playa Grande in Arecibo to collect sand samples from the egg chamber at oviposition. After the incubation period, samples of unhatched eggs and sand from the chamber floor were collected to analyze the fungi present. Fungi identified in the sand samples prior to hatching included Aspergillus, Penicillium, Cladosporium, and Fusarium. Post-hatching observations revealed additional fungal morphotypes, distinct from Fusarium, suggesting that other fungi may also infect the eggs.

## Poster Number: 75

## Investigating the Effect of Spatial Structure on Community Development in Cheese Rind Communities

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Small-scale spatial structure – including patch size, density, and location – has been shown to be important in the assembly of plant and animal communities. Much less is known about the importance of small-scale spatial structure in the formation of mixed-kingdom microbial communities. In this project, we used the cheese rind model community to determine how spatial structure impacts fungal and bacterial community structure and function. Two experimental setups (a four-species community of filamentous fungi and an eight-species community of filamentous fungi, yeast, and bacteria) were both arranged in two spatial treatments (homogeneous and heterogeneous) on cheese curd agar. The homogeneous treatment was inoculated at regularly-spaced points with patches of an even mixture of all strains while the biologically heterogeneous configuration was inoculated at regularly-spaced points with patches of individual strains. The density of all strains between the two spatial treatments were different for both the fungal and the mixed communities, and the spatial treatment accounted for nearly 40% of the difference in the relative abundance of species across the samples of all communities. Ongoing RNA sequencing is identifying the transcriptional differences between the two spatial treatments in one prevalent fungal community member. Given that these spatial treatments strongly influenced community composition, further experiments should be done to assess spatial structure in real cheese rinds in order to develop a strategy for accounting for spatial structure in laboratory experiments of microbial communities.

## Poster Number: 76

## Molecular Methods to Detect an Emergent Invasive Wood-Decay Fungus: Eliminating the Basidiocarp Bias

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Invasive species are a major threat to biodiversity. Reliable detection of emergent invasives is essential for successful surveillance efforts, especially for species with cryptic lifecycles, such as fungi. In North America, the Golden Oyster Mushroom (Pleurotus citrinopileatus; GOM) is non-native, edible, wood-decay fungus that has spread rapidly since escaping cultivation. Invasive fungi are typically detected by observations of basidiocarps; molecular tools can alleviate this bias by identifying DNA of interest from environmental samples. Quantitative PCR (qPCR) is a fast, sensitive, and relatively inexpensive molecular method for detecting and quantifying DNA. We developed a species-specific qPCR assay for GOM using the ITS2 gene region. We rigorously tested the qPCR assay for specificity in vitro using GOM isolates, closely related Pleurotus species, and other common wood-decay fungi. We then validated the qPCR assay using metabarcoding of 32 environmental samples from trees with and without GOM basidiocarps. The GOM-specific qPCR assay was reliable at detecting GOM, and did not amplify any other Pleurotus or wood-decay fungi. Additionally, metabarcoding data confirmed that the qPCR assay was sensitive enough to detect GOM even when DNA copy number was low and a basidiocarp was not present. Our GOM-specific qPCR assay is a valuable tool with a wide range of applications for this emergent invasive. The qPCR assay can help with current surveillance efforts thus increasing our limited knowledge of GOM's invasion ecology, including the tree species it can colonize, when GOM colonizes trees, how quickly colonization occurs, and if GOM plays a role in tree death.

### Poster Number: 77

### Characterizing the Soil Microbiome of Invasive Halophytes in Disturbed and Non-Disturbed Sites

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Tamarix sp. of the Tamaricaceae are an invasive tree common in riparian areas across the South West United States which can outcompete native Salicaceae trees. Tamarix sp. are drought-adapted halophytes with the capacity to concentrate salt in their foliar tissue. At the end of a growing season, the senesced leaves contribute to increased salinity in the topsoil giving this organism an advantage over native plants. In order to examine the effect of Tamarix sp. on the soil microbiota we collected soil along a gradient of distance from Tamarix sp. trunks in areas with different disturbance history and shade aspects. Soil samples were tested for macronutrient content and salinity. Serial dilutions of the soil were used to observe culturable microbes. We found differences in salinity, nitrate content, and bacterial and fungal community compositions based on proximity to Tamarix sp. and disturbance status. The undisturbed plots had the highest alpha diversity of bacteria within the canopy and lowest outside the canopy, while the disturbed plots had intermediate values. Additionally, we have employed ITS/16S metabarcoding to characterize the full microbial communities associated with each site, finding that the most abundant species of fungi across samples are plant pathogens, with the exception of Pseudogymnoascus desctructans, the cause of White Nose Syndrome in bats.

### Poster Number: 78

### Identification and Characterization of Regulators of Germination Initiation in the Human Fungal Pathogen Cryptococcus neoformans

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Cryptococcus is an invasive human fungal pathogen that causes severe meningitis in immunocompromised people. Spores are infectious propagules that when inhaled can germinate into yeast and spread to other tissues of the body. Spores must germinate to cause disease; therefore, we are especially interested in understanding the molecular mechanisms underlying germination to identify targets for inhibition. To identify key pathways and processes important for germination, we evaluated a collection of single gene deletion mutants for phenotypes in germination. We discovered that hgr2Δ and isp2Δ spores show an unexpected “early” germination phenotype in which mutant spores initiate and complete germination ~2 hours earlier than wild type spores. Hgr2 is a sequence-specific High Mobility Group Domain transcription factor. Isp2 is a protein found to be enriched in spores relative to yeast that has no conserved domains. Because hgr2Δ and isp2Δ spores showed the same germination phenotype, we hypothesized that Hgr2 and Isp2 regulate similar molecular pathways in germination. To test this hypothesis, we carried out RNA-seq analysis on hgr2Δ and isp2Δ mutant spores during germination and discovered that they have strikingly different transcriptomes. These preliminary data suggest that they function in independent regulatory pathways. To further test and refine our hypothesis, we will create hgr2Δ isp2Δ double mutant spores and evaluate their phenotypes under diverse germination conditions. By comparing wild type, hgr2Δ, isp2Δ, and hgr2Δisp2Δ spores, we will determine the similarities and differences between Hgr2 and Isp2 regulation and gain insights into the fundamental pathways that function to regulate initiation of germination.

### Poster Number: 79

### Transcriptional Decoupling of Filamentation in Candida albicans

Siobhan Dietz, University of Wisconsin, Madison

Candida albicans is a diploid yeast that is a normal part of the gut, oral, vaginal, and skin microbiomes in humans. Despite this largely commensal lifestyle, C. albicans is a major pathogen causing systemic infections among immunocompromised individuals and vaginal yeast infections in otherwise healthy people. This ability to colonize, disseminate, and persist across diverse host niches is due, in part, to the immense genetic diversity within the species, which produces strains with a range of pathogenic potential. Two phenotypes critical for virulence in the host are filamentation and epithelial damage. Here, we investigated the genetic basis for the opposing filamentation/damage phenotypes between two strains. One strain, 529L, displays canonically “commensal” phenotypes (non-filamentous/non-damaging), and the other strain, SC5314, is widely considered a “pathogen” (filamentous/damaging). RNA-sequencing of these two strains incubated on human oral epithelial cells along a time course revealed that despite massively different phenotypes, these strains display similar temporal patterns of gene expression over time. Strikingly, genes that regulate filamentation and their downstream effectors were expressed similarly in both strains. Additionally, a core filamentation network showed the same pattern of expression across the time course for both strains. This data suggests that the lack of filamentation associated with commensalism in 529L is not due to altered transcriptional regulation but likely the result of a post-transcriptional or structural defect. By investigating individual genes related to these phenotypes we will further uncover how intra-species diversity within Candida albicans contributes to the commensal-pathogen spectrum.

**Poster Number: 80**

### Characterizing the Endophyte-To-Pathogen Transition in Colletotrichum Spp.

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Recent research has increasingly revealed that many fungi once thought to be solely disease-causing agents exist in far more complex associations with plants. Some of these organisms, known as facultative pathogens, can shift between asymptomatic colonization (endophytism) and disease induction (pathogenicity) for reasons that remain elusive. Understanding the mechanisms behind this transition is crucial for effective disease management, and the fungal genus Colletotrichum—which includes species spanning a spectrum from benign endophytes to aggressive pathogens—serves as an ideal model for study. In recent years, outbreaks of Colletotrichum siamense, a major causal agent of strawberry anthracnose crown rot (ACR), have been reported in the northeastern United States. Initial field assessments indicate that C. siamense can exist both as an endophyte and as a necrotrophic pathogen within genetically uniform hosts in close spatial proximity. Field screening of C. siamense across various strawberry varieties revealed stark differences in disease outcomes, ranging from near immunity to full mortality, yet asymptomatic colonization remained consistently present at similar frequencies. This suggests that disease variation is not due to true resistance but rather to differences in C. siamense's ability or tendency to shift from an endophytic to a pathogenic state. This work aims to disentangle the mechanisms governing this transition, improving our understanding of Colletotrichum ecology and informing better strategies for managing these fungi as agricultural pathogens.

**Poster Number: 81**

### Unraveling the Impacts of Heat and Drought on Dryland Soil Ascomycota

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Ecosystem resistance is challenged by climate change. Soil degradation, particularly in drylands is expected to intensify, threatening the unique microbial communities in biological soil crusts (biocrusts). Fungi likely play important roles in these communities, by processing nitrogen, phosphorus, and carbon, yet their responses to heat and drought remain largely unknown. To better understand how climate change may affect biocrust fungi, we isolated fungal species found in biocrusts of semi-arid grasslands in central New Mexico. We subjected cultures to gradients of heat and desiccation in the laboratory by varying media thickness and incubating them at 25, 30, 35, and 40°C, then measured growth every 24h for 7d. We measured fungal traits, including exopolysaccharide production and melanin pigment, which can be important for drought resistance. Fungi varied in growth rates in response to heat and drought, with both sensitivity and resistance to heat and/or desiccation, which correlated with the expression of exopolysaccharide and melanin production. Results suggest that shifts in biocrust communities under future heat and drought could alter fungal traits that promote resistance to climate change.

**Poster Number: 82**

### Local co-adaptation shapes the Quaking Aspen mycobiome in the Intermountain West

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Plant-associated microbial communities play a crucial role in enhancing plant resilience to environmental stressors, including drought. However, the extent to which plant-microbe co-adaptation and microbial adaptation to local conditions contribute to patterns of soil community composition remains unclear. This study investigates how aridity influences symbiotic interactions of Quaking Aspen (Populus tremuloides) trees by examining microbial community composition and aspen physiology along an elevational precipitation gradient in the Intermountain West. Using DNA metabarcoding of root and soil samples, we characterize and quantify the aspen mycobiome across an array of sites in the San Juan National Forest, CO. We also use a field-based reciprocal transplant experiment to assess plant performance when paired with local or non-local microbial communities under drought conditions. We found that microbial communities vary along climatic and biological gradients, with increased ectomycorrhizal diversity and abundance at higher elevations. Several fungal taxa are identified as key indicators of droughted conditions. By integrating microbial ecology with plant physiology, this research advances understanding of plant-soil feedbacks under climate stress, informing conservation strategies for drought-vulnerable tree populations. Findings may have direct applications for assisted migration and restoration efforts, highlighting the role of microbial symbionts in enhancing plant resilience to climate change.

**Poster Number: 83**

### Source-Sink Dynamics and Gene Flow of Endophytes between Agricultural Fields and Field-Adjacent Plants

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Christine V. Hawkes, North Carolina State University

Because of the threat of climate change to global crop yield, we aim to leverage plant microbiomes to increase crop resilience. Previous work from our lab indicates the amount of vegetation surrounding a focal field is positively associated with foliar fungal endophyte diversity in crop plants, and preliminary analyses indicate that endophyte haplotypes are shared between these two pools. We hypothesize that endophytes from plants adjacent to agricultural fields form crop microbiomes. To test this hypothesis, we sampled foliar endophytes from wheat in seven fields in North Carolina and plants adjacent to those fields. We characterized bacterial and fungal communities using amplicon sequencing, and used whole-genome sequencing of cultured fungi for population analyses. We cultured a species tentatively identified as Stagonosporopsis present at high abundance in both wheat and adjacent hosts at all sites. Using this two-pronged approach, we can corroborate community-level source-sink analysis with patterns of abundance of specific haplotypes. Nestedness of wheat endophyte communities within adjacent communities at the same site along with shared haplotypes indicating gene flow between these host pools will support our hypothesis that crop microbiomes are formed from endophytes of plants growing near fields.

**Poster Number: 84**

### Decoding Fusarium oxysporum pathogenicity and variability with pangenome graphs

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The astounding diversity of the Fusarium oxysporum species complex (FOSC) presents a significant challenge for agricultural biosecurity, with over 100 lineages threatening the health of specialty and commodity crops globally. Various lineages within the species complex are known for their host specificity, while many others colonize plants as asymptomatic endophytes. The diverse pathotypes that constitute FOSC make strain differentiation a critical first step for disease prevention and management. However, the DNA markers routinely used to distinguish between pathogenic and asymptomatic FOSC lineages often perform poorly in diagnostic settings. To address this issue, we aim to develop state-of-the-art capabilities for differentiating FOSC strains with varying biosafety risks by designing long-read DNA barcodes that are diagnostic of specific pathogenic lineages. To achieve this goal, we are utilizing pangenome graphs, which offer distinct advantages for diagnostics over individual genome references by representing the full complement of coding and non-coding DNA sequences within a species. This approach provides a powerful framework for capturing genetic diversity across multiple strains, enhancing resolution in comparative analyses and surpassing traditional linear reference models. We are constructing benchmark pangenome graphs for Fusarium oxysporum strains to identify optimal strategies for capturing all possible genomic variations relevant to phylogenetic classification and pathogenicity. This work will enhance molecular diagnostics of phytopathogens by providing a critical resource for genetic barcode design and will be automated as an open-source bioinformatics tool. Rather than relying solely on genetic relatedness, this tool will differentiate strains based on key biosecurity traits such as host specificity and pathogenicity.

### Poster Number: 85

### Determining the surface composition of Cryptococcus neoformans spores

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The makeup of the exterior of a cell is a crucial determinant of how it will interact with its environment, such as a host organism during infection. The basidiomycete yeast Cryptococcus neoformans is a meningitis-causing pathogen of humans, especially in immunocompromised people. The surface composition of Cryptococcus yeast is generally understood – it has a cell wall composed of chitin, chitosan, and alpha- and beta-glucans, as well as a polysaccharide capsule that is primarily made up of glucuronoxylomannan (GXM). Though the yeast surface has been the subject of many studies, far less is known about the surface of Cryptococcus spores. Spores are the product of the Cryptococcus sexual reproduction cycle and are thought to be infectious particles in cryptococcal disease. Previous research has demonstrated that the exterior of spores, called the spore coat, contains some of the same components as the yeast exterior, including GXM, but also some spore-specific polysaccharides or arrangements of polysaccharides. Additionally, it is known that Cryptococcus spores and yeasts interact differently with host phagocytes, which in turn can produce different disease outcomes. By using techniques like fluorescence microscopy and flow cytometry, we are investigating the surface composition of the Cryptococcus spore and comparing it to that of the yeast. We will also examine the way the cell surface changes during spore germination. These early studies will lead to greater explorations into the biosynthetic pathways that produce these polysaccharides and assemble the spore coat.

### Poster Number: 86

### Determining the Host Range of Trichoderma Spp. on Cultivated Fungi and Fungal Pathogens

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Trichoderma species pose an interesting parallel in fungal research as they are both formidable pests in mushroom cultivation and widely employed as biocontrol agents against plant pathogens. Their ability to aggressively colonize and parasitize a wide range of fungal species makes them valuable in agriculture but challenging for commercial mushroom growers. In this study, we examined the growth dynamics of edible and medicinal fungi (golden oyster ‘Pleurotus citrinopileatus’, turkey tail ‘Trametes versicolor’, chestnut ‘Pholiota adiposa’, wine cap ‘Stropharia rugosoannulata’, lion’s mane ‘Hericium erinaceus’, and pink oyster ‘Pleurotus djamor’), alongside common fungal pathogens (Fusarium graminearum, Bipolaris sorokiniana, and Pyrenophora teres) and 11 Trichoderma spp. found in agricultural soils and in mushroom cultivation contaminants. We compared their growth across multiple culture media (V8, PDA, Mungbean, and Malt Extract). These initial growth assessments guided our inoculation strategy for Trichoderma challenge assays, where we co-cultivated Trichoderma isolates with both cultivated and pathogenic fungi to observe their interactions. Our findings contribute to understanding Trichoderma host range dynamics and provide insight into potential molecular and ecological factors influencing its dual role in fungal cultivation systems. This research has implications for both mushroom growers seeking mitigation strategies and agricultural biocontrol applications leveraging Trichoderma.

### Poster Number: 87

### Endosymbiotic Bacterium of Arbuscular Mycorrhizal Fungi May Affect the Growth of a Host Plant

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Multiple species of endosymbiotic bacteria have been identified within arbuscular mycorrhizal fungi, but their role in the biology of their host fungi is not fully understood. Arbuscular mycorrhizal fungi are becoming increasingly appealing as an alternative to mineral fertilizers, as these fungi can assist with crop nutrient uptake. However, more research into the biology of these fungi is needed to optimize their use in agriculture. This study focuses on Candidatus Moeniiplasma glomeromycotorum, an obligate endosymbiont with a highly reduced genome. The goal of this study is to determine how this bacterium affects the sporulation and gene expression of its host fungus, and in turn how this affects the growth, nutrient uptake, and gene expression of a host plant. We tested various strains of Rhizophagus clarus from the International Collection of Vesicular Arbuscular Mycorrhizal Fungi for the endobacterium, and compared how these strains affect the growth of Medicago truncatula in nutrient sufficient and phosphorus deficient conditions. We hypothesized that Candidatus Moeniiplasma glomeromycotorum is a conditional mutualist, and may provide benefits to its host fungus and plant host in low nutrient conditions.

### Poster Number: 88

### Infection rate, density, and Diversity of Laboulbeniales on Aquatic Beetles (Hydrophilidae, Dytiscidae) of Indiana through Time

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Anthropogenic land use changes have resulted in significant habitat loss and a decline in biodiversity, which in turn affects host-parasite interactions. The dilution effect hypothesis suggests that healthy and diverse ecosystems can mitigate the risk of disease by reducing interactions between hosts and parasites. This study aims to test the dilution effect hypothesis by looking at temporal trends in the prevalence, infection intensity, and species richness of Laboulbeniales, a group of ectoparasitic fungi, on aquatic beetles in Indiana. Given the extensive loss of Indiana’s forests and wetlands over the past 200 years, this system provides an opportunity to investigate how anthropogenic pressures influence parasitism. To assess long-term trends in infection, historical beetle specimens from the Purdue Entomological Research Collection and the Field Museum of Natural History will be screened for Laboulbeniales. Additionally, fresh specimens will be collected from historical sites for screening. Data on prevalence rates, infection intensity, and species richness will be gathered, with data points ranging from the late 19th century to 2025. We hypothesize that Laboulbeniales infection rates have increased over time due to habitat degradation, consistent with the dilution effect. This study will enhance our understanding of host-parasite dynamics in the Anthropocene and contribute to the documentation of Indiana’s fungal biodiversity.

### Poster Number: 89

### Restoring Restoration: Leveraging Fungal-Bacterial Hydrogel Beads to Improve Transplant Survivability of Gaillardia Aristata in Ecological Restoration

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A key factor to success in ecological restoration is the survival of native plants. Often, plants for these projects are grown under nursery or greenhouse conditions, and when they are transplanted at the

site, they face transplant shock stressors. Therefore, the hardiness of the plant during the transplant phase is critical for success. Certain soil fungi and bacteria hold potential to boost plant hardiness. However, research on how these early stage plant-bacterial-fungal interactions can impact restoration transplant success across different restoration sites is in its infancy, in part because soil belowground interactions are complex and understudied. To contribute fundamental knowledge on approaching ecological restoration from a belowground perspective, this study explores if hydrogel-encased arbuscular mycorrhizal fungi and beneficial bacteria, applied at seedling stage, can improve transplant survival rates. This project focuses on blanketflower (Gaillardia aristata); a drought-tolerant perennial plant with a long blooming period and high reseeding success. We aim to understand: (1) How does our selected hydrogel consortium (Rhizophagus intraradices, Funneliformis mosseae, Duganella sp., Phyllobacterium sp., Rhanella spp., and Azospirillum brasilense) impact early development of G. aristata in the pre-transplant stage; and (2) Does early-stage application of these microbial-embedded hydrogels increase transplant survival at the restoration site? Currently, G. aristata plants treated with hydrogels are demonstrating improved early-stage growth. Over the next months, a subset of G. aristata plants will be destructively harvested to measure plant biomass and root mycorrhization. The findings to be presented will focus on how the hydrogel consortium compares to other treatments.

**Poster Number: 90**

**Diversity of generalist entomopathogenic fungi infecting adult periodical (Magicicada spp.) cicadas**

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Periodical cicadas (Magicicada spp.) are remarkable for their synchronized mass (up to billions of adults) emergences, which, depending upon the species, occur every 13 or 17 years. Little, however, is known concerning the microbial pathogen dynamics of these insects whose adult stages occur decades apart. During emergence, cicada populations experience intense selective pressures from such pathogens which include entomopathogenic fungi. While some attention has been paid to the behavior-modifying obligate cicada fungal pathogen of the Massospora species, little is known concerning broad-host range "generalist" entomopathogenic fungi that may target periodical cicadas. Here, during the 2024 emergence of Broods XIII and XIX periodical cicadas in Illinois, over 150 cicada cadavers infected with generalist entomopathogens were collected from sites across the state. A total of 180 fungal isolates were derived from these samples (some cadavers resulted in more than one isolate), which were single colony purified. Examination of colonies on plates indicated a robust distribution of morphologies within the collected set, with growth and sporulation consistent with a variety of known entomopathogenic fungal genera, including Metarhizium, Beauveria, and Isaria. Most isolates (~95%) formed colonies (diameter 3-5 cm) on potato dextrose agar (PDA) plates within 10-15 d, although slow growers (diameter 2-3 cm, 20 d, 5%) were noted. Molecular analysis examining the translation elongation factor-a (Tef1-a) locus was performed to help determine the identities of the isolates. This study provides insights into the diversity and ecology of generalist entomopathogens associated with Magicicada spp., with potential implications for novel isolate and metabolite discovery.

**Poster Number: 91**

**Complex Community of Mycoviruses Associated with Populus Deltoides (Eastern Cottonwood) Leaf Blotching**

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In summer 2024, a Populus deltoides seedling exhibiting leaf blotching symptoms was investigated utilizing high-throughput sequencing (HTS). Total RNA was extracted from symptomatic leaf tissue and sequenced utilizing Illumina NovaSeqX technology. Trimmed reads were assembled utilizing rnaSPAdes and viral contigs were identified utilizing BlastX. Several novel mycoviruses belonging to the genera Alphafusarivirus, Mitovirus, and Narnavirus were identified. The complete genome sequences were determined by 3/5' RACE and Sanger technology. Based on the species demarcation criteria established by the ICTV these are all putative new virus species. Additionally, several contigs aligning to both mymonavirus and mononegaambi viruses were identified. Follow up experiments to validate the full length viral sequences and their taxonomic grouping are being performed and the results will be presented. The results of this experiment reveal not only several novel virus species but also highlight the complex community of mycoviruses that exist in the environment. Increasing studies are highlighting the impacts of mycoviruses on their fungal hosts, which can have major effects on the role of fungi in forests. Methods of biological characterization of these mycoviruses to better understand their ecological impacts will be discussed.

**Poster Number: 92**

### Mycelium-based packing peanuts produced using locally isolated fungi

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Styrofoam packing peanuts are widely used in packing applications due to their lightweight and cost-effectiveness. However, they cause significant environmental issues due to their non-biodegradable nature. This study focuses on developing fully compostable packing peanuts using fungal mycelium and locally sourced lignocellulosic waste materials. Two fungal strains of Trametes sp. and Ganoderma sp., isolated from Sri Lanka, were cultivated on corn seeds to produce spawn, which was then introduced to rice husk and Albizia sawdust substrates. The substrate-spawn mixtures were incubated in PVC molds (0.5-inch diameter, 1-inch length) for 7 days under dark, elevated $CO_2$ conditions, followed by 2 days in an oxygen-rich environment to achieve complete mycelial coverage. The resulting packing peanuts were dehydrated at 70°C for 6 hours and evaluated for key material properties, including dry density, shrinkage, water absorption, water contact angle (WCA), and compressive strength. Rice husk-based packing exhibited lower dry density (102 kg/m$^3$) and shrinkage (4.80%) compared to sawdust-based packing (165.28 kg/m$^3$, 8.30%). Additionally, rice husk-based packing showed higher hydrophobicity (WCA: 93.14°) and lower water absorption (6.68%). Sawdust-based packing exhibited greater compressive strength (0.053 MPa) than rice husk-based packing (0.044 MPa). While the compressive strength of the mycelium-based peanuts was lower than Styrofoam, they showed relatively high fire-retardant properties. These findings suggest mycelium-based packing peanuts as a sustainable alternative to Styrofoam, with further optimization needed for broader commercial use.

**Poster Number: 93**

### Investigating Pyrolyzed Carbon Accumulation as a Potential Mechanism for Pyrophilous Fungi Emergences in the Great Smoky Mountains

Mary Grace Graddy, NEON

Pyrophilous fungi thrive in fire-affected forests, with some species solely fruiting on burned substrates. However, the mechanisms governing phenology, distribution, and ecology remain unclear. One hypothesis suggests that pyrolyzed organic matter, particularly altered carbon compounds, may serve as specialized nutrients that enhance growth post-fire. Across fungal taxa, unique substrate utilization is well-documented, from Cordyceps species parasitizing specific insect hosts to coprophiles. Similarly, pyrophilous fungi may rely on fire-modified organic compounds for colonization and reproduction. Recent studies have investigated the ecological impacts of the 2016 Chimney Tops 2 Fire in the Great Smoky Mountains on fungal communities and soil organic matter across burn sites. Between 2017 and 2019, mycologists at the University of Tennessee documented 41 species of pyrophilous Ascomycota and Basidiomycota, with 28 taxa previously unrecorded in the region. Concurrently, Oregon State University researchers analyzed soil samples collected pre- and post-fire, revealing that pyrolyzed carbon concentrations significantly increased in severely burned plots; over the course of a year, these levels decreased in O-horizons while accumulating in M-horizons. This study examines the correlation between pyrolyzed carbon concentrations and pyrophilous fungal occurrences, exploring whether heightened carbon availability mechanistically facilitated emergences. Is pyrophilous fungal proliferation driven by pyrolyzed carbon accumulation in post-fire ecosystems?

## Poster Number: 94

## The Effects of Drought on Peanut Fungal Diversity.

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Peanuts (Arachis hypogea L.) are important crops for high-quality proteins, unsaturated fats, vitamins, and minerals like magnesium, potassium, and zinc. Stress such as drought results in reduced pod setting and a lower yield. It also weakens the plant's immune response, making it more vulnerable to susceptible pathogens such as Aspergillus flavus. This study aims to understand how water availability shapes the fungal microbiome community in different peanut habitats. Peanut roots, soil, and specialized reproductive organs known as pegs were sampled at harvest from drought-tolerant and drought-sensitive varieties under rain-out shelters and irrigated conditions. This multi-year experiment was conducted in 2022, 2023, and 2024 at the Plant Breeding Unit, Tallassee, Alabama. Fungal microbiome composition was determined by sequencing the Internal Transcribed Spacer (ITS) region. The analysis determined that the peanut habitats and water availability but not variety significantly affected the fungal composition. Interestingly, the fungal communities in the peg tissue were consistently affected by water availability in all three years. This is interesting because the above-ground pegs initiate the development of below-ground pods, and the exploration of the effect of drought on peg microbial communities may lead to insights into vertical inheritance or opportunistic pathogen invasion. Together, these findings highlight the importance of moisture availability in shaping the fungal community.

## Poster Number: 95

## Seasonal underground phenology of ectomycorrhizal fungi varies by group and host tree traits

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Ectomycorrhizal (ECM) fungi assimilate one-quarter of global fossil fuel emissions annually, are critical symbionts for tree health, and perform key ecosystem functions such as decomposition. The timing of underground fungal production is an ECM trait with large implications for ecosystem carbon budgets, however, our understanding of it remains limited. Here, we analyze intra-annual temporal patterns of ECM fungal abundance across five temperate mono-dominant forest stands in Illinois, USA. We assessed fungal relative abundances of soil cores collected at monthly intervals for one year based on ITS2 Illumina sequencing and DADA2 processing with FungalTraits database matching. We found that overall ECM fungal abundance remained relatively constant at ca. 17% of total fungal reads. However, individual genera differ in their timing of initial peak production: for example under evergreen hosts, Amphinema first peaked earlier in spring, Wilcoxina peaked later in autumn, and Tuber and Cortinarius peaked in summer. Similarly, most ECM fungal exploration types peaked earlier in spring, except for short-distance coarse types, which peaked later with evergreen hosts. These findings suggest that future studies with limited sampling capacity should consider sampling across multiple seasons to more accurately capture the dynamic nature of ECM fungal communities.

### Poster Number: 96

### Evolution of isocyanide natural products in Fusarium sporotrichioides, a cereal pathogen and wild grass endophyte

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Species in the genus Fusarium infect diverse plant hosts as either asymptomatic endophytes or mycotoxin-producing pathogens. Fusarium sporotrichioides is a common endophyte of wild grasses and one of the causative agents of Fusarium head blight disease in cereal crops, like wheat and barley. However, it is unclear how F. sporotrichioides has genetically differentiated between wild and cultivated hosts in different geographic ranges. We assembled and compared de novo genomes for 109 isolates collected from wild grasses and infected cereal crops worldwide over 60 years. We found that some isolates have twice as many isocyanide synthase gene clusters as closely related Fusarium species. Isocyanide synthases produce reactive isocyanide compounds that chelate metals and affect microbial communities. Fungal isocyanide production in planta can also contaminate animal feed and result in dangerous trace metal deficiencies after consumption. To clarify the threat fungal isocyanides pose to grasses and the animals that consume them, we characterized the diversification of isocyanide synthases in F. sporotrichioides. Comparisons across Sordariomycetes demonstrated that the large number of isocyanide synthases in F. sporotrichioides results from a complicated evolutionary history of gene loss and duplication. Because isocyanides are highly reactive, we also hypothesize that isocyanide biosynthesis will occur in specific intracellular compartments. Ongoing efforts include localizing isocyanide biosynthesis enzymes in live cells using fluorescence microscopy, chemically isolating novel isocyanides, and testing if isocyanides play a role in F. sporotrichioides interactions with a host. Together, this study clarifies the evolution of isocyanides in F. sporotrichioides and their role in host specificity.

### Poster Number: 97

### Isolation and Molecular Characterization of Endophytic Fungal Isolates from Cacao Trees (Theobroma cacao) in Colombia

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Phytopathogenic fungi, such as the basidiomycete Moniliophthora roreri, causal agent of moniliasis or frosty pod rot disease, cause significant losses in cacao (Theobroma cacao) production. Endophytic microorganisms can influence host plant health through various interactions, including potential antagonism against pathogens. Employing these endophytic fungi as biocontrol for pathogens is a strategy that could yield sustainable solutions for disease management. In this study, 116 endophytic fungal isolates were obtained from pods, leaves, stems, and branches of various cacao tree clones in Colombia. To identify these isolates to species, DNA will be extracted, and isolates will be sequenced at the ITS locus; additional genus-specific loci will also be amplified as necessary, depending on the ITS-

derived placement, and phylogenetic analyses will be conducted for select isolates to confirm identification. We will also conduct biochemical assimilation tests of isolates belonging to genera suspected of being antagonistic to better characterize their growth requirements. This study enhances the knowledge of endophytic fungal diversity in tropical ecosystems, specifically in cacao trees, and contributes to the investigation towards finding potential agents for biological control against pathogens such as M. roreri.

### Poster Number: 98

### Leotiomycetes in the Bog down in the Valley-O: Environmental Metabarcoding of Peatlands in Western Ireland

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Peatlands or Sphagnum Bogs cover ~3% of Earth's surface, yet they sequester ~25% of the global soil carbon. Within these environments, various levels of anthropogenic disturbances (conversion to agriculture lands, timber lots, extraction of peat for personal heating fuel) can degrade and diminish the quality of the environment and its ability to store soil carbon. These environments have been shown to be enriched for the Ascomycota class Leotiomycetes. Ecologically, Leotiomycetes function as symbionts and saprotrophs, yet their biodiversity is often overlooked due to their cryptic and diminutive sporocarps. To better understand the biodiversity of Leotiomycetes, and fungi writ large, eDNA was collected from water samples within different Peatlands in Western Ireland. Samples were amplified using amplicon metabarcoding for the ITS-2 (using primers fITS7 and ITS4) and the 28S Large Subunit (LSU; LR0R and JH-LSU-369rc) region and sequenced on a 2X300 Illumina MiSeq. The OTUs recovered, as well as patterns of community stratification, will be discussed.

### Poster Number: 99

### Behavior of Rose Downy Mildew (Peronospora sparsa) on Leaves and Flowers of a Variety of Plants in the Rosaceae

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Downy mildews on roses and brambles are sometimes considered the same species, Peronospora sparsa, and sometimes considered to be two species, P. sparsa on roses, and P. rubi on brambles. P. sparsa has also been reported from cherry laurel (Prunus laurocerasus). We have performed host range tests on detached leaves and petals of Rosa multiflora, Rubus strigosus, cherry laurel, Spiraea cantoniensis, Cydonia oblonga, and Amelanchier canadensis, among others, comparing susceptibility with that of miniature roses inoculated at the same time. Sporangia collected from miniature rose petals were used as inoculum (approx. 15,000 spores/mL water); a micropipette was used to put one or two 20 uL drops of suspension on each leaf or petal, incubating in moist chambers consisting of Petri dishes lined with moist Whatman Filter paper. After 8-10 days, the number of infected leaves or petals were counted. Miniature roses were most susceptible, and for other plants that became infected (like cherry laurel and raspberry), infection was generally greater on petals or exclusively on petals compared to leaves. Haustoria and oogonia were often observed in infected petals cleared in ethanol. Results suggest that while P. sparsa can weakly infect various weakly infect the leaves of plants in the Rosaceae, there was less host specificity observed in flower infections. It has not escaped our notice that our results immediately suggest a possible mechanism for adaptation to new hosts.

**Poster Number: 100**

# Think globally, Barcode locally: Nine Years of Macrofungi Sampling Reveals Extensive Biodiversity at the Ordway-Swisher Biological station, a Subtropical Site in Florida

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The Ordway-Swisher Biological Station (OSBS) is a 38-km2 reserve owned by the University of Florida and is part of the National Ecological Observatory Network (NEON). The reserve contains several iconic Florida habitats, such as sandhill, mesic hammock, and scrubby flatwoods. While plants and animals have been extensively studied at OSBS, the fungi remain poorly known. Fungal inventories are critical to increase knowledge of both fungal diversity and species ranges, and thus to provide foundational data for a wide array of applications in ecology and resource management. Here, we present the results of a nine-year effort to collect, preserve, and DNA barcode the macrofungi at OSBS. This effort generated >1,200 vouchered specimens and 984 ITS rDNA sequences, representing more than 546 species. Our sampling was dominated by Basidiomycota and revealed a high diversity of symbiotic ectomycorrhizal fungi, particularly species of Amanita, Cortinarius, and Russula. Sampling curves and both Chao1 and Jacknife1 richness estimators suggest that our DNA barcoding efforts captured only about half of the macrofungi species and that a more complete inventory would detect 897–1,177 macrofungi species at OSBS. Our sampling found more species of macrofungi at OSBS than the known number of vertebrate animal species at the reserve and our estimates also suggest that there are likely more macrofungi species than plants at OSBS. This study is the first comprehensive macrofungi inventory within a NEON site and highlights the importance of long-term monitoring to provide novel data on fungal diversity, community structure, conservation, biogeography, and taxonomy.