SYMPOSIUM 1: EXPANDING COMMON MYCORRHIZAL NETWORKS: NOVEL ANALYSES, METHODOLOGICAL ADVANCES, CONCEPTUAL DEVELOPMENTS, AND THE FUTURE OF NETWORK RESEARCH

Session Chairs: Ian R. Mounts¹, Beatrice M. Bock²
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Synopsis
Discussion on the current status of the common mycorrhizal network literature, including recent analyses and advances in terminology and concepts.

SYM01-001: CLARIFYING THE DEFINITION OF COMMON MYCORRHIZAL NETWORKS
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Abstract
The current use of the term ‘common mycorrhizal network’ stipulates a direct, continuous physical link between plants formed by the mycelium of mycorrhizal fungi. This means that a specific case (involving hyphal continuity) is used to define a much broader phenomenon of hyphae interlinking among roots of different plants. We propose a more inclusive definition of the CMN as a network formed by mycorrhizal fungi among roots of different plants, irrespective of the type of connection or interaction, and not limited to direct hyphal linkages. This approach leads to a hierarchy of concepts surrounding common mycorrhizal networks. This hierarchy is supported by the current reality of research, as shown in a systematic mapping exercise for arbuscular mycorrhizal fungi.

SYM01-002: EXAMINATION OF COMMON MYCORRHIZAL NETWORK EFFECTS ON PLANT BIOMASS, NUTRIENT CONCENTRATION, AND SURVIVAL THROUGH META-ANALYSIS
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Abstract
The conduct and communication of research on common mycorrhizal networks (CMNs) have experienced both a boom in interest and a thorough reevaluation over the past three decades. Reevaluation has focused on the presentation of available data to the general public, alternative explanations for experimental results, and an apparent context-dependency in CMN effects. Open questions remain in CMN research regarding the effects of networks on plant functioning and survival. While previous reviews have addressed issues with communication and interpretation of results, they have remained largely narrative. We conducted a series of meta-analyses on 20 CMN field studies to examine network connectivity on receiver plant biomass, survival, and nutrient concentration, using mixed-effect meta-regression to quantify environmental and experimental factor influence on effect size magnitude. Results emphasize the context-dependence of CMN effects on plant responses, as effect sizes did not differ significantly from zero on average, but were highly variable, with a full-range of positive, neutral, and negative effects.

SYM01-003: CONTEXT DEPENDENCY IN DIVERSE EFFECTS OF COMMON MYCORRHIZAL NETWORKS
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Abstract
Although gaining much attention in recent years, it is unclear whether mycorrhizal fungi distribute meaningful amounts of resources among trees in ways that increase the fitness of the receiving trees. To this end, we performed several experiments, including shaded and non-shaded pairs of inter- and intra-species Pinus halepensis and Quercus calliprinos saplings growing outdoors in forest soil. The effects of belowground connections were examined by tree performance and non-structural carbohydrates (NSC) pools. Additionally, we monitored the carbon (C) flow from a 13CO2 labeled donor tree to the final recipient tree. We were able to demonstrate belowground C transfer, most prominently from pines to shaded oaks, and identify the main fungal symbionts involved in C transfer by DNA stable isotope probing (DNA-SIP). Collectively, our findings indicate that the effects of belowground C transfer are evidently context-dependent, and they manifest in nuanced alterations in plant NSC that are not readily apparent through conventional growth metrics.

SYM01-004: POSITIVE CONTROLS FOR COMMON MYCORRHIZAL NETWORKS
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Abstract
There are hundreds of examples of net carbon transfer through common mycorrhizal networks; they are called mycoheterotrophic plants. For both arbuscular mycorrhizas and ectomycorrhizas, mycoheterotrophic plants provide evolutionarily and geographically widespread examples of: a) mycorrhizas that function in reverse, whereby carbon is transferred from neighbouring green plants via mycorrhizal fungi to non-photosynthetic plants, b) plant specificity to mycorrhizal fungi, with fungi acting as hosts to plants, and c) of functional variation in carbon transfer within common mycorrhizal networks, with initial mycoheterotrophy (non-photosynthetic mycorrhizal seedlings that develop into photosyntetic mature plants), partial mycoheterotrophy (plants that supplement their photosynthesis with mycorrhizal carbon) and full mycoheterotrophy (non-photosynthetic mycorrhizal plant species). Over the last three decades, the study of common mycorrhizal networks and the study of mycoheterotrophy have grown largely independently, but the direct biological links cannot be ignored, and should provide insights into one of the most methodologically challenging and controversial areas in plant ecology.
**SYM01-005: EXPLORING THE POTENTIAL FOR COMMON NON-MYCORRHIZAL NETWORKS**
Beatrice Bock1,2, Nancy Johnson1,2, Catherine Gehring1,2
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**Abstract**
The “Wood Wide Web” has captured pop-culture attention because of the fascinating fungal networks which the term describes, wherein mycorrhizal fungi may allow for the flow of resources among the plants they connect. While this field has focused on mycorrhizal fungi, other types of fungi, including fungal endophytes, can also act as mutualists with plants yet have not been explored for their capacity to form common networks among plants. This talk will discuss the literature basis for the potential of fungal endophytes to transport nutrients among plants, as well as preliminary evidence from recent experiments which suggests the same phenomenon.

**SYM01 Discussant**
Dr. David Hibbett
Clark University, Worcester, MA USA

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**SYM02-002: FUNGI DETECTIVES: THE BIODIVERSITY, ECOLOGY AND EVOLUTION OF FUNGI FROM A STUDENT ANTIBIOTIC INVESTIGATOR'S PERSPECTIVE**
Chinyere Knight
Tuskegee University, Tuskegee, USA

**Abstract**
Antibiotic resistance is a threat to animal, human, and environmental health. To boost systemic change in STEM, the integration of research courses into the curriculum is highly recommended. Although, the total number of bioactive fungal products represents 38% of all microbial products, only 300,000 species out of an estimated 5.0 million species of fungi have been identified. Thus, investigating understudied fungi are certain to elucidate novel secondary metabolites. The purpose of this project was to co-develop and implement the Mycological Curriculum for Education and Discovery (Myco-Ed), a Course-based Undergraduate Research Experience at Tuskegee University (TU). Specific aims of Myco-Ed were to enable students to: (1) Culture fungi from the Dr. Lafayette Frederick Collection; which houses unique basidiomycete and ascomycetes. (2) Confirm the identity of specimens using ITS1/ITS4 molecular markers; (3) Submit novel strains for genome sequencing and analysis to the Joint Genome Institute (JGI) MycoCosm; and (4) Practice comparative genomics using R studio and the JGI MycoCosm platform to investigate secondary metabolites for antibiotic use. Six unique fungal strains *Aleurodiscus thailandicus*, *Heterobasidion araucariae*, *Hydnoporia laricicola*, *Diatrype lijiangensis*, *Peniophora crassitunicata* and *Efibula americana* were identified and will be metabarcoded by JGI and deposited in MycoCosm. Bioinformatics protocols were developed, and students were trained to retrieve and analyze antibiotic sequences from MycoCosm, NCBI Blast, and utilizing R studio. Protocols have been archived in Protocol.io. The preservation and characterization of specimens from a historical collection has transitioned a traditional undergraduate biology course into Myco-Ed. Future studies will assess teaching and learning goals.

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**SYM02-003: TWISTING INSTRUCTION TO BROADEN LEARNING IMPACTS IN MYCOLOGY**
Emily Cantonwine
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**Abstract**
One of the unique aspects of student-centered instruction is that subject-specific content serves two roles: it is the foundation for knowledge construction and the medium for skill development. This presentation will discuss a partially flipped (twisted) student-centered instructional approach used in Biodiversity of Macromycetes, a 16-person, primarily undergraduate course taught at Valdosta State University. The course’s skill-based objectives, such as efficient use of resources, attention to detail, critical thinking, knowledge synthesis, and oral communication, are addressed using homework assignments and in-class activities that account for >50% of lecture time. During the first half of the semester, students research assigned species within the Friesian macrofungi groupings and present their work to the class. From these presentations, the class develops a list of vocabulary words and diagnostic summaries that become examinable content. In the second half of the semester,
higher levels of classification are examined using a similar approach, and students reorganize species by phylogeny. A final presentation integrates lecture knowledge and skills with a DNA barcoding collection project from lab. In addition to facilitating student activities and assessing work, the instructor guides critical thinking, serves as a real-time fact-checker, models curiosity, and provides just-in-time instruction. Students report increased confidence with public speaking, greater awareness of conceptual interconnections, and enhanced intrinsic motivation, among other things. The pros and cons of twisted instruction and tips on how to tweak or twist other assignments will be shared.

**SYM02-004: THE FOREST MYCOBIOME: DNA-BASED STUDY A TRUFFLE ORCHARD**

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**Abstract**

Successful truffle farming requires expertise across many fields such as horticulture, soil microbiology, and mycorrhizal biology. As part of a graduate course in Microbial Ecology and Evolution, Duke students visited an operational Tuber borchii truffle farm operated by Burwell Truffles where students had opportunity to observed truffle dogs in action and also learn about methods used by farmers to grow and harvest truffles. For their class project, students designed a study to characterize and compare fungal and bacterial communities on mycorrhizal root tips, bulk roots and bulk soil from the truffle orchard and adjacent forest using both culture-dependent and culture-independent methods. Students also performed analyses of variation in edaphic characteristics to examine how soil texture and pH influence microbial diversity, composition, and truffle production. RESULTS: both orchard (high pH) and natural (low pH) pine forest soil and root mycobiomes were dominated by ectomycorrhizal (ECM) fungi. Tuber borchii was the 14th most abundant fungal species within the study, easily detected within truffle orchard but absent from natural forest samples which were collected within 100 M of the orchard. Truffle plantation management had a large effect on soil mycobiome composition within the truffle orchard which had lower numbers of fungi by almost half (200 ASVs) vs. the natural forest (400 ASVs). Furthermore, very few ECM species overlapped between orchard vs. the natural forest communities. Bacterial species diversity (800 ASVs) higher in both managed vs natural plots, but also had very different community composition. This talk will describe methods and analyses used by the class to provide training in basic mycology techniques including microscopy, culturing, DNA sequencing and metabarcoding studies used to study soil fungal communities associated with cultivated truffles.

**SYM02-005: MYCO-ED: MYCOLOGICAL CURRICULUM FOR EDUCATION AND DISCOVERY**

Stephen Mondo1, Sara Branco2, Amy Honan3, Andrew Wilson4, Kerrie Barry5, Lotus Lofgren6, Chinyere Knight6, Sara Gremillion6, Jane Stewart6, Ami Wangelene6, Alisha Quandt6, Jayson Talag6, Ellen Dow7, Gerald Cobian8, Victoria Bunting9, Christopher Bivins10, Geoff Zahn13, Tanya Cheeke16, Kurt LaButti1

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**Abstract**

In a collaborative effort, mycologists from diverse institutions are developing Myco-Ed, a Course-based Undergraduate Research Experience (CURE) to train undergraduate students in fungal biology and comparative genomics. The learning outcomes for students include fungal culturing, experimental design, DNA amplification, and how to conduct comparative genomic analyses. Students in undergraduate mycology courses isolate fungi, assay them under specific conditions, document phenotypic responses, and harvest fungal tissue for genome sequencing. Harvested tissue from species without a corresponding genome are first passed to the Arizona Genomics Institute for DNA extraction and then to the Joint Genome Institute (JGI) for genome sequencing. Next, 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 also modular, allowing instructors to incorporate any aspect of the curriculum that fits their teaching goals. The MycoEd CURE has been successfully piloted in five classrooms. As a result of the pilot, we have already targeted over 20 fungal species for genome sequencing and released several genomes via the JGI MycoCosm platform. Having already created freely available course materials and protocols, we aim to scale this project to cover a wide range of institutions, introducing a diverse student body to mycology and genome science. Beyond providing training for the next generation, we hope to inspire students to pursue careers within the field of mycology by allowing them to meaningfully contribute to the advancement of our field.
Abstract
Fungal infections have escalated from a rare curiosity to a major cause of food insecurity as well as human mortality around the globe. This is in part due to a scarcity in the number of antifungals available to combat mycotic disease in both humans and plants, making the discovery of novel bioactive compounds and determining their mode of action of utmost importance. The development and application of chemical genomic assays using the model yeast *Saccharomyces cerevisiae* as well as the human fungal pathogen *Candida albicans* has provided powerful methods to predict the mechanism of action of diverse molecules in a living cell. Here, we describe how high-throughput small molecule screens can be coupled with chemical genomic assays to identify compounds with efficacy against diverse fungal pathogens. Specifically, we highlight examples where this approach led to the identification and characterization of compounds with efficacy against the human fungal pathogen *C. albicans* and the plant fungal pathogen *Fusarium graminearum*. Overall, this work describes novel and promising antifungal strategies that can be developed further to combat agriculturally- and clinically-relevant fungal pathogens.

SYM03-002: COMPARATIVE ANALYSIS OF ROS RESISTANCE ACROSS YEAST SPECIES IDENTIFIES GENE TARGETS FOR INDUSTRIAL AND HEALTH APPLICATIONS
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Abstract
Reactive oxygen species (ROS) are frequently encountered by yeasts during routine metabolism, as well as during interactions with other organisms, particularly in the context of plant or animal pathogens. We sought to characterize the variation in resistance to ROS across the yeast subphylum *Saccharomycotina* and identify the genetic mechanisms underlying this trait. Through measuring the relative growth of 284 yeast species in the presence of low or high tert-butyl hydroperoxide concentrations, we were able to identify the most resistant and sensitive species. We employed a machine learning classification model using a random forest algorithm to classify species as resistant or sensitive and to identify gene families which were predictive of this trait. The most predictive genes included two families of reductases and, interestingly, were enriched in gene families related to cell wall organization. We functionally confirmed that the overexpression of the old yellow enzyme reductase resulted in increased resistance to ROS and that some mutants in cell wall genes were hypersensitive to ROS. Altogether, this work highlights new insights on genes that are related to ROS resistance and has many potential applications depending on the yeast species of interest. Since ROS have such broad implications, this knowledge could be used to target ROS resistance in yeast pathogens to increase the antifungal drug repertoire including through using combination therapies. On the other hand, yeasts used for industrial scale aerobic oleochemical or protein bioproduction could be modified to be more resistant to ROS and more robust for industrial processes.

SYM03-003: THE PAN-GENOMIC EFFECTECTOME OF THE FUSARIUM SAMBUCINUM SPECIES COMPLEX
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1University of Toronto, Toronto, Canada. 2Agriculture Canada, Ottawa, Canada. 3Carleton University, Ottawa, Canada

Abstract
The Fusarium sambucinum species complex (FSAMSC) comprises prominent phytopathogenic fungi that collectively place a severe burden on global agriculture. Understanding the interaction between host plants and fungi is crucial to delineate mechanisms of plant defence and mitigate agricultural losses. Many phytopathogens deploy suites of secreted proteins, called effectors, to modulate host immunity and promote colonization; however, fungal phytopathogenic effectors are poorly understood compared to those of bacterial phytopathogens. To promote the characterization of FSAMSC effectors, we developed a pan-genomic effectomete for this species complex using a combination of bioinformatics tools. Our pipeline led to the prediction of 125,777 candidate-secreted effector proteins (CSEPs) from 195 isolates, including 235 conserved (“core”) effector families. A subset of core families demonstrated diversifying selection, and we hypothesized that these epitopes may be critical to host recognition and are thus likely to interact with host defence factors. We developed structural comparisons to known fungal effectors using AlphaFold and Foldseek, and used virulence assays to demonstrate effector-like function for a subset of conserved effectors. Host interaction partners of fungal effectors will be identified via proximity-based labelling with TurboID, to ultimately resolve a plant-pathogen interaction network.
SYM03-004: CONDUCTING GENETIC INTERACTION ANALYSIS IN CANDIDA ALBICANS' STRESS RESPONSE GENES BY USING CRISPR-CAS9-BASED GENE DRIVE SYSTEM
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Abstract
Candida albicans is a commensal organism, typically found in the oral mucosa, the gut, the vaginal mucosa, and the skin of humans and other mammals. C. albicans is also an opportunistic fungal pathogen that may cause superficial to severe invasive and systemic infections, depending on the status of an individual's immune system. Cells need to adapt to environmental stressors to survive, and this ability is dependent on the speed and robustness of their stress responses. For C. albicans, stress response factors can also modulate antifungal drug resistance, as antifungal drugs can impart different forms of stress on the fungal cell. Understanding C. albicans stress responses would be prudent in novel antifungal drug discovery. We exploit a genetic approach using the CRISPR-Cas9-based genome editing platform to map out genetic interactions between fungal genes, targeting stress response genes with roles in fungal cell survival. The proposed research aims to dissect the genetic interactions underpinning C. albicans’ response to diverse stressors. This proposed research will use cutting-edge genomic technologies to explore the genetic mechanisms by which C. albicans survive amidst a constantly changing environment. Leveraging this platform, we will have the ability to gain previously inaccessible biological insight into the complex genetic interaction networks in C. albicans, and discover fundamental processes in fungal biology, including stress tolerance.

SYM03-005: LEVERAGING GENETIC DIVERSITY IN SCHIZOPHYLLUM COMMUNE IN UNLOCKING THE FUNCTIONAL POTENTIAL OF FUNGAL FILMS
Viraj Whabi, Jianping Xu
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Abstract
Fungal mycelium, renowned for its robust fiber structure, is gaining widespread attention as a sustainable alternative to traditional plastics and textiles. Strain optimization offers the opportunity to improve these mycelial materials by systematically selecting specific phenotypes that have ideal mechanical and physiochemical properties. Schizophyllum commune is a cosmopolitan mushroom species with over 23,000 mating types and is a great model to explore due to its remarkable phenotypic diversity reflected in its varied color, size, and structure. This study focuses on four monokaryotic strains of S. commune sourced globally, and their set of twelve dikaryotic progeny, each with their own unique combinations of nuclear and mitochondrial DNA. First, growth differences among strains were observed by growing strains over 7 days at 30°C. Subsequently, mycelial mats from each strain were cultivated through liquid-state fermentation for 12 days, followed by treatment with crosslinkers and dehydration to form films. These varied fungal films were then tensile tested to map out the spectrum of stiffness and elasticity. Preliminary results show that different strains create different films; some flexible and some stiff. The observed variance in different karyotype and genetic lineages of S. commune demonstrates that it is possible to optimize and tailor mycelial materials to fit conventional materials applications. Future plans look to compare surface morphology and chemical composition to better understand the depths at which macro-scale phenotypic differences are controlled by their micro-scale counterparts.

SYM03-006: ENVIRONMENTAL RESERVOIRS OF A WILDLIFE PATHOGEN (PSEUDOGYMNOASCUS DESTRUCTANS) DECREASE IN THE ENDEMIC PHASE IN NORTH AMERICA
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Abstract
The skin disease white-nose syndrome is caused by the fungal pathogen Pseudogymnoascus destructans (Pd) and has killed millions of bats in North America since it was first documented in 2006. Environmental reservoirs of Pd in caves and mines are considered a threat to the persistence of bats in North America due to the potential for repeated re-infection of bats in subsequent years. Environmental reservoirs increase over the first 1–4 years after Pd invasion in North American hibernacula, but long-term patterns of Pd environmental persistence are unknown. We swabbed hibernaculum walls eleven years after the invasion of Pd into Maritime Canada in 2011 and found that Pd prevalence decreased from a high of 40.6% in the first year after Pd detection (Apr 2012) to 1.7% in Apr 2022. Prevalence also decreased on hibernating bats. It is unknown if the patterns we documented in eastern Canada have also occurred in other hibernacula in eastern North America (Pd-endemic zone) in sites with different bat species composition and surviving bat colony sizes. We will present preliminary data from an ongoing study on Pd environmental reservoirs in other areas of eastern North America. If bats are no longer being exposed to Pd environmental reservoirs in hibernacula in the Pd-endemic zone, then treatments designed to reduce those reservoirs should be carefully considered given the high likelihood of negative non-target effects on hibernacula ecosystems.

Session Chairs: Lluvia B. Vargas-Gastélum1, Donald M. Walker2
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SYM04-001: CUTANEOUS CHEMISTRY: HOW SMALL MOLECULES DIRECT BACTERIA-FUNGI INTERACTIONS
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Abstract
The human skin microbiome is vital for skin health, yet the intricate interactions, including the role of bioactive metabolites in colonization resistance, remain largely uncharacterized. Particularly, the cross-kingdom interactions between bacteria and fungi on the skin, as well as the impact of metabolites on colonization resistance against fungi, remains limited. To tackle this question, we hypothesize that bacterial metabolites stabilize the skin microbiome through inhibition of fungal colonization. We conducted high-throughput screening, identifying an Actinobacteria skin bacterium that produces metabolites inhibiting fungal pathogens. Genomic analysis was performed to search for potential biosynthetic gene clusters predicted to encode in the genome, which may be responsible for metabolite biosynthesis. RT-qPCR was employed to assess differences in antifungal production between varying growth conditions. Upon chemical extraction and purification, we identified non-toxic yet active fractions against C. albicans and C. auris both in vitro and in vivo. Carbone, a compound shown to inhibit fungal hyphae formation but not growth, was found in addition to other structures in other bioactive fractions not containing carbone. We then assessed different growth conditions and found low and high production conditions of the antifungal molecules. Three biosynthetic gene clusters were identified. Intriguingly, a polyketide gene was observed to be upregulated by 76-fold (p < 0.001) when the skin bacteria was fermented in the high production condition (solid media after five days of growth), suggesting a polyketide could be contributing to the antifungal activity. Future directions would be elucidating the chemical identity of the bioactive molecules.

SYM04-002: DISCOVERY AND CHARACTERIZATION OF THE GLOBAL PATTERNS AND DETERMINANTS OF ANAEROBIC FUNGAL DIVERSITY IN THE HERBIVOROUS GUT
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Abstract
We examined global anaerobic gut fungal (AGF) diversity using a combination of culture-independent, culture-based, and -omics approaches. Through scientific collaborations and citizens participation, thousands of fecal samples were obtained and analysed. The dataset covers canonical placental hosts, as well as representatives of three non-canonical hosts (marsupials, tortoises, and ostriches). We expand global AGF diversity by identifying 57 novel genera. AGF communities in placental mammals were structured according to host and gut type. In contrast, communities in marsupials were small, stochastic, and potentially acquired from placental foregut fermenters. AGF communities in tortoises were dominated by three novel, deep branching genera, two of which (Eustudomyces gen nov., and Astrotudomyces gen nov.) were isolated and characterized. These genera displayed high aerotolerance, wide temperature range, and limited substrate utilization potential. Further, gene content analysis demonstrates a limited CAZyme machinery, a dearth of HGT-acquired genes, and lack of cellulosomal production potential. AGF communities in ostriches were dominated by two genera (Piromyces and uncultured NY9). Transcriptomics-enabled molecular timing demonstrated a remarkable correlation between host and fungal evolution. Estimates of 107-110 Mya for tortoise genera, 44-58 Mya for hindgut genera and 22-32 Mya for foregut genera were obtained. Such estimates correspond to herbivory evolution in the Testudaincæae, evolution of hindgut families (Equidae, Elephantidae, and Trichechidae), and evolution of the ruminant families Bovidae, Cervidae, and Giraffidae, respectively. Our results expand the global estimates of AGF diversity, documents its occurrence in novel hosts, and provides an ecologically and evolutionary-grounded model to explain the observed patterns of AGF diversity.

SYM04-003: EXPLORING THE SKIN MICROBIOME OF ENDANGERED AXOLOTLS SPECIES AND THE EFFECT OF A FUNGAL PATHOGEN ON ITS DIVERSITY AND STRUCTURE.
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Abstract
The structure and function of animal-associated microbial communities are shaped by multiple ecological and evolutionary processes acting at different spatial and temporal scales. Specifically, members of the skin microbiome in amphibians play an important role protecting their hosts against fungal disease such as chytridiomycosis. This skin disease is caused by the pathogenic fungus Batrachochytrium dendrobatidis and is responsible for population declines and extinctions of amphibian species worldwide. In this study we explored the diversity and structure of skin microbial communities (bacteria and fungi) of eight amphibian species from the genus Ambystoma. These species are commonly known as axolotls, are endemic species from Mexico and are highly threatened by many anthropogenic factors and chytridiomycosis. We evaluated...
the presence of the pathogen *B. dendrobatidis* across all amphibian species and determined whether infection status was correlated with skin bacterial and fungal diversity and structure. We determined that Bd infection was highly variable across *Ambystoma* species and that microbial skin communities were clearly differentiated among host species. In addition, we found that Bd infection intensity was significantly correlated with skin fungal diversity across hosts. Our study suggests a relevant link between the fungal skin microbiome and pathogen infection in amphibians.

SYM04-004: ANAEROBIC GUT FUNGI IN REPTILIAN HERBIVORES: EXPLORING NOVEL HOSTS AND TAXA

Carrie Pratt1, Casey Melili1, Adrienne Jones1, Emily Chandler1, Darian Jackson1, Emma England1, Yan Wang2, Steve Hartson1, Janet Rogers1, Mostafa Elshahed1, Noha Youssef1

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Abstract

Anaerobic gut fungi (AGF, Neocallimastigomycota) are a basal fungal phylum found in the digestive tracts of mammalian herbivores. Here we uncovered their presence in non-mammalian hosts, specifically tortoises. Culture-independent surveys identified a unique AGF community within tortoises, with three novel deep-branching genera representing >90% of sequences in 9 out of 11 fecal samples from nine tortoise species. Representatives of these genera were successfully isolated under strict anaerobic conditions. Twenty-nine fungal isolates were obtained from tortoises, revealing two distinct clades with significant sequence divergence from their closest cultured relatives. These isolates have been characterized and proposed as two novel genera (Testudinimyces and Astrotestudinimycetes).

Transcriptomics-enabled analyses suggest an ancient evolutionary divergence of these tortoise-associated AGF, estimated at 104-112 million years ago. This pushes the evolutionary divergence of these tortoise-associated AGF, estimated at 104-112 million years ago. This pushes the establishment of tortoise-Neocallimastigomycota symbiosis from the late to the early Cretaceous period. The tortoise-associated AGF exhibited limited capacity for plant polysaccharide metabolism and lacked genes encoding several carbohydrate-active enzyme families. This reduced metabolic capacity is attributed to the scarcity of horizontal gene transfer in tortoise-associated AGF genomes compared to their mammalian counterparts. These findings shed light on the phylogenetic diversity, ecological distribution, evolutionary history, fungal-host nutritional symbiosis, and gene acquisition dynamics within Neocallimastigomycota.

SYM04-005: INTERKINGDOM DYNAMICS IN THE GUT MICROBIOME OF AN AMPHIBIAN MODEL SYSTEM

Jason Dallas1, Kylie Moe2, Reed Alexander3, Mitra Ghotbi1, Kaitlyn Murphy4, Lluvia Vargas-Gastélum4, Kerry McPhail2, Joseph Spatafora4, Jason Stajich2, Donald Walker1

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Abstract

The gut microbiome is a complex community, but experimental approaches to examine the impact of specific microbial taxa on the overall community structure are limited to a small subset of model organisms. Filamentous fungi in the genus *Basidiobolus* are ubiquitous members of the herpetile gut and are hypothesized to play an important role in fungal-bacterial interactions in the microbiome. We used a novel experimental system with wood frogs (WF; *Lithobates sylvaticus*) to identify how the addition of *Basidiobolus* affected the gut microbiome. Following metamorphosis, captive-reared WF were fed fruit flies inoculated with one of two putative *Basidiobolus* species cultured from the feces of wild Plethodontid salamanders. Afterward, all WF were fed uninoculated fruit flies for three months, and WF feces were collected daily for metabarcoding and amplicon sequencing of 16S rRNA and ITS1 rDNA. All *Basidiobolus*-fed WF tested qPCR positive following the single feeding while all control frogs remained *Basidiobolus*-free. However, *Basidiobolus* was lost after one month in 60% of frogs suggesting that this fungus requires consistent reinoculation for long-term persistence in the gut, likely reflecting the lifecycle of the fungus within the host. The gut bacterial composition was largely influenced by maternal effects (*r* = 0.74, *P < 0.001) and the *Basidiobolus* treatment (*r* = 0.18, *P < 0.001), while the latter had a strong effect on mycobiome assemblage (*r* = 0.22, *P < 0.001). Utilizing our novel experimental system, we controlled the *Basidiobolus* inoculation into WF and were able to determine that *Basidiobolus* structures bacterial-fungal interactions in the gut microbiome.

SYM04-006: DID WOOLLY MAMMOTHS EAT TRUFFLES?

Bryn Dentinger1,2, Alexander Bradshaw1,3, Paul Kirk3, Laura Suz2, Selina Brace1, Ian Barnes2

1Natural History Museum of Utah, University of Utah, Salt Lake City, USA. 2School of Biological Sciences, University of Utah, Salt Lake City, USA. 3Royal Botanic Gardens, Kew, Richmond, United Kingdom. 4Natural History Museum, London, United Kingdom

Abstract

Little is known about the fungal component of the diets and gut microbiomes of extinct megafauna. Ancient DNA analysis of gut contents extracted from Lyuba, an exceptionally well-preserved ~42,000 year old baby mammoth, was conducted using shotgun metagenomics. Taxonomic assignment using k-mer based approaches with a custom reference database, including ~1500 fungal genomes, revealed the majority of sequences belong to *Bacteria*. Many of these are likely post-mortem colonizers and modern contaminants. After filtering out likely mammoth-derived DNA sequences through alignment to the Asian elephant genome, 33% of the remaining eukaryotic sequences were classified as Fungi. Fungi detected included typical dung-associated Ascomycota,
Basidiomycota, and Mucoromycota as well as other taxa likely encountered in the Pleistocene environment. However, the most abundant fungus was the summer or Burgundy truffle, *Tuber aestivum*. Analysis of the sequences assigned to *T. aestivum* exhibit patterns of cytosine lesioning consistent with expectations for ancient DNA. Lyuba’s death in late spring overlaps with the known seasonality of *T. aestivum* and prior analyses of the plant material in Lyuba’s stomach had fragments of plants that form mycorrhizae with *T. aestivum*. Taken together, our evidence supports the hypothesis that woolly mammoths ate truffles. To our knowledge, this is the first evidence of truffle consumption by woolly mammoths, or any pachyderm, and could enhance efforts to resurrect the woolly mammoth by revealing more completely their natural diets.

**SYM04 Discussant**

Lluvia B. Vargas-Gastélum  
*Oregon State University, Corvallis, OR, USA*

**SYM05-001: ZOOSPORIC EUFUNGI, THEIR HISTORY, AND BIODIVERSITY: A PRIMER**

D. Rabern Simmons  
*Purdue University, West Lafayette, USA*

**Abstract**

Basal lineages of zoosporic eufungi are of increasing interest in the 21st century as “dark fungi” have become more important in our interpretation of the mycological world. However, the wider mycological community may not be exposed to the study of these fungi, given their relative obscurity and the paucity of their experts. In spite of this, a new generation of mycologists has made extensive taxonomic revisions and scientific advances during the study of these organisms, which we now recognize as constituting multiple phyla of the Fungi. Specialists in these fungi remain few, however, and outdated misconceptions on the importance and influence of these fungi may block additional mycologists from including them in their own research. This presentation seeks to instill a renewed appreciation of the basal fungal lineages, their taxonomic revisions, their recent phylogenetic and phylogenomic examinations, and their pathogenic and commensal interactions on vertebrate, invertebrate, and algal hosts.

**SYM05-002: WHAT SHALL WE CALL THE EARLY DIVERGING FUNGAL LINEAGES?**

Tim James  
*University of Michigan, Ann Arbor, USA*

**Abstract**

In recent years, the term early diverging fungi or basal fungi has come to be commonly used to describe all fungi outside of the subkingdom Dikarya. These lineages, including the lineages formerly known as Zygomycetes and Chytridiomycetes, form a paraphyletic grade of phylum or class-level branches that hold a tremendous amount of phylogenetic diversity and are being increasingly appreciated for their novel traits. In this talk, I will discuss the question of whether the term early diverging or basal fungal lineages is evolutionarily appropriate due to the implicit assumption that some extant taxa are evolutionarily more derived, as was historically used with the term “higher fungi”. At issue is the fact that, since nearly all phyla have diverged from each other many hundreds of millions of years ago, all phyla are essentially early diverging. How instead should we refer to this heterogeneous group of interesting fungi? I will discuss the possible advantages of switching our terminology for the early diverging fungal lineages and will discuss options that involve creating new names, resurrection of old names, and the possibility of staying the course.

**SYM05-003: DIPLOID-DOMINANT LIFE CYCLES CHARACTERIZE THE EARLY EVOLUTION OF FUNGI**

Kevin R. Amses1,2, D. Rabern Simmons1,3, Joyce E. Longcore4, Stephen J. Mondo4, Kensuke Seto4, Gustavo H. Jerônimo4, Anne E. Bonds5, C. Alisha Quandt5, William J. Davis5, Ying Chang6, Brian A. Federici6, Alan Ku06, Kurt LaButti5, Jasmyn Pangilinan5, William Andreopoulos5, Andrew Tr ист6, Robert Riley6, Hope Hundley6, Jennifer Johnson6, Anna Lipzen6, Kerrie Barry6, B. Franz Lang6, Christina A. Cuomo6, Nicolas E. Buchler1,2, Igor V. Grigoriev7, Joseph W. Spatafora7, Jason E. Stajich8, Timothy Y. James8

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**Abstract**

The majority of described fungal species are contained in two phyla: the Ascomycota and the Basidiomycota, together called Dikarya. As a result, and despite the fact that we now appreciate that Fungi comprises numerous phylum-level lineages, our understanding of the biology of the kingdom is highly influenced by traits known in Dikarya. That is, traits well represented in Dikarya or Burgess truffle, *Tuber aestivum* exhibit patterns of cytosine lesioning consistent with expectations for ancient DNA. Lyuba’s death in late spring overlaps with the known seasonality of *T. aestivum* and prior analyses of the plant material in Lyuba’s stomach had fragments of plants that form mycorrhizae with *T. aestivum*. Taken together, our evidence supports the hypothesis that woolly mammoths ate truffles. To our knowledge, this is the first evidence of truffle consumption by woolly mammoths, or any pachyderm, and could enhance efforts to resurrect the woolly mammoth by revealing more completely their natural diets.

**SYM05 Discussant**

Lluvia B. Vargas-Gastélum  
*Oregon State University, Corvallis, OR, USA*
evolutionary trends in non-Dikarya fungi, we conducted genome-scale phylogenetic analysis of 69 newly generated draft genome sequences of zoosporic (flagellated) lineages of true fungi. Our phylogeny supports five lineages of zoosporic fungi and places the Blastocladiomycota, which is unique in its alternation between haploid and diploid generations, as branching closer to the Dikarya than to the Chytridiomycota. Our estimates of heterozygosity based on genome sequence data indicate that lineages of zoosporic fungi are characterized by diploid-dominant life cycles involving regular mitotic division of diploid nuclei. The mapping of additional traits shared between Fungi and Metazoa suggests that these ancestral traits have been subject to extensive but incomplete parallel loss across zoosporic lineages. Together, our results indicate a gradual transition in the genetics and cell biology of fungi from their ancestor with animals and caution against assuming that traits well represented in Dikarya are typical of other fungal lineages.

**SYM05-004: CRYPTIC BIOLOGY OF HARPELLALES FUNGI – ECOLOGY, EVOLUTION, AND BEYOND**

Yan Wang  
*University of Toronto, Toronto, Canada*

**Abstract**

Harpellales fungi represent a diverse group thriving as obligate symbionts in insect guts, comprising 38 genera and over 300 species. Since their first documentation in 1929, their presence has been globally reported. Other than certain instances, Harpellales rarely harm their hosts under natural conditions, and are often regarded as commensals. With the aid of comparative genomics, we started to unravel intriguing evolutionary hallmarks of these gut-dwelling fungi. For example, previous studies unearthed an interkingdom transfer event involving a mosquito-derived polyubiquitin gene integrated into the genome of *Zancudomyces culisetae* (Harpellales), offering unprecedented insights into host-fungus interactions. Additionally, potential whole-genome duplication events were suggested to have occurred within several lineages of Harpellales. The draft quality of Harpellales genomes, however, has posed significant challenges hindering comprehensive investigations into these phenomena. To surmount this hurdle, our laboratory has recently assembled several reference-quality genomes of Harpellales. In this symposium talk, I will share our recent findings regarding Harpellales, highlighting how these discoveries offer fresh insights into the intricate relationships between insects and fungi. I will also discuss how our findings shed light on the cryptic biology of microbial fungi thriving in extreme environments, such as insect guts.

**SYM05-005: SINGLE-CELL GENOMIC ANALYSES ON OLPIDIUM-LIKE CHYTRIDS: WHAT IS THE “TRUE” OLPIDIOMYCOTA?**

Kensuke Seto1, Timothy James2  
1*Faculty of Environment and Information Sciences, Yokohama National University, Yokohama, Kanagawa, Japan.* 2*Department of Ecology and Evolutionary Biology, University of Michigan, Ann Arbor, MI, USA*

**Abstract**

The genus *Olpidium* is one of the chytrid genera characterized by an endobiotic and holocarpic thallus, namely a simple thallus composed of only a zoosporangium without rhizoids. This highly reduced morphology suggests it could easily have evolved multiple times by degenerate convergent evolution from more typical chytrid morphology. Molecular phylogenetic analyses showed that plant root parasitic *Olpidium* spp. are phylogenetically distinguished from major zoosporic fungal phyla. Recent fungal taxonomy places *Olpidium* in the independent phylum, Olpidiomycota. However, *Olpidium* includes parasites of other organisms such as algae, fungi, and micro-invertebrates. Re-examination of these parasites is important to reveal the phylogenetic diversity of *Olpidium*. In this study, we sequenced genomes of *Olpidium*-like chytrids infecting rotifers and desmid algae by single-cell techniques and examined their phylogenetic position by genome-scale phylogenetics. We found seven lineages of *Olpidium*-like chytrids: three lineages on rotifers or rotifer eggs and four lineages parasitic on desmid algae. Our phylogenomic analysis showed that these *Olpidium*-like chytrid lineages were not related to *O. bornovanus* parasitic on cucumber root and were instead distributed among three other phylum-level clades. One rotifer parasitic lineage was placed in Blastocladiomycota and another two lineages on rotifers and rotifer eggs were in a putative novel phylum-level clade sister to the clade of Blastocladiomycota and Sanchytriomyctota. In contrast, the four lineages of desmid algal parasites were positioned in the order Rhizophydiales (Chytridiomycota) and were related to *Batrachochytrium* and its allied taxa. These results showed the polyphyletic nature of the genus *Olpidium*, which requires taxonomic revision of the genus.

**SYM05-006: DIVERSITY OF “AMPHIBIOUS FUNGI” AND ITS EVOLUTIONARY IMPLICATIONS**

Yousuke Degawa  
*Faculty of Environment and Information Sciences, University of Tsukuba, Ueda, Nagano, Japan*

**Abstract**

Considering the evolutionary process of kingdom Fungi, Zoopagomycota is a key taxon as they are the first fungi lost flagellum and adapted to the land environments. A newly described genus *Unguispora* Ri & Degawa (Kicxellales, Kicxellomyctina) discovered from the excrements of cave cricket has a novel lifestyle intermediate between the gut-inhabiting and saprotrophic fungi. For this taxon, we propose a new ecological group “amphibious fungi” (Ri et al. 2022), defined by the following characters. 1. Sporangiola has a specialized structure to attach the surface of the host arthropod gut. 2. Sporangiospore germinates under anaerobic condition in the gut. 3. Yeast-like secondary spore propagation in the gut. 4. Vegetative mycelial growth and sporangiospore...
formation outside of the host gut (on the excrements).  
5. Sporangiospores are immersed in a liquid droplet at maturity which can adhere to the surface of host body and go back to the gut. So far, as members of amphibious fungi, about 20 species have been provisionally recognized which have these characters in common to some extent. At the present, from polyneopteran insects (Orthoptera and Dermaptera) and Myriapoda (Diplopoda and Chilopoda), amphibious fungi are detected, namely *Unguispora*, *Pinnaticoemansia*, *Aenigmatospora* (*Mononema*) and *Myconymphaea* respectively. Based on preliminary molecular analyses, all of these amphibious genera phylogenetically placed at primitive positions within the Kicxellales. Then, at least within this order, an evolutionary trend can be understood in which they shifted their habitats from inside to outside of the gut well adapted to the terrestrial environments.

**SYM05 Discussant**
D. Rabern Simmons
Purdue University, West Lafayette, Indiana, USA
PAR11-001: WEATHER AND LEAF AGE SEPARATELY CONTRIBUTE TO TEMPORAL SHIFTS IN FOLIAR FUNGAL COMMUNITY STRUCTURE
Jacob Heil, Leonora Bittleston
Boise State University, Boise, USA

Abstract
Microbial communities living on plant leaves can positively or negatively affect plant health and thus, by extension, can influence the functioning of whole ecosystems. Most research into the leaf microbiome consists of single snapshots, and little is known about how microbial communities change over time with shifting weather and host characteristics. To remedy this, we characterized the fungal community from sagebrush (Artemisia tridentata) leaves over the course of an entire year using both culturing and an ITS high-throughput sequencing approach, combined with quantitative PCR. The sagebrush leaf microbiome is currently undescribed, and may play a role in the health of the vast sagebrush steppe ecosystem. We collected temporal, environmental, and host-related data every two weeks for a full year to determine the factors structuring this community. Changes in alpha diversity occurred quickly and were mostly driven by the age of a community and the air temperature. Surprisingly, total fungal abundance and species richness were not positively correlated and respond differently, sometimes oppositely, to variables measured. Changes in beta diversity were seasonal and driven by leaf type, leaf age, and air temperature. The largest changes were seen during spring and fall, when weather conditions shifted more dramatically. Sagebrush leaves were a continual reservoir for at least twenty genera of fungi. Nine different genera showed differential abundances with air temperature, δ13C, leaf type, and leaf age. Our findings demonstrate the necessity for longer-term, repeated sampling to capture the rapid change of communities in response to both the environment and their host.

PAR11-002: HOW FUNGAL ENDOPHYTE COMMUNITIES COLONIZE AND ALTER PLANT HOST CHEMISTRY IN THE WILDFLOWER WHITE SNAKEROOT
Noelle Visser, Natalie Christian
University of Louisville, Louisville, USA

Abstract
Throughout a plant’s growing season, leaves are colonized by diverse communities of endophytic fungi. The fungal communities that assemble 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. We used culture-based methods to describe foliar endophytic fungal communities throughout the growing season of white snakeroot (Ageratina altissima), a native Kentucky wildflower known for its toxicity to macro-herbivores. At each sampling point, we collected a new leaf and a leaf that flushed the previous month. We found endophyte communities changed through the growing season. Dominant fungal endophyte genera throughout the growing season included Colletotrichum, Arthrinium, and Daldinia. We then tested how endophyte inoculation alters host secondary chemistry. We inoculated endophyte-free white snakeroot seedlings with one of five treatments: 1) a dominant endophyte 2) another dominant endophyte 3) a community of common endophytes, 4) a heat-killed endophyte, and 5) sterile water as a control. We extracted phenolics from leaf tissue and performed liquid chromatography-mass spectrometry. Comparing phenolic profiles across the five 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. Additionally, abundance of individual phenolic compounds varied between treatments. 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.

PAR11-003: GEOGRAPHICAL STRUCTURE OF GENOTYPIC VARIATION IN EPICHLOË BRACHYELYTRI, THE SEED-TRANSMITTED ENDOPHYTE OF THE GRASS BRACHYELYTRUM ERECTUM.
Christopher Schardl1, Patrick Calie2, Rachel Sneed1, Simona Florea1, Padmaja Nagabhyru1, Robert Hirsch1, Andrew Tapia1
1University of Kentucky, Lexington, KY, USA. 2Eastern Kentucky University, Richmond, KY, USA

Abstract
Brachyelytrum erectum is an understory grass in temperate forests of eastern North America, and Epichloë brachyelytri (ord. Hypocreales, fam. Clavicipitaceae) is a seed-transmissible endophyte unique to this hosts. A sequenced isolate of E. brachyelytri produces three bioprotective alkaloids: the loline-related 1-acetamidopyrrolizidine, the ergot-alkaloid chanoclavine I, and the pyrrolopyrazine peramine. The determinant genes for these alkaloids were screened by PCR in a survey of 20 populations (≥ 20 plants each), in Kentucky and Indiana. Endophyte symbiosis was common (median = 87 %, range = 5–100%). Only loline-alkaloid genes showed presence/absence polymorphism (LOL+ vs. LOL–). Adding a mating-type screen identified all four genetic combinations: MTA LOL+, MTB LOL+, MTA LOL– and MTB LOL–. Of these, both LOL+ genotypes dominated the survey area, but LOL– genotypes were present (at ≥ 50%) in six populations of central Kentucky. Genome sequences indicated that all LOL– isolates lacked six out of seven LOL genes, but retained lolF, which in turn had two alleles. In LOL– isolates the different lolF alleles were associated with different mating types, whereas LOL+ strains had all possible combinations of lolF alleles and mating-types. The findings suggest a scenario whereby a LOL deletion occurred in a sexual cross in or near Kentucky’s Red River Gorge, resulting in an MTA LOL– genotype that dispersed westward, and an MTB LOL– genotype that dispersed to the southwest. The distribution of LOL– genotypes may reflect a selective advantage to LOL– strains in certain environments such as ecological transition zones.
PAR11-004: FIELD-ADJACENT PLANTS AS RESERVOIRS FOR FOLIAR ENDOPHYTES OF WHEAT
Mara DeMers, Christine Hawkes
North Carolina State University, Raleigh, USA

Abstract
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 including wheat. We hypothesize that fungi are sourced from plants adjacent to the field to form the wheat microbiome. To test this hypothesis, we sampled fungi from wheat leaves in seven fields in North Carolina along with leaves of plants growing adjacent to those fields. Herbaceous plants were selected based on abundance in plots along a 50 m transect parallel to the field edge, while trees were selected based on abundance within 500 m. After surface sterilizing leaf samples, we cultured 12593 fungi from 31800 leaf pieces. Using a combination of morphotyping and ITS amplicon sequencing, we tentatively identified a species of Stagonosporopsis as the only abundant taxon occurring in both wheat and adjacent host plants at all sites, so this taxon was selected for population genomic analyses. Preliminary sequencing suggests the presence of an accessory chromosome (AC) in our populations similar to a S. rhizophila AC associated with plant-fungal interactions. After assembling a reference genome to facilitate SNP calling, we will compare haplotypes between host pools to estimate gene flow from adjacent plants to wheat. We will also evaluate the potential for an AC to modulate endophytic interactions with host plants in our sampled populations.

PAR11-005: EVIDENCE THAT COFFEE-ASSOCIATED PHYLLOSHERE FUNGI CAN MOVE FROM PLANTATION TO ADJACENT FOREST
Jeffrey A. Lackmann1, Bénédicte Bachelot2, Priscila Chaverni3,4,5, Catherine A. Lindell6, Laura Aldrich-Wolfe1
1 North Dakota State University, Fargo, USA 2 Oklahoma State University, Stillwater, USA 3 Universidad de Costa Rica, San José, Costa Rica 4 Centro de Investigaciones en Productos Naturales (CIPRONA), San José, Costa Rica 5 Bowie State University, Bowie, USA 6 Michigan State University, East Lansing, USA

Abstract
Tropical forests are important reservoirs of biodiversity yet face intense fragmentation threats from agriculture, producing forest-agriculture borders across which organisms can move. Investigation of this movement often frames forests as reservoirs of fungi that alter the fungal communities and pathogen loads of crops. We inverted this approach and investigated if coffee-associated phyllosphere fungi are spilling over to leaves of understory trees in adjacent forests. We established transects 100 m in either direction from a coffee-forest border at eight sites in southern Costa Rica with coffee plantations adjacent to forest fragments. We sampled and imaged leaves from five individual coffee trees, three Rubiaceae, and two non-Rubiaceae understory trees, respectively, at 10, 25, 50 and 100 m from the forest-coffee border. Using metabarcoding, we characterized leaf phyllosphere and airborne fungal communities along the transects via leaf tissue sampling and ambient air spore collectors. We cross-referenced taxa in our dataset detected in both coffee plantations and adjacent forest with known endophytes of coffee with and without putative pathogenesis. Phyllosphere communities included many rare taxa alongside relatively few dominant taxa. Roughly ~28% of the OTUs in the dataset were detected in coffee and forest. Several fungal genera with known endophytic (asymptomatic) and pathogenic (symptomatic) associates of coffee attenuated in forest plants with phylogenetic distance from coffee. This novel approach demonstrates the microbial porousness of ag-forest borders and implies that cropland can increase incidence of crop-associated fungi in plants of adjacent forests. The influence of such fungi on forest plant communities remains unexplored.

PAR11-006: PATHOGENIC AND NON-PATHOGENIC FUNGI ASSOCIATED WITH CULTIVATED AND WILD CACAO IN THE PERUVIAN AMAZON
National University Toribio Rodríguez de Mendoza de Amazonas, Chachapoyas, Peru

Abstract
Cacao is the source of one of the most beloved commodities in the world, chocolate. However, the fungi associated with it are vastly understudied, especially in the heart of its center of diversity, the Peruvian Amazon. During the last three years, the Díaz-Valderrama mycology and plant pathology lab has made a lot of progress in documenting the pathogenic and non-pathogenic fungi associated with cacao. We found that in Amazonian remote areas, the most common problem is the thread-blight disease caused by a new species of Marasmius, M. infestans nom. prov. 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, evidence of outcrossing, and revealing its invasive Amazonian routes using an Approximate Bayesian Computation approach. Moreover, we found the causal agents of cacao dieback disease, besides the globally common L. subglobo, associated with it are vastly understudied, especially in the heart of its center of diversity, the Peruvian Amazon. During the last three years, the Díaz-Valderrama mycology and plant pathology lab has made a lot of progress in documenting the pathogenic and non-pathogenic fungi associated with cacao. We found that in Amazonian remote areas, the most common problem is the thread-blight disease caused by a new species of Marasmius, M. infestans nom. prov. 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, evidence of outcrossing, and revealing its invasive Amazonian routes using an Approximate Bayesian Computation approach. Moreover, we found the causal agents of cacao dieback disease, besides the globally common Lasiodiplodia theobromae, are L. iraniensis and L. subglobo, for the first time reported in this crop in the world. 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 Peruvian cacao phyllosphere. All this is just a little taste because most likely there are many fungi left to discover from cacao in the Peruvian Amazon.
Heterokaryon strains of *Drummondii* in AM symbiosis. 80 experimental units of the effect of nuclear organization on carbon sequestration is unknown. This project seeks to investigate (homokaryotic or heterokaryotic) lead to enhanced carbon differing AM fungal strains or nuclear organizations improve atmospheric carbon sequestration. Yet whether Multiple studies have demonstrated that AM fungi can when two genomes segregate among co-existing nuclei. their nuclei carry the same genome, or heterokaryons these symbionts are categorized as homokaryons when significantly improve plant growth and fitness. Strains of with the roots of ~80% of terrestrial plants that can significantly improve plant growth and fitness. Strains of these symbionts are categorized as homokaryons when their nuclei carry the same genome, or heterokaryons when two genomes segregate among co-existing nuclei. Multiple studies have demonstrated that AM fungi can improve atmospheric carbon sequestration. Yet whether differing AM fungal strains or nuclear organizations (homokaryotic or heterokaryotic) lead to enhanced carbon sequestration is unknown. This project seeks to investigate the effect of nuclear organization on carbon sequestration in AM symbiosis. 80 experimental units of *Sorghum x drummondii* were inoculated with either homokaryon or heterokaryon strains of *Rhizophagus irregularis*, a model AMF species, in a growth chamber experiment. During growth, the chamber was pulsed with isotopically-labelled 13CO2 to trace the flow of carbon through the plant, fungus and soil. Overall, AMF inoculation significantly increased root and total dry mass, and AMF strain had a significant effect on root dry mass in the plant. 13C analyses of soil and plant tissue samples are currently under way to assess carbon sequestration among strains. This project represents a stepping stone towards identifying AM fungi with potential for applications as bio-stimulants for enhanced carbon sequestration, with the goal of informing large-scale agricultural and ecosystem restoration projects in their choice of AM fungal inoculation options to optimize crop yield and carbon capture.

PAR12-002: ABSTRACT WITHDRAWN AT THE REQUEST OF THE SUBMITTER.

PAR12-003: FUNGAL PATHOGEN AND SAPROTROPH RESPONSE TO CLIMATE, FIRE AND VEGETATION TYPES IN NORTH AMERICA
Haley Burrill1, Carolyn Delevich1, Heather Dawson1, Jeremy Collings1, Marcos Caiafa2, John Conery3, Bitty Roy4, Jeff Diez3, Neda Arad5, Elizabeth Arnold1, Serita Frey1, Peter Kennedy3, Jean Lodge6, Jana U’Ren7, Matt Smith3, Andrew Wilson8

1University of Oregon, Eugene, USA. 2University of Florida, Gainsville, USA. 3University of Arizona, Tucson, USA. 4University of New Hampshire, Durham, USA. 5University of Minnesota, St. Paul, USA. 6University of Georgia, Athens, USA. 7Washington State University, Pullman, USA. 8Denver Botanic Gardens, Denver, USA

Abstract
Fungal pathogens and saprotrophs can be highly influenced by fire, host specificity, and climate. To understand these factors across a greater geographical scale, we sampled litter and soil from 8 ecoregions across North America encompassing inherent climate gradients in fall and spring, 2022 and 2023. Where possible, each ecoregion included burned and unburned plots, and oak, conifer, and grassland vegetation types. We extracted DNA from soil and litter compartments, amplified fungal ITS1 region via PCR, then sequenced on Illumina. Climate data were acquired via NEON and LTER weather stations. We used a Bayesian model selection approach to identify major drivers of fungal response to climate and fire across ecoregions. We found fungal compositional differences among ecoregions, as well as significant differences among vegetation types. Fungal pathogen composition differed among vegetation types, more strongly in the soil than litter, with the opposite result for saprotrophs. Saprotroph diversity increased with precipitation, indicating that climate differences between ecoregions will likely impact ecosystem services provided by saprotrophic fungi. Despite known fungal sensitivities to fire, we did not find a fire effect on diversity for either functional group. Increasing pH and decreasing C:N generally predicted higher fungal diversity and effects of soil moisture differed between functional group and sampling compartment. The differential responses to climate and fire suggests that the distributions of pathogenic and saprotrophic fungi are more sensitive to moisture, pH, and nutrients, than fire in these regions. Our findings can guide inferences on how fungi-mediated ecosystem services may shift with changing climate.

PAR12-004: LINKING MICROBIAL RESILIENCE AND ECO-SYSTEM RECOVERY: A FIVE-YEAR STUDY FOLLOWING A CHAPARRAL WILDFIRE
M. Fabiola Pulido-Chavez1, Elizah Stephens2, Aral Greene2, Meg Kargul2, Sameer S. Saroa2, Loralee Larios2, Peter M. Homyak1, Sydney I. Glassman3
1University of California-Irvine, Irvine, USA. 2University of California-Riverside, Riverside, USA. 3University of California-Riverside, Riverside, USA

Abstract
Soil microbes, crucial for ecosystem health, nutrient cycling, and vegetation regeneration, face significant impacts from high-severity wildfires in fire-adapted
PAR12-005: ABSTRACT WITHDRAWN AT THE REQUEST OF THE SUBMITTER.

PAR12-006: ATMOSPHERIC DEPOSITION THREATENS RUSSULA DIVERSITY IN AN ENDANGERED SPRUCE-FIR ECOSYSTEM

Chance Noffsinger1, Slavomir Adamčík2, Brandon Matheny1
1University of Tennessee, Knoxville, USA. 2Slovak Academy of Sciences, Bratislava, Slovakia

Abstract

The spruce-fir ecosystem of the southern Appalachian Mountains is endangered and receives the highest amounts of nitrogen deposition in this region, which negatively impacts the growth, composition, and function of soil organisms. Russula is an important genus of ectomycorrhizal fungi that associates with red spruce (Picea rubens) and Fraser Fir (Abies fraseri); however, no systematic analysis of the genus has been completed in the region. We compared Russula collected from spruce-fir habitats of the southern Appalachian Mountains with collections in the TENN herbarium and reference material from North America and Europe, using an in-depth morphological study and multilocus phylogenetic analysis. Additionally, we sampled 71 soil cores to understand the molecular diversity of Russula belowground as well as species’ ecological preferences. Preliminary analysis has tentatively identified 36 species-level clades from basidiomata in the spruce-fir ecosystem. Eight of these species are distributed across eastern North America, four species appear to have intercontinental distributions that extend into spruce-fir habitats of Europe, and the remaining species require further investigation. Additionally, 27 Russula OTUs were identified using ITS2 sequences from soil samples. Some of the Russula species studied are undescribed based on unique morphological characters and distinct molecular composition. We also determined that pH and nitrogen deposition are negatively influencing the community structure and diversity of Russula within this system, potentially leading to the local extirpation of species. This work has provided valuable information regarding the Russula species present in the spruce-fir ecosystem and how aboveground and belowground diversity differ for large ectomycorrhizal genera.

PAR13-001: SUCCESSFUL ENRICHMENT OF THOUSANDS OF GENOME-WIDE NUCLEAR LOCI FROM PNEUMOCYSTIS IN WILD RODENTS WITH LOW INFECTION LOADS

Spenser Babb-Biernacki1, Jacob Esselstyn1, Vinson Doyle2
1Louisiana State University Museum of Natural Science, Baton Rouge, USA. 2Louisiana State University AgCenter Department of Plant Pathology and Crop Physiology, Baton Rouge, USA

Abstract

Characterizing diversity in the ascomycete genus Pneumocystis, a group of obligate symbionts found only in mammal lungs, has long challenged researchers. A major impediment is the low infection loads in wild animals, which are typically immunocompetent and able to limit colonization by Pneumocystis. Because this makes isolating Pneumocystis DNA difficult, most diversity in the genus is characterized by only mitochondrial DNA sequences, with sporadic examples of success sequencing a few nuclear loci. This reliance on mitochondrial DNA precludes formal description of most species in the genus. Here, we present a leap forward in our capacity to study Pneumocystis: a probe set targeting ultraconserved elements (UCEs) in Pneumocystis and other members of the Taphrinomycotina. From the nuclear genomes of eight Pneumocystis taxa as well as Taphrina deformans and Schizosaccharomyces pombe, we designed a set of 32,844 probes targeting 2,704 UCE loci. We tested this probe set on 16 wild rodent lung samples, with Pneumocystis content ranging from 0.000001% to 0.015%. After dual rounds of hybridization, Pneumocystis DNA was successfully enriched in all samples. 0.66% to 98% of sequencing reads belonged to Pneumocystis, which assembled into 6 - ~2,000 UCE loci per sample. From these loci, we produced a well-supported phylogenetic tree that is largely concordant with relationships inferred from mitochondrial data. This probe set potentially transforms our ability to study Pneumocystis diversity and relationships in this dark branch on the tree of life.
PAR13-002: NEW SPECIES OF EUROTOMYCETES ASSOCIATED WITH VACCINIUM MYRSINITES FROM THE FLORIDA SCRUB ECOSYSTEM
Alexis Faulborn¹, Aaron David², Emily Walsh¹, Jing Luo¹, Ning Zhang¹
¹Rutgers University, New Brunswick, USA. ²Archbold Biological Station, Venus, USA

Abstract
Eurotomyces is a large class in Ascomycota, but limited sequence data make it difficult to delineate taxa within. It is believed that some of the fungal species in this class live symbiotically with plants, characterizing them as fungal endophytes. The phylogenetic placement and taxonomy of most fungal endophytes has not been explored greatly, even though molecular sequencing and high-throughput methods are increasing in advancements. Understanding this class could prove crucial for animal, plant, and ecosystem health applications. Taxonomy of Eurotomyces is highly contested and has shifted significantly over time. Here, we propose a new species of Eurotomyces based on six isolates (FLBS3-R9, FLBS3-R11, FLBS3-R13, FLBS3-R25, FLBS3-R31, and FLBS3-R35) isolated from the root of apparently healthy blueberry (Vaccinium sp.) plants collected from a scrub ecosystem in Archbold Biological Station during November 2023. To validate the new species, we analyzed ITS, SSU (18S), LSU (28S), BENA, and RPB2 sequence data, and compared morphological and ecological characteristics. This study at Florida scrub is part of a project of investigating the impact of climate variation on mycobiome dynamics along a latitudinal transect from Maine to Florida.

PAR13-003: PINIBARRENIALES, A NEW ORDER OF SORDARIOMYCETES FROM PINE BARRENS ECOSYSTEM
Jing Luo, Emily Walsh, Alexis Faulborn, Kevin Gao, James White, Ning Zhang
Rutgers University, New Brunswick, USA

Abstract
Pinibarrenia chlamydospora sp. nov., isolated from the roots of highbush blueberry in the New Jersey Pine Barrens, is described and illustrated. Based on multi-locus phylogenetic analysis, as well as morphological and ecological characteristics, Pinibarreniales and Pinibarreniaceae are established to accommodate this novel lineage in Sordariomycetidae, Sordariomycetes Pinibarreniales, Tracylliales and Vermiculariopsiellales are proposed to be included in the subclass Sordariomycetidae. Pinibarreniales likely have a wide distribution and formed association with Ericaceae plants that live in acidic and oligotrophic environments because its DNA barcode matches with environmental sequences from other independent ecological studies. The plant-fungal interaction experiment revealed negative impacts on Arabidopsis, indicating its pathogenicity. This uncovered new fungal lineage will contribute to a better understanding of the diversity and systematics of Sordariomycetes.

PAR13-004: TAXONOMIC REVISIONS AND INSIGHTS INTO THE ECOLOGY AND MATING SYSTEMS OF LORCHELS (DISCINACEAE, PEZIZALES) USING WHOLE GENOME ANALYSES
Alden Dirks¹, Timothy James¹, Andrew Methven², Andrew Miller², Michelle Orozco-Químe¹, Sundy Maurice³, Gregory Bonito¹, Judson Van Wyk¹, Alexander Bradshaw⁴, Francis Martin⁵, A. Elizabeth Arnold⁶, Joseph Spatafora⁷
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Abstract
Lorchels, also known as false morels (Gyromitra spp.), are iconic due to their brain-like mushrooms and production of gyromitrin, a deadly mycotoxin. Molecular phylogenetic studies have hitherto failed to resolve deep-branching relationships in the lorchel family, Discinaceae, hampering our ability to settle longstanding taxonomic debates. We newly generated 72 draft genomes from mushroom samples and cultures that covered all major clades in Discinaceae and conducted phylogenomic analyses to infer the early evolutionary history of lorchels. In addition, we utilized comparative genomics to search for signatures of trophic status and mapped mating type loci to better understand lorchel reproductive biology. Our phylogenomic tree had high gene tree concordance and bootstrap support, facilitating genus-level taxonomic revisions in Discinaceae. We recognized a single genus, Gyromitra, encompassing 10 subgenera. Paradiscina melaleuca and Marcellelina donadinii formed their own family-level clade sister to Morchellaceae. Genome size and CAZyme content agreed with a mycorrhizal lifestyle for the hypogeous species formerly classified as Hydnotrya, while the other clades possessed properties of a saprotrophic habit. Gyromitra species were found to be predominantly heterothallic, but a single occurrence of colocalized mating type idiomorphs in Gyromitra esculenta was an anomaly that requires follow-up study. Our genomic dataset will facilitate investigations into the gyromitrin biosynthesis genes and their evolutionary history. Additional sampling of Geomorriaceae and Helvellaceae, closely related families with no publicly available genomes, could facilitate comprehensive studies on the evolution of hypogeous growth and ecological diversity in a morphologically intriguing and economically important group of Pezizales fungi.

PAR13-005: CHARACTERIZING THE UNKNOWN DIVERSITY OF PSEUDOGYMNOASCUS IN NORTH AMERICAN BAT HIBERNACULA: DESCRIPTION OF 15 NEW TAXA
Abigail Ireland, Stephanie Kivlin, Karen Hughes
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Abstract
Pseudogymnoascus, (Pseudeurotiaceae, Leotiomycetes), is a globally-distributed genus of saprophytic and dermatophytic fungi, the diversity of which has scarcely been explored. In light of the ecological and economic devastation caused by P. destructans (White-nose fungus), P. destructans is a globally-distributed saprophytic and dermatophytic fungi, the diversity of which has scarcely been explored. In light of the ecological and economic devastation caused by P. destructans (White-nose fungus), P. destructans is a globally-distributed saprophytic and dermatophytic fungi, the diversity of which has scarcely been explored. In light of the ecological and economic devastation caused by P. destructans (White-nose fungus), P. destructans is a globally-distributed saprophytic and dermatophytic fungi, the diversity of which has scarcely been explored.
ARSENIY BELOSOKHOV described. Present in ecosystems across North America and yet to be indicates a great diversity of additional species are widely phylogeny, species richness, and distribution. The evidence for studying the genus Retiarius, expanding the current characteristics. This research will serve as a benchmark of three new species, each with unique morphological Arctic. A multi-locus phylogeny supports the distinction but only at low frequency in samples from the Canadian lichens and adjacent substrates of forested ecosystems on lichens. We detected Retiarius at high frequency on isolated Retiarius in axenic culture from pollen deposits from forested ecosystems in North America. We also presence of Retiarius on lichens and adjacent substrates of lichens have revealed hyphae infecting pollen grains. We developed genus-specific primers to screen the of lichens have revealed hyphae infecting pollen grains. Retiarius (Orbiliomycetes) is an anamorphic hyphomycete that traps airborne pollen grains with aerial hyphae. Only four species are known, described from South Africa and Hungary. Retiarius has been widely reported in Europe, with scattered records worldwide including one from North America. In recent years, Retiarius has been detected in lichen metagenomes from western North America. In addition, microscopic observations of pollen grain deposits on the undersurfaces of lichens have revealed hyphae infecting pollen grains. We developed genus-specific primers to screen the presence of Retiarius on lichens and adjacent substrates from forested ecosystems in North America. We also isolated Retiarius in axenic culture from pollen deposits on lichens. We detected Retiarius at high frequency on lichens and adjacent substrates of forested ecosystems but only at low frequency in samples from the Canadian Arctic. A multi-locus phylogeny supports the distinction of three new species, each with unique morphological characteristics. This research will serve as a benchmark for studying the genus Retiarius, expanding the current phylogeny, species richness, and distribution. The evidence indicates a great diversity of additional species are widely present in ecosystems across North America and yet to be described.

PAR13-006: THE POLLEN-ASSOCIATED FUNGAL GENUS RETIARIUS (ORBILIOMYCETES): UBIRIQUOUS AND DIVERSE HYPHOMYCETES IN NORTH AMERICA.

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1University of Alberta, Edmonton, Canada. 2Canadian Museum of Nature, Gatineau, Canada

Abstract
Fungi can obtain nutrients from a variety of sources, including some which penetrate and degrade pollen grains. Retiarius (Orbiliomycetes) is an anamorphic hyphomycete that traps airborne pollen grains with aerial hyphae. Only four species are known, described from South Africa and Hungary. Retiarius has been widely reported in Europe, with scattered records worldwide including one from North America. In recent years, Retiarius has been detected in lichen metagenomes from western North America. In addition, microscopic observations of pollen grain deposits on the undersurfaces of lichens have revealed hyphae infecting pollen grains. We developed genus-specific primers to screen the presence of Retiarius on lichens and adjacent substrates from forested ecosystems in North America. We also isolated Retiarius in axenic culture from pollen deposits on lichens. We detected Retiarius at high frequency on lichens and adjacent substrates of forested ecosystems but only at low frequency in samples from the Canadian Arctic. A multi-locus phylogeny supports the distinction of three new species, each with unique morphological characteristics. This research will serve as a benchmark for studying the genus Retiarius, expanding the current phylogeny, species richness, and distribution. The evidence indicates a great diversity of additional species are widely present in ecosystems across North America and yet to be described.
ORPHIDIOMYCES OPHIDIICOLA
BACTERIAL INTERACTIONS INFLUENCE THE GROWTH OF PAR21-002: SNAKE SKIN LIPIDS AND FUNGAL-

Kaitlyn Murphy1, Mitra Ghotbi1, Jason Dallas1, Justin Miller2, Charlotte Van Moorleghem2, Robert Mason3, Joseph Spatafora3, Frank Pasmans4, An Martel1, Raoul van Damme3, John Niedzwiecki5, Clay Stalzer1, Ori Bergman1, Emily Stone7,1, Donald Walker1

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Abstract

The incorporation of biological scale (i.e., microbial to whole-organism) into studies of host-microbiome interactions is essential for identifying factors contributing to host health. Integration of heterogeneous data types characterizing host skin chemistry, and microbial interactions that might predict disease state, will improve our ability to manage wildlife epidemics. Within the host-microbiome-pathogen system, host microenvironment and chemical composition are often overlooked. For example, reptilian skin is composed of complex lipid structures rich in cholesterol that likely influence the skin microbiome community composition. In this study, we test the hypothesis that the intimate relationships between host skin chemistry and bacterial microbiome affect growth of the infectious agent (Ophidiomyces ophidiicola) responsible for snake fungal disease. Analyses of culture dependent and independent methods suggest that host skin chemistry, particularly the presence of specific lipids, and bacteria isolated from free-ranging snake skins influence the growth of O. ophidiicola. However, the O. ophidiicola genome contains biosynthetic gene clusters that may suppress host lipid production, potentially allowing for fungal colonization of snake skin. Our results highlight the importance of integrating host chemistry into studies of bacterial-fungal interactions in disease ecology and illustrate a variable range of competitive to cooperative interactions between a fungal pathogen and host microbiome.

PAR21-003: IDENTIFICATION OF SPIDER FUNGAL PATHOGENS AND CHARACTERIZATION OF THE SURROUNDING FUNGAL ENVIRONMENTAL COMMUNITY

Ross Joseph, Abolfazl Masoudi, Nemat Keyhani

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Abstract

Fungi in the family Cordycipitaceae infect insects and arachnids, employing sophisticated mechanisms and behavioral manipulation to invade and ultimately kill their hosts. However, their diversity in many geographical regions remains under sampled particularly with respect to fungal pathogens of arachnids. Here, we located five spiders infected by pathogenic fungi on forest trees in central Florida resulting in the isolation of three purified fungal strains. Sequencing of the ITS, LSU, SSU, and TEF1 regions revealed two isolates, UFSI_3 and UFSI_4 clustering closely with Parengyodontium album and one isolate, UFSI_5, clustering most closely with Gibellula species, with the latter forming a distinct separate branch, suggesting that this isolate may represent an undescribed species within this genus. Interestingly, the fruiting structures on the spiders from which Parengyodontium was isolated and those on the spider from which Gibellula was isolated were extremely similar in appearance. In culture, the Gibellula isolate appeared to form rudimentary fruiting structures and purple-pigmented spores, while the Parengyodontium isolates were primarily smooth and white, but with some yellow pigmentation of hyphae and darkening of the media surrounding colonies. Phenotypic and morphological aspects of these fungi are presented. Environmental sampling using Illumina based ITS amplicon sequencing of surrounding soil, leaf litter, and above-ground plant tissues is presented, with varying levels of fungal diversity at different trophic levels seen. These data combine invertebrate pathogen identification via characterization of infected specimens with surrounding environmental sampling to provide a more complete picture of the ecological context of these fungi.

PAR21-004: FUNGI TAKE UP AND STORE SALMON NITROGEN

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Abstract

The return of Pacific salmon from ocean to freshwater spawning grounds transfers marine-derived nutrients (MDN) from marine to terrestrial ecosystems. Although studies have demonstrated the presence and significance of MDN for animals, plants, and soils, the significance of MDN for fungi and their potential role as an MDN sink in the soil has been almost entirely overlooked, even though fungi play a crucial role in organic matter decomposition and nutrient cycling. We examined how a multi-decadal salmon carcass deposition experiment affected fungal, soil, and plant δ15N, C:N, and δ13C using stable isotope analysis and genetic sequencing along salmon streams in SW Alaska. Fungi absorbed and retained MDN in fungal tissue for years following the long-term carcass deposition, suggesting a potentially significant MDN sink in fungi. Carcass deposition significantly decreased fungal C:N, showing ecological significance of MDN for fungal functioning. Plants and soil also retained MDN from carcass deposition, showing that MDN persists in soil, fungi, and plants for years. Long-distance and medium-distance ectomycorrhizal fungal foragers, typically not prevalent at sites with high N availability, were the only functional groups present and incorporating MDN at the site of carcass deposition, likely due to their ability to maintain a large network structure and efficiently mine nutrient hotspots. These findings show that MDN flows through the soil, plants, and fungi of riparian forests and persists in these components for years, with ecologically significant effects for fungi, and demonstrates that fungi must be considered for accurate MDN assessment in riparian systems.
PAR21-005: REDUCED FUNCTIONAL FUNGAL COMMUNITIES IN TWO SPECIES OF SLOTHS (BRADYPUS VARIEGATUS AND CHOLEOEPUS HOFFMANNI) SUGGEST A LINK TO SLOW DIGESTION

Priscila Chaverri1,2,3, Mariana González4, Darling Mora-Rojas5, Andrea Calvo-Obando4, Esteban Escalante-Campos4, Esteve Mesén-Porras4, Daniela Wicki-Emmenegger5, Diego Rojas-Gätjens6, Judith Avey-Arroyo5, Andrés Moreira-Soto6,7, Jan Felix Drexler6,8, Efrain Escudero-Leyva4,2, Max Chavarría4,9,2

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Abstract

Sloths, known for their ruminant-like polygastric digestive systems, possess the slowest digestion among mammals, with passage rates ranging from 11 to 30 days, averaging 16 days. Low metabolic rate, little food intake, and extremely low-energy diet have been linked to the slow rate of digestion. However, to date, there are no comprehensive studies that have characterized the sloth’s gut microbiome and its potential role in digestion. Because the rate of digesta passage in sloths is significantly slower than in ruminants and other herbivores (ca. 5–20x less), this study hypothesized that effective cellulose and lignin-degrading taxa (i.e., fungi) would be scarce in the sloth’s gut microbiome. Therefore, the aim of this study was to describe the gut microbiomes of three-toed (Bradypus variegatus) and two-toed (Choloepus hoffmanni) sloths to begin to unravel their link to slow digestion. Utilizing shotgun metagenomics, metatranscriptomics, and fungal metabarcoding (ITS 1 and 2 nrDNA), microbial composition and functionality were analyzed. As expected, bacteria predominated (95%), followed by viruses (~3%). Fungi accounted for only 0.05–0.1% of metagenomic reads and 0.1% of transcripts. Functional analysis revealed minimal CAZY abundance (1.7–1.9% in metagenomes, 0.2% in metatranscriptomes), with no fungal CAZys detected. Neocallimastigomycota, typical in ruminants and ruminant-like animals, were negligible in metagenomic data (5–15% of fungal reads, 0.003–0.006% of total microbial biomass), and absent in metatranscriptomic or ITS metabarcoding data. These findings provide insight into the factors influencing sloths’ slow digestion.

PAR21-006:
ABSTRACT WITHDRAWN AT THE REQUEST OF THE SUBMITTER.

PAR22-001: YEAST SEXES OR MATING TYPES? THE STORY IN METSCHNIKOWIA SPECIES

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Abstract

Filamentous Ascomycetes (Pezizomycotina) may produce gametangia that are interpreted as male or female, but sexes are generally considered absent in ascomycetous yeasts. In haplontic Metschnikowia species (Saccharomycotina), sexual reproduction begins with the conjugation of two morphologically identical yeast cells of complementary mating types. The nucleus of one cell moves into the other, from which emerges a protuberance within which the now diploid nucleus will undergo meiosis and give rise to two needle-shaped ascospores. The originating cell can therefore be regarded as an ascus mother cell, i.e., as female. Whether the mating type locus is also responsible for sex determination was not known. Based on the higher evolutionary rate of the α-pheromone and the less diffusible nature of the αpheromone, it was reasonable to hypothesize that mating type α cells are male. A precedent also exists in the basidiomycetous yeast Cryptococcus neoformans (Agaricomycotina), where the θconjugant donates its nucleus to a mating type θ partner that then gives rise to a dikaryon. The early stages of the mating reaction were observed in three large-spored Metschnikowia species, using fluorescent-labelled mating types. In every case, the sexes were distributed randomly with respect to the mating types. Authors interested in yeast sexual reproduction should therefore exercise care in their use of terminology, as mating types are not the same as sexes.

PAR22-002: IMBALANCED NUCLEAR RATIOS IN DIKARYONS – THEORETICAL PREDICTIONS

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Abstract

In fungal dikaryons, two genetically distinct nuclei cohabitate a single contiguous mycelium. When formed as a product of mating during a sexual life cycle, karyogamy between the different nuclear types is postponed until immediately prior to meiosis and spore formation. From an evolutionary perspective, dikaryons are frequently considered functionally equivalent to diploids because in many species equal numbers of each nuclear type are strictly enforced. However, some members of Ascomycota and Basidiomycota have an imbalanced ratio between the two nuclear types. These imbalanced ratios are genetically determined and affected by environment. As the relative expression level of genes in separate nuclei can be correlated with their relative abundance, biased nuclear ratios have the potential to affect mycelial fitness. Biased nuclear ratios may also be reflected in asexual spores, allowing for the possibility of nuclear conflict. Using deterministic mathematical models, we generate predictions for when imbalanced nuclear ratios are favoured to evolve in the context of nuclear conflict and heterozygous gene expression modification. We find that
the dominance level of heterozygous alleles determines whether the alteration of gene expression favours or disadvantages biased nuclear ratios. We also find that although imbalanced nuclear ratios can enhance local adaptation by increasing the expression of locally beneficial alleles, a cost to sexual spore production caused by biased ratios is critical for preventing selfish nuclei from taking over a population. These results suggest a limited parameter space exists for which maintenance of biased nuclear ratios is evolutionarily favoured.

**PAR22-003: IDENTIFICATION AND CHARACTERIZATION OF THE MATING-TYPE LOCI IN ESCOVOPSIS, A MYCOPARASITE IN THE FUNGUS-GROWING ANT SYMBIOSIS.**

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**Abstract**

Asexual eukaryotic lineages have long been assumed to be evolutionarily dead ends, doomed to eventually go extinct without meiotic recombination to break up linkage between deleterious and beneficial alleles. In addition, sex is thought to be especially favored during parasite-host arms race as meiotic, also known as the red queen hypothesis for the maintenance of sexual reproduction. *Escovopsis* spp. (Ascomycota; Hypocreales; Hypocreaceae) are specialized parasites on the fungal gardens of fungus-growing ants and has been previously thought to be asexual as no sexual cycle or complete MAT (mating-type) locus has been described. Using 24 previously sequenced high-quality genomes spanning nine species, we identified both the Mat-1 (α) and Mat-2 (a) loci. Correct annotation of these loci using MAKER was inconsistent, and individual genes or the entire locus was often missed. We instead manually annotated the MAT locus of each strain. In the case of Mat-1-1-1 (an α domain transcription factor), this annotation was validated using a previously generated transcriptome. The MAT loci were highly syntenic across strains and species, as was the gene structure (number and location of introns and overall length). The functional protein domains for both Mat-1-1-1 and Mat-1-2-1 (an HMG domain transcription factor), including the specific residues that bind to DNA, were also conserved. Taken together, these data suggest that *Escovopsis* may not be an ancient asexual, although future studies are needed to confirm the presence of a sexual cycle.

**PAR22-004: A LIGHT IN THE DARK: EVALUATING THE IMPACT OF LIGHT EXPOSURE ON ZYGOSPORE PRODUCTION IN LINNEMANIA ELONGATA (MORTIERELLOMYCOTINA)**

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**Abstract**

Sexual reproduction is critical to the evolution of eukaryotes, but biotic and abiotic factors mediating fungal sexual compatibility are unevenly resolved across fungal lineages. In the Dikarya, both the pheromones (small peptides) and pheromone receptors (G-protein coupled receptor kinases) determining sexual compatibility are known. In the early-diverging phylum Mucoromycota, studies focused on the subphylum Mucoromycota have revealed sexual pheromones (trisporoids) critical to sexual spore (zygospore) production, but corresponding receptors are unknown. In both the Dikarya and the Mucoromycotina, perception of light plays a complex role in initiating or inhibiting sexual reproduction depending upon the intensity and wavelength of light exposure, and blue-light receptors involved in sex have been identified. Biological and chemical data support the hypothesis that trisporoids also mediate sexual compatibility in the Mucoromycota subphylum Mortierellomycotina, and Mortierellomycotina zygospore production is repressed in strong, full-spectrum light. However, Mortierellomycotina zygospore production in compatible co-cultures exposed to different wavelengths of light has not been quantified. We leveraged a novel microfluidic device to visualize and quantify zygospore production in compatible co-cultures of *L. elongata* exposed to different wavelengths of light. Linnemannia elongata (Mortierellomycotina) is well-positioned to address this gap in knowledge because mating assays produce visually distinct zygospores and variation in zygospore quantity depends upon isolated isolates and environmental conditions. Zygospore count data from custom-built microfluidic mating chambers equipped with LEDs with dominant emission wavelengths of 467, 525, 590, and 624 nm will be presented. Discussion will center on contextualizing the results within the current knowledge of light-mating interactions within the Mucoromycota.

**PAR22-005: PARALLEL EVOLUTION IN GENE EXPRESSION DURING THE SPORE GERMINATION OF THE MYCOPARASITES, TRICHODERMA ASPERELLOIDES AND TOLYPOCLADIUM OPHIOGLOSSOIDE**

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**Abstract**

Mycoparasitism evolved independently multiple times in the kingdom of fungi. However, little is known about the genes that govern the virulence traits essential for pathogenic mycoparasitism. The conidial germination provides the initial means of these fungi to sense and interact with the hosts. Analyzing gene expression during this process gives us opportunities to reveal the genetics underlying mycoparasitism. This study focuses on sordariomyceteous mycoparasites, *Trichoderma asperelloides* and *Tolypocladium ophioGLOSSOide*, offering a powerful framework to understand the evolution of mycoparasitism. We ascertained genome-wide gene expression associated with spore germination in *Tr. asperelloides*, *To. ophioGLOSSOide*, and four other Sordariomycetes encompassing non-pathogenic or pathogenic species affecting plants or insects. For all six species, gene expression was quantified at key initiation and establishment of fungal infection, including four conidial germination stages: fresh conidia, onset of polar growth, doubling of the long axis, and first hyphal branching. By reconstructing the ancestral expression pattern, 27 genes were identified to have undergone parallel evolution. To investigate the gene regulatory
networks, Bayesian networks were constructed for these genes and known mycoparasitic genes. This allowed the identification of regulatory rewiring that associated with the mycoparasitism, revealing seven regulatory gene pairs unique to the mycoparasites. One specific gene pair with high degree of parallelism exhibited high upregulation in mushroom powder media and includes a gene encoding a chitin degradation enzyme. The findings supporting the analysis of lineage-specific expression changes from ancestors of these fungi with diverse life histories identified genes that likely contributed to parallel-evolution in their fungal pathogen-host association.

PAR22-006: RECONSTRUCTING THE EVOLUTIONARY HISTORY OF HOST PREFERENCE IN RHIZOCTONIA SOLANI UNVEILS A SHIFT TO SPECIALIST IN ONE OF ITS SUBPOPULATIONS
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Abstract
Rhizoctonia solani, a soil-borne fungal pathogen associated with numerous plant diseases, has a major negative impact on global agriculture. The diversity of R. solani has been historically assessed based on its morphology, which has led to the identification of 14 anastomosis groups (AGs) across different plant hosts, classifying it as a generalist pathogen. Although much work has been focused on controlling this pathogen, our understanding of the evolutionary mechanisms governing its host range remains limited. We investigated the evolutionary history of host preference in R. solani using publicly available sequences collected over the last 30 years. We aligned 4,443 R. solani rDNA-ITS GenBank sequences and 40 sequences (N = 4, 483) of recent isolates collected in Nebraska from various host species for Maximum Likelihood (ML) and Bayesian inference (BI) phylogenetic analyses. A subset of 535 sequences was created from the original dataset and a new record belonging to the genus Xanthagaricus was added to the position of all species are provided. The morphological and molecular phylogenetic analyses showing the position of all species are provided. The morphological and molecular phylogenetic analyses based on the nuc rDNA internal transcribed spacer region (ITS) and partial 28S region resulted in eight new species and a new record belonging to the genus Xanthagaricus with strong bootstrap and Bayesian inference values. The new species are X. ahmadii, X. dunensis, X. haroonabadii, X. khanewalensis, X. nigrodiscus, X. olivaceosquamulosus, X. swabensis, X. rubelleocephalus, and the new record is X. necopinatus. Detailed descriptions, color photographs, line drawings, and phylogenetic trees showing the position of all species are provided. With the addition of these species, the number of known species of Xanthagaricus from Pakistan increases to thirteen. Our research indicates that there is a need for additional mycological field trips to explore the hidden macro-fungal treasures of Pakistan.

PAR23-002: WILD LAMELLATE EDIBLE MUSHROOM DIVERSITY OF NORTH WEST HIMALAYAS
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Abstract
The threat of losing the natural resources like wild edible mushrooms due to population pressure and to utilise the local agrowaste, fungal forays were planned to identify the edible mushrooms and collect ethnomycological information of the potentially edible taxa in Northwest Himalaya with an aim to domesticate them. Based on these surveys 90 taxa of such identified mushrooms were found to be potentially edible. In the present paper emphasis is laid on providing an identification key based on morphological features to be of use for common man. Vegetation of the area mainly comprises of the conifers and broad-leaved trees. The best season
for the collection of such mushrooms being between July to September. Dominant agars of the Sub Tropical Forests are Amanita vaginata, A. fritillaria, A. farinosa, A. chepangiana, A. banningsianaR. brevipes var. brevipes, R. parazurea, R. aquosa, Lactifluus echinus, Lactarius subpurpureus while in the Temperate Forests Xerula redicata, Lentinus velutinus, L. connatus, L. tigrinus, L. squarrosulus, Amanita hemibapha, A. flavoconia, R. parazurea, R. aquosa, R. densifolia var. densifolia, Lactarius salmoneus are dominant. The common edible taxa being Agrocybe parasitica, Agaricus bernardii, A. silvaticus, A. augustus, A. arvensis, Amanita hemibapha var. ochracea, A. banningsiana, A. chepangiana, A. vaginata, Volvopilectus gloiocephalus, Russula cyanoxantha, Lentinus transitus, L. tigrinus, L. squarrosulus, L. kashmirinus, L. tuberregion, Lactarius rubrilacteus, Pleurotus sapidus, Pluteus subcervinus. Pure cultures of the selected mushroom were raised on PDA and trials for Lactarius salmoneus cyanoxantha, Lentinus transitus, L. tigrinus, L. squarrosulus A. vaginata, Volvopilectus gloiocephalus, Russula cyanoxantha, Lentinus transitus, L. tigrinus, L. squarrosulus, L. kashmirinus, L. tuberregion, Lactarius rubrilacteus, Pleurotus sapidus, Pluteus subcervinus. Pure cultures of the selected mushroom were raised on PDA and trials for

PAR23-003: EXOBASIDIUM ON LYONIA: A PUTATIVE SPECIES AND A NEW HOST REPORT
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Abstract
Exobasidium species are biotrophic fungal pathogens that infect plants in the order Ericales. Although Exobasidium species are found on economically important host plants, including blueberries, cranberries, and azaleas, the Exobasidium pathogens on hosts in natural habitats are less well studied. Here we report new observations of Exobasidium species from hosts in the genus Lyonia. We documented a new host for E. ferrugineae. This pathogen was originally described from Lyonia ferruginea, but we found galls caused by this fungus on a related host, L. fruticosa. These two Lyonia species often co-occur across Florida and southern Georgia. We also documented a putatively new species of Exobasidium from the Dominican Republic that causes extensive leaf and stem galls on the endemic shrub, Lyonia macrocarpa. We examined the morphology of galls, asexual cultures, and fungal micromorphology along with molecular phylogenetic data from the ribosomal ITS and 28S. ITS and LSU data demonstrate this taxon is unique but closely related to E. ferrugineae. A literature review suggests that this same fungus may have been mistakenly reported from Haiti as “Exobasidium vaccini” by Ciferri (1961).

PAR23-004: AN IMPROVED MULTI-LOCUS PHYLOGENY OF HERICINUM IN NORTH AMERICA, NEW SPECIES, AND THEIR PRODUCTION OF ERINACINE A
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Abstract
Previously reported phylogenetic studies of Hericium using sequence data from the nuclear ribosomal internal transcribed spacer (ITS) region have produced phylogenies where species delimitations, treatment of cryptic species, and interspecific relationships generally are unresolved. Multi-locus analysis using sequence data from ITS and adjacent large ribosomal subunit (LSU), translation elongation factor 1-alpha (tef1) and RNA polymerase subunit 2 (rpb2) genes has produced a phylogeny in which species were resolved into monophyletic groups that includes the type species H. coralloides plus H. americam, H. alpestre, H. abietis, H. cirrhatum, H. erinaceus, and two recently described species in the H. erinaceus species complex, H. carolinense and H. asiaticum. Analyses of the mycelial extracts by liquid chromatography-mass spectrometry from five of these species showed evidence for the production of erinacine A, a cyathane-diterpenoid with a demonstrated therapeutic potential in the treatment of neurodegenerative diseases. These findings provide evidence that should erinacine A continue to be of research interest, species other than the commercially available H. erinaceus may be alternative sources of this compound. Clearly defined species limits within Hericium, provided by an improved phylogeny, will be valuable in natural products discovery, pharmacological applications, and breeding for commercial cultivation of these edible and medicinally valuable mushrooms.

PAR23-005: THE PLUTEUS NANUS COMPLEX IN NORTH AMERICA: HIGH SPECIES DIVERSITY AND REGIONAL ENDEMISM.
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Abstract
We studied the taxonomy, species delimitation and biogeography of the taxa in the Pluteus nanus complex present in North America. Eleven species in this group have been described from North America, and 10 species originally described from Europe or South American have been reported in Canada, Mexico and/or the USA. We sequenced 114 North American collections and included them in our global phylogenetic studies for this group. Based on molecular data none of the species originally described from Europe or South American have been described from North America, and 10 species in this group have been described from North America. Eleven species in this group have been described from North America.
Abstract

Cryptic diversity is the existence of two or more taxa considered as a single taxon, as they share perceptible attributes but differ in less conspicuous traits. This phenomenon is caused by four evolutionary processes: recent divergence, parallelism, convergence and stasis. Here we present three new species of *Thelephora s. l.* that resemble the previously described *Thelephora versatilis* found with Polygonaceae and Nyctaginaceae trees. Although statistical analyses did not reflect differences, the time-calibrated divergences and ancestral area reconstruction were tested to infer underlying speciation processes.

Methods: Fruit bodies were sampled in tropical deciduous forest of southeastern Mexico. Additional specimens were obtained from herbaria and personal donations. Micromorphological descriptions and measurements were recorded for statistical analyses. Locations of all samples were mapped. nrITS and nrLSU sequences were obtained and aligned with a voucher-type matrix to perform phylogenetic analyses. Molecular dating and ancestral areas reconstruction were tested to infer underlying speciation processes.

Results: Collections showed flabelliform-resupinate to eroded mesopodal-coralloid morphologies, and were found with Polygonaceae and Nyctaginaceae trees. Phylogenetic analyses showed three independent lineages related to *Thelephora versatilis* and *T. pseudoversatilis*. Although statistical analyses did not reflect differences, micromorphology provided notable distinctness, leading us to propose three new species: *T. renispora*, *T. canela* and *T. chiapaneca*. Time-calibrated divergences and ancestral area reconstruction suggest homoplastic and homologous pathways aided by allopatry and sympatry.

Conclusions: Integrative taxonomy can help to overcome ambiguous morphologies and sampling understudied regions can bridge the gap between estimated and described richness. Lastly, *Thelephora-Tomentella* is comprised of poorly differentiated taxa, and hence, it could serve as a focal group to enhance methodologies for solving species complexes.

PAR31-001: THE RECOVERY OF ECTOMYCORRHIZAL FUNGAL COMMUNITIES AFTER 26 YEARS OF EXPERIMENTAL NITROGEN DEPOSITION

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Abstract

The impacts of increased nitrogen deposition on ectomycorrhizal fungal communities are well documented, but if and how these fungi recover after the cessation of nitrogen deposition is less known. In this study, we examined the recovery of ectomycorrhizal fungal communities after 26 years (1989 to 2016) of experimental ammonium sulfate application at the Bear Brook Watershed Experiment in Maine. Organic horizons, rhizospheres, and bulk soils (53 each) were sampled in 2016 and again in 2022 then subjected to Illumina MiSeq sequencing of the internal transcribed spacer (ITS) regions. Results indicate that the richness of ectomycorrhizal fungal species returned to the levels of control plots six years after the cessation of experimental application. Further, the recovery occurred in eight “nitrophobic” ectomycorrhizal fungal genera led by increases in Cortinarius and Amanita. Concomitant decreases in experimental vs control watershed nitrogen levels (but not sulfur) suggests that the ectomycorrhizal fungal recovery we documented was due to the effect of lowered nitrogen availability. This study is one of the first clear cut demonstrations of ectomycorrhizal fungal recovery after the cessation of nitrogen deposition.

PAR31-002: ARE MYCOHETEROTROPHS ACTUALLY PARASITIC? INVESTIGATING PROXIMITY-BASED ABUNDANCE OF TOMENTELLA FUSCOCINEREA RELATIVE TO CORALLORHIZA STRIATA

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Abstract

Mycoheterotrophs are non-photosynthetic plants that engage in symbiotic relationships with fungi, and are typically described as parasitic on their fungal hosts. Our research focuses on two distinct mycoheterotrophic plants, Sarcodes sanguinea from the Eudicot lineage and Corallorhiza striata from the Monocot lineage, and their respective ectomycorrhizal fungal hosts, Rhizopogon ellenae and Tomentella fuscocinerea. Research by Bidartondo et al. (2000) showed that *S. sanguinea* may enhance the abundance *R. ellenae*, potentially indicating a mutualistic relationship. Our study extends this investigation to *C. striata*, comparing its interactions with *T. fuscocinerea*, to assess whether such potentially mutualistic associations are more widespread across mycoheterotrophs. Utilizing environmental DNA (eDNA) metabarcoding, we investigated the relative abundance of these fungi in proximity to their mycoheterotrophic partners. Through soil eDNA fungal metabarcoding from rhizosphere soil and ectomycorrhizal root tips, we aimed to replicate Bidartondo et al.’s findings. We then extended this investigation to assess the proximity-based abundance
of T. fuscocinerea relative to C. striata. Our findings suggest that the relationship between mycoheterotrophs and their fungal hosts may not be solely parasitic but context-dependent, with potential mutualistic interactions differing across species. This study contributes to a nuanced understanding of mycoheterotrophs, highlighting the complexity of these plants’ ecological interactions.

PAR31-003: ECTOMYCORRHIZAL FUNGAL COMMUNITY RICHNESS AND COMPOSITION ON CORYLUS AMERICANA LARGELY MIRRORS THAT OF CO-OCCURRING OAKS AND PINES
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Abstract
Despite being a common understory shrub in both pine and oak forests throughout eastern North America, the ectomycorrhizal (ECM) fungal communities on American hazel (Corylus americana) have yet to be well characterized. To address this gap, we sampled roots from cores containing both hazel and pine in two stands at the Cedar Creek Ecosystem Science Reserve (CCESR) in Minnesota, USA: a stand dominated by Pinus resinosa (red pine) and one dominated by Pinus strobus (white pine). Additionally in a third stand, we sampled roots from hazel and adjacent Quercus ellipsoidalis (red oak) seedlings or Quercus macrocarpa (white oak) seedlings at CCESR. Using high throughput sequencing of the ITS2 region, we found that ECM fungal community richness was not significantly different among hazels and associated trees, with the exception of white pine—communities from white pine-associated hazels had overall higher richness than white pine communities. ECM fungal community composition also did not significantly differ among hazels and their associated oak or pine trees. Further, while communities on both oaks and their associated hazels did not significantly differ, communities on red pine and their associated hazels were significantly different from communities on white pine and their associated hazels. Collectively, these findings suggest that ECM fungal communities of Corylus americana are highly flexible and can have a similar compositional makeup as that of surrounding trees.

PAR31-004: GRADIENTS IN PEATLAND MYCORRHIZAL TYPES, AND THE GEOGRAPHIC DISTRIBUTIONS OF PEATLAND ERICOID MYCORRHIZAL FUNGI
Louis Lamit1, Nate Basiliko2, Christopher Schadt1, Susannah Tringe3, Mark Waldrop4, Evan Kane5, Erik Lilleskov6
1Syracuse University, Syracuse, USA. 2Lakehead University, Thunder Bay, Canada. 3Oak Ridge National Laboratory, Oak Ridge, USA. 4Department of Energy, Joint Genome Institute, Berkeley, USA. 5Geology, Minerals, Energy, and Geophysics Science Center, US Geological Survey, Moffett Field, USA. 6School of Forest Resources and Environmental Science, Houghton, USA. 7USDA Forest Service, Northern Research Station, Houghton, USA

Abstract
Peatlands are carbon accumulating wetlands, including acidic nutrient-poor bogs to circumneutral mineral-rich fens. The abiotic conditions and vegetation that vary among water-logged peatland habitats present unique environments for fungal diversity and a gradient of conditions that may affect mycorrhiza functioning. We used a metabarcoding dataset from across Earth’s peatlands to test if the relative abundance of mycorrhizal fungal types (ecto [EMF], ericoid [ErMF], arbuscular [AMF]) track peatland habitat gradients, and to examine the distributions of ErMF lineages. Mycorrhizal fungi shifted along the bog-fen gradient, with ErMF dominant in bogs and poor fens, and AMF more frequent in rich fens. EMF were more common in moderate and low pH peatlands, but were partial to drier sites with abundant woody hosts. These patterns were most distinct across northern peatlands. Known ErMF lineages showed broad distributions across the Northern Hemisphere, were they were more species rich than in the Southern Hemisphere. Dominant mycorrhizal types shifted along peatland gradients in ways broadly analogous to mycorrhiza distributions in uplands, but are set apart by the variation in saturation among peatland sites. Our results highlight the broad distributions of many ErMF taxa, while the dearth of ErMF in the Southern Hemisphere may be driven by the lower abundance of Ericaceae in these sites or a lack of taxonomic description of Southern Hemisphere ErMF. This work suggests the possibility for developing a holistic framework for understanding gradients in peatland mycorrhiza types from fungal and plant perspectives, and emphasizes the need for work with Southern Hemisphere ErMF.

PAR31-005: EFFECTS OF MULTIPLE MICROBIAL MUTUALISTS ON SHAPING PLANT-FUNGAL DISEASE ECOLOGY
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Abstract
Understanding the impact of microbial interactions on plants is critical for maintaining healthy native ecosystems and sustainable agricultural practices. Despite the reality that plants host diverse microbiomes that include many mutualists and pathogens, few studies have examined how interactions among multiple microbial mutualists could impact plant response to fungal pathogen stress. Rhizobia and arbuscular mycorrhizal fungi symbioses are considered to be among the most important symbioses on Earth due to their diverse roles in plant health and resilience. Our
study uses a controlled greenhouse experiment where we planted 960 germinants (8 plant genotypes x 8 microbial treatments x 15 replicates) in a completely randomized block design with a factorial manipulation of the presence/absence of an arbuscular mycorrhizal fungi (Rhizophagus irregularis), rhizobia (Ensifer melliloti), and a fungal root pathogen (Fusarium oxyporum) in the model legume Medicago truncatula. We measured consequences for plant performance (including leaf health, branching, and height) and microbial abundances. We found that there are non-additive effects of multiple mutualists on plant performance metrics and that host genotype shapes microbial interactions. We also identified putative gene candidates using gene regulatory networks that may underpin how multiple mutualistic interactions modulate plant responses to pathogens by investigating changes in functional gene expression across the plant and fungal transcriptomes. Overall, this work elucidates the interactions between mycorrhizal fungi and nitrogen-fixing bacteria and how they shape plant-fungal disease ecology.

PARALLEL SESSION 3-2: FUNGI AND ANIMALS 2

PAR32-001: ENVIRONMENT AND DIET INFLUENCE FUNGAL GUT MYCOBIOMES OF AGASSIZ DESERT TORTOISE (GOPHERUS AGASSIZII) IN CALIFORNIA
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Abstract
Gopherus agassizii ( Mojave Desert Tortoise) is a keystone species for dispersing native desert plant seed and providing habitat with their burrows. These tortoise populations are faced with challenges from habitat modification, human disturbance, and microbial pathogenesis. We evaluated microbiomes in wild free-ranging and captive pen-raised animals to characterize their gut microbial structure and composition and to assess how these factors relate to their health. We extracted DNA from desert tortoise fecal samples and paired soil samples collected from the environment. Fecal samples were collected opportunistically from animals who voided during routine health assessments, as paired with separate soil samples collected in tandem. We sequenced amplicons of the 16S rRNA gene and fungal ITS2 region using an Illumina MiSeq and compared the host microbiome to the soil communities in landscapes inhabited by these animals. 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 fungal 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. Although a small core microbiome was present, and shared across all tortoises, fungal consortia showed lower taxa richness than coexistent bacterial communities. Findings from this study will help provide valuable information about tortoise microbiomes and the ecological resilience of these tortoise populations.

PAR32-002: TOWARDS UTILIZING MOLECULAR GENETICS TO EXAMINE FUNGAL COLONIZATION OF THE AMBROSIA BEETLE MYCANGIA
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Abstract
Ambrosia beetles are globally distributed insects that burrow into the xylem of trees and farm fungal symbionts as their sole source of nutrition. During dispersal, these beetles transport viable propagules of their fungal crop within specialized transport organs termed mycangia. Mycangia select for their specific fungal symbiont, however the mechanism(s) and dynamics of this process remain obscure. Some ambrosia fungi have emerged as devastating tree pathogens in agricultural and forestry sectors, increasing the urgency of studying vector-microbe dynamics within these systems. The ambrosia fungus Harringtonia lauricola is the causal agent of laurel wilt disease, affecting members of the family Lauraceae, including avocado in the United States. This fungus can switch hosts from its original invasive vector, Xyleborus glabratus, into mycangia of native Xyleborus species, complicating management of laurel wilt and expanding its geographic and host tree range. Methods for transformation and the genomic sequence of H. lauricola are available. To better understand the molecular genetics and cell dynamics of the H. lauricola-beetle mycangia interaction, we generated targeted deletions of the perilipin gene, an important regulator of lipid homeostasis. Perilipin:eGFP fusion strains allowed visualization of lipid droplet dynamics within cells. Changes in cell physiology between wild type and mutant strains were tracked and alterations in the dynamics of mycangial colonization of mutant strains were observed quantitatively by image cytometry and qualitatively by cryosectioning of colonized beetles. These experiments reveal the contribution of lipid regulation to H. lauricola environmental adaptation both in vitro and within the mycangia of ambrosia beetles.

PAR32-003: ADAPTABILITY OF EMERALD ASH BORER (AGRILUS PLANIPENNIS) GUT MICROBIOME STRUCTURE IN RELATION TO HOST TREE SPECIES OF FRAXINUS SPP. IN NORTH AMERICA
Judith Mogouong1, Claire Yager1,2, Kathryn Bushley1,2
1Cornell University, ITHACA, USA. 2USDA ARS, ITHACA, USA

Abstract
The Emerald Ash Borer (EAB) is one of the biggest threats to North American forests and is a specialist infesting ash trees (Fraxinus spp.), including susceptible native ash species. Although various strategies have been tested to stop the spread of EAB, efficient control is still challenging. The microbiome plays a crucial role in the survival and wellbeing of both plant and insects hosts. In wood- and phloem-feeding insects such as EAB, the larval
Abstract

The majority of terrestrial biomass is wood, and specialized wood-decaying fungi release carbon stored in wood. Due to vast fluxes of carbon from wood, wood decomposition impacts global carbon cycles and climate. However, fungal succession and competition determines decomposition rates. Fungus farming ambrosia beetles are among the first to colonize dying trees. They inoculate wood with a variety of fungal symbionts. Beetle-associated fungi were historically thought to increase wood decay and carbon release, but recent research suggests that in some contexts they may slow decay through competition with wood-decaying fungi. Due to international trade, invasive non-native ambrosia beetles are spreading around the globe. It is unknown if non-native beetles and their fungi change decomposition rates in the invaded regions or if these impacts vary among tree species. Our study utilized surveys of local ambrosia beetle communities, a beetle exclusion experiment, and DNA metabarcoding to observe the ambrosia symbiosis and measure its impact on fungal community assembly and wood decomposition in logs from four disparately related tree species. We tested the hypothesis that non-native fungi associated with recently introduced and hyperabundant non-native ambrosia beetles suppress wood decay and compete with native fungi. Most observed ambrosia beetles were non-native. Ambrosia beetles readily colonized all 4 hardwood tree species (American Beech, Red Maple, Bitternut Hickory, and Southern Magnolia). We compare fungal community composition between ambrosia beetle exposed and excluded logs, and the implications for wood decomposition rates are discussed. As non-native symbioses invade, it is imperative that we understand the native ecosystem’s unexplored response.

PAR32-004: THE AMBROSIA BEETLE MYCOBIOME AND ITS IMPACT ON WOOD DECOMPOSITION
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Abstract

The Emerald Ash Borer (EAB; Agrilus planipennis), an invasive phloem feeding beetle from Asia, now threatens all native North American ash species. We hypothesized that while the phloem microbiome structures may differ across ash tree species, the larva gut harbors a relatively consistent core gut microbiome. To address this question, samples collected from State Parks near Ithaca (NY) were used for metabarcoding targeting both ITS1 and 16S barcode regions (Illumina PE300 platform) and metagenomic (Illumina shotgun platform) sequencing, as well as widely-targeted metabolomics to evaluate the taxonomic and functional variations involving associated microbes and occurring in distinct sample types. Our findings will help illuminate the role of fungi and other microbes in the successful invasion of this beetle.

PAR32-005: MICROBIOME OF NORTH AMERICAN ASH FOR BIOCONTROL OF EMERALD ASH BORER
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Abstract

Ash (Fraxinus) are economically and culturally important trees in North America, and host to numerous native wood boring beetles and their parasitoids. However, little is known about their microbiota and, more specifically, endophytic or pathogenic fungi that may grow in the living phloem and leaves. The Emerald Ash Borer (EAB; Agrilus planipennis), an invasive phloem feeding beetle from Asia, now threatens all native North American ash species. We hypothesized 1) that increasing infestation with EAB will decrease endophyte diversity and abundance in ash phloem and 2) that ash trees may harbor endophytes that are entomopathogens of EAB. To investigate these questions, we collected infested and uninfested phloem, insect frass, and insects in two regions of New York. Cultured fungal isolates included several potential entomopathogens from families Cordycipitaceae, Ophiocordycipitaceae, and Clavicipitaceae, as well as other insect-associated fungi that may be plant pathogens (Ophiostomataceae) or saprophytic wood rot (Peniophoraceae) fungi. Several entomopathogenic taxa were isolated not only from insects, but also from galleries, frass, and even uninfested ash phloem, suggesting they may grow within healthy phloem as entomopathogenic endophytes. Our findings will elucidate the diverse fungi in this system, identifying fungi with potential roles in ash decline, as well as entomopathogenic endophytes, which could offer novel options for biocontrol of this invasive insect.
PAR33-002: ENGINEERING LIVING MATERIALS WITH FUNGI AND BACTERIA

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Abstract
Engineered living materials are composed of inert substances containing living organisms that benefit from the organism’s structure, metabolic processes, and other functional properties. This study aims to create new living materials based on symbiotic relationships between fungi and bacteria grown in wood. Our goals are for these materials to display increased strength, lifespan, carbon capture, and self-healing capabilities compared to their uninoculated counterparts. Tensile strength testing was used to determine the effectiveness of fungal and bacterial inoculations on material properties and on suitability as sustainable living materials.

PAR33-003: DOMESTICATION STUDIES OF LENTINUS TIGRINUS: SPAWN PREPARATION

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Abstract
Lentinus is a well-known genus possessing a number of edible taxa, Lentinus sajor-caju, L. squarrosulus and L. polychorus are commercially cultivated species of this genus. In present paper, the spawn preparation studies of wild collected Lentinus tigrinus from North Kashmir are discussed. This edible fungus is collected by natives for cooking, thus, to reduce the local pressure on this natural resource, its domestication studies were initiated, the pure cultures were raised and physical parameters were standardized. Trails for the spawn preparation were started by using the four locally available grains viz. wheat, bajra, jowar and maize. The grains were surface sterilized, three replicates of each type of grains boiled for 10, 20, 30 and 40 minutes were inoculated. The observations for best vegetative growth depending on the characters like thickness of mycelium on grains, rate of linear growth of mycelium on grains, viability of boiled grains till the mycelium fully engulfs them, were noted down on daily basis. It was inferred from the observation that the wheat grains boiled for 30 minutes gave the best results for spawn preparation of L. tigrinus. Later, by taking these results as a base for mass production, the packets for spawn were prepared.

PAR33-004: THE MYCOBIOME OF ELECTRONIC CIGARETTES: POTENTIAL RESERVOIR FOR INFECTIOUS AGENTS

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Abstract
Previous research regarding e-cigarette use impacts on human health has focused on lung injury caused by inhalation of vaporized materials, the effects on innate immunity, and/or metal toxicity related to e-cigarette cartridges. Given the enclosed plastic design and alternating temperature cycles (leading to condensation) we hypothesize pathogenic yeasts colonize the interior of e-cigarettes, potentially leading to negative impacts on user health. In this study, a combination of culture-based and Illumina sequencing methods were employed to examine fungal pathogen presence by sampling from e-cigarette mouthpieces used by twenty-five adult individuals in Gainesville, Florida. Results from Sanger sequencing (ITS1 of the rDNA) of cultures confirmed the presence of several pathogens including: Rhodotorula spp., Aureobasidium melanogenum, Cystobasidium minutum, Meyerozyma guilliermondii, Mucor circinelloides, and Papiliotrema flavescens. At least eight additional fungal pathogens were detected with Illumina sequencing of the ITS1 amplicon. None of the fungal pathogens were detected in oral mycobiome analyses suggesting these pathogens are originating from environmental sources rather than the user’s mouth, establishing in the conducive microhabitat of the e-cigarette mouthpiece. The most frequently isolated pathogen, Cystobasidium minutum, was evaluated for pathogenicity in immunocompetent wildtype (C57BL/6J) mice, which showed hypersecretion of mucin and associated molecular and serological markers characteristic of chronic bronchitis. These results are the first to investigate the potential linkage between infectious disease agents and e-cigarette devices. Further studies are warranted to evaluate the potential roles that these and other microbial taxa may have on users’ respiratory and/or overall health.

PAR33-005: THE INFLUENCE OF GLYPHOSATE USE ON FUNGAL COMMUNITY COMPOSITION AND DECAY CAPABILITIES

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Abstract
Glyphosate is the most widely used herbicide worldwide. As an organophosphorus pesticide, it inhibits essential aromatic amino acid biosynthesis in plants, a metabolic pathway also present in bacteria and fungi. Unlike bacteria, the effects of glyphosate on fungi are not well studied. Reports of stimulatory/inhibitory effects vary widely by taxa and are often contradictory, with most research focused on microbial activity in agricultural soils. Detailed HTS data on fungal community response to glyphosate application are lacking and vitally important; fungal co-occurrence networks can be profoundly affected. The effect of glyphosate on wood decay, an essential ecosystem service primarily performed by basidiomycetes, has received little attention. To explore this, we designed a study to address the questions “does repeated long-term/short-term glyphosate application impact soil and wood fungal communities” and “does glyphosate exposure alter wood decay processes?”

An AWPA E-7 stake test was established using a matched-pair plot design (glyphosate/no glyphosate) with four blocks at each of three sites. Southern pine stakes were installed with harvests every six months for five years. At each sampling: (1) eight stakes/plot were visually rated for decay progression and returned; (2) two surface soil samples with organic material removed, before and after glyphosate application, and one stake were collected.
However, whether plant-fungus associations existed in facilitating terrestrialization of the earliest land plants.

Fungi have coevolved with land plants and their algal ancestors, the streptophyte algae. Therefore, fungal pectinase and xyloglucanase genes can be used as markers to infer potential interactions between early plants and fungi. We used a comparative phylogenetic approach to reconstruct evolutionary histories of fungal enzymes, utilizing available genomes of terrestrial and chytrid fungi, which share a common ancestor that predates plant terrestrialization. However, bioinformatic predictions of pectinase and xyloglucanase genes in chytrids continue to rely largely on experimentally characterized sequences from terrestrial fungi. We utilized high-performance anion-exchange chromatography with pulsed amperometric detection (HPAEC-PAD) to detect breakdown products of plant cell wall polysaccharides and enzyme assays to quantify enzyme activity. Here we present evidence for enzyme function beyond bioinformatic inferences in the poorly known chytrid fungi.

Abstract

Fungi have a powerful influence on plants’ traits, and there has been a recent surge of efforts to harness them to aid in agriculture and plant conservation through mycobiome transplantation. But research on these interactions has largely focused on one fungus at a time; a perspective that is never encountered in nature. Mycobiome transplantations are increasingly seen as a viable intervention for steering ecosystem recovery and succession, as well as influencing the fitness of host organisms. But they have shown mixed results in practice, and it is unclear why some transplants succeed and others fail. If we want to move beyond the “hope and pray” method of transplanting fungal communities, we need process-based understanding and predictive modeling for how entire donor fungal communities interact with hosts, the environment, and resident microbial communities. One major challenge in predicting community transplantations is that models must be able to handle multiple response variables while accounting for potentially thousands of interactions between resident and donor communities. Here, I present the CommunityAssemblR R package to facilitate large-scale simulations of microbiome transplantation under defined biotic interactions within existing ecological theory. These simulated data sets are being used for supervised training of DeepInsight convolutional neural net (CNN) models that can detect key ecological processes such as niche overlap, antagonism, and facilitation. Once trained, these CNN models can be used to detect these processes in real experimental situations so that we can better understand what factors are key for determining transplantation success.

Abstract

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PAR41-003: EVOLUTION OF TRANSPORTABLE ELEMENTS IN ARBUSCULAR MYCORRHIZAL FUNGI: INSIGHTS INTO GENOME VARIABILITY AND GENE REGULATION

Jordana Oliveira1, Catrina Lane1, Ariane Nicol2, Nicolas Corradi3
1University of Ottawa, Ottawa, Canada. 2Queen’s University, Kingston, Canada

Abstract
Arbuscular mycorrhizal fungi (AMF) are plant symbionts that provide nutrients from the soil to their hosts in exchange for carbohydrates and lipids. AMF exhibit low morphologic variability and no sign of plant specificity, raising questions about how these organisms have adapted to the wide spectrum of host species. Recent genomic analysis has revealed that AMF species harbor a significant portion of transportable elements (TEs), which play crucial roles in promoting genome variability by generating new copies and insertions. However, the average 60% of TEs in AMF genomes remain unknown. We hypothesize that investigating the TE content can unveil hidden AMF diversity and detect the impact of these sequences in promoting genetic variability. To achieve this, we constructed a library using 26 AMF species, identifying the presence of transposition domains in consensus sequences. The annotation of TEs revealed that the major groups of AMF share patterns of transposition, with ancestral Paraglomeralea exhibiting lower TE content and smaller genome sizes compared to more derived groups like Archeosporalea, Glomeralea, and Diversisporalea, which show clade-specific expansions. Moreover, a significant proportion of TE insertions are located in exons in all species, suggesting an impact of these repetitive sequences on protein diversity through exonization processes. Expression analysis in the model species Rhizopagus irregularis showed a fourfold increase in upregulated TEs during symbiosis compared to extraradical mycelium, indicating a role of TEs in communicating with the host. We propose that TE variability in AMF may contribute to the evolution and diversification of genes, influencing their successful symbiotic relationships with plants.

PAR41-004: FIRST GENOMIC AND ITS SEQUENCES OF GENUS BLASTOCLODIA (BLASTOCLODIOMYCOTA: BLASTOCLODIALES: BLASTOCLODIACEAE) FROM AN ANAEROBIC SPECIES B. SPRINGSHIEMII

Yi-Hong Ke, Eva Schwarz, Michelle Orozco-Quime, Timothy James
University of Michigan, Ann Arbor, USA

Abstract
Blastocladia is a genus of zoosporic fungi that is widely distributed across the world. The collections of Blastocladia spp. have been made on submerged rosaceous fruits and submerged twigs in America, Europe, Africa, Asia, and Oceania. However, neither ITS sequences nor genome sequences are available for the whole genus so far. In this study, we obtained an axenic culture of B. springshiemii from tomato baits and sequenced the genome using Oxford Nanopore. The species is previously believed unable to perform aerobic respiration and thus an obligate fermenter producing large amounts of lactic acid in culture. The genome sequence suggests the genome is diploid. The assembly size of the nuclear genome is 30.589 Mbp containing 13,715 gene models. The assembly of the mitochondrial genome is 85.703 kbp in a circular configuration, containing all 14 conserved protein-coding genes and 1 ribosomal protein S3 gene commonly present in fungal mitochondrial genomes, suggesting the species is indeed capable of undergoing oxidative phosphorylation. RNAseq of cultures in different conditions confirms differential transcriptomic profiles in response to the oxygen level. The cryo-preservation attempts of the cultures are successful and the isolates are available for request through the Collection of Zoospores Eufungi at University of Michigan (CZEUM). The new genomic and ITS sequences and the culture will serve as important resources to understand the biochemical pathways and the evolution of aquatic anaerobic fungi, as well as to identify the genus from environmental sequencing.

PAR41-005: THE GENOME AND LANDSCAPE OF CRONARTIUM HARKNESSII VARIANTS IN ALBERTA

Laura Manerus, Rhiannon Peery, Janice Cooke, Samuel Beck
University of Alberta, Edmonton, Canada

Abstract
Cronartium harknessii (J.P Moore) Meinecke, the causative agent of western gall rust, impacts both forest health and lumber yield. C. harknessii is found throughout the ranges of lodgepole pine (Pinus contorta Dougl. ex Loud var latifolia) and jack pine (Pinus banksiana Lamb.), as well as in the hybrid zone where the ranges of lodgepole and jack pine overlap in Alberta and the Northwest Territories. Recently, we have described two genetically distinct variants of C. harknessii: a more virulent western variant whose range coincides with lodgepole pine, and a less virulent eastern variant whose range coincides with jack pine. A whole genome comparison from assemblies of C. harknessii east and west variant representatives has revealed significant structural differences. We hypothesize that these differences have led to possible divergence of these two variants who have evolved differing virulence relationships with their pine hosts in addition to possible genomic and temporal barriers to reproduction. Functional annotation of these structural differences will allow us to identify candidate genes responsible for this differing virulence. In parallel, we are conducting a fine-scale analysis of the population structure of C. harknessii sampled across a transect spanning genetically pure lodgepole pine in western Alberta across the hybrid zone to genetically pure jack pine in eastern Alberta. To aid these analyses, we are developing a variant-discriminating PCR assay. The outcomes of these population genetic analyses will reveal host-specificity behaviours of each variant and what, if any admixture has occurred within a species only speculated but not observed to sexually reproduce.
PAR41-006: POPULATION GENOMIC ANALYSES REVEAL DEEP POPULATION SUBDIVISION IN RHIZOCTONIA SOLANI AG-1 ISOLATES ASSOCIATED WITH DIFFERENT CROPS IN NORTH AMERICA AND THE CARIBBEAN
Juanita Gil1,2, Kensy Rodriguez1, Vanina Castroaguadín4, Camila Nicollil, Felipe Dalla Lana1, Xin-Gen Zhou5, Sara Thomas-Sharma7, Terry Spurlock2, Jim Correll2, Pierre Gladieux7, Alejandra Rojas1
1Michigan State University, East Lansing, USA. 2University of Arkansas, Fayetteville, USA. 3Louisiana State University, Baton Rouge, USA. 4USDA-ARS Mycology & Nematology Genetic Diversity & Biology Laboratory, Beltsville, USA. 5Texas A&M, Beaumont, USA. 6PHIM INRAE, Montpellier, France

Abstract
Rhizoctonia solani is a species complex classified into anastomosis groups based on hyphal compatibility. AG-1 is an important group and further divided into subgroups based on differences in host range and molecular diversity. Rhizoctonia solani AG1-IA is the causal agent of sheath blight in rice and aerial blight in soybean, two devastating diseases. Currently, there is limited resistance to rice blight in rice and aerial blight in soybean, two devastating diseases. Monitoring genetic variability and addressing host-pathogen dynamics in R. solani AG1-IA is necessary to understand the origin and colonization history of the pathogen. We sequenced 16S R. solani isolates, representing four subgroups of AG-1, collected over three decades (1993 to 2022) from different hosts and states in the United States, as well as other countries in North America and the Caribbean. The genetic diversity of the AG1-IA subgroup was determined using high-quality single nucleotide polymorphisms (SNPs). Illumina reads were mapped to the genome of R. solani AG1-IA isolate HG81, achieving an overall alignment rate of up to 92% within the AG1-IA subgroup. Mapping percentages between subgroups were below 55%. The population genetic structure of the AG-1 group was inferred with clustering approaches based on ca. 1.8M biallelic SNPs. These analyses revealed that isolates from Arkansas showed less genetic variability and were distinct from those from Cuba, Texas, and Louisiana. Population structure had a clear geographical component, although signs of recent admixture were observed. Our work contributes to a better understanding of the genome-wide variability of R. solani AG1-IA.

PAR42-001: IMPORTANCE OF LIVE SOIL INOCULATION FOR ROOT-ASSOCIATED FUNGI CONSERVATION AND RESTORATION EFFORTS IN TROPICAL ECOSYSTEMS
Luisa F. Chavarro1, Mariana Carrillo-Ramirez1, William J. Bravo1, Santiago Madriñan1, Lina Caro1, Adriana Corrales4,2
1Universidad de los Andes, Bogotá, Colombia. 2Center for Research in Microbiology and Biotechnology-UR (CIMBIUR), Faculty of Natural Sciences, Universidad del Rosario, Bogotá, Colombia. 3Wildlife Conservation Society, Bogotá, Colombia. 4Society for the Protection of Underground Networks, SPUN, Dover, USA

Abstract
Root symbiotic fungi are highly diverse and perform key roles in tropical forest but have been historically overlooked in ecosystem restoration. Therefore, there is a knowledge gap about soil fungi composition, diversity and their potential applications in tropical reforestation and restoration efforts. Symbiotic relationships with root-associated fungi, including arbuscular mycorrhizal (AM) and ectomycorrhizal (ECM) fungi, play a fundamental role in seedling survival by improving nutrient uptake and increasing pathogen defense. To understand more about the role for these fungi in seedling grown for restoration purposes, we run two independent greenhouse experiments with seedlings of two trees: Coccoloba uvifera (ECM plant) and Juglans neotropica (AM plant). We grew seedlings in regular commercial nursery soil and with 6% inoculation of live soil from local conspecific adults. In addition to seedling growth, we characterized the fungal communities in their roots by amplifying the ITS2 region usingillumina miseq. We found, for both species, that seedling that were inoculated with live soil showed a higher growth rate and associated with a more diverse fungal community than seedling grown on commercial nursery soil. Our results highlight the importance of including the soil microbiome in propagation processes to increase seedling growth, health, and survival and as an effective strategy for restoring soil microbial communities in tropical ecosystems.

PAR42-002: SOIL FUNGAL COMMUNITY SUCCESSION DURING AFFORESTATION OF MID WESTERN AGRICULTURAL LAND
Kathryn Maley, Mary Catherine Aime
Purdue University, West Lafayette, USA

Abstract
Land use conversion significantly alters soil communities, and soil fungi are particularly susceptible to these changes. Conversion of agricultural land to forest, a process known as afforestation, could offset the negative effects of deforestation and habitat fragmentation. Many afforestation sites are established as monoculture tree plantations, but most natural forest systems are heterogeneous communities with regions dominated by different tree species. These local differences in composition may drive fungal community assembly during forest development. Whether a tree species forms arbuscular mycorrhizas (AM trees) or ectomycorrhizas (ECM trees) can affect its inter- and intraspecific
Further, grain yield between the biofertilizer and results further supported that poor nutrient conditions or in beads, and slight variations across species. Additionally, there was a significant increase (P < 0.01) in mycorrhizal establishment in treatments that received the consortia in beads, and slight variations across species. Additionally, results further supported that poor nutrient conditions or high fertilized soils greatly impact root-fungal interactions. Further, grain yield between the biofertilizer and conventional fertilizer was comparable, and the hydrogels helped maintain soil water retention, suggesting that with further research, bacterial-fungal hydrogel biofertilizers may offer an alternative.

PAR42-005: EFFECTS OF FUNGICIDE SEED TREATMENTS ON SOIL MICROBIOME ACROSS YEARS
Marianna Araujo Alves Gomes de Souza1, Marcos Paulo da Silva2, Samantha Rigo Segalin3, Sherif Adam Sharfadine4, Quirong Fan5, J. Alejandro Rojas1
1Michigan State University, East Lansing, USA. 2Syngenta Seeds, Malta, USA. 3University of Arkansas, Fayetteville, USA. 4USDA-ARS, Oxford, USA

Abstract
Pythium spp., Rhizoctonia solani, Thielaviopsis basicola, and Fusarium spp. are the primary pathogens associated with Cotton Seedling Disease Complex, affecting cotton production worldwide. Although fungicides are a useful tool for controlling soilborne diseases, their use may represent a potential risk to soil health. This study aimed to understand the impact of fungicide seed treatment combinations on fungal populations at the cotton seedling development stage. For that reason, plants and soil samples were collected from 2019-23 for Judd Hill and 2021-23 for Marianna, Arkansas, to monitor species that are associated with this disease complex and to conduct bioassays under controlled conditions.
Treatments consisted of no fungicide (T1), metalaxyl (T2), penflufen (T3), and a mix of prothioconazole, myclobutanil, penflufen, metalaxyl (T4). Total DNA was extracted from soil and roots, and the primers ITS1F and ITS2 were used to amplify the ITS1 region of the rDNA, and sequencing was carried out on an Illumina MiSeq system. A bioassay under controlled conditions using soil collected from both locations was conducted to monitor the effect of seed treatment on root and soil microbes under two temperatures, 18 and 25°C. After 25 days, roots were collected and plated on 3 different types of media to isolate seedling disease complex pathogens. DNA was extracted from the mycelia and primers ITS1F and ITS4 were used to amplify the ITS region. While seed treatments filter fungal communities, location, and temperature cause variation in fungal communities.

PAR42-003: ABSTRACT WITHDRAWN AT THE REQUEST OF THE SUBMITTER.

PAR42-004: THE BENEFICIAL IMPACT OF MIXED BACTERIAL-FUNGAL HYDROGEL BIOFERTILIZERS ON MYCORRHIZATION OF TRITICUM AESTIVUM ROOTS: A GREENHOUSE STUDY
Korena Mafune, Mari Winkler, Rosemary Randall, Jillian Rogers
University of Washington, Seattle, USA

Abstract
Both nitrogen and phosphorus fertilizers are currently indispensable for high yield crop production. However, the sourcing and production is extremely unsustainable and outside of the safe-operating space for planetary boundaries. Although it is possible to increase industrial N-production, P-mining, and the application, alternatives are greatly needed for a sustainable future. One potential alternative is a highly-efficient, multi-functional biofertilizer that harnesses the power of fungi and bacteria to promote a healthy soil. To better understand how bacterial-fungal interactions can be harnessed to potentially help meet these goals, we’ve created a novel hydrogel biotechnology in the form of biodegradable beads that encase mixed bacterial-fungal consortia. In the first large-scale trial, we applied various types of hydrogel beads that contained three different species of arbuscular mycorrhizae with a consortia of P-solubilizing, N-fixing, and plant growth promoting bacteria to *Triticum aestivum* (wheat) in a greenhouse study. Post senescence, wheat grain, foliage, and roots were harvested. Roots were analyzed for mycorrhization using a modified grid-line intersect technique. Results show that all three species of mycorrhizae (*Rhizophagus irregularis*, *R. intraradices*, and *Funneliformis mosseae*) successfully established. There was a significant increase (P < 0.01) in mycorrhizal establishment in treatments that received the consortia in beads, and slight variations across species. Additionally, results further supported that poor nutrient conditions or high fertilized soils greatly impact root-fungal interactions. Further, grain yield between the biofertilizer and conventional fertilizer was comparable, and the hydrogels helped maintain soil water retention, suggesting that with further research, bacterial-fungal hydrogel biofertilizers may offer an alternative.
PAR43-002: A MESS OF MERISMODES: CLARIFYING TAXONOMIC CONCEPTS IN A GENUS OF CYPHELLOID FUNGI

Bruce Malloch, Greg Thorn
Western University, London, Canada

Abstract

Merismodes (Agaricales, Cyphellopsidaceae) is a cosmopolitan genus of saprotrophic fungi associated with dead, standing branches of Angiosperms. This genus is characterized by the production of minute cupulate basidiomata frequently found in association with old pyrenomycetes. Presently, taxonomic concepts within this group are poorly resolved and in need of revision. The aim of this study is to clarify species concepts in North America using ITS phylogeny, in addition to morphological and ecological evidence. Sixty-five specimens were collected or borrowed with emphasis on Canadian material. Sequence data were obtained primarily from living cultures derived from recent collections, with some attempts to extract, amplify and sequence DNAs from older voucher specimens. Our results indicate there are at least five species of Merismodes in North America, with species exhibiting a range of substrate specificities. Merismodes confusa and M. fasciculata are sister taxa, rather than a single species as some authors have suggested based on their similar morphologies. Fully resolving species concepts in the genus is not currently feasible without type studies of European species. There may also be several additional North American species for which we were unable to acquire sequence data due to scarcity of material.

PAR43-003: A SECONDARY ACCOUNT OF THE NORTH AMERICAN SPECIES OF RHIZOPOGON

Aljia Mujic, Thelmalyn Montenegro, Matt Gordon, Emeline Pano, Darci Rivers-Pankratz
1California State University, Fresno, Fresno, CA, USA. 2Molecular Solutions, LLC, Portland, OR, USA. 3USDA Forest Service, Region 6, Portland, OR, USA

Abstract

Rhizopogon is a genus of truffle-forming fungi that forms mutualistic ectomycorrhizal (ECM) mushroom-forming fungi that so far has eluded intrafamilial phylogenetic resolution based on morphology and multi-locus datasets. In this study, we present a genome-wide molecular dataset of 1764 single-copy gene families from a global sampling of 418 Boletaceae specimens. The resulting phylogenetic analysis has strong statistical support for most branches of the tree, including the first statistically robust backbone. The enigmatic Phylloboletellus chloephorus from non-ECM Argentinian subtropical forests was recovered as a new subfamily sister to the core Boletaceae. Time-calibrated branch lengths estimate that the family first arose in the early- to mid-Cretaceous and underwent a rapid radiation in the Eocene, possibly when the ECM nutritional mode arose with the emergence and diversification of ECM angiosperms. Biogeographic reconstructions reveal a complex history of vicariance and episodic long-distance dispersal correlated with historical geologic events, including Gondwanan origins and inferred vicariance associated with its disarticulation. Together, this study represents the most comprehensively sampled, data-rich molecular phylogeny of the Boletaceae to date, establishing a foundation for future robust inferences of biogeography in the group.
PAR51-001: INVESTIGATING DRIVERS OF THE COMPOSITION OF TREE-ASSOCIATED MYCORRHIZAL FUNGAL COMMUNITIES IN THE NORTHERN UNITED STATES

L. McKinley Nevins1, Tanya E. Cheeke2, Geselle Sotelo1, James A. Lutz2

Abstract

Mycorrhizal fungi are crucial symbionts to temperate forest trees, providing essential functions like water and nutrient transport. The assembly of fungal communities is shaped by processes such as environmental filtering, which favors species suited to local conditions. Increasing climate change-induced droughts in the northwest US will alter availability of water and soil nutrient resources, likely influencing future fungal community composition.

PAR51-002: SEEING THE FOREST FOR THE FUNGI: DO INSECT-INDUCED FOREST DISTURBANCES AFFECT MACROFUNGAL DIVERSITY IN OLD-GROWTH EASTERN HEMLOCK STANDS?

Rebecca Mader1, Matthew Smith2, Keith Egger3, Allison Walker1

1Acadia University, Wolfville, Canada. 2Kejimkujik National Park and National Historic Site, Maitland Bridge, Canada. 3University of Northern British Columbia, Prince George, Canada

Abstract

Fungi are important decomposers and mutualists which are vital for maintaining forest health. Fungi are sensitive to vegetation changes, so fungal diversity can shift during forest succession. In Kejimkujik National Park and National Historic Site (KNPNHS) of Nova Scotia, Canada, old-growth populations of a key forest foundation tree species, eastern hemlock (Tsuga canadensis), are threatened by an invasive insect—the hemlock woolly adelgid (Adelges tsugae). To understand how old-growth hemlock macrofungal communities respond to insect disturbances, we investigated the effects of a 2002 – 2006 pale-winged grey moth (Iridopsis ephyraria) outbreak on macrofungal diversity in KNPNHS. We collected macrofungi in KNPNHS hemlock plots from July to November, 2022 – 2023—634 specimens were taken. For historic comparison, we used specimens from Acadia University’s E. C. Smith Herbarium collected from the same plots in 1990 – 1995. Specimens were identified using ITS rDNA barcoding, phylogenetic analysis, and microscopy. Identifications are ongoing with 144 species recorded to date, mainly in the genera Amanita, Cortinarius, and Russula. Hypogeous fungi and species previously unrecorded in Eastern Canada were also identified. We will detect significant changes in KNPNHS fungal diversity before and after the I. ephyraria disturbance using diversity indices and data on hemlock defoliation and environmental variables from each plot and year. Our results expand current knowledge of macrofungal diversity.
in old-growth T. canadensis stands and will illustrate how macrofungal communities respond to ecosystem disturbances, illuminating the future of forest macrofungi in KNPNHS as A. tsuga infestations intensify.

PAR51-003: PRIME TIME FOR PINE DECOMPOSITION: ECTOMYCORRIZHIAL FUNGI ENHANCE LITTER DECAY IN A TEMPERATE RED PINE FOREST
Lang C. DeLancey1, Moira J. McCarthy1, François Maillard2, Sarah E. Hobbie2, Peter G. Kennedy3
1University of Minnesota, Department of Ecology, Evolution, and Behavior, St. Paul, USA. 2University of Minnesota, Department of Plant & Microbial Biology, St. Paul, USA

Abstract
The suppression of organic matter decomposition by ectomycorrhizal fungi (EMF), a.k.a. the ‘Gadgil effect’, is often linked to variation in leaf litter chemistry, especially as it relates to nitrogen (N) and carbon (C) chemistry. To date, however, the litters of a limited number of plant species have been tested, hindering our ability to predict EMF effects on C cycling at the ecosystem scale. Here, we compared needle decomposition of both a novel (red pine; Pinus resinosa) and previously tested (white pine; P. strobus) species for 12 months in control plots and plots where EMF were suppressed via trenching in a red pine stand in Central Minnesota, USA. In addition to tracking mass loss, we analyzed litter bags for C- and N-acquisition enzyme expression. Contrary to our hypotheses, leaf litter decomposed 13% more over one year in the presence of EMF and roots, an effect that was more pronounced for red pine litter. These decomposition changes were associated with increased N-acquisition and decreased litter %N and proteins. These results suggest that while litter N content may influence EMF-saprotroph interactions, EMF suppression of decomposition does not necessarily follow in low-N, recalcitrant litter types, even in temperate pine forests.

PAR51-004: DESCRIBING AND MONITORING A POTENTIAL FUNGAL PATHOGEN OF ANDEAN WOODLANDS
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1University of Colorado Boulder, Boulder, USA. 2La Universidad Nacional Toribio Rodríguez de Mendoza de Amazonas, Chachapoya, Peru

Abstract
Endemic to the Andean Mountain range are the highest elevation growing trees of the world. Polylepis woodlands are endangered, heavily fragmented, and becoming threatened by a potential fungal pathogen. Paraleptosphaeria polylepis (Leptosphaeriaceae, Pleosporales) 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 an undescribed species of Paraleptosphaeria in Perú growing on Polylepis albicans and P. weberbaueri. The abundance of this causal agent has doubled in 59 plots established in June 2019 and revisited in December 2023 and January 2024. The results of this study show that fungal presence in these plots is linked with north facing slopes, lower elevations, and the presence of human disturbance (logging and trails). Here, we also describe morphological, ecological, and genetic diversity of this suspected fungal pathogen in Perú compared to its described Bolivian counterpart. Ultimately, this study will aid in better understanding the ecology, distribution, and impact of this fungus as well as which regions of the Andes may be most susceptible to this potential emerging disease.

PAR51-005: INVESTIGATING THE EFFECTS OF THE BLEWIT MUSHROOM LEPISTA NUDA ON THE COMMUNITY COMPOSITION OF ITS SOIL ENVIRONMENT.
Katarina Kukolj, Greg Thorn Western University, London, Canada

Abstract
This study aims to investigate the effects of the edible saprotrophic Blewit mushroom (Lepista nuda) on the community composition of its soil environment in coastal regions of Newfoundland, Canada. Previous studies have discovered Blewit antimicrobial properties including hyphal penetration of bacteria, yeasts, and green algae, and the reduced incidence of disease on plants with Blewit culture filtrates/extracts. However, field studies on the effects of Blewit mycelium on soil organisms are lacking. Therefore, this study includes sampling soil at various time points from known natural Blewit patches and nearby treatment plots inoculated with Blewit mycelium, in comparison to plots without Blewits. Arthropod, nematode, bacterial and fungal members of the soil community will be identified and their relative abundance determined by metabarcoding analyses of soil-extracted DNAs. It is predicted that soils colonized by Blewit mycelium will have simplified communities of soil microbes and soil invertebrates compared to soils without Blewit. This could possibly be due to dominance, antibiosis, and predation of other community members, as their mycelium has been observed to grow in dense mats through soil and because of their known antibiotic properties. These results will tell us how Blewits affect these communities and if potential crop pests and plant pathogens are significantly reduced by growth of Blewit mycelium, essential for understanding the potential of Blewits in the agricultural industry as an environmentally friendly biopesticide and potential co-crop.

PAR51-006: METABARCODING ANALYSIS REVEALED ENVIRONMENTALLY-DRIVEN MYCOBIOME WITHIN THE ROOTS OF DAPHNE ARBUSCULA SHRUBS
Miroslav Caboň1, Zuzana Gajdošová2, Zuzana Kolaříková2, Radka Sudová2, Jana Rydlová2, Slavomír Adamčík3, Michaela Caboňová4, Jaromír Kučera1, Marek Slovák1,3
1Plant Science and Biodiversity Centre, Slovak Academy of Sciences, Bratislava, Slovakia. 2Institute of Botany, Czech Academy of Sciences, Prague, Czech Republic. 3Faculty of Natural Sciences, Charles University, Prague, Czech Republic

Abstract
Fungi engage in a wide array of ecological interactions with rock-dwelling plants, ranging from beneficial mutualism and asymptomatic endophytism to saprotrophy and
detrital parasitism. In these challenging environments, the endobiotic communities of fungi may play a crucial role in the long-term survival and adaptation of plants. Despite the apparent influence of the endobiome on plant fitness and survivability, there is a significant gap in understanding how microclimatic conditions affect root-associated fungal communities. In this study, we investigated fungal assemblages within the root systems of the endangered endemic shrub Daphne arbuscula, which dwell in rock habitats characterized by dynamic microclimates often reaching extreme ecological conditions. A total of 36 root samples were collected from six populations of Daphne arbuscula, growing in areas with contrasting microclimatic conditions (colder versus warmer) within the Muránska Planina Mts region of Central Slovakia. Fungal diversity was assessed using Illumina amplicon sequencing, targeting both the universal fungal barcode ITS2 rDNA region and V4/V5 region of SSU rDNA used for the definition of AM fungal taxa. We revealed extensive colonization of the Daphne roots by diverse taxonomic fungal groups attributed to different ecological guilds, predominantly plant pathogens, dark septate endophytes (DSE), and arbuscular mycorrhizal fungi (AMF). Notably, differences in taxonomic composition and ecological guilds emerged between colder and warmer microenvironments. Apart from omnipresent AMF, shrubs on warmer sites exhibited a prevalence of plant pathogens, while colder sites were characterized by a dominance of DSE.

PARALLEL SESSION 5-2: Fungal Interactions: Other

PAR52-001: Photobiont Subsidies Correlate with Genomic Profiles in Lichen Fungal Symbionts
David Diaz Escandon, Toby Spribille
University of Alberta, Edmonton, Canada

Abstract
One of the highest risks of living in a symbiosis is becoming dependent. Once a function becomes redundant, it is subject to relaxed selection, ultimately resulting in irreversible consequences. Lichens—typically characterized as a photosynthetic partner and a fungal symbiont—are generally thought to be nutritional symbioses where the fungus is subsidized by photosynthetically derived carbon. Yet the subsidies received from the different photosynthetic partners—glucose or sugar alcohols—are not metabolically interchangeable, suggesting different selection pressures. Here, we contrasted the different molecular subsidies using 216 lichen genera from newly generated lichen fungal genomes and data available at NCBI. Together with literature and genomic data, we assigned major photosynthetic partners to each lichen symbiosis and summarized them by the major subsidy-type molecule based on the literature. We used carbohydrate-active enzymatic machinery as a proxy for fungal metabolic ability to get carbon outside the symbiosis. Finally, we mapped the directionality of these transitions through the photosynthetic partners’ turn-over across all ascomycotan fungi. Subsidy-type molecules correlated with distinct enzymatic profiles of lichen fungi, suggesting that the underlying relationships involved in these lichen symbioses also differ.

PAR52-002: Virus-Host Interactions in Saccharomyces Yeasts
Primrose Boynton1, Rahul Unni2, Eva Stukvenbrook2, Onur Erik Kavlak3
1Wheaton College, Norton, MA, USA. 2University of Tübingen, Tübingen, Germany. 3University of Kiel, Kiel, Germany. 4Freie Universität Berlin, Berlin, Germany

Abstract
Fungal viruses can have a variety of impacts on hosts, including altering host fitness (positively or negatively) and establishing new host phenotypes. Saccharomyces killer viruses are among the best-studied fungal viruses: these viruses are most famous for coding secreted toxins that can kill nearby sensitive yeasts. However, killer toxins are only effective under very specific environmental conditions, raising questions about the roles of viruses and toxins in natural environments such as the forest floor. We are exploring interspecific and intraspecific mechanisms that maintain killer virus-Saccharomyces host interactions. We discovered that, in the absence of sensitive yeasts, removing forest Saccharomyces paradoxus viruses from hosts had a variety of fitness effects and that these effects depend on host/virus pairings and the environment. We are further exploring the potential for viruses to act as selfish genetic elements in their hosts and the effectiveness of killer toxins on competition in realistic natural environments. Our results will broadly inform the ecology and evolution of fungal-virus systems, especially systems that, like the Saccharomyces killer system, have diverse fitness effects.

PAR52-003: Life on a Tremella: Unexpected Genome Reduction in the Fungicolous Ascomycete Sporothrix Epigloea
Carmen Allen1, David Díaz-Escandón1, Sarah DeLong-Duhoń2, Gulnara Tagirdzhanova1, Alejandro Huereca3, Shauna Reckseidler-Zenteno4, Andrew Forbes2, Toby Spribille1
1University of Alberta, Edmonton, Canada. 2University of Iowa, Iowa City, USA. 3The Sainsbury Laboratory, Norwich, United Kingdom. 4Athabasca University, Athabasca, Canada

Abstract
Sporothrix epigloea is a ophiostomatoid fungus known to exclusively grow on the fruiting bodies of Tremella white jelly fungus (T. fuciformis or T. yokohamensis). First considered “setae” of a new pilose genus of jelly fungus (Nakaiomyces), the structures were later discovered to be perithecia of an ascomycete. Using a comparative genomics approach, we found that S. epigloea genomes were smaller than any other Sporothrix genome and reduced in carbohydrate-active enzymes (CAZymes), proteases, biosynthetic gene clusters, and sugar transporters. Notably, the suite of CAZyme families degrading both plant and fungal cell wall components was reduced in S. epigloea compared to its sampled non-fungicolous relatives. At the same time, 27 orthologue groups were acquired in S. epigloea, including a lytic polysaccharide monoxygenase (LPMO) with no previously established activity or substrate specificity. Phylogenetic analyses suggest that the LPMO was acquired in S. epigloea through HGT from Hypocreales. Our findings question the assumption that S. epigloea is a mycoparasite...
PAR53-001: GLOBAL MOVEMENT OF COFFEE LEAF RUST PATHOGEN (HEMILEIA VASTATRIX) POPULATIONS
Terry Torres Cruz, M Catherine Aime
Purdue University, West Lafayette, USA

Abstract

*Hemileia vastatrix* is the causal agent of the recurrent coffee leaf rust (CLR) epidemics that have affected all major coffee growing regions of the world. It most recently invaded Hawaii in late 2020 and was reported in Florida in late 2021. While *H. vastatrix* was likely accidentally introduced to Hawaii from Central America or the Caribbean islands, the source of its introduction to Florida remains unknown. Our objectives are to determine the origin of the CLR introduction to Florida, assess if these new invasions are all caused by one invasive *H. vastatrix* strain or if there are multiple genotypes involved, and analyze the overall historical movement of genotypes worldwide. Population structure of *H. vastatrix* will be determined via 12 simple sequence repeat (SSR) markers for a global set of nearly 600 *H. vastatrix* isolates collected from coffee plantations across most of CLR’s geographic range. This includes Central Africa, Southeast Asia, the Caribbean, and South and Central America between 2014 and 2023, along with key historical CLR samples dating from the 1800’s to 2004. We will use a minimum spanning network analysis to trace the most probable pathway of *H. vastatrix* introduction to Florida. Our study uses SSRs to explore global movement of *H. vastatrix* and analyze genotypic diversity of this rust. Increased understanding of CLR population genetics can provide important insights into its epidemiology and evolutionary potential.

PAR53-002: COMPARATIVE GENOMICS AND TRANSCRIPTOMICS OF THE SELECT AGENT
CONIOThYRIUM GLYCINES PROVIDE CLUES AS TO HOW IT IS ADAPTED TO CAUSE A DEVASTATING DISEASE OF SOYBEAN
Rachel Koch Bach1, Harun Murithi2,3, Steven Clough4,5
1USDA ARS, Foreign Disease-Weed Science Research Unit, Frederick, USA. 2ARS Research Participation Program through the Oak Ridge Institute for Science and Education, Oak Ridge, USA. 3International Institute of Tropical Agriculture, Nairobi, Kenya. 4USDA ARS, Soybean/Maize Germplasm, Pathology, and Genetics Research Unit, Urbana, USA. 5University of Illinois, Department of Crop Sciences, Urbana, USA

Abstract

Soybean red leaf blotch is a devastating fungal disease that can cause up to 70% yield loss. The causal agent is the ascomycete *Coniothyrium glycines* and is thus far known only from the African continent. The value of soybean in the United States, combined with the potential destructiveness of *C. glycines*, make it a pathogen of potentially high consequence and is one of two fungal species listed as a Select Agent by the USDA Animal Plant Health Inspection Service (APHIS) in the Agricultural Bioterrorism Protection Act. Although *C. glycines* is a very important plant pathogen, little is known regarding its biology, how it infects its host, or how it evolved to cause disease in soybean. To gain a
preliminary understanding of how this species adapted to cause a devastating disease of soybean, we sequenced the genomes of 24 recently collected *C. glycines* isolates from numerous African countries along with six phylogenetically related species. We also compared transcriptomes of multiple isolates at different growth stages. Herein, we will discuss insights gleaned from the comparative genomics and transcriptomics studies, including gene families that may be important in the adaptation of *C. glycines*, as well as the putative role that secondary metabolites might play in the biology of this species.

**PARS3-003: OUTCOMES OF COMPETITIVE DYNAMICS OF FUSARIUM GRAMINEARUM AND F. POAE ON WHEAT HEADS**

Imane Laraba, Briana K. Whitaker, Susan P. McCormick, Christina Cowger, Peter Oppenheimer, Martha M. Vaughan

1Agriculture and Agri-Food Canada, Ottawa, Canada. 2USDA-ARS National Center for Agricultural Utilization Research, Mycotoxin Prevention and Applied Microbiology Unit, Peoria, USA. 3North Carolina State University; USDA-ARS, Plant Science Research Unit, Raleigh, USA. 4North Carolina State University, Raleigh, USA

**Abstract**

Although *Fusarium graminearum* (Fg) is the pathogen responsible for most Fusarium head blight (FHB) outbreaks on wheat in North America, several other weaker pathogens (e.g., *F. poae* [Fp]) co-exist within the same head or field in certain agroclimatic settings. The implications of the competitive dynamics between Fg and Fp within the same head for FHB development and mycotoxin contamination remain poorly understood. Here, we evaluated whether pre-inoculation with Fp two days prior to Fg or co-inoculation of the two pathogens would impact Fg disease outcomes. We hypothesized that disease outcomes would be dependent on 1) the Fg population/chemotype (NA1/15-ADON and NA2/3-ADON), 2) the wheat variety (Alslen and Norm), and 3) wheat immune responses. Our preliminary results indicate pre- and co-inoculation of Fp with both NA1 and NA2 Fg strains resulted in significantly greater disease severity and deoxynivalenol (DON) toxin accumulation on cultivar Alslen heads compared to treatments of Fg alone. Similarly, on cultivar Norm heads, pre- and co-inoculation of Fp with the NA2 Fg strain caused higher FHB severity and DON contamination relative to NA2 Fg reference inoculation. For the NA1 strain treatments, no consistent statistically significant difference was noted in disease development and DON accumulation between pre- or co-inoculated heads as compared to the reference treatments of Fg strain inoculated alone. Analyses assessing the level of the plant defense phytohormones salicylic and jasmonic acids and expression patterns of their biosynthetic genes are underway to gain insight into the mechanisms underlying the observed disease outcome differences.

**PAR53-005: DESIGN AND OPTIMIZATION OF A QP-CR-BASED ASSAY FOR THE SPECIES-SPECIFIC IDENTIFICATION OF CALICIOPSIS PINEA**

Rebecca Harkness, Timothy Miles
Michigan State University, East Lansing, USA

**Abstract**

*Caliciopsis pinea* is the causal agent of Caliciopsis Canker Disease (CCD on *Pinus strobus*). qPCR-based markers exist for *C. pinea* detection from fungal and infected plant tissue that are now known to be cross-reactive with a closely related species of *Caliciopsis*. Since molecular identification tools are limited, current diagnostic methods rely on observations of symptoms and subsequent visual identification of fungal ascomata on the host. However, disease may be present with no visible signs of the pathogen. Therefore, this study aims to develop a species-specific qPCR-based detection assay for *C. pinea* from fungal and infected plant tissue. Previous phylogenetic investigations identified the internal transcribed spacer (ITS) region as an informative region at the species level, and was selected as the target for assay development. Isolates were tested for intra- and interspecific variation in detection (n = 63), comprising 9 species of *Caliciopsis* among other prominent pine pathogens. *C. pinea* was discriminated at the species level and the limit of detection was determined to be 10fg of target DNA. The assay was also tested on air samples collected with a rotating arm sampler as well as infected plant material. The reaction could detect *C. pinea* spores in the background of DNA from other aerial particulate, and was also able to detect the pathogen from infected plant material. This assay will be useful in diagnostic and epidemiological studies for detection and monitoring of *C. pinea*.
of VOCs was shaped by plant variety, with suppressed VOCs under AMF colonization and herbivory. AMF colonization improved plant biomass. Our results indicate that mycorrhization, herbivory, and plant variety can alter emissions of tomato VOCs and further shape volatile-mediated plant-insect interactions. More understanding of these mechanisms could help identify novel and sustainable approaches to pest management.

PAR61-002: BACTERIA AND FUNGI ARE DIFFERENTIALLY AFFECTED BY FUNGAL NECROMASS CHEMISTRY BUT SHARE SIMILAR FUNCTIONAL GROWTH CAPACITIES

Achala Narayanan1, François Maillard2, Briana Beatty3, Jessie Novak3, Jeffrey Gardner3, Jonathan Schilling3, Jennifer Pett-Ridge3, Peter Kennedy3

1University of Minnesota, St Paul, USA. 2Lund University, Lund, Sweden. 3University of Maryland, Baltimore County, Baltimore, USA. 4Lawrence Livermore National Laboratory, Livermore, USA

Abstract

Dead microbial biomass (i.e. necromass) represents ~1/3 of organic carbon (C) in forests and contributes to long-term soil C storage. Necromass is consistently inhabited by a microbial community (i.e. the necrobiome) that consumes, decomposes, and recycles necromass C. There is growing interest in how necromass decomposition capacity is partitioned across microbial domains, and whether resource use predicts necrobiome assembly. In this study, we characterized the growth profiles of soil and necrobiome bacteria and fungi. We grew 60 bacterial and 60 fungal strains isolated from both Hyaloscypha bicolor necromass and surrounding soil on 24 C substrates. Substrates included four H. bicolor necromass types with varied chemistry, fungal cell wall polymers and simple sugars. Growth on each substrate was evaluated after 5 days using the WST-8 stain (fungi) or by OD (bacteria). We hypothesized that fungi and bacteria would be specialized to grow on distinct substrates, with fungi preferentially growing on whole necromass and polymers, and bacteria more limited to growth on simple sugars. Contrary to our expectations, we found that bacterial and fungal isolates had largely overlapping substrate use patterns. While both microbial groups were able to grow on necromass, our results suggest that fungal growth was more limited by necromass melanin content and bacterial growth by necromass C:N. Further, neither phylogeny nor isolation habitat strongly predicted substrate use. Collectively, these results suggest that necromass microbial community assembly is not strongly shaped by substrate niche partitioning, and that other ecological factors, such as bacterial-fungal interactions, may be better predictors of necrobiome composition.

PAR61-003: DIVERSITY OF TREMELLALEAN PERTUSARIA-ASSOCIATED FUNGI IN NORWAY AND THE ROLE OF SECONDARY METABOLITES IN HOST-SPECIFICITY

Mika Kirkhus1,2, Andreas Frisch1,3, Ann Evankow1,3, Rakel Blaalid1, Raffaele Zane1, Mika Bendiksby3, Marie Davey5

1Norwegian University of Science and Technology, Trondheim, Norway. 2University of Bergen, Bergen, Norway. 3Natural History Museum University of Oslo, Oslo, Norway. 4Nord University, Steinkjer, Norway. 5Norwegian Institute for Nature Research, Trondheim, Norway

Abstract

The basidiomycete genus Tremella includes a number of species parasitic on lichens whose sexual stages form conspicuous galls on lichen thalli, but whose asexual yeast stage can persist asymptomatically on their hosts. We used ITS2 metabarcoding of fungarium specimens to investigate tremellalean fungi associated with asymptomatic lichen thalli from 13 Pertusaria species occurring in Norway. All hosts were chemotyped using thin layer chromatography to identify secondary metabolites, and negative-binomial general linear models were used to analyse infection success by the Tremella axa. Twelve of the 13 host species and almost three quarters of the specimens analysed hosted tremellalean fungi, including Pertusaria species not previously reported as hosts of these fungi. Despite an apparent lack of one-to-one host specificity, occurrences of the five most frequent OTUs in the dataset were nonetheless non-random across the 13 host species investigated, suggesting these OTUs are not universally capable of infecting all Pertusaria species. We found a strong correlation between reductions in tremellalean infection rates and Pertusaria containing the secondary metabolites thiophaninic acid, fumarprotocetraric acid, and/or gyrophoric acid. Our experiments led to the conclusion that asymptomatic Tremella infections are much more common and genetically diverse within Pertusaria than originally thought. We further demonstrate that the haploid yeast phases of Tremella are able to colonize a wide variety of hosts, where host phenotype likely influences infection success.

PAR61-004: UNVEILING VIRULENCE FACTORS IN ARmillaria SPECIES

Pratima Devkota, Raymond Hammerschmidt

Michigan State University, East Lansing, USA

Abstract

Armillaria solidipes is known to cause Armillaria root rot (ARR) in various woody tree species, posing challenges for effective management strategies due to a lack of understanding of its pathogenesis and virulence. In this study, we investigated the role of Cell Wall Degrading Enzymes (CWDEs) and toxins in A. solidipes pathogenesis. Culture filtrates from two A. solidipes isolates were analyzed, revealing the production of pectinases and ligninolytic enzymes. Pectinases exhibited higher activity initially compared to ligninolytic enzymes. Furthermore, a root and foliage dip treatment assay conducted on Prunus spp. leaf and root tissue showed necrosis in susceptible species, suggesting the presence of toxic compounds in the filtrates. These findings indicate that CWDEs and toxins likely contribute to A. solidipes pathogenesis, highlighting their potential importance in ARR management strategies.
PAR61-005: REPERTOIRS OF SECONDARY METABOLITE BIOSYNTHETIC GENE CLUSTERS IN INSECT AND NEMATODE PARASITIC FUNGI
Kathryn Bushley1, David Showalter2, Rodrigo Olarte3, Stephen Rehner4
1USDA-ARS, Ithaca, USA. 2Oregon Department of Forestry, Salem, USA. 3University of Minnesota, St. Paul, USA. 4USDA-ARS, Beltsville, USA

Abstract
Fungi have diverse host-associations and ecologies, including as pathogens of invertebrates such as insects, nematodes, and mites. Many of these fungi also known colonize plants as endophytes and provide protection against invertebrate pests either via direct parasitism or secretion of bioactive metabolites. Fungal parasites of invertebrates harbor a highly diverse repertoires of secondary metabolite biosynthetic gene clusters (SMBCs), as well as genes involved in degradation of carbohydrates (CAZymes) or protein (proteases) resources of distinct invertebrate hosts. Yet, the evolutionary processes that giving rise to or maintain the diversity of SMBCs, as well as their chemical products and potential functions for these fungi remain largely unknown. We explore broad-scale evolutionary processes leading to diversification of SMBCs, as well as CAZyme and protease gene content, among insect and nematode pathogens in the order Hypocreales. We focus on entomopathogenic fungi in the genus Beauveria and host-shifts between nematode and insect parasites in the genus Hirsutella. Our results shed light on how distinct repertoires of SMBCs, CAZymes, and proteases within the genomes of these fungi may shape the interaction of these fungi with distinct insect, nematode, or plant hosts during their life cycle. We highlight the potential role of transposable elements and repeat content in driving diversification of these gene families.

PAR61-006: LOSS OF 1-8DHN MELANIN IN EXOPHIALA DERMATITIDIS AND ITS EFFECT ON CELL MORPHOLOGY AND STRESS
Kamaldeep Chhoker1, Steven Harris2
1University of Manitoba, Winnipeg, Canada. 2Iowa State University, Iowa, USA

Abstract
Exophiala dermatitidis is a polymorphic black yeast found in various habitats such as soil, on exposed rock surfaces and man-made environments including sinks, and saunas. E. dermatitidis is also an opportunistic pathogen of humans where it can cause phaeohyphomycosis and skin infections. 1-8DHN melanin found in E. dermatitidis has been shown to provide various functions such as protecting against cell lysis, converting visible UV energy into heat and also being responsible for infections. The E. dermatitidis genome sequence has revealed the presence of genes responsible for production of melanin via three different pathways but not much is known about the coordinated regulation of these pathways. This study aims to examine how the absence of melanin affects growth, colony morphology, and stress response in E. dermatitidis. Albino mutants lacking the ability to produce melanin were obtained using UV irradiation. Based on genome re-sequencing and SNP analysis, all the albino mutants showed variants in the PKS1 gene including mutations ranging from missense base substitutions to frameshifts and short deletions. When grown on different media types and with various carbon sources, some albino mutants were able to recover melanin production whereas other albino mutants were able to accumulate carotenoids (pink color). Ultimately, comparative transcriptomics will be used as a tool to investigate regulatory differences between mutants that could conceivably account for variation in pigmentation phenotypes. This study also leverages the availability of albino mutants to characterize the types of carotenoids produced by E. dermatitidis and the factors that regulate their synthesis.

PAR62-001: FUNGAL DIVERSITY AND FUNCTION IN METAGENOMES SEQUENCED FROM EXTREME ENVIRONMENTS
Alisha Quandt1, Cliff Bueno de Mesquita2, Lara Vimercati1
1University of Colorado, Boulder, USA. 2Joint Genomes Institute, Berkeley, USA

Abstract
Fungi are increasingly recognized as key players in various extreme environments. Here we present an analysis of publicly-sourced metagenomes from global extreme environments, focusing on fungal taxonomy and function. The majority of 855 selected metagenomes contained scaffolds assigned to fungi. Relative abundance of fungi was as high as 10% of protein-coding genes with taxonomic annotation, with up to 289 fungal genera per sample. Despite taxonomic clustering by environment, fungal communities were more dissimilar than archaeal and bacterial communities, both for within- and between-environment comparisons. Abundant fungal classes in extreme environments included Dothideomycetes, Eurotiomycetes, Leotiomycetes, Pezizomycetes, Saccharomycetes, and Sordariomycetes. Broad generalists were the most abundant fungal genera in most of the extreme environments, while several specialist zoosporic taxa were common in cryosphere water and hot springs. Abundances of genes involved in adaptation to general, thermal, oxidative, and osmotic stress were greatest in soda lake, acid mine drainage, and cryosphere water samples.

PAR62-002: ASSESSMENT OF FUNGAL DIVERSITY IN THE POWDER RIVER BASIN COAL BED USING A SUBSURFACE BIO-SAMPLER
Quinn Moon1, Michelle Orozco-Quime1, Elliott Barnhart2, Jason Stajich3, Timothy James1
1University of Michigan, Ann Arbor, USA. 2USGS, Helena, USA. 3University of California, Riverside, Riverside, USA

Abstract
The deep terrestrial crust contains persistent microbial ecosystems, however, the ecology and diversity of fungi inhabiting deep biospheres is poorly understood. Further, there is a lack of empirical studies that investigate in situ fungal anaerobic degradation of subterranean carbon
deposits, including biogenic conversion of coal into methane. In this study, we employed a novel Bio-sampler approach to assess the total diversity and culturable diversity of fungi native to a coal bed ecosystem in the Powder River Basin- a location of active microbial degradation of coal deposits. Using a Bio-sampler, sterilized coal was placed into a 150 m deep well for ~6 months, allowing for fungal colonization of the submerged coal fragment. Several fungi have been isolated from the enriched sample, including Penicillium cf. ortum, a known biodegrader of coal and genome sequencing is being used to identify metabolic potentials related to subsurface life. We plan to further validate the Bio-sampler methodology as a viable approach to determining fungal community composition in low fungal biomass aquatic ecosystems. Ultimately, we aim to determine the fungal diversity of a terrestrial crust ecosystem and highlight its potential implications for biogenic degradation of subsurface carbon deposits.

PAR62-003: ELUCIDATING THE IMPACT OF EARLY COLONIZERS ON FUNGAL COMMUNITY DYNAMICS OF ROCK FACES THROUGH AN INNOVATIVE NGS PROTOCOL Daniel B. Raudabaugh, M. Catherine Aime Purdue, Department of Botany and Plant Pathology, Lafayette, USA

Abstract
Researchers utilize high throughput sequencing technology to analyze microbiome community composition and structure. However, the short sequence reads generated by this method often lead to a high percentage of unclassified sequences, hindering species identification. To address this, a new protocol was designed to increase sequence length, reduce unclassified sequences, and enhance taxonomic determination confidence. The protocol was tested by examining the mycobiome of rock face colonizers, including lichens, mosses, and rock ferns, hypothesizing that community composition is influenced to a greater extent by early colonizers than environmental factors. Moss, lichen, and rock fern samples were collected from two adjacent rock faces in West Virginia, differentiated by colonization maturity. DNA was extracted, PCR performed, and sequencing conducted using Illumina MiSeq. Data processing involved DADA2 and Decipher for OTU clustering and taxonomy assignment against the NCBI database. Results identified 2986 OTUs, with 1071 fungi, including dominant species like Chytridiomycota spp. Taphrina spp., and Mortierella sp. Statistical analysis revealed significant correlations between fungal presence and colonization age, host/tissue type, and a combination of both factors. Notably, the new protocol reduced unclassified sequences by 50%, with only 20 sequences remaining unclassified at the phylum level, indicating its effectiveness. This protocol provides a valuable tool for studying fungal microorganisms, promising further exploration of unique fungal genera in similar environments.

PAR62-004: PREDICTING FUNGAL COMMUNITY FUNCTIONAL POTENTIAL FROM ITS RRNA SEQUENCING Kathryn Atherton, Zoey Werbin, Daniel Segrè, Jennifer Bhatnagar Boston University, Boston, USA

Abstract
The most common method to characterize fungal communities is to sequence the ITS rRNA genes. While these methods can tell us the taxonomic composition of a community, they do not directly tell us about the functional profile of the community. Metagenomic or metatranscriptomic datasets can provide this functional information but can be more than double the cost of amplicon sequencing. Phylogenetic Investigation of Communities by Reconstruction of Unobserved States (PICRUSt2) was developed to predict prokaryotic metagenomic contents from 16S rRNA sequences, but a comparable tool for fungal communities has not yet been created due to a lack of high-quality, annotated genomes representing fungal phylogeny. Leveraging the Joint Genome Institute’s rapidly expanding MycoCosm database of fungal genomes, we have produced a tool to infer functional profiles of fungal communities from ITS rRNA sequences. Validation of the results of this tool against metatranscriptomic sequencing and functional data will highlight knowledge gaps in gene annotation and transcription. This tool will allow for the assessment of gene-based fungal community functional profiles with amplicon sequencing, improving whole microbial community functional characterizations when used in combination with PICRUSt2’s bacterial methods.

PAR62-005: A TARGET ENRICHMENT APPROACH FOR ENHANCED RECOVERY OF SYNCHYTRIUM ENDOBIOTICUM NUCLEAR GENOME SEQUENCES Hai Nguyen1, Ekaterina Ponomareva1, Kasia Dadej1, Donna Smith2, Melissa Antoun2, Theo van der Lee3, Bart van de Vossenberg4 1Agriculture and Agri-Food Canada, Ottawa, Canada. 2Canadian Food Inspection Agency, Charloettetown, Canada. 3Wageningen University and Research, Wageningen, Netherlands. 4Dutch National Plant Protection Organization, Wageningen, Netherlands

Abstract
Synchytriunm endobioticum is a chytrid (Chytridiomycota) that causes potato wart disease. Because of its obligate nature, DNA extraction from samples usually results in low S. endobioticum DNA concentration and/or highly contaminated with DNA coming from other microorganisms and the potato host, which leads to sub-optimal recovery of its nuclear genome during Illumina sequencing. In this study, we developed a hybridization-based target enrichment protocol, using specifically designed 180,000 molecular baits, to enhance S. endobioticum DNA recovery while off-target organisms DNA remains uncaptured. Compared to non-enriched samples, target enriched samples showed an increase in sequenced bases mapped to the S. endobioticum nuclear genome, as well as, yielded sequencing data with higher nuclear genome coverage and better genome assemblies with more S. endobioticum genes detected. Our approach provides a valuable tool for enhancing genome sequencing and NGS-based molecular detection & characterization of S. endobioticum.
PAR62-006: CHYTRID AND THRAUSTOCHYTRID BIODIVERSITY ACROSS WATERSHEDS IN MAINE: INSIGHTS FROM A THREE-YEAR MULTI-METHOD SURVEY
Peter Avis, Jessica Hayden, Etain Cullen, Erin Grey, Joyce Longcore
University of Maine, Orono, USA

Abstract
Chytrids and thraustochytrids are important in aquatic ecosystems, playing essential ecological roles as parasites and decomposers. Their distribution, taxonomy, and ecological functions are poorly understood, however. To better understand the biodiversity of these fungi in Maine, we integrated eDNA metabarcoding with traditional baited culturing surveys across four freshwater to marine watersheds. To date, we have isolated over 100 organisms mostly represented by chytrids isolated from freshwater samples whereas thraustochytrids dominated the marine samples. From 18S metabarcoding, we found 535 chytrid ASVs spanning many major chytrid lineages. In contrast we found only 81 thraustochytrid ASVs which may be explained by the greater number of freshwater samples analyzed to date. In the current dataset, we only found four “matches” -- where the culture sequences are the same (or very nearly the same) as eDNA sequences (i.e. ASVs). This indicates that eDNA metabarcoding can greatly expand the documented biodiversity of these fungi. We will discuss large-scale biodiversity patterns over time and space that emerged from this study, as well as the benefits and limitations of both survey methods. Overall, we found that merging traditional and eDNA methods is crucial for understanding the biodiversity of these important fungi.

PARALLEL SESSION 6-3:
SPECIAL SESSION - DIVERSITY, EQUITY, AND INCLUSION IN MSA

Abstract
Diversity, Equity, and Inclusion are cornerstones in our society. This year, the DEI committee will present the results from the efforts in DEI across the society, as well as providing insights into the recent surveys across the society members. In addition, the DEI committee will present a keynote talk on SPORES, the society’s program to invite and integrate undergraduate students interested in Mycology in our Society. Finally, we invite members of the society into a conservatory in the hidden elements of diversity, to discuss invisible disabilities and how we, as a society, can become more inclusive.

Sessions:
1. Advances on Diversity, Equity, and Inclusion within our society (10 minutes) - Dr. Fabiola Pulido (UC Irvine) and Dr. Javier Tabima Restrepo (Clark University)
2. The SPORES program and its benefits in MSA (25 minutes) - Dr. Terry Torres Cruz (Purdue University)
3. Hidden disabilities in MSA, a conservatory (25 mins) - Panelist TBD
POS01-001: BIOMATERIALS AND APPLICATIONS IN SUBARCTIC FOOD SYSTEMS
Meg Waite
University of Alaska Fairbanks, Fairbanks, USA

Abstract
Rural arctic and subarctic regions of Alaska currently lack adequate infrastructure for local waste management and recycling. As a result, plastics easily end up in landfills as well as contaminating local food networks. While there is a need to increase local agriculture in Alaska, many residents enjoy subsistence methods of harvesting and hunting. Plastics and synthetic materials impact soil, water, animal, and human health by getting into these vital ecosystems. Biomaterial containers as replacements to plastics used in food systems are a potential solution. The project demonstrated testing a locally harvested fungi, a red-belted conk, or Fomitopsis pinicola, and recording observed physiological properties for materials making, as well as regrowth of its mycelium or root systems. From this research project, biomaterials may be created and tested using sustainably sourced plant matter, fungal mycelium, and nutrients found naturally in the local environment. The polypore was harvested on University of Alaska Fairbanks’ Troth Yeddha’ campus. Exploratory student-led research was conducted to compare hyphal density of this species mycelium to other species, some known to Alaska and found elsewhere. Cold water flash immersion was performed in a lab to determine if mycelial regrowth was possible with this species, and this experiment produced some positive observations. More research is needed to understand the different property elements of lignocellulosic “white rot” and cellulolytic “brown rot” fungi, such as Fomitopsis pinicola, as well as testing soil with any mycelium seedling trays or planter pots and understanding any effects on soil decomposition.

POS01-002: TOWARDS MYCOREMEDIATION: FUNGAL DECOMPOSITION AND ASSIMILATION OF METAL-OXALATE COMPOUNDS AS A SOLE ENERGY SOURCE
Viviana Gaytan, Sophia Lee, Nhu Nguyen
University of Hawai’i at Manoa, Honolulu, USA

Abstract
Fungi face harsh environmental conditions that threaten their survival, and thus they have developed mechanisms to resist these conditions. Challenging environmental conditions are opportunities for innovation. For example, unique mechanisms, such as resistance strategies often arise when microbes are in a heavy metal contaminated environment. Fungi have developed strategies to not only break down certain organic-metal molecules, such as metal-oxalates, but can also use them as sole carbon sources. We tested this capability on a suite of soil fungi and identified the genes associated with this process. We found that many fungal species are resistant to high concentrations of manganese, and rather than inhibiting their growth it would seem to assist it. Our experiments suggest that the mechanism for tolerance is associated with their capability to decompose manganese oxalate, along with calcium oxalate, a common molecule in soil. These fungi were able to use these metal-oxalates as a sole carbon source. Their ability to decompose these compounds is dependent on the OxDD gene that we have sequenced and characterized for these fungi. We anticipate that our study will contribute to future bioremediation efforts, especially in soils where manganese levels can be toxic to plants.

POS01-003: VALORIZATION OF TEXTILE WASTE VIA FUNGAL BIOTECHNOLOGY: INNOVATIVE STRATEGIES FOR PADDED MATERIAL RECYCLING
Catherine Bélanger, Félix-Antoine Bérubé-Simard, Marilee Thiffault, Audrey Gaudreau
Biopterre, La Pocatière, Canada

Abstract
The challenge of managing non-compact padded materials, such as mattresses and upholstered furniture, is significant, with their disposal and storage presenting considerable hurdles. While the recycling of components like wood and metals is straightforward, the textile fibers embedded within these items (mixes of synthetic polyester and natural cotton) pose substantial difficulties. Biopterre’s research project aims to develop two innovative valorization techniques for these textiles, employing both terrestrial and marine fungi renowned for their adeptness at decomposing a variety of materials and environmental pollutants, alongside their capability to foster the creation of sustainable products. The project’s first method of valorization harnesses submerged fermentation, utilizing fungi’s fiber-decomposition abilities to potentially reincorporate textiles back into the production cycle. This approach not only presents an eco-friendly avenue for managing hard-to-recycle textiles but also holds the promise of mitigating the environmental ramifications of such waste accumulation. Furthermore, the project delves into the development of mycomaterials—composite materials crafted by integrating textiles with fungi growth on substrates, aimed at producing value-added items like thermal insulation and acoustic panels. These mycomaterials promise not just a reduction in waste but also a sustainable and eco-conscious alternative to the traditional materials currently prevalent in construction and industry. Ultimately, this research seeks to devise groundbreaking valorization strategies for textiles from bulky padded materials by leveraging the transformative potential of fungi. This initiative is poised to make a substantial impact on waste reduction, environmental conservation, and the enrichment of biotechnological knowledge in managing synthetic textiles, thereby aligning with broader sustainability goals.

POS01-004: BIODIVERSITY AND GROWTH OF FUNGI ON MARINE PLASTICS FROM NOVA SCOTIA
Arwen Estrada Pérez, Sarah J. Adams, Allison K. Walker
Acadia University, Wolfville, Canada

Abstract
An estimated 1.8 million pieces of garbage including plastics are found on the seafloor of the Bay of Fundy, Canada. This can have a negative effect on marine ecosystem health. Recent studies have suggested the use of fungi as plastic biodegradation agents. Field collections were made at three Nova Scotia beaches: Kingsport, Houston’s Beach, and Scots Bay. Fungal
culturing from marine plastics was performed, as was ITS rDNA barcoding for identification. We then tested four fungi isolated from marine plastics (Cladosporium cladosporioides, Alternaria alternata, Pleospora herbarum, and Trichoderma hamatum) for their capacity to biodegrade PP (polypropylene) and LDPE (low density polyethylene), the two most common plastics in the North Atlantic Ocean. Four growth conditions were tested in 90 day plastic degradation trials: salt water agar, artificial salt water, artificial salt water in shaker flasks, and empty Petri plates. Plastic biodegradation was assessed using SEM analysis. Preliminary results indicate higher colonization of plastic by all four fungi in artificial salt water in shaker flasks, highlighting the roles of aeration and mechanical degradation. Our study provides new insights as to how to best use marine-derived fungi as biodegradation agents targeted towards marine plastics.

POS01-005: DOMESTICATING A WILD EDIBLE AGARIC: MACROCYBE GIGANTEA (MASSEE) PEGLER & LODGE
Gagan Brar, Munruchi Kaur
Department of Botany, Punjabi University, Patiala, India

Abstract
Macrocybe gigantea was collected growing in large caespitose clusters from wild. This being a potentially edible taxa, in the present study an attempt has been made to explore the conditions that support its cultivation under controlled laboratory conditions. With an aim to domesticate it, various solid and liquid media were evaluated of which Malt Extract Agar (MEA) and Glucose Peptone Medium (GPM) were chosen as best solid and liquid media respectively, vegetative growth was found to be best at temperature 30ºC and pH 5.0 with an incubation period of 23 days and the mycelial growth was comparatively faster under dark exposure. Different easily available grains in market such as Wheat, Jowar, Bajra and Maize grains were tried for spawn preparation, wheat grains boiled for 30 minutes gave the best vegetative growth and was taken up for the mother spawn preparation. For fruit body production, different locally available agrowastes such as wheat straw, paddy straw and rice husk were taken up in combinations. Among the different agrowastes tried, paddy straw gave maximum biological efficiency. Huge flushes of the mushroom came up in the paddy straw bags in comparison to the wheat straw and combination of wheat and paddy straw. Thus, a proper protocol for the cultivation of this wild agaric has been successfully completed.

POS01-006: PRESENCE OF MYXOMYCETES IN A SOUTHERN BOTTOMLAND HARDWOOD SWAMP IN SOUTH CAROLINA
Brogin Van Skoik
Morris College, Sumter, USA

Abstract
The presence of Myxomycetes in Southern Bottomland Hardwood Swamps is understudied and not well known. Several substrates were sampled to search for the presence of myxomycetes in a Southern Bottomland Hardwood Swamp. Tree bark, Bryophyte (mosses and liverworts) mats found on trees, and leaf litter found in the water were collected from Sparkleberry Swamp located in the midlands of South Carolina. The presence of six species of myxomycetes was determined with collections of substrates incubated using the moist chamber culture method. Twenty-one of the fifty cultures (42%) collected from tree bark/Bryophytes had the presence of fruiting bodies or plasmodium of myxomycetes. Four of the 15 cultures (26%) collected from leaf litter in the water had the presence of fruiting bodies or plasmodium of myxomycetes. This data provides evidence for the presence of myxomycetes in Southern Bottomland Hardwood Swamps, but species richness and abundance are yet to be determined.
POS01-008: POTENTIAL DISTRIBUTION OF THELEPHORA RENISPORA NOM. PROV. (THELEPHORACEAE), A NEW CRYPTIC SPECIES OF ECTOMYCORRHIZAL FUNGI
Mariana Avila-Muñoz1, Julieta Alvarez-Manjarrez1, Oscar Zarate-Martinez4, Ezequiel Alberto Cruz-Campuzano4,5
1Laboratorio de Micología Integral, Instituto de Biología, Universidad Nacional Autónoma de México, Mexico City, Mexico. 2Department of Botany, University of Tartu, Tartu, Estonia. 32Posgrado en Ciencias Biológicas, Universidad Nacional Autónoma de México, Mexico City, Mexico

Abstract
Introduction: One way to quantify the ecological niche or chorology of a species is through species distribution modeling (SDM). In our study, we estimate the potential distribution of a new ectomycorrhizal species, Thelephora renispora nom. prov. This species is putatively associated with Polygonaceae and Nyctaginaceae and inhabits tropical dry forests in Mexico. We aim to contribute with knowledge towards conservation of this species and the forests where it develops.

Methods: Sporomes sampling was made in June and September 2023 in the state of Chiapas, Mexico. Additionally, herbarium specimens with resupinate-clavarioid morphology were retrieved from XAL (INECOL), ENCB (IPN) and FLAS (UF) herbaria. Specimens were identified using the ITS region. Using bioclimatic, topographic, edaphological and lithological information (obtained from CHIELSA Bioclim, SoilGrids and INEGI) we quantified the potential niche of the species. Principal component analysis was applied to summarize and identify the environmental space where the species distributes.

Results and Discussion: From a PCA we identified two components that together explain 70.1% of the variance: the first one explains 37.5% of the variance and is related to air temperature, while the second component explains 32.6% and is composed of precipitation variables. This suggests that T. renispora has a preference for warm and humid climates.

Conclusions: The most significant environmental variables for the occurrence of T. renispora are situated within air temperature and precipitation components. These results contribute to the ecological knowledge of ectomycorrhizal fungi in tropical ecosystems, which could influence conservation measures of these fungi in the future.

POS01-009: FIRST DOCUMENTATION OF TRICHOMYCETES FUNGI IN THE GREATER TORONTO AREA: INSIGHTS INTO ENVIRONMENTAL FACTORS AND INSECT HOST VARIATIONS
Sümhithaa Srima1, Maija Lehn1, Yan Wang1,2
1University of Toronto, Scarborough, Canada. 2University of Toronto, Toronto, Canada

Abstract
Trichomycetes are obligate gut symbionts of aquatic insect larvae and nymphs and they are commonly found in freshwater ecosystems, including lakes and rivers. Extensive research has been conducted on their occurrence in insect larvae all over the world, but little is known from the Greater Toronto Area. It is also unclear if the fungal distribution has been affected by abiotic environmental variables, such as TDS (Total Dissolved Solids), pH and temperature, and biotic variables such as insect host prevalence. To address this research gap, we conducted a local survey to explore potential relationships between environmental variables and the diversity and distribution of Trichomycetes fungi in the Greater Toronto Area. This comparative study primarily focuses on watersheds in the well-preserved Rouge National Urban Park (RNUP) and the anthropogenic Highland Creek region (HLC) which predominantly passes through a residential area. A total of 27 sites were visited, which varied in their landscapes or vegetation. Aquatic insect samples were collected from these sites along with measurements of the environmental variables. A variety of fungal species, including Smittium culicis, Ejectosporus sp., Stachyliina lenticia, and Stachyliina thauamaleidurum were identified and reported for the first time from the GTA watersheds. A canonical correspondence analysis (CCA) suggests that in RNUP and HLC, the variance of aquatic insects was related to changes in pH, while the prevalence of Trichomycetes species was related to all three environmental variables (pH, TDS, and Temperature). More details of the ongoing research, including network analyses between insect hosts and Trichomycetes, will also be presented.

POS01-010: THE ROLE OF MICROBIAL INOCULATION ON POST-FIRE MICROBIAL COMMUNITY RESILIENCE AND ECOSYSTEM RECOVERY
Taylor Bright1,2, Mia Maltz3, Esbeiry Cordova-Ortiz4, Brendan O’Brien5, Maya Elson5, Janel Luke6, Jennifer Van Gelder1, Alisa Wilson1, Vanessa Robertson-Rojas1, Chelsea Carey5, Sydney Glassman6
1CoRenewal, Cathedral City, USA. 2Fungal Diversity Survey, Sebastopol, USA. 3University of Connecticut, Storrs, USA. 4UC Riverside, Riverside, USA. 5UC Santa Cruz, Santa Cruz, USA. 6Camp Fire Restoration, Paradise, USA.
7The Understory Initiative, Medford, USA. 8Point Blue Conservation Science, Petaluma, USA

Abstract
The West Coast of the United States has witnessed an alarming increase in the frequency of wildfires, primarily attributed to global change-induced factors such as heightened drought, fire-suppression, logging, and invasive species. These wildfires not only pose immediate threats, but also have far-reaching consequences on the carbon storage capacity of ecosystems. A significant portion of California’s catastrophic wildfires have occurred since 2015, raising critical questions about the potential for system recovery and the feasibility of mitigation efforts. An avenue for addressing these challenges is post-fire microbial inoculation, such as introducing microorganisms from unburned sites into fire-affected soils. This may enhance carbon sequestration or ameliorate impacts of wildfires on human communities and ecosystems. We investigated the effects of microbial inoculation on the resilience of post-fire microbial communities and the overall recovery of ecosystems in coniferous forests from California to Oregon, as well as California grassland and coastal sage scrub ecosystems, which enabled us to examine the intricate dynamics of microbial establishment and community composition. Soil chemistry, heavy metals, and plant and microbial communities were analyzed to assess the influence of inoculation methods on post-fire microbial community dynamics. Microbial communities varied over time since fire, which may correspond to soil nutrient dynamics over time since wildfire occurred. These findings shed light on the role of microbial inoculation...
in promoting ecosystem recovery and the resilience of microbial communities following fire events. Findings from this study contribute to our understanding of post-fire ecological processes and provide insight for ecosystem management strategies aimed at restoring fire-affected landscapes.

POS01-011: WHAT HAPPENS WITH BACTERIA IN THE ROOTS AFFECTS WHAT HAPPENS WITH FUNGI IN THE LEAVES
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Universidad de Costa Rica, San Pedro, Costa Rica

Abstract
The impact of plant-bacteria symbioses in roots on plant-fungal interactions in distant tissues, such as leaves, remains a significant knowledge gap, particularly for tropical legume trees. We analyzed the ITS sequences of fungal endophytes in eight tropical Fabaceae tree species, varying in their nodulation capacities and subfamily affiliation, to investigate the relationship between root nodulation and the endophytic community composition. We determined that nitrogen-fixing bacteria in root nodules significantly shaped fungal endophytes, while subfamily affiliation had a less pronounced effect. Notably, non-nodulating plants hosted a substantially richer and more diverse fungal community, boasting 72 taxonomic orders and 130.5 fungal amplicon sequence variants (ASVs) compared to 45 orders and 42.7 ASVs in nodulating plants, respectively. Moreover, a striking 40% of fungal orders were found exclusively in non-nodulating hosts. In this study we demonstrate that interactions between leguminous trees and nitrogen-fixing root bacteria significantly influence the fungal endophytic communities. Our findings contribute valuable insights into the complex interplay between plants and microorganisms, particularly in the context of tropical forest ecosystems.

POS01-012: FUNGAL CONCENTRATIONS IN LEAF LITTER ALONG MICROCLIMATE AND ELEVATION VARIATIONS AMONG PSEUDOTSUGA MENZIESII AND TSUGA HETEROPHYLLA
Gabriel Velador Madera, Abigail Neat, Posy Busby
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Abstract
Fungal endophytes are found in the leaves of all terrestrial plants. Endophytes infect leaves from the environment, with spores typically originating from the leaf litter. However, the relative concentration of fungal inoculum in litter associated with varying hosts and environments is poorly known. In this study, we evaluated the concentration of fungal colony forming units in leaf litter of Douglas Fir (Pseudotsuga menziesii) and Western Hemlock (Tsuga heterophylla), two species of conifer trees native to the Pacific Northwest. Litter for this study was collected from both high and low elevation sites and varying microclimates at the HJ Andrews Experimental Forest in the Western Oregon Cascades. After leaf litter was moist-incubated, we generated a 1:1 litter:water slurry to collect the microbial community from the leaf litter. The leaf slurry dilutions were then plated on PDA treated with streptomycin and tetracycline. After five days of incubation, fungal colony counting revealed that fungal concentrations were significantly higher in high elevation leaf litter relative to low elevation leaf litter for both Douglas Fir and Western Hemlock species. However, the fungal concentrations between dry, intermediate, and wet microclimates did not differ. Our ongoing studies address the functional consequences of this variation for seedling growth and survival.

POS01-013: LEAD (PB) TOLERANCE IN THE ECTOMYCORRHIZAL FUNGI SUILLUS BREVIPES AND S. TOMENTOSUS
Matt Johnson, William Leary, Jessica Fletcher, Sara Branco
University of Colorado Denver, Denver, USA

Abstract
Soil lead (Pb) contamination is widespread and negatively affects organisms. Some fungi can thrive in soils with high metal content. Lead contamination levels are high in the Rocky Mountains due to historical mining activity, however it is not clear if fungal species from this region are Pb-tolerant. We investigated Pb tolerance in Suillus tomentosus and S. brevipes isolates from Pb contaminated and non-contaminated sites in Colorado. We expected isolates from contaminated sites to display high levels of Pb tolerance, and isolates from non-contaminated sites to be Pb sensitive. We also hypothesized both species would show similar levels of Pb tolerance that would positively correlate with tolerance to other metals. Unexpectedly, there was no correlation between Pb soil contamination and Pb tolerance in either species. We however found that S. tomentosus is more Pb tolerant than S. brevipes and that both species show large intra-specific variation regarding Pb tolerance. We found no relationship between growth rate and Pb tolerance in both species. There was a positive correlation between Pb and zinc tolerance only for S. brevipes and no correlation between Pb and cadmium tolerance for either species. Our results show that even though some S. brevipes and S. tomentosus isolates display Pb tolerance, it is difficult to predict where tolerance arises. Pb tolerance in Suillus from the Rocky Mountains is an important finding, as these fungi can be used as a tool for the recovery of local habitats impacted by Pb contamination.

POS01-014: CLIMATE CHANGE-INDUCED SHIFTS IN MEDITERRANEAN FUNGAL FRUITING PHENOLOGY
Rachel DeMay, Derek Johnson
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Abstract
Climate change is impacting yields, timing, and patterns of fungal fruiting around the world. Autumnal fruiting seasons have been delayed to later in the year, and the duration of the fruiting season has lengthened or compressed depending on the system. This carries consequences for the many roles that fungi fill as plant symbiotes and decomposers in forest ecosystems, and the numerous wild edible fungi that are economically important around the world. Spain, where mycophagy and economic value of edible mushrooms are particularly important, is experiencing increasingly frequent and severe droughts, threatening the fruiting of forest mushrooms. We used a 27-year (1995-2021) dataset of mushroom fruiting from a Scots pine forest in Soria, Spain, to assess long-term
changes in mushroom fruiting season length and peak across taxonomic and functional groups of mushrooms and the relationships between mushroom fruiting phenology and climate variables. Among mycorrhizal fungi, litter-decaying saprotrophic fungi, and the economically-important edible genera Boletus and Lactarius, the length of the fruiting season has trended downward over the course of the study. Conversely, the fruiting season length of wood-decaying saprotrophic fungi did not have a clear trend. Understanding the long-term trends and climatic drivers of fungal fruiting patterns provides insight into future ecosystem and economic consequences of climate change effects on fungal fruiting and forest management.

**POS01-015: MYCELIAL MAINFRAMES AND FUNGAL FACTORIES; ASSESSING VARIATIONS IN CELLOBIASE ACTIVITY IN THREE FUNGI UNDER DIVERSE GROWTH CONDITIONS; A COMPARATIVE STUDY ON THE EFFICIENCY OF AGRICULTURAL BY-PRODUCTS IN ENZYME PRODUCTION FOR OPTIMAL CELULOSIC BIOFUEL**

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**Abstract**

Cellulosic biofuel production using fungi presents a promising frontier to conventional longer-range agricultural products. This investigation shows the potential of leveraging agricultural by-products to produce the crucial cellobiase enzyme via fungal cultivation. By conducting comparative analyses on cellobiase activity across three distinct yet accessible species—Pleurotus djamor, Hericium erinaceus, and Agaricus bisporus—under varied growth conditions, including the incorporation of molasses and sucrose as well as temperature adjustments, this study aims to elucidate optimal strategies for enhancing enzyme output for biofuel conversion. Analysis regarding enzymatic activity from dish-grown samples showcases the potential for applicative study in quickly deriving strains. The research reveals nuanced interactions between fungal strains and their substrates, some samples highlighting pronounced growth and cellobiase production in molasses-enriched environments and at elevated temperatures; concurrently, others emerged as a top performer in enzymatic activity but suffered increased propensity for bacterial contamination and poor growth performance. DNA barcoding confirmation of the species identity of our fungal subjects facilitates a deeper understanding of their phylogenetic relationships and the genetic basis underlying their enzymatic responses. These insights pave the way for the strategic selection of fungal strains and growth conditions that maximize cellobiase production, advocating for a less conventional, more holistic approach to biofuel enzyme generation.

This research underscores the transformative potential of fungi in the biofuel sector, championing the use of agricultural residues not only as a feedstock for enzyme production but also as a substrate for bioconversion, thereby promoting a sustainable and integrated biofuel production paradigm.

**POS01-016: MICROBIAL COMMUNITY PROCESS MODELING WITH CONVOLUTIONAL NEURAL NETWORKS**

Tayler Fearn, Geoffrey Zahn
Utah Valley University, Orem, UT, USA

**Abstract**

The facilitated restoration of degraded ecosystems often depends on outplantings of desirable plant species. Recent work has shown that mutualistic microbes are crucial to outplanting success and thus microbiome transplantation has emerged as an important tool for conservation and restoration work. However, inconsistent efficacy and lack of reproducibility warrants further investigation into the “rules” of microbial and environmental interactions that determine microbiome transplantation outcomes. Our goal is to develop a modeling framework for predicting microbiome transplantations. As a first step, we are training Convolutional Neural Network (CNN) models to detect ecological processes in simulated community data sets. By transforming pre- and post-transplantation microbial community matrices into spatial representations, CNNs can reveal the underlying simulated ecological processes. This approach allows us to train supervised models to aid in predicting key biotic interaction patterns that govern microbial communities during transplantation. This offers a promising pathway toward informed and conditioned improvements in microbiome transplantation and is fundamental for developing next-generation modeling paradigms for these complex interactions. With greater predictability in microbiome transplantation, we can improve success rates in habitat restoration and agricultural interventions.

**POS01-017: APPLYING DATA SCIENCE PRINCIPLES TO FACILITATE HIGHLY REPRODUCIBLE COLLABORATIVE RESEARCH**

Carolyn Delevich1, Peter Kennedy2, Jana U’ren3, Bitty Roy4, Betsy Arnold5, John Conery1
1University of Oregon, Eugene, USA. 2University of Minnesota, Minneapolis, USA. 3Washington State University, Pullman, USA. 4University of Oregon, Eugene, USA. 5University of Arizona, Tucson, USA

**Abstract**

Collaboration is fundamental to scientific advancement. Our diverse catalog of fungi would not exist without cooperation among mycologists. While the benefits of collaboration are evident, we lack a clear roadmap to navigate the mire of multi-source data, cryptic naming conventions, and idiosyncratic analysis pipelines that may lurk beneath the surface. An idyllic union of mycologists can quickly devolve into a mess of murky data, or worse, a complete aversion to collaboration. To mitigate such outcomes, I formulated clear and reproducible methods to manage, analyze, and store data in a mid-size (~10 PIs) collaborative project. This framework outlines common data issues in collaborations, like merging data from multiple sources. These challenges are common across data-driven domains, and the field of data science is particularly poised to overcome them. Using data science principles, I addressed these challenges by developing software tools that programmatically collect, clean, and analyze multi-source data. This approach minimizes error, bias, and time that is otherwise unavoidable with human-led tasks. I implemented this
framework on the CliMush project, a group of 10 core researchers studying the impact of climate on macrofungi across the United States. Given the project’s scale, we faced data-related hurdles, like integrating data across multiple sequencing technologies, community scientists, and long-term environmental monitoring. I will share my framework for facilitating collaborative research, along with the open-source tools I developed that support this framework. I hope these tools will minimize the mess, maximize reproducibility, and pave the way for more frequent (and fun!) collaborations in mycology.

POS01-018: BRIDGING BELOW AND ABOVE: EXPLORING AMF IMPACT ON POLLINATOR NETWORKS AND POLLEN NUTRITION IN NORTH-CENTRAL TEXAS GRASSES
Isabella Szebelledy, Adam Mitchell
Tarleton State University, Stephenville, USA

Abstract
Grassland ecosystems face challenges in mitigating biological diversity loss and its effects on ecosystem structure and function. Arbuscular mycorrhizal fungi (AMF) play pivotal roles in ecosystem health and function for grasslands through uptake of nutrients and improved plant performance; however, the magnitude of this relationship may be confounded by environmental stochasticity, host plant identity, and fertilizer inputs. In addition, global, long-term studies show declines in pollinator insect abundance; although conservation strategies recommend additional studies on pollinator-plant relationships to highlight mechanisms of decline at local scales, the loss of native, high-quality floral resources are highlighted as a prominent factor, which may be correlate with loss of AMF diversity in degraded grassland ecosystems. Although primarily wind-pollinated, grasses nonetheless provide valuable resources for pollinator health, including nesting structure and pollen as supplemental feed when other resources are limited, particularly during drought. We seek to assess the efficacy of AMF on pollinator communities associated with Texas grasslands by: (1) quantifying insect pollinator networks associated with a suite of native grasses with AMF infection, and (2) assess AMF infection on grass pollen productivity and nutritive value at early and late flowering stages. We used a randomized split plot design under 4 treatment combinations: mycorrhizal inoculum (+/-) and nutrient load (fertilizer +/-), using 5 species of native warm-season perennial grasses. I will collect data on soil and plant characteristics, pollen chemical composition, and pollinator frequency and diversity. We will provide a baseline for understanding aboveground-belowground trophic interactions and guide pollinator conservation efforts in grassland ecosystems.

POS01-019: DYNAMICS OF PINE ECTOMYCORRHIZAE AFTER ROOT DISTURBANCE
Gavin Kernaghan, Britanie LeFait LeFait, Ayesha Hussain
Mount Saint Vincent University, Halifax, Canada

Abstract
A large proportion of the carbon fixed by forest trees is allocated below ground to ectomycorrhizae (ECM), but the decomposition and recruitment rates of ECM formed by individual fungal species are unknown. To investigate the post-disturbance dynamics of individual ECM, sections of humus were excised from pine-forest floors, severing all roots in July. Humus sections were replaced immediately and then randomly sampled over time as roots decomposed. Previously undisturbed (control) humus samples were also collected at selected time points. Decomposing ECM and ECM regenerating on roots growing into the humus segments were identified by ITS sequencing. Clavulina coraloides ECM decomposed most rapidly, and most other ECM (e.g., Suillus, Russula) were also degraded by the first fall, although some Cenococcum ECM remained intact for one year after disturbance. Recruitment of new ECM began in the spring following the disturbance and was tracked into the fall of the second year. These new ECM were mainly formed by members of the Russulaceae (Lactarius, Lactifluus and Russula). Only a small number of new Cenococcum ECM were formed, and this occurred at the very end of the experiment. We found that ECM formed by different fungi decompose and recruit at different rates following disturbance. Cenococcum is especially slow to decompose and also slow to recruit, resulting in a very slow turnover rate. Differences in ECM turnover among fungal species may impact local rates of carbon cycling in forest soils.

POS01-020: BIODIVERSITY AND ECOLOGY OF SALT MARSH GRASS ROOT ENDOPHYTES FROM THE MINAS BASIN, NOVA SCOTIA
Charlotte Peng1, Kendra Sampson1, Gavin Kernaghan2, Allison Walker1
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Abstract
Salt marsh grass species provide foundational habitat for recreational and commercial fisheries, and contribute to tidal wetland carbon sequestration. Tidal wetland plant root endophytes remain understudied in these threatened habitats and may contribute to salt marsh plant restoration success. We cultured and identified non-mycorrhizal root endophytes of a key salt marsh grass species, Sporobolus pumilus (formerly Spartina patens) (salt marsh hay), from one restored and one natural Nova Scotia salt marsh. Higher root fungal diversity was noted at the natural salt marsh. Sporobolus pumilus was also propagated from seed in tissue culture and roots were experimentally inoculated with four S. pumilus root endophytes: Paralulworthia candida, Falciphora sp., Dimorphospora foliicola, and Ophiophaerella aquatica. Plant survival and growth (root, leaf, and shoot lengths, and total plant weight) with and without endophyte inoculation were assessed after 28 days of growth under controlled conditions. Preliminary results indicate plant growth promotion by some root endophytes. This study will aid in improving native salt marsh plant propagation and restoration techniques.
POS01-021: ASSISTED MIGRATION OF LOCALLY ADAPTED PSEUDOTSUGA MENZIESII AND ITS INTERACTIONS WITH THE SOIL FUNGAL COMMUNITY
Joseph M. Gagne1, Emily Johnson1, Robyn Banasky1, Posy E. Busby1, Richard Cronn1, Michael Nelson1, Rose Roberts1, Robert A. Slesak1, Joseph W. Spatafora1, F. Andrew Jones1
1Department of Botany and Plant Pathology, Oregon State University, Corvallis, OR, USA. 2Department of Forest Ecosystems and Society, Oregon State University, Corvallis, OR, USA. 3Pacific Northwest Research Station, U.S. Department of Agriculture Forest Service, Corvallis, OR, USA. 4Department of Agriculture Forest Service, Olympia, WA, USA. 5University of New Hampshire, Durham, NH, USA. 6University of Minnesota, St. Paul, MN, USA. 7University of Arizona, Tucson, AZ, USA. 8University of Georgia, Athens, GA, USA. 9Denver Botanic Gardens, Denver, CO, USA.

Abstract

Pseudotsuga menziesii (Douglas fir) is an ecologically and economically valuable tree species worldwide, particularly in western North America. Understanding how management techniques like assisted migration of locally adapted genotypes may affect and be affected by soil fungal communities is critical, especially in the face of anthropogenic climate change. We sampled soil and sequenced fungi from the United States Forest Service’s Seed-Source Movement Trial, a network of nine common P. menziesii gardens in Oregon and Washington. We collected soil from three of these gardens in Oregon where genotypes of locally adapted P. menziesii from twelve different source regions across the Northwestern U.S. were planted reciprocally in 2008. We sequenced the ITS2 region of the soil fungi using Illumina MiSeq. A synthetic DNA spike-in was added as an internal standard to estimate fungal load. We report results on the extent to which fungal communities vary by source region and garden location, and how these are correlated with the tree growth metrics of height and canopy cover. This exploratory data set will be used to inform decisions for future sampling and analysis of all nine common gardens to elucidate how assisted migration of P. menziesii and soil fungal communities may influence the other and help inform strategies regarding climate smart forestry practices in response to rapid climate change.

POS01-022: FUNGAL CONTRIBUTIONS TO THE BIRCH EFFECT: INSIGHTS FROM MICROFLUIDICS IN DRYLAND ECOSYSTEMS
Yi-Syuan Guo1, Karl Weitz2, Mary Lipton1, Leslie Shor2, Arunima Bhattacharjee1
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Abstract

Dryland ecosystems are one of the largest biomes on the earth and are highly vulnerable to drought and rewetting events that decrease species richness and crop diversity. These ecosystems are currently expanding due to climate change. Therefore, understanding the effects of drought and rewetting cycles on the soil microbiome is crucial for accurately predicting and mitigating the impact of climate change on ecosystems and carbon cycling. The Birch Effect, a direct result of drying and rewetting cycles, leads to the efflux of carbon dioxide (CO2) which can be monitored using real-time mass spectrometry (RTMS). During prolonged periods of drought, soil fungi transport and retain water within soil pores which helps sustain microbial life. However, the contribution of soil fungi to CO2 efflux during dry-rewetting cycling and the associated pore-scale biogeochemistry remains unclear. Here we propose to use soil micromodels to investigate the Birch Effect through simulated drought and rewetting cycles. Emulated soil micromodels were initially employed to inoculate fungi and monitor their growth with and without access to minerals. The micromodels were then dried out to examine the effect of dried fungi on moisture retention in the pores. Following a sufficient drying period, RT-MS was utilized to quantify the CO2 release upon rewetting the micromodels with deionized water. This approach provided insights into the fungal hydraulic lift and consequently the contributions of soil fungi to the Birch Effect.

POS01-023: THELEPHORALES DIVERSITY ACROSS NORTH AMERICA: GENUS AND SPECIES LEVEL COMPOSITION BY HABITAT AND ECOREGION FROM SOIL METABARCODING DATA.
Klaudia Sowrizal1, Carolyn Delevich2, Haley Burriill2, Marcos V. Caiafa1, Heathen A. Dawson2, Jeffrey M. Diez2, John Conery2, Serita D. Frey4, Peter G. Kennedy3, A. Elizabeth Arnold4, Jana U’Ren’, D. Jean Lodge2, Matthew E. Smith3, Bitty A. Roy2, Kristofor Voss1, Andrew W. Wilson9
1Regis University, Denver, CO, USA. 2University of Oregon, Eugene, OR, USA. 3University of Florida, Gainesville, FL, USA. 4University of New Hampshire, Durham, NH, USA. 5University of Minnesota, St. Paul, MN, USA. 6University of Arizona, Tuscon, AZ, USA. 7Washington State University, Pullman, WA, USA. 8University of Georgia, Athens, GA, USA. 9Denver Botanic Gardens, Denver, CO, USA.

Abstract

The Thelephorales are considered to be important ectomycorrhizal fungi in forest ecosystems globally, yet the patterns and processes that shape their diversity and distributions remain poorly understood. We address this research gap by conducting an exploratory analysis of Thelephorales fungi across various habitat types (grassland, oak forest, and Pinaceae forest) throughout North America. The Climush project is a collaborative multi-year, systematic sampling of macrofungal diversity across 7 field sites located throughout the United States, intended to evaluate sexual (sporocarp and spore trap data) and asexual (soil and endophyte metabarcode data) diversity and distribution in relation to environmental factors including fire disturbance. Using metabarcoding data from soil samples, Thelephorales diversity was assessed at the genus and species levels by patterns of molecular operational taxonomic units (MOTUs). Notably, these fungi were either absent or very rare in burn sites and in grassland habitats. In terms of species diversity, we observed significant richness within the genus Tomentella, supporting the concept of genus-level hyper-diversity within Thelephorales. Genus and species level linear regressions are evaluated across habitats and ecoregions. The results provide valuable preliminary insights into Thelephorales diversity and distribution. We identify significant cryptic diversity in the Thelephorales associated with non-burned forests that is not apparent in fire disturbed habitats. This has significant conservation and management implications for forest fungal communities and lays the groundwork for future research.
POS01-024: WHERE THE RED QUEEN SLEEPS: HOW A CURIOUS MICROFUNGAL CLASS CAN HELP CHARACTERIZE COEVOlUTIONARY RELATIONSHIPS
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Abstract
Spread primarily through sex, members of the microfungal class Laboulbeniomycetes are parasitic on arthropods, where they form tiny, three-dimensional thalli on the host exoskeleton. While the study of Laboulbeniomycetes has had a renaissance in the age of molecular methods, so too has the Red Queen Hypothesis, a coevolutionary theory aimed at characterizing how biotic interactions shape the evolutionary trajectory of “players” over time. While the central dogma of “laboulbeniology” is that labouls do not cause a fitness disadvantage to the host in the wild, here we report the first genome annotation data of a Laboulbeniomycete genome, indicating the possibility of past antagonistic relationships with host species. Some of the genes predicted are homologous with those of highly pathogenic entomopathogenic species, such as Cordyceps. To understand why these seemingly benign parasites possess genes associated with pathogenicity, we reviewed recent advances in molecular methods for detecting Red Queen associations, and propose a new model we call “Sleeping Red Queens”. Using Laboulbeniomycete evolutionary history, we predict that antagonists who have adapted to each other over time to a benign state can “re-awaken” or transition to a more antagonistic mode due to environmental changes. The “Sleeping Red Queen” model of Laboulbeniomycetes is supported by research on laboul ecology under artificial conditions. With promising advances in next-generation sequencing, we believe our Sleeping Red Queen model will be advantageous for interpretation of future genomic and bioinformatic data of Laboulbeniomycetes.

POS01-025: EFFECTS OF LEAD (PB) ON PINUS-SUILLUS MUTUALISM
William Leary, Matthew Johnson, Sara Branco, Jessica Fletcher
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Abstract
Soil metal contamination due to anthropogenic activity negatively impacts organisms. However, some species evolved tolerance and can persist in metal-contaminated sites. We recently found lead (Pb) tolerance in Suillus tomentosus and S. brevipes, two mycorrhizal fungi commonly found in the American West that live in mutualistic associations with pine trees. It is unclear whether and how Suillus Pb tolerance impacts pine partner survival/health in Pb-contaminated environments. Here, we performed a pilot study to investigate the ability of P. contorta seedlings inoculated with Pb-sensitive S. tomentosus and S. brevipes isolates to tolerate a range of Pb concentrations. We found all pines could tolerate Pb. Notably, S. brevipes significantly improved pine biomass at low Pb levels, while inoculation with S. tomentosus had no effect. Further research will expand our studies to include Pb-tolerant Suillus isolates to assess whether they further minimize the effects of pine Pb toxicity.

POS01-026: A NEW SPECIES OF PERIGLANDULA SYMBIOTIC WITH THE MORNING GLORY IPOMOEA TRICOLOR
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Abstract
Ergot alkaloids are chemicals produced exclusively by fungi and are important for their use in pharmaceuticals and their toxic impacts on livestock. Ipomoea tricolor is a common plant species in the family Convolvulaceae (morning glory). Limited sequence data and HPLC analysis of ergot alkaloid presence in plant tissues provide evidence of a fungal symbiont in I. tricolor despite no identified or externally visible fungus. Our goal is to isolate and describe this fungus, which we hypothesize represents a new species. Observation of fungal hyphae on evacuated seed coats from I. tricolor and subsequent transfer onto malt extract agar resulted in cultures of the symbiont isolated from the plant. The fungus grew slowly as white hyphae and sometimes aggregated into synnema-like structures, both of which lacked spores. Sequences of PCR products from this culture were most similar to the preliminary sequence data available for the morning glory symbiont. Using PCR and enzymatic digests, the same fungus was detected in I. tricolor roots, hypocotyls, cotyledons, leaves and stems at varying frequencies. Since we were able to culture the fungus, we isolated sufficient DNA to sequence the genome with illumina technology. Phylogenetic analyses based on multiple genes indicated that the symbiont of I. tricolor was distinct from, but related to, the two described species of Periglandula previously observed in other species of morning glories. Based on these data and observations, we conclude that the symbiotic fungus of I. tricolor is a distinct species of Periglandula and propose the name Periglandula clandestina sp. nov.

POS01-027: GETTING TO THE ROOT OF THE PROBLEM WITH TERRESTRIAL ORCHID CONSERVATION: IDENTIFYING THE FUNGAL SYMBIONTS OF RAM’S-HEAD LADY SLIPPER (CYPRIPEDIUM ARIETINUM) IN NOVA SCOTIA
Katie King1, Gavin Kernaghan3, Allison K. Walker1
1Acadia University, Wolfville, Canada. 2Mount Saint Vincent University, Halifax, Canada

Abstract
Cypripedium arietinum is an endangered orchid found in Eastern North America. It relies on symbiotic fungi for seed germination and nutrient transfer, although we have yet to identify the fungal partners involved. The Nova Scotian population is disjunct and found in a different habitat type than most other known populations, factors which may influence the fungi that associate with C. arietinum. We have begun to isolate and identify these fungi from the Nova Scotian population. A preliminary assay of root samples collected in Fall 2023 will be repeated in Spring 2024. Roots were examined for pellets and dissected to isolate fungi onto selective media. Fungal DNA was also extracted from root tissue for PacBio next generation sequencing. Seed collections are planned for ex situ seed baiting trials for fungi, and the fungi found in the tissues of any germinated protocorms will be similarly identified using culture and molecular techniques. We have isolated two fungi one of which has been identified as Saitozyma podzolica. PacBio sequencing results from roots returned
conducted predominantly on one species, Research on the chemical composition of toxin droplets attempts have been made to identify the Pleurotus for fungal consumption. Although recent burst when disrupted by passing nematodes, immobilizing microdroplets produced on aerial hyphae. The droplets metabolites. These metabolites are contained within liquid nematodes through the production of toxic secondary mushrooms—possesses the unique ability to paralyze Pleurotus these fungi, the microfauna as a means of nutrient supplementation. Of to possess diverse mechanisms to trap and digest Abstract The genus Basidiobolus has been identified for its distinct secondary metabolism compared to other early diverging zygomycete fungi. These metabolites function in communication, sensing the environment, symbiotic interactions, and as virulence factors. There is ongoing research into how metabolites may aid in entry, colonization, nutrient acquisition, immune cell response, and tolerance to antifungal drugs in animal hosts. This project focuses on the responses of B. ranarum, a potentially pathogenic species, to strong selective pressures of three common antifungal drugs used in the treatment of zygomycoses (Amphotericin B, Fluconazole, and Itraconazole). Response was measured by culture growth and sporulation rate. Our preliminary results show that B. ranarum does not only appear to be resistant to the antifungals, but also may have a faster grow rate when exposed to these compounds. These results have strong implications on antifungal resistance and potential impacts for human health.

POS01-030: CHARACTERIZING THE DIVERSITY AND SPATIOTEMPORAL STRUCTURE OF BACTERIAL-FUNGAL RELATIONSHIPS IN THE GUT MICROBIOME OF HERPTILES Alexander J. Rurik1, Mitra Ghotbi2, Jason W. Dallas3, Chloe Cummins3, N. Reed Alexander2, Kaitlyn M. Murphy3, Llvia Vargas-Gastélum2, Joseph W. Spatafora2, Kerry L. McPhail3, George F. Neuhaus4, Jason E. Stajich4,5, Leila Shadmani6, Donald M. Walker1
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Abstract Herptiles (reptiles and amphibians) are among the most threatened vertebrate groups. Estimates suggest that 21% of reptiles and 41% of amphibians are threatened with extinction. Considering a healthy gut microbiome as a crucial element of herptile conservation approaches is essential, as dysbiosis in the microbiome may cause adverse health effects for the host. Understanding the
complexity of stable 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 herptiles. We have determined that filamentous fungi (genus *Basidiobolus*) are dominant members of the herptile microbiome and that *Basidiobolus* diversity structures the bacterial community. By examining the bacterial and fungal assemblages in the herptile gut across space, host phylogeny, and life history, we aim to better understand the unique role that ubiquitous members like *Basidiobolus* play in the herptile gut. To date, we have characterized bacterial and fungal assemblages using metatranscriptomics and amplicon sequencing of 16S rRNA and ITS1 rDNA in 90 herptile species, many of which have never had their gut microbiome studied and/or are species of conservation concern. Expected results include the taxonomic characterization of the gut fungal and bacterial assemblages of over 90 host species, comparisons of alpha and beta diversity, an investigation of the co-occurrence of *Basidiobolus* and other microbial taxa, and an exploration into spatial relationships of herptile microbiomes.

**POS01-032: FRUITING-BODY INHABITING BACTERIA: THEIR SUCCESSION AND GLOBAL DIVERSITY PATTERNS**
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**Abstract**

Fruiting-body forming fungi are important source of food and medicine worldwide, and their growth and health are known to depend on various microbial communities. Although several studies have examined the structure of these communities, our understanding of their succession and functional potential during fruiting-body development, as well as the global determinants of their diversity, remains limited. Here we used high-throughput sequencing to characterize the bacterial communities and their associated potential functions in three different developmental stages of a model fungal species *Cantharellus cibarius*. We also examined global diversity and community composition of bacteria inhabiting fruiting-bodies of different fungal genera in relation to climate, soil, and host factors. Our results reveal that certain functional groups, such as those related to nitrogen fixation, persist in fruiting-bodies during maturation but are later replaced by putative parasites/pathogens. We identified a core global fruiting-body microbiome, accounting for 30% of sequence reads, comprising a few bacterial genera such as *Halomonas*, *Serratia*, *Bacillus*, *Cutibacterium*, *Bradyrhizobium*, and *Burkholderia*. Our analysis further revealed the significant role of fungal host phylogeny in shaping the bacterial communities, while the effects of climate and soil factors remained negligible. The findings suggest that the communities of fruiting-body inhabiting bacteria and free-living bacteria are structured by contrasting community assembly processes, and fungal-bacterial interactions are important determinants of fruiting-body inhabiting bacterial community structure.

**POS01-033: GENOMIC AND METABOLOMIC ANALYSIS OF THE GOLDEN OYSTER MUSHROOM AND INSIGHTS INTO THE BIOSYNTHESIS OF NEMATODE PARALYZING NEUROTOXIN**
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**Abstract**

*Pleurotus citrinopileatus* Singer is a wood-decaying saprotroph that was introduced to North America from East Asia and has become invasive. The members of the genus *Pleurotus* are also reported to trap and consume nematodes. The mycelium of *P. citrinopileatus* produces a toxin droplet, which paralyzes the nematode upon contact. Recently, the toxin was suggested to be a volatile ketone, 3-octanone, and was found to use a sensory cilia-dependent mechanism to paralyze the nematode accompanied by an influx of calcium ions. However, the intensity of the calcium ion influx induced by the ketone was lower than that induced by the toxin droplet. *Pleurotus* is also reported to attract nematodes toward the traps, but the mechanism of this attraction has not been studied. Thus, the identity of metabolites in the toxin droplet and their biosynthesis remains questionable. Results from LC-MS analysis of toxin droplets suggest that the neurotoxin could be a polyketide. In addition to metabolomic analyses, we are working to elucidate the biosynthetic pathway of the *P. citrinopileatus* neurotoxin using genomic data from long read sequencing. Understanding the chemical nature of the toxin and other metabolites could provide the basis for development of new anti-helminthic drugs for controlling plant and animal parasitic nematodes.

**POS01-034: INVESTIGATING THE ROLE OF HOST-ASSOCIATED MICROBIAL COMMUNITIES IN PSEUDOTSUGA MENZIESII SEEDLING RESPONSE TO DROUGHT STRESS**
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1Oregon State University, Corvallis, USA. 2Marquette University, Milwaukee, USA

**Abstract**

Plants harbor diverse microbial communities both belowground in the soil and aboveground in the foliage, and these plant-microbe interactions can range from mutualistic to pathogenic. The habitat-adapted symbiosis hypothesis argues that plant-fungal mutualisms are common in abiotically stressful environments and supports the persistence of both fungi and their plant host. Here, we explore the related hypothesis that plants and associated microbes sourced from extreme climates exhibit greater resilience to abiotic stress relative to those found in mesic climates. We test this hypothesis through a reciprocal inoculation greenhouse experiment using Douglas-fir (Pseudotsuga menziesii) seedlings sourced from across an elevation gradient present in the Western Oregon Cascade
Range. This elevation gradient also represents a climate gradient, with the low elevations defined by a longer growing season, less extreme temperature fluctuations, and greater relative humidity compared to the higher elevations. Six populations of *P. menziesii* seedlings sourced from across the gradient were inoculated with foliar microbes, soil microbes or no microbes, with microbial communities sourced from a high elevation site or a low elevation site. Half of the seedlings were then subjected to a month-long drought event, after which we recorded plant physiological measurements including height, total biomass, stomatal conductance, fluorescence, and mycorrhizal colonization rates. This data analysis is ongoing, and in total will allow us to explore if *P. menziesii*-associated microbial communities either inhibit or increase a seedling’s ability to withstand drought stress, if this outcome varies based on climate origin, and potential physiological mechanisms associated with the outcomes we observe.

**POS01-035: BIOTROPHY IN USTILAGO MAYDIS, AN INTERPLAY OF CARBON, IRON AND GLUTATHIONE METABOLISM.**

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**Abstract**

*Ustilago maydis* is a biotrophic pathogen of maize and the causal agent of corn smut disease. We recently showed that a combination of glucose plus the C4-photosynthesis related organic acid malate induced the genetic program for biotrophy in *U. maydis in vitro*. Observed phenotypic changes included accelerated growth, formation of an extracellular matrix and the induction of melanin biosynthesis usually observed during sporulation. RNAseq identified iron-sulfur cluster containing (IRC) genes including the iron-regulon controlling protein glutaredoxin Grx4 as differently regulated in glucose plus malate (GM). Grx4 uses IRC's and glutathione as co-factors to fulfill its gene expression regulating function. Interestingly, iron-uptake as well as glutathione biosynthesis genes were also differently regulated in GM. Here we report the involvement of Grx4 and the glutathione synthase (Gsh2) in iron and GSH metabolism, as well as the impact of the carbon source malate alone or in combinations on growth, ESP and melanin formation in *U. maydis*. Iron, GSH and malate were able to individually increase growth of the respective deletion mutants. But especially their combinations increased growth and could partially rescue the genetic defects of Δgrx4 or Δgsh2. Either chemical or genetic disturbance of Grx4 and Gsh2 functions further impaired normal melanin formation. Δgsh2 in contrast to Δgrx4 showed normal mating. However, increased filamentation on mating medium was observed for Δgsh2. The virulence of the Δgrx4 strains was strongly impaired. In conclusion, *in vitro* biotrophy mimicking conditions, induced by mixed carbon sources, rely on proper iron and GSH metabolism in *U. maydis*.

**POS01-036: OPTIMIZING A MACHINE LEARNING MODEL TO IDENTIFY GENE FAMILIES PREDICTIVE OF OXIDATIVE STRESS RESISTANCE ACROSS THE SACCHAROMYCOTINA SUBPHYLUM.**

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**Abstract**

To understand variation in resistance to reactive oxygen species (ROS) across diverse yeasts, we employed a comparative approach using machine learning to identify gene families associated with high ROS resistance among 284 yeast species, with representation across each order in the yeast subphylum Saccharomycotina. We grew each species in two different concentrations of a ROS-inducing drug to create a combined dataset for use in our model. The 20% of species that grew poorest in the low drug concentration were classified as ROS-sensitive, and the 20% of species that grew best in the high drug concentration were classified as ROS-resistant to maximize biological accuracy. Random Forest feature selection method was used to select the 50 most predictive gene families out of 73,000 to build a binary classification model. The gene families with the highest predictive importance were both reductases, and a GO-term enrichment analysis revealed that the 50 selected gene families were enriched for cell wall organization. To understand the contribution each important feature has on the classification of individual species, we utilized Shapley Additive exPlanations, or SHAP values. This analysis revealed that the old yellow enzyme reductase family was predictive of ROS sensitivity if there was one copy or less, but predictive of ROS resistance if there were two copies or more. Through validation that increasing the copy number of OYE increased ROS resistance in a ROS-sensitive species, we underscore the biological relevance of machine learning models, which are poised to become increasingly important for mining ever-expanding datasets.

**POS01-037: AN IMPROVED GENOME ASSEMBLY OF LENTINUS TIGRINUS AND MAPPING OF A DIMORPHIC ALLELE.**

Thomas Roehl, Javier Tabima, David Hibbett

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**Abstract**

*Lentinus tigrinus* is a white rot agaric in the Polyporales that grows on water-associated wood. In North America, the species is dimorphic, with agaricoid (exposed gills) and secotioid (closed off gills) forms coexisting and widespread across the continent. The secotioid form is absent from Europe and European species additionally have a partial veil. Although a genome was previously generated using Illumina for an inbred strain of North American *L. tigrinus*, that genome is highly fragmented. We use a hybrid assembly of short- and long-read data to generate an improved assembly of the *L. tigrinus* genome. Furthermore, we generate genomes using wild strains from the United States and Europe, which allows preliminary investigation into whether North American and European
L. tigrinus are conspecific. Finally, past work identified 900 genes across four scaffolds as associated with the secotioid allele. We map these regions to the reference genome and suggest possible identities for the secotioid allele.

**POS01-038: INTRA-SPECIFIC DIVERSITY IN TRANSCRIPTOME AND PLANT RESPONSE IN ARBUCULAR MYCORRHIZAL FUNGI**

Ken Mugambi, Nicolas Corradi  
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**Abstract**  
Arbuscular mycorrhizal fungi form mutualistic associations with approximately 80% of all terrestrial plant species, stimulate plant growth, and enhance plant tolerance to biotic and abiotic stress. AMF are multinucleate, with individual spores carrying up to 20,000 nuclei in some species. Recent complete genome sequencing of *Rhizophagus irregularis* strains showed that these model plant symbionts are characterized by significant variability in chromosomal size, genes, and repeat content elements. While the genome assemblies provide considerable insights into the genome diversity in *R. irregularis* strains, it remains to be explored how this diversity correlates with variation in transcriptome to plant responses. We hypothesize that *R. irregularis* strains might regulate different gene sets, as well as produce different mRNA isoforms in the presence of the same plant host, and are related to variation into plant phenotypic responses. Five *R. irregularis* strains (DAOM 197198, A1, B3, C2, and 4401) were grown *in-vitro* in the presence of two hosts in root organ cultures of *Daucus carota* (*Carrot*), and *Cichorium intybus* (*Chicory*). The total RNA of colonized roots in these conditions was sent for illumina sequencing, and the next steps will involve obtaining a fine-scale transcriptome map of these strains. The same set of five strains are being cultured in growth chambers in the presence of two plant hosts: Leek (*Allium ampeloprasum*) and Sudan grass (*Sorghum × drummondii*). Through this, we will examine if different strains alter plant response, and we will also obtain a detailed view of isoform variability from colonized roots of these strains.

**POS01-039: EVALUATION OF SPOROCARP EVOLUTIONARY RELATIONSHIPS AND MATERIAL PROPERTIES**

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**Abstract**  
Some fungi form complex ordered structures made up of condensed layers of filaments (hyphae) known as sporocarps (mushrooms). Despite a vast body of knowledge on sporocarp morphology, material properties like their impressive strength relative to their low density remain understudied in favour of metabolic properties. There exist few available English papers that assess sporocarp material properties, none of which seek to understand how these properties relate to the evolutionary relationships among sporocarps. There is a lack of cohesion within literature as to which testing standards, sample preparation methods, and mathematical models are appropriate for the characterization of sporocarp properties. Collected sporocarps of several species have been prepared into cubes cut from the context (middle) layer and subjected to compressive loading to estimate plateau stress and densification strain. A phylogenetic tree will be constructed based on the barcode DNA sequences from the sporocarps to determine their evolutionary relatedness. Closely related species with dissimilar material properties may suggest that among their differences are genes which significantly contribute to sporocarp, microstructure, and mechanical properties. This may help to elucidate contributors to the ‘mechanical evolution’ of sporocarp structure. The activation of such genes in lab-grown fungi could improve these properties for producing mycelium-based leather and other potential bioproducts of different strengths. The methods and data produced serve to advance the standardization of fungal materials testing and the modelling of their mechanical behaviour, contributing to our understanding of the influence of mechanical constraints on fungal evolution.

**POS01-040: DISCOVERY OF FUNGAL CARBONYL SULFIDE (COS) ASSIMILATION AND THE ROLE OF COS HYDROLASE**

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**Abstract**  
Filamentous fungi exhibit remarkable sulfur assimilation capabilities, utilizing diverse forms of sulfur compounds, both inorganic and organic, as sulfur sources. However, existing research has primarily focused on water-soluble sulfur compounds as sources of sulfur. Meanwhile, carbonyl sulfide (COS), the most abundant sulfur-containing gas in the atmosphere, is ubiquitously present in the troposphere with average concentrations around 500 parts per trillion by volume (pptv). In the recent study, our research group has shown that the filamentous fungus *Trichoderma harzianum*, isolated from forest soil, has the ability to take gaseous carbonyl sulfide (COS) into its cells, degrading it and assimilating it as a sulfur source. Furthermore, we have discovered the COS hydrolase (COSase, COS + H₂O → H₂S + CO₂), the first such fungal enzyme identified in this fungus, indicating that this enzyme might be involved in the gaseous assimilation process. This finding implies that processes like carbon fixation and nitrogen fixation for the assimilation of gaseous compounds also exist for sulfur. In this study, we further investigated the physiological aspects of COS assimilation in *Trichoderma harzianum*, additionally focusing on the detailed biochemical characteristics and the physiological role of fungal COSase, which is considered a key enzyme in this process.
**POS01-041: EUKARYOME: THE RRNA GENE REFERENCE DATABASE FOR IDENTIFICATION OF ALL EUKARYOTES**

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**Abstract**

Molecular identification of micro- and macro-organisms based on nuclear markers has revolutionised the understanding of their taxonomy, phylogeny, and ecology. Today, research on the diversity of eukaryotes in global ecosystems heavily relies on nuclear ribosomal (rRNA) markers. Here we present a manually curated reference database EUKARYOME for nuclear ribosomal 18S rRNA (SSU), Internal Transcribed Spacer (ITS), and 28S rRNA (LSU) markers for all eukaryotes, including metazoans (animals), protists, fungi, and plants has presented. It is particularly useful for identification of arbuscular mycorrhizal fungi as it bridges the four commonly used molecular markers – ITS1, ITS2, SSU V4-V5, and LSU D1-D2 subregions. The key benefits of this database over other annotated reference sequence databases are that it is not restricted to certain taxonomic groups and it includes all rRNA markers. EUKARYOME also offers a number of references long-read sequences that are derived from (meta)genomic and (meta)barcoding - a unique feature that can be used for taxonomic identification and chimera control of third-generation, long-read, high-throughput sequencing data. Taxonomic assignments of rRNA genes in the database are verified based on phylogenetic approaches. The reference datasets are available in multiple formats from the project homepage, http://www.eukaryome.org.

**POS01-042: TWO NEW XYLOGRAPHA SPECIES AND NOTEWORTHY RECORDS FROM JAPAN AND MEXICO.**

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**Abstract**

Xylographa (Fr.) Fr. (Baeomyctales, Ostropomycetidae) is a dead wood-obligate genus of lichen- fungi that forms thin thalli often associated with goniocysts, and lireliform plants. The internal transcribed spacer region of Xylographa lactucae is a common member of the mycobiome of commercially grown romaine lettuce in the United States. Romaine lettuce is a leafy vegetable crop commonly implicated in foodborne pathogen outbreaks. Current detection methods of foodborne pathogens on leafy greens is often costly or time-consuming. Thus, the development of new molecular tools for such detection is needed. This study is part of a larger project that seeks to develop *S. lactucae* as a living biosensor for leafy greens. Here, we aim to develop species-specific primers for *S. lactucae* to allow rapid detection of the yeast, and then test our primers on lettuce and various other leafy green vegetables. The internal transcribed spacer region of *S. lactucae* was used as the source sequence for primer development. Primers were designed using the Primer3 software via the web interface. Gradient polymerase chain reaction was used to determine the optimal annealing temperature without cross-reactivity with closely related *Sporobolomyces* species. The optimal cycle number required to enable precise detection of *S. lactucae* was tested against the same related species. These primers...
were tested on lettuce slurries for targeted detection of *S. lactucae*. This work provides a valuable tool for future investigations into the ecological dynamics of this yeast in diverse environments, with implications for food safety and microbiome studies.

**POS01-045: TAXONOMIC DETERMINATION OF THELEPHORA TERRERSTRIS EHR. EX FR. SENSU LATO IN MEXICO**

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**Abstract**

**Introduction:** In 1793, Ehrhart proposed the species *Thelephora terrestris* from Europe, as the type species of the genus *Thelephora* Ehrh. ex Willd. (1787) (Thelephoraceae, Basidiomycota). There is a very incipient description of the specimen. Until 1914, Burt described the macro- and micromorphology, and in 1968, Corner provided a more detailed description. *T. terrestris* has been reported in Mexico, however there is insufficient information about its taxonomy. As a result, there are several herbaria records, which upon observation and analysis, exhibit notable macroscopic and microscopic differences.

**Methods:** We got loans from the largest herbaria in Mexico, of specimens named as *Thelephora terrestris*. Taxonomic determination involved describing macroscopic and microscopic. We amplified and sequenced the ITS DNA region. For the contaminated and DNA fragmented specimens we designed specific primers for *Thelephora*. We performed phylogenetic analysis with sequences recognized as *Thelephora terrestris* from UNITE database. Statistical analyses were conducted using the measurements obtained from microscopy.

**Results and discussion:** We studied 24 herbaria specimens and found differences in both macroscopic and microscopic morphology. In general, the measurements obtained from microscopy, fall within the ranges reported by Burt and Corner. However, the ranges provided by these authors are so wide that it is difficult to precisely determine the taxonomy of this species. We obtained 13 sequences corresponding to *Thelephora*, and in a preliminary phylogenetic analysis, we found that at least two species are new.

**POS01-046: ENDLESS FORMS MOST COLOURFUL: GEOGRAPHIC TRENDS IN THE FRUITING BODY COLOURATION OF AGARICALES (BASIDIOMYCOTA)**

Gayathri Venkatraman, Alison Davis-Rabosky, Timothy James
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**Abstract**

Fruiting bodies of Agaricomycetes are well known to exhibit a wide range of colours, and yet the adaptive value of colouration in mushrooms has been challenging to establish. Fungal pigments are energetically expensive to produce, and while previous but limited research has shown that some of these pigments serve as antioxidants and antibiotics, the functional significance of mushroom colouration for a majority of species is unknown. Which genera exhibit the greatest and least diversity in colouration; if and how colouration correlates to their lifestyle; and whether colour as a trait shows a phylogenetic signal also remains to be elucidated. In order to gauge the functional, ecological and evolutionary significance of mushroom colouration, it is first necessary to establish what patterns of distribution are exhibited by coloured species, which genera show the greatest diversity in colouration and what the geographic and ecological correlates relating to colouration are. Here, as a first step to understanding the diversity and patterns of variation in fungal colouration, I perform a global meta-analysis of Agaricales using public databases such as iNaturalist and Mycoportal to quantify and characterise mushroom colouration, the geographic distribution of coloured assemblages, their correlation to different environmental factors and the phylogenetic patterns of adaptive coloration.

**POS01-047: MYCOLOGY CLASSROOMS AS MOLECULAR BARCODING AND INVENTORYING OPPORTUNITIES: METHODS AND RESULTS**

Arthur Grupe1, Elisabeth Paluch1, Todd Osmundson1, Matthew Smith2, C. Alisha Quandt3, Jessie Uehling4
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**Abstract**

Incorporating practical molecular genetics skills training into mycology classroom learning exercises is an important part of our job as educators. As researchers, cataloging and describing the wealth of fungal diversity with limited funding for basic species inventories produces a challenging situation. A practical solution to achieve both of these goals is through utilizing mycology classrooms as molecular barcoding and inventorying opportunities. Here we present some of the results of such related activities, including budgets, protocols and materials lists. Additionally, links to resources for quick and efficient incorporation of these activities into new or existing courses are provided. Using biological materials in collections format engages students with course materials and underscores their potential as future mycological researchers. Workflows for integrating Sanger DNA sequencing, bioinformatics for DNA based identification, and accessioning class collections into herbaria will be discussed.

**POS01-048: EXPLORING MICROFUNGAL DIVERSITY ON IMPATIENS MARIANAE AT LAS CRUCES BIOLOGICAL STATION IN COSTA RICA**

Julianna Harden1,2, Terry Torres-Cruz3,4,5
1Cornell University, Ithaca, USA. 2Organization of Tropical Studies (OTS), San José, Costa Rica. 3Organization for Tropical Studies (OTS), San José, Costa Rica. 4Pennsylvania State University, University Park, USA. 5Purdue University, West Lafayette, USA

**Abstract**

Fusarium is a diverse genus of microfungi widely known for affecting agricultural crops. Despite being most commonly known for its pathogenic behavior, recent studies have identified Fusarium species with environmental benefits. *Impatiens marianae* (Balsaminaceae) is abundant on hiking trails at the Las Cruces Biological
Station in San Vito, Costa Rica. Despite its ecological niche occurring in multiple countries, there are no studies on this plant’s fungal diversity. Our study explored the diversity of microfungi on the leaves, rhizomes, and roots of *I. marianae* in a selectively logged primary forest at Las Cruces aiming to discover potential new species of *Fusarium* with novel applications. Full plants were collected in triplicate from three sites at Las Cruces.

Tissues (roots, rhizomes, and leaves) were washed with tap water and rinsed 3x with distilled water. Five 2x2 mm pieces of tissue were put onto Nash-Snyder Agar and incubated at room temperature for 6-8 days. Pure cultures were transferred to potato dextrose agar. A total of 106 fungal cultures were isolated: representing 80 morphotypes. Twenty-seven morphotypes were recovered from roots, 25 from rhizomes, and 37 from leaves. Isolates were identified morphologically to infer their distribution in *I. marianae*. Further molecular work is needed to determine potential novel species. Exploring fungal diversity in under-researched regions of the world is vital. Species discovery can reveal new scientific information useful for conservation policy and novel applications (e.g. environmental bioremediation efforts).

**POS01-049: INVESTIGATING THE MECHANISMS AND ECOLOGICAL IMPACT OF MYCORRHIZAL-SAPROTROPHIC INTERACTIONS**

Yuzhe Yuan, Rytas Vilgalys
*Duke University, Durham, USA*

**Abstract**

Many land plants engage in mutualistic associations with mycorrhizal fungi, establishing complex symbiotic networks within the rhizosphere. Previous studies have demonstrated that ectomycorrhizal fungi (EMF) can suppress the activity of saprotrophic (SAP) fungi, thereby inhibiting organic matter decomposition. However, the underlying mechanisms structuring these interactions remain poorly understood. This study aims to characterize interactions between pine-associated EMF and co-occurring SAP fungi using a series of *in vitro* pairwise bioassays. We hypothesize that EMF with long-distance exploration types and SAP fungi from mineral horizons will exhibit the strongest levels of inhibition, as measured by a reduction in growth rate and total biomass. EMF associated with and without pine seedlings will be grown in competition with SAP species, and EMF competitive ability will be altered via limiting carbon transfer from the host using light deprivation. We hypothesize that reducing ECM carbon access will increase SAP’s competitive ability. Furthermore, we hypothesize that EMF will modulate their transcriptional activity upon exposure to SAP fungi, resulting in altered enzyme secretion profiles. Analyzing these species-specific interactions will illuminate the ecological consequences of SAP inhibition, including its impact on successional dynamics and nutrient cycling in forest ecosystems.
POSTER SESSION 2

POS02-001: THE EFFECT OF MICROENCAPSULATION ON THE VIABILITY OF FUNGI
Erica Babusci, Amelia Foley, Claudia Gunsch
Duke University, Durham, USA

Abstract
EPA Superfund sites are characterized as locations with hazardous levels of contaminants that require engineered solutions to protect environmental and human health. Polyaromatic hydrocarbons (PAHs) are a group of chemicals that have mutagenic and carcinogenic properties, often prevalent in these Superfund sites. Due to their accumulative and persistent nature in the environment, it is often difficult to remediate PAHs. Mycoremediation is a strategy that utilizes fungi to remove PAHs in a minimally invasive and cost-effective manner. The use of fungi is advantageous because they are resilient in low-nutrient conditions, produce large quantities of reductive enzymes, and can easily compete with other microbes. However, in-situ mycoremediation applications have shown minimal success due to the planktonic cultures’ inability to properly establish within the novel environment. In this project, we aim to develop an encapsulation protocol that better protects the fungi from harsh environmental conditions to improve establishment success, viability, and fitness over longer periods of time. Previously, a library of PAH degrading bacteria and fungi strains have been identified from a PAH contaminated Superfund site. Current methods have been developed to encapsulate the bacteria in the biodegradable polymer sodium alginate, via extrusion. We aim to adapt this protocol to encapsulate fungi, currently focusing on species from the genus Trichoderma, by comparing the growth and viability of planktonic and encapsulated fungal cultures. Methods for quantifying the growth and release of fungi from the microcapsules are under development. These data are essential for determining if current bacterial encapsulation methods are translatable to fungi.

POS02-002: GROWTH CHARACTERISTICS AND HEAVY METALS BIOACCUMULATION BY DESERT FUNGUS PODAXIS PISTILLARIS
Ryan Cotter1, Ming-Min Lee2, Emmanuel Salifu3, Caitlyn Hall
1W.A. Franke Honors College and Chemical and Environmental Engineering Department, University of Arizona, Tucson, AZ, USA. 2School of Plant Sciences, University of Arizona, Tucson, AZ, USA. 3School of Sustainable Engineering and the Built Environment, Arizona State University, Tempe, AZ, USA. 4W.A. Franke Honors College and Biosystems Engineering Department, University of Arizona, Tucson, AZ, USA

Abstract
Two strains of Podaxis pistillaris were evaluated for their ability to tolerate and bioaccumulate copper and zinc for potential soil remediation. Contaminant concentrations were chosen to reflect those found in copper mine tailings in Arizona to consider how effectively P. pistillaris could remediate these mining wastes in-situ. Cultures were germinated from the spores of fruiting bodies collected from urban areas in Tucson, Arizona. Two tolerance assays were tested with a range of concentrations of copper sulfate pentahydrate and zinc sulfate heptahydrate over 3 weeks. Throughout the growth period, the mycelial growth area of each plate was evaluated to determine the tolerance to contaminant concentration. At the end of the experiment, biomass and spent growth media were analyzed to quantify the total heavy metal sequestration. Tolerance is expected to have a negative correlation with higher initial concentrations and the amount of heavy metal sequestered. These results will provide valuable insights into how P. pistillaris interacts with heavy metal contaminants and its potential for soil remediation in arid and semi-arid environments.

POS02-003: THE KAPOOSE CREEK FUNGAL CULTURE COLLECTION AND FUNGARIUM
Michael Ranieri1, Branden Walle2, Stewart McLellan1, Olivia Carter1, Nikoo Mansourian1, Dinuri Punchihewa1, Dima Zada1, Michaela Hughes-Butler1, Yasamin Ghasemi1, Julia Naccarato1, Nicole Arango1, Timsy Bhand1, Adele Girgis-Gabardo1, Janet De Gouw2, Telmah Lluka1, Julia Deisinger1, Eric Brown1,2
1McMaster University, Hamilton, Canada. 2Kapoose Creek Bio, Vancouver, Canada

Abstract
Natural products have long played an important role in modern medicine, inspiring many of the drugs we currently use. Fungi are an important source of these natural products, and past efforts have tapped them as a resource to find compounds that can meet unmet medical needs. Much of this past work has focused on soil- and marine-derived species, with less attention paid towards other species and sources. To find new chemistry, it is paramount that researchers look to less evaluated species and underrepresented sources. The Kapoose Creek Fungal Culture Collection and Fungarium have been sourced from diverse biomes around Kapoose Creek as well as other places within Canada. The collection encompasses over 500 fruiting bodies and 4,500 fungal cultures, highlighting the area’s unique biodiversity. These cultures originate from a broad range of sources, including endophytes from plants, feces from local fauna, insect tissues, soil samples, and, most significantly, macrofungal fruiting bodies. Current efforts to characterize this collection focus on leveraging high throughput nanopore sequencing technology to look at multiple fungal barcode regions in parallel to characterize the collection effectively and robustly. This insight into the diversity of the collection will inform downstream applications in the discovery of novel chemistry.
POS02-004: EXPLORING THE EFFECT OF CHEMICAL PRE-TREATMENT OF LDPE AS A POTENTIAL APPROACH FOR ACCELERATING FUNGAL DEGRADATION OF LDPE PLASTIC FILM
Jacob Simmons1, Leah Karwick1, Marina Eshbaugh2, Samantha Semler3, Thomas Chrzanowski2, Josephine Wee1, Gamini Mendis2, Luciana Aronne2
1Penn State University, State College, USA. 2Penn State University, Erie, USA.

Abstract
Plastic pollution is ubiquitous and continues to worsen as human consumption persists at unprecedented levels. Therefore, it is necessary to find effective and cost-efficient methods of disposal to mitigate this problem. One solution is bioremediation, the use of biological organisms to degrade pollutants. This study aims to assess the ability of filamentous fungi, Aspergillus niger, Aspergillus terreus, and Phanerochaete chrysosporium to degrade abiotically pretreated low-density polyethylene (LDPE) film. By pretreating LDPE with UV radiation or acid-assisted microwave degradation, we seek to test the hypothesis: chemical pretreatment results in enhanced functional groups on LDPE that accelerate fungal degradation. We developed SHIFT, a culture-based method for optimizing fungal biomass in a chemically rich medium prior to transferring into a starvation medium where LDPE is the sole carbon source. FTIR suggests formation of hydroxyl groups (3600-3000 cm-1), monosubstituted C=C bonds (1700-1600 cm-1), and conjugated nitro groups (1600-1500 and 1400-1350 cm-1). SEM showed the formation of pits across the treated LDPE strips, and XPS results demonstrate a decrease in carbon content on the surface and an increase in elements such as oxygen, nitrogen, and phosphorus compared to untreated LDPE. Chemical pre-treatment with nitric acid under microwave conditions demonstrates changes in LDPE film primarily in the hydroxyl (3200-3500 cm-1) and the carbonyl (1600-1750 cm-1) regions. Preliminary experiments suggest laccase and cutinase enzymatic activity that could help explain differences in fungal degradation. Observations from this study indicate that chemical pre-treatment may be necessary for fungal degradation. Outcomes from this work will provide optimized methods and baseline data for combining microbial and chemical remediation for accelerating plastic degradation.

POS02-005: FROM AIR TO LEAF: UNRAVELING AEROBIOTA, ENDOPHYTES, AND LEAF LITTER COMMUNITIES
Diana Avila, Jessica Moody, Gerald Cobian
California State University, Chico, Chico, USA.

Abstract
Fungi are essential and abundant in the environment. Understanding community assembly processes of fungi will allow us to better understand community composition, which potentially influences environmental processes. In this study, we aim to investigate the fungal aerobiota community at the Big Chico Creek Ecological Reserve and compare it to fungal endophyte and leaf litter communities to offer insight into the processes that drive fungal community assembly and ultimately environmental processes. By utilizing two types of spore traps, we will collect and sequence fungal spores from both the air and rainwater from three sites at the Big Chico Creek Ecological Reserve. After obtaining all our samples we will extract DNA and amplify the fungal ITS region to characterize fungal communities associated with the atmosphere, rainwater, foliar fungal endophytes, and leaf litter. Alpha and beta diversity will be assessed to determine what roles airborne fungi play in the community assembly of foliar endophytes and leaf litter communities. Understanding the roles that aeromycota play in the community assembly processes of foliar fungal endophytes and leaf litter communities can help us understand varying communities will influence environmental processes.

POS02-006: SOIL FUNGAL COMMUNITIES ALONG A MONTANE TEMPERATE-BOREAL ECOTONE
Rachel L. Benway1, Jordan Tourville2, Martin Dovciak3, Louis J. Lamit4
1Syracuse University, Syracuse, USA. 2Appalachian Mountain Club, Boston, USA. 3State University of New York College of Environmental Science and Forestry, Syracuse, USA.

Abstract
As the climate changes, the species composition of many biomes will change in response, resulting in far-reaching alterations in biodiversity, nutrient cycling, and other ecosystem services. In mountainous regions, this will likely lead to altitudinal shifts of many plant species’ ranges. For example, in the northeastern U.S., lower elevation temperate tree species are predicted to replace upper elevation conifer species. The majority of research on climate driven range shifts focuses on plants, while fungi are largely overlooked, despite the fact that they too will likely experience range shifts. We are applying DNA metabarcoding and quantitative PCR to soil collected from elevation gradients on three mountains in three northeastern states (New York, Vermont, New Hampshire), to characterize patterns of soil fungal community change with elevation. We predict total fungal diversity will decrease with elevation, but that specific functional groups may show divergent patterns. For example, ectomycorrhizal fungal diversity may be greatest in high elevation montane conifer forests where host basal area is greatest, while arbuscular mycorrhizal fungal diversity will be greatest in low elevation temperate forests where their hosts are more common. Additionally, fungal community species composition should change dramatically along elevation gradients, tracking shifts in plant communities, temperature, soil moisture, and soil pH. Gaining a deeper understanding for patterns of mycorrhizal fungal communities along elevation gradients could increase the accuracy of predictions about how these forests will respond to climate change and can help to inform management decisions as these ecosystems undergo climate influenced changes over the next several decades.
POS02-007: DIVERSITY AND GEOGRAPHIC DISTRIBUTION OF THE THELEPHORACEAE FAMILY (BASIDIOMYCOTA) IN MEXICO
Verónica Rebollo-Osorio, Julieta Alvarez-Manjarrez
Laboratorio de Micología Integral, Instituto de Biología, UNAM, Ciudad de México, Mexico

Abstract
The Thelephoraceae family has been estimated with world-wide high diversity, like Tomentella has 41,565 OTUs. The widespread occurrence of these fungi can be attributed because they can function as ectomycorrhizal and saprotrophs. Despite their ecological relevance, scarce research on these organisms, combined with ecosystems degradation, presents challenges for fungal biodiversity conservation. Our aim was to evaluate the effect of several biogeographic and edaphic variables on the Thelephoraceae diversity in Mexico. We used the 60 sites from Mexico of the soil fungi data from the Global Soil Mycobione consortium. We added biogeographic province, to the metadata. We calculated diversity indexes. We mapped the distribution for each genera within Thelephoraceae. Providing information on vegetation and climate in Mexico. The effect of all the variables will be analyze by PERMANOVA. We discovered 640 OTUs in Mexico from the Thelephoraceae family. Our phylogenetic analysis showed a new genus to be described. We identified: Amaurodon, Odontia, Polyozellus, Pseudotomentella, Thelephora, Tomentella, Tomentellopsis and the probable new genus. The genera with the highest abundance were Tomentella and Thelephora. They were abundant in the states of Coahuila, Yucatan, Oaxaca, and Quintana Roo.

POS02-008: FUNGAL BIOPROSPECTING IN HOSTILE ENVIRONMENTS FOR NEW BIOTECHNOLOGY: THE ST. LAWRENCE RIVER CASE STUDY
Félix-Antoine Simard, Catherine Belanger, Pierre Bouchard, Marilée Thiffault
Bioterre, La Pocatière, Canada

Abstract
The fungal kingdom is vast and contains many different species with a wide variety of useful properties, supported by enzymes and their associated metabolites (primary and secondary). These properties are, among others, inherent to their genetic plasticity and ability to rapidly adapt to new hazardous and difficult to colonize environments. Therefore, fungal bioprospection in hostile environment have tremendous potential for solving urgent global issues (medicine, environmental sustainability, food security, etc.). To offer innovative solutions to the companies that approach us to develop new eco-responsible biotechnological processes, we have undertaken bioprospecting campaigns in hostile environments, particularly the St. Lawrence estuary. Indeed, its physicochemical parameters (variation in osmotic pressure and depth, low temperature, strong current, pH, etc.) suggested the possibility of discovering new fungi (psychro-, halo-, osmo- and/or contaminant-tolerant). Sampling campaigns on this emblematic Quebec River have enabled us to acquire several fungal tools that are very useful for 1- biomonitoring the St. Lawrence estuary against various stresses (global warming, environmental contaminants, exotic invasive species, etc.) and 2- isolating fungal species with great biotechnological potential. Among these, it is possible to highlight specimens which are particularly effective for producing various biomolecules of interest, such as biocides (Epicoccum nigrum), melanin (Cadophora sp.), mycoprotein (Paradendriphiella salina), mycomaterials (Isaria farinosa), degradation of contaminants (Lulwana sp.), and many others. Thus, the fungal biodiversity of the St. Lawrence River is a good example that supports the idea that hostile environments are real gold mines for the development of innovative bioprocess.

POS02-009: PARASITIC FUNGI AS MEDIATORS OF MARINE CARBON CYCLING: EXPLORING THE IMPACT OF FUNGAL PARASITISM ON THE GROWTH AND METABOLISM OF BLOOM-FORMING DIATOMS
KJE Hickman1,2, Sara Shapiro1, Harriet Alexander2
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Abstract
Diatoms are single-celled primary producers inhabiting the open ocean, converting sunlight into carbon that serves as the base of the marine food web. Alongside other phytoplankton, diatoms fix organic carbon and cycle silica, offering a foundational contribution to marine carbon cycling. Prior observations suggest that parasitic fungi and other heterotrophic protists may capitalize on the explosive biomass production that occurs during phytoplankton blooms as a source of readily available substrate, particularly in polar environments. These activities redirect the flow of carbon through the food web, a phenomenon referred to as the “fungal shunt,” and is emerging as an important concept in our understanding of the marine carbon cycle. We co-isolated a putative fungal parasite and host diatom from the Scotian shelf in the fall of 2023. Cross-infection experiments indicate a broad host range that spans disparate pennate diatoms, but an apparent inability to infect centric diatoms. We tested the impact of parasitism on diatom growth and metabolism using a pennate diatom host, Asterionella spp. We hypothesize that transcription patterns will vary between early- and late-stage growth in infected cultures beyond the variability observed in their uninfected counterparts. Preliminary data suggest that the parasite lives dormant during host exponential growth with infection taking off in late exponential. This type of parasite may cause phytoplankton blooms to terminate early, with variable impacts based on host species’ susceptibility. These data point to the important role of parasitic fungi as top-down controls on phytoplankton populations and carbon flow through marine food webs.

POS02-010: PRIORITY EFFECTS OF FOLIAR FUNGAL ENDOPHYTES IN LEAF LITTER DECOMPOSITION
Tawny Aeriel Bolinas, Gerald Cobián
California State University, Chico, Chico, USA

Abstract
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 primary objective of this project is to investigate and determine which of these fungi are involved in the decomposition of leaf litter after leaves have fallen from trees. Since fungal endophyte 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, this project will aim to 1) determine how fungal endophytes influence the composition of leaf litter fungal communities through priority effects; 2) investigate the efficiency of fungal endophytes as leaf decomposers; and 3) determine how fungal endophyte communities and leaf decay communities change over time. By understanding the influence of fungal endophytes on leaf litter decomposition and the carbon cycle, the results of this project could have important implications for understanding and managing ecosystem services.

POS02-012: FOLIAR ENDOPHYTIC FUNGI OF PSEUDOTSUGA MENZIESII
Birgitta Woods, Abbey Neat, Posy Busby
Oregon State University, Corvallis, USA

Abstract
Foliar endophytic fungi (FEF) are nonpathogenic microbes that inhabit above ground plant tissue with varying functional impacts on their hosts. In a previous experiment, we demonstrated that Douglas-fir (Pseudotsuga menziesii) seedlings inoculated with a P. menziesii foliar microbial community exhibited increased growth and drought tolerance. However, this was only true for seedlings sourced from high elevation populations, not low elevation populations. In the present study, we are testing the hypothesis that P. menziesii seedlings from high elevations are characterized by a greater abundance and diversity of fungal leaf endophytes than seedlings sourced from low elevations. This study was executed through a reciprocal inoculation greenhouse experiment in which seedlings from across the same elevation gradient, located in the Western Oregon Cascades, were grown in a greenhouse and inoculated with a P. menziesii foliar microbial community from either the highest or the lowest site. Needles were collected after inoculation, surface sterilized, cut into segments, placed on agar for culturing, and individual fungal endophytes later identified by sequencing the ITS region. Data analysis is ongoing. We will present results testing the hypothesis that trees from different populations interact with microbes differently depending on the environmental conditions in which they originated.

POS02-013: PREDICTING FUNGAL COMPETITIVE SUCCESS IN DECAYING WOOD: IMPACT OF INOCULUM POTENTIAL
Aiym Bakytbaikyzy, Jonathan Schilling
University of Minnesota, Saint Paul, USA

Abstract
Eighty percent of Earth’s aboveground biomass is stored in wood, and fungi are its main decomposers. Fungi competing for the same wood substrates have two main distinct nutritional modes: white rot (lignin-degrading) and brown rot (lignin-avoiding). Recalcitrant particulate lignin left behind by brown rot likely gets sequestered into the soil, rather than being released into the atmosphere as CO2 via fungal respiration. Since lignin constitutes a substantial 40% of the total wood carbon, competition between brown and white rot fungi has significant consequences for carbon cycling. To determine the competitive success of Fomitopsis betulina (the sole brown rot decaying birch), we set up a fully factorial field experiment to test the effects of three variables: 1) log sterility (endophytic presence), 2) soil sterility (presence of more combative species), and 3) the presence of the F. betulina inoculum. After decay, we calculated ratios of lignin loss to density loss (>0.8 for white rot) to infer rot type. We ran ITS2 and 16S sequencing to establish community composition before (targeting endophytes) and after decay. We found that inoculum potential had a significant effect on F. betulina’s success, while log sterility and soil sterility did not, suggesting that inoculum potential overrides assembly history. Inoculum potential also had a significant effect on bacterial alpha and beta diversity. Thus, we developed a system, in which to test the colonization success of brown rot, carbon consequences in birch, and relationships between the prevailing rot type and subsequent colonizer dynamics, including bacteria.
**POS02-014: FUNGAL COMMUNITY RESPONSES TO EXPERIMENTAL WARMING IN A POOR FEN**
Miranda Murray1, John Hribljan2, Rodney A. Chimner2, Evan S. Kane3, Erik Lilleskov2, Louis J. Lamit1
1Natural History Museum of Utah & School of Biological Sciences, University of Utah, Salt Lake City, USA. 2Biology Department, Duke University, Durham, USA

**Abstract**
Peatlands are critical global carbon stores; despite covering just 3% of Earth’s surface, they sequester 15–30% of Earth’s soil carbon. Global change stressors associated with climate change such as increased temperatures and drought conditions may shift the balance of carbon fluxes, turning peatland ecosystems from carbon sinks to carbon sources. Fungi are essential in carbon mobilization and stabilization in peatlands as free-living saprotrophs and root-associated symbionts, yet we have a poor understanding of how peatland fungi are impacted by climate change. Our aim was to examine the effects of elevated temperature on fungal community structure, within the context of heterogeneous peatland microtopography. In a poor fen in Michigan’s Upper Peninsula, 1m² plots were established in hummock and lawn microforms and subjected to heating with infrared lamps or designated as controls. Cores were collected after two seasons from the 10-20 cm soil depth, and fungal communities were characterized with DNA metabarcoding. Ongoing data analyses are addressing the following predictions. We expect heating to shift fungal composition and reduce diversity, although the effect will be modest relative to distinctions between hummocks and lawns. Importantly, microform will likely modulate the influence of heating. If heating creates drier conditions, communities in lawns that typically experience wetter conditions may change more than those in hummocks, whose drier ambient conditions may have prefiltered sensitive species. Alternatively, if short term heating does not strongly change moisture, the more saturated lawn communities may be buffered from the stresses of increased heat relative to hummock communities.

**POS02-015: EFFECTS OF CHANGING FORESTS ON THE GENETIC DIVERSITY OF BOLETUS EDULIS**
Alexander Housley1, Keaton Tremble2, Bryn Dentinger2
1Natural History Museum of Utah & School of Biological Sciences, University of Utah, Salt Lake City, USA. 2Biology Department, Duke University, Durham, USA

**Abstract**
Climate change, drought, and resource overexploitation have had a drastic impact on forest ecosystems, especially in places like California, where drought is frequent, yet how these aboveground environmental impacts affect ectomycorrhizal (ECM) mutualists belowground is currently unknown. This project focuses on the widespread ECM fungus Boletus edulis Bull. (porcini) to investigate how ecosystem changes have affected the genetic diversity of natural B. edulis populations over time. We generated a population genetic dataset using whole-genome shotgun sequencing of fungarium specimens collected in California over the past 100 years. This dataset will be used to test the hypothesis that forest fragmentation has had little impact on B. edulis genetic diversity because of its wide global distribution and capacity for spores to travel long distances. Preliminary results will be presented.

**POS02-016: UTILIZING PRESENCE ONLY PREDICTION TO MODEL MORCHELLA DIMINUTIVA DISTRIBUTION**
Spencer Baldwin, Barbara Shock
Lincoln Memorial University, Harrogate, USA

**Abstract**
Morels (Morchella spp.) are recognized for their cultural importance and culinary use; however, some species remain understudied. Morchella diminutiva was formally described in 2012, but little follow up research has occurred. To determine the ecology of M. diminutiva, in situ experiments should be conducted. Utilizing GIS analyses we can create predictive species distribution models to guide future environmental collections and research. The purpose of this study is to develop a predictive model and test the model with mycelia eDNA collections at predicted locations. Using Maxent, we can identify which environmental factor(s) best predicts M. diminutiva growth. After implementing the worldclim bioclimatic data set, we found that coldest quarter mean temperature was the strongest predictive variable with a model AUC of .899. A hotspot map of M. diminutiva predicted distribution was also generated. In summer 2024, we will test the efficacy of the model by collecting soil samples from areas with high, medium, and low presence predictions and screening these samples with molecular techniques. Following field sampling we plan to develop a linear regression model as well as identify the correlation coefficient of prediction to observed presence. These data will assist in understanding the ecology of M. diminutiva as well as provide a workflow for the study of other cryptic species, including plants or wildlife.

**POS02-017: FACTORS AFFECTING ECTOMYCORRHIZAL COMMUNITY ECOLOGY IN THE KICKAPOO VALLEY, WISCONSIN U.S.A.**
Jacob Hansel
University of Wisconsin La Crosse, La Crosse, USA

**Abstract**
The Kickapoo Valley in southwest Wisconsin, U.S.A. is a unique ecosystem comprised of old growth and early successional forests that rely on symbioses with the ectomycorrhizal (ECM) community to thrive. To understand how the ECM symbiosis affects the health and stability of this ecosystem, tree, soil bacterial, and ECM community composition was surveyed in 23 plots in the Kickapoo Valley; soil characteristics were also examined. The surveys identified 6 distinct tree communities, which varied along a north to south gradient, with significant differences observed among slope aspects. Soil texture varied among loam, sandy loam, and silt loam. Carbon utilization metabolic assays of the soil bacterial communities showed high functional diversity amongst the surveyed plots. The greatest range of carbon substrate utilization was found in tree communities with significant understory debris. Future analyses include identifying ECM fungi isolated
from tree roots in the soil samples to determine ECM fungal community composition on the levels of individual trees, individual soil cores, and entire plots. Tree, fungal, and soil bacterial communities will be identified using Illumina sequencing. Results of these analyses will provide an overview of the factors that affect the interactions of ECM trees, fungi, and soil bacteria of the forested ecosystems within the Kickapoo Valley that can be applied to other temperate forested ecosystems worldwide.

**POS02-018: FUNENDO: A COMPREHENSIVE GLOBAL FUNGAL ENDOPHYTE REPOSITORY**

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**Abstract**

In the past two decades, endophyte studies have grown exponentially due to their ecological significance and ability to produce metabolites that modulate the host plant’s physiology or have pharmacological properties. However, according to our knowledge, no global database of fungal endophytes exists to study their distribution, taxonomic and ecological diversity, host and organ specificity, or phylogenetic host preference. In the present study, we compiled a list of fungal endophytes from articles in English and Chinese, extracted from the Web of Science, Scopus, PubMed, and published and unpublished data in GenBank repository and FungalTraits dataset. The ITS sequences, host species, plant organ types, and geographical distribution were included as metadata. More than 100,000 fungal records were amassed from approximately 4,500 studies, encompassing around 4,300 fungal species, 1,789 genera, 522 families, 165 orders, and 47 classes. Our results indicate that although the fungal endophytes belong to ten different phyla, Dikarya encompasses more than 90% of the total number of endophytic fungi records. Taken together, 4329 plant species have been reported to host fungal endophytes. Plant leaves represent the predominant source of endophytes, followed by branches and roots in frequency of reports. The United States, China, and India are the countries where fungal endophytes are most commonly documented. Initial statistical analyses suggest significant variations in fungal endophyte distribution across various ecoregions in the globe. Statistically distinct phylogenetic clusters of endophytes are associated with particular host species across diverse ecological niches and environments.

**POS02-019: MYCORRHIZAL COMMUNITIES OF NATURAL AND RESTORED ATLANTIC WHITE CEDAR SWAMPS IN SOUTHEASTERN MASSACHUSETTS**

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**Abstract**

Atlantic white cedar (Chamaecyparis thyoides) swamps are a threatened wetland ecosystem in the eastern coastal plain of the US that are increasingly being restored. These systems have unique features in terms of plant community composition, mycorrhizal fungal type, and peat-forming soils, but their mycorrhizal and soil fungal ecology is not well researched. This study examines the potential difference in fungal ecology between restored and natural Atlantic white cedar swamps, and what factors are driving that difference. This is being done through DNA metabarocking of arbuscular mycorrhizal fungi and the broader fungal community, quantifying mycorrhizal colonization of roots, and analysis of abiotic and biotic factors that might be driving the difference between restored and natural cedar swamp fungi (e.g., pH, depth to water table, plant community composition, cedar canopy cover and basal area, and soil N and P chemistry). This research aims to uncover unique fungal biodiversity hidden in these rare ecosystems, and the results will directly benefit conservation and restoration efforts underway in southeastern Massachusetts.

**POS02-020: ROOT ASSOCIATED FUNGAL COMMUNITIES DIFFER BETWEEN PHOSPHORUS-RICH VERSUS POOR SOILS IN CENTRAL PANAMA BUT DO NOT ACCOUNT FOR DIFFERENCES IN SEEDLING GROWTH RATES**

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**Abstract**

Soils of the Panama Canal watershed vary almost as much in phosphorus as those of the entire Amazon Basin. This variation is associated by high compositional turnover, with >50% of tree species showing strong preferences for high or low phosphorus soils. The traits underlying P specialization remain unclear. We used a pot experiment to determine whether low phosphorus specialists obtain greater benefits from mycorrhizal communities associated with low phosphorus soils. We grew seedlings of 9 tree species differing in P requirements in sterile soil collected from either a low (283 ppm total P) or high (794 ppm total P) phosphorus site, and then added 150 g of either live or sterile inoculum (soil and roots) collected from beneath one of four tree species from each site. We found that seedlings always grew faster in the high P soil, and that the impact of inoculum source was generally small. However, in the low P soil, seedlings grew faster with live vs sterile inoculum, and contrary to expectation, had 2-3 fold faster growth rates with live inoculum from the high P versus low P soil. Metagenomic sequencing of roots indicated that these differences could be attributed to distinct AMF communities in the high vs low P soils. In addition to
AMF, seedlings were also infected with Mucoromycotina but only in the low P soil and inoculum combination. In conclusion, root associated fungal communities vary with inoculum source and soil type, but cannot account for observed species performance and distribution patterns.

POS02-021: THE CHANGING SOIL MYCOBIOME DURING AMERICAN GINSENG (PANAX QUINQUEFOLIUS) CULTIVATION.
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Abstract
Various species of ginseng (Panax) have been used for several thousand years in herbal medicine. American ginseng (Panax quinquefolius) which is native to the understory of deciduous forests in eastern North America, became endangered in the wild due to overharvesting, which led to the development of its commercial cultivation. Commercial cultivation, however, can lead to root rot and associated reduced crop yield when ginseng is replanted in the same field where it had been grown previously, a disease syndrome known as Ginseng Replant Disease (GRD). To better understand the etiology of this syndrome, we investigated the soil mycobiome at planting and harvest of cultivated American ginseng in a newly planted garden and 3–14 years post-harvest from former ginseng gardens. Using single-molecule real-time sequencing (Pacific Biosciences), we generated ~600 bp sequence reads from the nuclear ribosomal internal transcribed spacer (ITS). These longer sequence reads improved discrimination among closely related fungi, such as differentiating species of Ilyonectria and Fusarium. Fusarium oxysporum and F. solani, which are known plant pathogens, increased in relative abundance after ginseng harvest from a new garden, whereas F. equiseti decreased in a replant garden. These variations in the relative abundance of particular fungal species enabled us to distinguish between newly planted ginseng gardens, a former ginseng gardens, and a replant garden. These patterns could be useful for development of a diagnostic tool for identifying sites previously exposed to ginseng cultivation.

POS02-022: BEYOND ECTOMYCORRHIZAL SPECIALIZATION: UNVEILING THE COMPREHENSIVE FUNGAL COMMUNITY COMPOSITION IN CENTRAL CALIFORNIA’S OAK SAVANNAS
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Abstract
California’s oak savannas, hallmarked by Quercus species, are critical yet declining ecosystems where fungal diversity plays a pivotal role in forest health and nutrient cycling. This study extends prior work on ectomycorrhizal fungi, particularly the Cortinarius genus, to a comprehensive assessment of the broader fungal community associated with these habitats. Utilizing soil samples from an elevational gradient across five Sierra Nevada sites, we applied high-throughput Illumina sequencing of the ITS1 region, targeting the complete spectrum of soil fungal operational taxonomic units (OTUs). The approach enables a detailed characterization of the fungal communities, while advanced bioinformatic processing and statistical analyses, including ANOVA and ordination, aim to discern patterns of diversity and community structure. The focus of the ongoing analysis is to elucidate why Quercus douglasii hosts a notably diverse ectomycorrhizal consortium compared to other oak species. We hypothesize that the interaction between host-specific traits, environmental conditions, and community dynamics influences fungal diversity. Anticipated outcomes include identifying key factors driving fungal distribution across different oak hosts, their adaptation to environmental gradients, and determining the ecological implications of these associations. This investigation offers crucial insights into the conservation of oak savannas, highlighting the intricate links between fungal diversity and ecosystem services. Results will provide a nuanced understanding of community composition, inform sustainable management practices, and contribute to the broader ecological narrative of Californian forest systems. The knowledge gained will be vital for preserving these biodiversity hotspots in the face of ongoing environmental changes.

POS02-023: MAPPING TO PROTECT AND CONNECT: SCIENCE AND OUTREACH AT THE SOCIETY FOR THE PROTECTION OF UNDERGROUND NETWORKS (SPUN)
Camille Truong, Adriana Corrales, Bethan Manley, Rachel Pringle, Justin D. Stewart, Michael E. Van Nuland, Kellie Walther, E. Toby Kiers
Society for the Protection of Underground Networks (SPUN), Dover, USA

Abstract
Soil-inhabiting fungi are among the most species-rich groups of organisms on Earth and are indispensable drivers of ecosystem composition and functions. The Society for the Protection of Underground Networks (SPUN) is a science-based initiative that aims to map and safeguard the mycorrhizal networks that regulate Earth’s climate and ecosystems. In collaboration with local researchers and communities, SPUN leads efforts to explore mycorrhizal biodiversity and advocates for the inclusion of fungi in conservation and climate agendas. We combine geolocated databases of mycorrhizal sequencing data with ecological and environmental variables to generate spatial predictions of mycorrhizal diversity using machine learning. This method allows us to quantify and map the uncertainty of these predictions and identify under-sampled ecoregions to guide future mycorrhizal research across the globe. To improve the accuracy of our models, we work with local researchers to physically sample soils in ecosystems identified by our models as having the highest uncertainty values. These data are then fed back into our models, improving our predictions. So far SPUN has led or funded expeditions in 40+ countries, including Chile, Kazakhstan and Lesotho. In collaboration with GlobalFungi, we have processed over 2.8 billion SSU and ITS amplicon sequences. Our prediction maps indicate that >90% of mycorrhizal biodiversity hotspots are unprotected under current regulations. Such information is critical for governments, policymakers, NGOs, and others, to include mycorrhizal fungi in conservation agendas. Additionally, our Science Associate program includes more than 350 members from 30+ countries, providing support, networking opportunities and capacity building in understudied regions.
POS02-024: NUCLEOTYPE SELECTION IN NEUROSPORA CRESSA HETEROKARYA
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Abstract
Syncytial fungi can house tens, even hundreds of nuclei within large hyphal compartments. These nuclei are totipotent, creating the possibility for conflicts between nuclei over resources. We aim to study the extent to which resources are held in common among genetically diverse nuclei. To test whether different nucleotypes may have different division rates, we use heterokaryon constructed from two auxotrophic mutants of the fungus Neurospora crassa. We vary the level of interdependence between the two populations by growing mycelia on media that partly or fully supplement either or both nucleotypes. Our results show that when one of the auxotrophs is completely supplemented, eliminating its dependence upon the other nucleotype, then the proportions of nuclei become skewed. This indicates that selection can occur at the level of nucleotypes within a syncytium, illuminating broader mechanisms for how new nucleotypes can emerge and evolve.

POS02-025: IDENTIFICATION OF AN UNKNOWN FUNGUS THAT IS LETHAL TO SANDFLY COLONIES
Natasha Goldson, Priscilla Chaverri
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Abstract
This research was conducted to show the importance of this unknown fungus and its relation to sandflies. In doing so there will an analysis of the type of fungi that is killing the sandflies. Leishmaniasis is a disease that sandflies carry and infects their host by biting them. This raises some concern especially for military personnel due to them having to travel to tropical countries. To distinguish the type of fungus present, DNA extraction and PCR sequencing and analysis will be conducted.

POS02-026: BEHAVIOURAL PROFILING OF FUNGAL SECONDARY METABOLITES FOR NEUROACTIVE COMPOUND DISCOVERY
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Abstract
Natural products have unmatched structural and functional diversity, refined over millions of years of evolutionary trial-and-error within their biological systems. While fungi have seen therapeutic use across human history, these microbes are relatively underexplored due to limitations with laboratory cultivation. Our laboratory has assembled a fractionated fungal extract library, derived from fungi foraged largely from a remote and temperate rainforest on Vancouver Island, Canada. The objective of this research is to identify novel neuroactive fungal metabolites from this library using a high-throughput behavioural assay with the model organism Caenorhabditis elegans. We hypothesize that neuroactive phenotypes from fungal metabolites can be identified using a comparative set of known neuroactive drugs. To achieve this objective, we are carrying out behavioural screens using a diverse collection of known neuroactive compounds. Here, behavioural responses to compound exposure are quantified into a profile of 256 behavioural features using Tierpsy Tracker, an open-source software that tracks individual and multi-worm behavioural phenotypes such as swimming dynamics, morphology, and trajectory. We aim to use machine learning methods to create a comprehensive functional map of neuroactive drugs in order to understand the activity and mechanism of neuroactive fungal metabolites. This project represents an exciting opportunity to discover novel neuroactive natural products derived from fungi, using an unconventional whole-animal behavioural model.

POS02-027: FUNGI, FRIEND OR FOE: THE ROLE OF ZANCUROMYES CULISETAE ON Aedes aegypti DEVELOPMENT
Jessica Cho-Ah-Ying, Paige Van Rooy, Yostina Farag, Chiung Joyce Wu, Yan Wang
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Abstract
Research on animal gut microbiomes has suggested that microbes can play a variety of roles in influencing their host’s behaviour and development. However, fungi, as one of the major components of the animal gut community, remain under-investigated. Zancudomyces culisetae is one of the most frequently encountered species of insect gut-dwelling fungi across the globe and has been used as a model to pioneer our understanding of these cryptic microbes. While historically regarded as commensals, the obligate associations between insects and their gut-dwelling fungi present a shifting symbiotic capacity sliding towards mutualistic or parasitic relationships under certain circumstances. In this study, we will use Z. culisetae and Aedes aegypti to study how the gut-dwelling fungus influences host growth and development under both nutrient-rich (fed) and nutrient-poor (starving) conditions. Host development parameters, such as body length, head length/width, and thorax length/width will be measured in each condition with or without the presence of the gut fungus. Survivorship will also be examined in starving conditions when larvae fail to pupate. In fed conditions, time to pupate and time spent in the pupal stage before adulthood will be examined. Preliminary results will be presented.

POS02-028: ACROSS 160 YEARS OF EXPERIMENTAL RESEARCH: A QUEST FOR LICHEN RESYNTHESIS
Arseniy Belosokhov, Toby Spribille
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Abstract
Lichens are regarded as exemplary avatars of symbiotic relationships. Emerging as entangled interactions between fungi, algae, and a variety of microorganisms, they serve as a never-ending source of insight that stimulates our understanding of symbiosis. Given their nature, lichens naturally prompted numerous experiments aiming to establish a routine process for their disassembly and subsequent reassembly from their constituent parts (a process often referred to as ‘resynthesis’). This experimental practice, though straightforward in theory, has proven to be exceptionally challenging. Despite over 160 years of research and a series of milestone
experiments, the achievement of true resynthesis remains in question. We reviewed a century and a half of literature on lichen resynthesis studies in more than 350 papers, including reported successes, failures and methods used. We assessed the reported results against modern standards for sterile methods in microbiology and thresholds for success based on natural stages of lichen development.

**POS02-030: THE EFFECT OF AN ENDOSYMBIOTIC BACTERIUM ON THE ARBUSCULAR MYCORRHIZAL FUNGUS RHIZOPHAGUS CLARUS AND A HOST PLANT**

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**Abstract**

The bacterium ‘Candidatus Mомнiiplasma glomeromycotorum’ is a recently discovered widespread obligate endosymbiont of the arbuscular mycorrhizal fungus *Rhizophagus clarus*. However, little is known about the effect this bacterium has on its fungal host or the impact of the endosymbiosis on a plant host. Previous work in our lab found tentative fitness advantages in strains of *R. clarus* containing the bacterium. Spore germination and hyphal branching rates were higher in strains containing the bacterium than in strains without the bacterium. This study investigates the impact of the bacterium on host plant growth using the model system *Medicago truncatula*. The objectives are to measure how plant biomass and nutrient uptake are affected, and the impact on gene expression of the plant and fungus when the endobacterium is present. *M. truncatula* will be inoculated with endobacteria-containing and endobacterium-free strains of *R. clarus*. Strains are taken from the International Collection of (Vesicular) Arbuscular Mycorrhiza Fungi, and bacterial presence is confirmed using PCR. Plants are exposed to phosphorus-sufficient or phosphorus-deficient fertilizer, and plant growth responses are measured. RNA sequencing will be performed on plant root cells containing arbuscules to identify differentially expressed genes associated with bacterial endosymbiosis. Based on our previous results, we predict that strains of *R. clarus* containing the bacterium will be associated with increased plant biomass and nutrient uptake, especially in phosphorus-deficient conditions. This study may contribute to building a predictive framework for applications of AMF in agricultural systems and ultimately reduce the dependency on chemical fertilizers.

**POS02-031: CHARACTERIZING THE GUT MICROBIOME OF EASTERN HELLBENDERS (CRYPTOBRANCHUS ALLEGANIENSIS ALLEGANIENSIS) IN A HEADSTART PROGRAM**

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**Abstract**

Amphibians are the most threatened group of vertebrates globally, with 41% of amphibians at risk of extinction. Recent declines in amphibians have been ascribed to a myriad of anthropogenic and environmental causes, including climate change, emerging infectious diseases, and habitat loss. Consequently, population declines have stimulated an increase in captive breeding and headstart programs as a management strategy for the conservation of imperiled amphibian species. Nevertheless, a comprehensive understanding of the complex interkingdom interactions in the gut microbiome of amphibians must be elucidated for effective implementation of conservation strategies, especially considering that disturbance-induced dysbiosis of the gut microbiome can adversely impact host health. Hellbenders (*Cryptobranchus alleganiensis*), the largest species of salamander in North America, have experienced persistent declines across their historic range in recent decades and are now listed as threatened or endangered in many states, including Tennessee. Due to these population decreases, Nashville Zoo began a headstart program in 2015, where wild-collected hellbender eggs are reared in captivity prior to reintroduction. By using metabarcoding and high-throughput amplicon sequencing with bacterial 16S rRNA and fungal ITS1 rDNA markers, an increased understanding of the composition and intricate bacterial-fungal interactions within the gut microbiome of an imperiled amphibian species will be elucidated. Anticipated results will include a characterization of the bacterial-fungal gut assemblages of pre-release hellbenders in captivity and post-release individuals in the wild, with the aim of informing headstart programs on the potential to rewild the gut microbiome.
Abstract

The order Mucorales in the Mucoromycota Fungi is responsible for the fungal disease mucormycosis, a condition with increasing incidence and a mortality rate exceeding 85% in some forms. However, we lack basic understanding of Mucorales biology, evolution, and pathogenesis in the human body. Endosymbiotic bacteria are common in the Mucorales, and are known to facilitate their pathogenicity in plants and animals by contributing secondary metabolites to their fungal hosts, but many questions remain as to the diversity and maintenance of bacterial populations in fungi. Rhizopus microsporus (Rm) is one of the most common agents of mucormycosis, and many of its strains harbor endosymbiotic bacteria. These bacteria, often Mycetohabitan spp. (formerly Burkholderia), exert control over fungal reproduction and provide the fungus with metabolites that help it evade macrophagic destruction. This integrated relationship suggests vertical transmission of endosymbionts, but we believe that horizontal transfer must occur between Rm strains, since endosymbionts would disappear from Rm lineages otherwise. Therefore, our goal in this project is to film interactions between Rm and associated Mycetohabitan species. We will constitutively express fluorescent proteins in the Mycetohabitan endosymbiont and Rm host using a CRISPR-Cas9 homologous recombination system. We will then film fungal bacterial interactions on a microfluidic device to enable visualization of single hyphae. We hope to provide direct evidence of horizontal transfer of endosymbionts between Rm strains. This research will suggest mechanisms of bacterial sorting and exchange within fungal hosts and inspire avenues for future investigations.

POS02-034: BIOPROSPECTING FUNGAL ANTAGONISTS OF SOYBEAN CYST NEMATODES
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Abstract

Understanding the interactions of fungi with plant pathogens in the soil can help us discover sustainable approaches to manage the yield loss they cause. This project focuses on bioprospecting fungi as potential biocontrol agents for the soybean cyst nematode (SCN) Heterodera glycines. SCN is the most devastating soybean pest in the U.S., estimated to cause more than twice as much yield loss as any other disease. Prior research found two potential nemathophagous fungi prevalent in Ohio soils and enriched when soybean cyst nematode abundance was high. To isolate these fungi, we collected 11 soil samples from soybean fields with a high abundance of SCN (> 600 SCN eggs/100cm3 of soil) in Ohio. A high throughput isolation approach was used with three media types to increase isolate diversity. Each sample had five replicates per media type, totaling 165 plates. Six hundred fifty isolates were recovered from these plates and organized into 235 morphotypes. These morphotypes ranged from 1 to 51 isolates per group. A representative of each morphotype was selected and placed in long-term storage using two different approaches. Ultimately, 25 morphotypes did not survive long-term storage, leaving 210 isolates in our collection. We use the molecular barcodes TEF1 and ITS to identify the taxonomy of these fungi. These fungi will then be tested for SCN antagonistic activity based on the production of extracellular chitinases and proteases and through SCN egg colonization assays. Ultimately, this research will support discovering potential biocontrol agents against SCN.
POS02-035: A TRANSCRIPTOMIC INVESTIGATION OF ZN TOLERANCE IN SUILLUS LUTEUS
Jessica Fletcher1, Alexander Smith1, Janne Swinnen2, Karl Jonckheere2, Anna Bazzicalupo3, Sunny Liao4, Greg Ragland1, Jan Colpaert3, Anna Lipzen3, Sravanthi Tejomurtula4, Kerrie Barry1, Igor Grigoriev4, Joske Ruytinx1, Sara Branco1
1University of Colorado Denver, Denver, USA. 2Vrije Universiteit Brussel, Brussels, Belgium. 3Royal Botanic Gardens, Kew, United Kingdom. 4University of Florida, Quincy, USA. 5Hasselt University, Hasselt, Belgium. 6Joint Genome Institute, Berkeley, USA

Abstract
Zinc (Zn) is a micronutrient required for metabolism, growth, and reproduction. However, in excess it disrupts cell function and can lead to death. We investigated the genetic basis of Zn tolerance in Suillus luteus, an ectomycorrhizal fungus associated with pine trees. Previous research found tolerant and sensitive isolates, and candidate genes for metal tolerance. We compared the transcriptomes of a Zn-tolerant and a sensitive isolate in the presence/absence of Zn stress to investigate genes actively involved in tolerance. The isolates showed overall distinct transcriptomes. The Zn-sensitive isolate showed significant gene expression changes upon Zn exposure, with downregulation in genes involved in transmembrane transport and metal binding, and upregulation in genes related to stress responses. The Zn-tolerant isolate showed little response to Zn exposure. Zn induced upregulation of stress response and Zn binding genes and downregulation in transport genes in both isolates. In addition, we found that genes downregulated in the sensitive isolate Zn response were already being expressed at significantly lower levels in the tolerant isolate in no Zn conditions, indicating tolerance is likely constitutive and expressed independently of metal exposure. We also found expression of chromatin rearrangement and DNA binding genes in the tolerant isolate, which suggests epigenetic regulation of constitutive Zn tolerance. This research deepens our understanding of the molecular mechanisms involved in Zn tolerance in Suillus species and paves the way for further studies highlighting the importance of ectomycorrhizal fungi in host plant symbiosis and environmental stress.

POS02-037: EXTENSIVE AND INDEPENDENT EVOLUTION OF SECONDARY METABOLISM GENES ACROSS THE EARLY DIVERGING FUNGAL GENUS BASIDIOBOLUS
Jasper Carleton1, Liam Cleary1, Emily Newman1, Maddie Hincher2, Javier Tabima Restrepo1
1Clark University, Worcester, USA. 2Massachusetts General Hospital, Boston, USA

Abstract
Secondary metabolism (SM) is responsible for the biosynthesis of biologically and medically important compounds with roles in antibiotics, toxicity, plant virulence, and response to environmental cues. In the fungal kingdom, SM is best characterized within Dikarya, where ascomycete fungi are well known producers of alkaloids, peptides, polyketides and terpenes. Conversely, the prevailing hypothesis is that zygomycete fungi do not produce a comparable diversity of secondary metabolites. An exception of this is the genus Basidiobolus (Entomophthorales; Basidiobolaceae), characterized by harboring a large number of secondary metabolite genes with potential roles of antibiotics, metal capture and host immune response modulation. We present computational, evolutionary, and functional predictions of SM across different species and isolates from the genus Basidiobolus, showing that SM genes are predicted across all described species in the genus. In addition, we show that while SM core gene abundance appears to be dependent on taxonomic group, two SM core genes are found across all species. These results illustrate the unexpected diversity of SM across early diverging fungal species.

POS02-038: DESIGN AND DEVELOPMENT OF QUANTITATIVE PCR ASSAY FOR DETECTION AND QUANTIFICATION OF XYLARIA NECROPHORA, THE CAUSAL AGENT OF SOYBEAN TAPROOT DECLINE
Qiurong Fan, Alejandro Rojas
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Abstract
The soybean taproot decline is an emerging disease in the southern United States, with distribution in Alabama, Arkansas, Louisiana, Mississippi, Missouri, and Tennessee. The causal agent of this disease is the ascomycete fungus Xylaria necrophora. It can target the soybean root system, causing the roots to turn charcoal-colored and the taproot to decline and break when plants are uprooted. Foliar symptoms include yellow interveinal chlorosis and necrosis. Infection can occur early in the season, causing seedling death. Adjacent plants with lower infection levels can cover it up and disease remains unnoticed until late in the season. Current identification approaches of X. necrophora are mainly based on root and culture morphology, and phylogenetic characterization comparing the internal transcribed spacer, partial sequence of the second largest unit of RNA polymerase II, partial alpha-actin and partial beta-tubulin with reference sequences of Xylaria from previously published studies. These methods are time-consuming, enforcing the need for an improved diagnostic assay. In this study, we designed a TaqMan-based qPCR assay targeting the Xylaria necrophora species-specific internal transcribed spacer region for detection and quantification of this pathogen. The limits of detection for assay targeting pathogen along and assay multiplexing pathogen and plant internal control are both at 10fg/ul. This assay will be an applicable tool for detecting Xylaria necrophora affecting soybean.

POS02-039: ASSESSING ASSORTATIVE MATING BY PHENOTYPE IN A DIMORPHIC FUNGUS, LENTINUS TIGRINUS
Sofie Irons, David Hibbett, Javier Tabima, Thomas Roehl, Carlos Perez-Gazca, Olive Peterson, August Waggerner
Clark University, Worcester, USA

Abstract
Lentinus tigrinus is a white-rot wood decaying fungus known to grow in close proximity to bodies of water that are periodically flooded. The fruiting bodies produced by L. tigrinus are phenotypically dimorphic: agaricoid (hymenophore with exposed gills) and sectoid (hymenophore with enclosed gills at maturity). Based on previous studies, this dimorphic quality is controlled by a single locus that exhibits Mendelian inheritance, with the
Recent discoveries; characterized to produce abundant ergot alkaloids and the closest relative to Aspergillus leporis migraines, and other conditions. Produced by fungi and are used to treat dementia, ergot alkaloids are pharmaceutically important chemicals.

Abstract

West Virginia University, Morgantown, USA
Jessica Fuss, Daniel Panaccione

Aspergillus aspearensis

POS02-040: ERGOT ALKALOID BIOSYNTHESIS IN ASPERGILLUS ASPARENSIS
Jessica Fuss, Daniel Panaccione
West Virginia University, Morgantown, USA

Abstract

Ergot alkaloids are pharmaceutically important chemicals produced by fungi and are used to treat dementia, migraines, and other conditions. Aspergillus aspearensis is the closest relative to Aspergillus leporis, a fungus recently characterized to produce abundant ergot alkaloids and to have significant pathogenic potential. Considering the relatedness of A. aspearensis to A. leporis, we tested whether it could produce ergot alkaloids and parasitize the model insect Galleria mellonella. High-performance liquid chromatography (HPLC) analysis demonstrated that A. aspearensis accumulates lysergic-derived ergot alkaloids including lysergic acid alpha-hydroxyethylamide (LAH) and lysergic acid. This alkaloid profile was similar to that of A. leporis but not identical. We sequenced the genome and found it contained two ergot alkaloid synthesis gene clusters both of which appeared to be functional. Accumulation of LAH by A. aspearensis varied when the fungus was cultured on 15 different media; malt extract supported high concentrations. When spores of A. aspearensis were injected into larvae of the insect model, larvae died at a significantly faster rate than control larvae injected with buffer. The fungus produced ergot alkaloids during insect pathogenesis; later it produced sclerotia and spores on corpses, indicating that it can complete its life cycle in an insect. Aspergillus aspearensis was not an effective pathogen when exposed to intact insects, however, suggesting the pathogenesis observed represents a pre-adaptation to animal virulence. Lysergic acid-producing Aspergillus species are rare and are recent discoveries; A. aspearensis is a new source of ergot alkaloids and may be useful for studying and producing these important chemicals.

POS02-041: QUANTIFYING DATA DISPARITIES BETWEEN TROPICAL AND NON-TROPICAL FUNGI: GENETICS, TAXONOMY, CONSERVATION, AND CITIZEN SCIENCE
Jeffery Stallman1, Rachel Koch2, Danny Haelewaters3, M. Catherine Aime1
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Abstract

Biodiversity discovery of the estimated 2.5 million species of fungi is ongoing and it has been suggested that the majority of undescribed species occur in tropical environments. Unfortunately, tropical regions are underrepresented in fungal studies. In this poster, we use data from public repositories to quantify the discrepancies in DNA sequence data, species descriptions, conservation data, and citizen science data that exist between non-tropical and tropical fungi in NCBI, MycoBank, IUCN, and iNaturalist. All repositories have at least double the information on non-tropical fungi compared to tropical fungi. Additionally, geographic biases in conservation and community science data are more pronounced in fungi than in plants and animals. These data discrepancies contribute to a bias in the understanding of many aspects of fungal diversity, such as taxonomy, biogeography, ecology, and conservation.

POS02-042: TAXONOMIC PLACEMENT OF ENTORRHIZOMYCOTA
Yongjie Zhang1, Saleh Rahimlou2, Timothy James2
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Abstract

Entorrhiza s.l. is a group of fungi that are obligate, gall-forming root parasites of plant families Juncaceae (rush) and Cyperaceae (sedge). They are found all over the world but have been rarely studied due to their hidden lifestyle, which does not cause visible effects on host plants. Traditionally, this fungal lineage was classified under the subdivision Ustilaginomycotina of Basidiomycota. A new phylum, Entorrhizomycota, was proposed in recent years to accommodate this group of fungi based on a five-gene phylogenetic analysis. The placement of Entorrhizomycota in the fungal tree of life, however, is still controversial. It is considered a close sister group either to the rest of Dikarya or Basidiomycota. Unfortunately, the lack of genome data has hindered our understanding of its exact placement. To address this issue, this study performed genome sequencing of several individuals of this group of fungi to gain insight into its phylogenetic position, using phylogenomic approaches.
POS02-043: NEW SPECIES OF LACHNUM (LACHNACEAE, HELOTIALES) FROM PANAMA
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Abstract
The genus Lachnum is a diverse group of fungi within the family Lachnaceae (Helotiales, Leotiomycetes), and comprises approximately 251 species with cosmopolitan distribution. Lachnum is distinguished by stipitate to sessile cup or disc-shaped apothecia with granulate hairs, and is commonly associated with a variety of substrates including the dead wood or leaves of ferns and coniferous or broad-leaved trees. As part of a field expedition focused on Leotiomycetes, several undescribed Lachnum specimens from Panama were collected, sequenced, and examined for morphological features. Three new species were identified based on micro- and macromorphological characteristics in conjunction with phylogenetic analyses. All three species display a blue amyloid reaction at ascus apices with Melzer’s reagent and KOH pretreatment. This study will greatly increase the known diversity of Central American discomycetes and contribute to our understanding of known distributions and substrates within Lachnum.

POS02-044: A NEW SPECIES OF ENTYLOMA (ENTYLOMATALES, EXOBASIDIOMYCETES) ON THE ORNAMENTAL PLANT ERYNGIUM PLANUM EXPANDS THE E. ERYNGIUM SPECIES COMPLEX
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Abstract
The plant genus Eryngium (Apiaceae) includes various species used as condiments, ornamentals in gardens, or as elements in floral arrangements. In recent years, there has been a surge in interceptions from South America at U.S. ports of entry, leading to the subsequent destruction of these plants due to the presence of an unidentified species of Entyloma (Entylomatales, Exobasidiomycetes). Despite the resemblance of host samples to Er. planum, the limited plant material complicates host identification. Moreover, the morphology of teliospores and the asexual state does not align with any published species on Eryngium. This study aimed to identify and characterize this unknown Entyloma sp., ascertain its phylogenetic relationship with other Entyloma species on Eryngium, and verify the identity of the host plant. Morphological and phylogenetic (ITS nrDNA) analyses were performed, in context with known species of Entyloma. ITS nrDNA was also used to attempt the identification of the host. Initial findings reveal that the unidentified Entyloma sp. forms a distinct and well-supported clade separate from other species on Eryngium and Er. aff. planum. Its closest relatives include En. carmeli, En. eryngii, En. eryngii-cretici, En. eryngii-planii, En. lagoeciae, and En. scandicis. Morphologically, it resembles En. argentiniense; however, no molecular data is available for that species and its host is Er. nudicaule. Therefore, a new species of Entyloma is proposed. The host plant was identified as Er. planum. This research increases knowledge of Entyloma diversity and contributes to understanding the dynamics of pathogen movement and potential invasion into new territories.

POS02-045: EVOLUTIONARY DRIVERS OF RUSSULA DIVERSITY IN ECTOTROPHIC ANDEAN TROPICAL MONTANE FORESTS OF COLOMBIA
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Abstract
The Colombian portion of the Andes Mountain range shows elevations ranging between ca. 1000 to 3000 m asl and hosts natural tropical montane forests dominated by ectomycorrhizal trees: Quercus humboldtii and Trigonobalanus excelsa (Fagaceae). These endemic ectotrophic forests are unique in the South American subcontinent, due to the biotic floristic exchange with North and Central America. Based on macrofungi and metabarcoding data, Russula is among the most common and abundant fungi forming ectomycorrhiza in this type of forests. Recent studies uncovered a high species number of russulas in these Colombian tropical ecosystems. In some Russula lineages, there are multiple evidences of vicariance connected to a recent migration of oaks from Panama in glacial periods of late Pliocene to early Pleistocene. However, other Russula lineages suggest that the Colombian diversity of ectomycorrhizal fungi was present much earlier in Miocene due to a migration of the ectomycorrhizal host tree Trigonobalanus excelsa before the oak migration. In addition, presence of some closely related sister species of lineages not detected in Panama suggests recent sympatric evolution of some Russula lineages in Colombia.

POS02-046: DELIMITING GENERA IN PHAKOPSORACEAE S.L. (PUCCINIALES)
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Abstract
Of the estimated 5.1 million species of fungi, only 150,000 species (~3%) have been described. In subphylum Pucciniomycotina alone, only 16% of an estimated 54,000 species have been described. For the largest order in Pucciniomycotina, Pucciniales (rust fungi), recent family-level revision has divided the previous family Phakopsoraceae into Crossopsoraceae (suborder Uredinieae) and Phakopsoraceae s.s. (suborder Raveniiineae). However, polyphyletic genera exist between both families which is problematic. Thus, in this study
we aim to delimitate genera of the Crossopsoraceae (Pucciniales, Uredinieae) and Phakopsoraceae (Pucciniales, Raveneliineae) into monophyletic clades and delimit genera. To do this, concatenated DNA sequences from multiple loci (LSU, SSU, and CO3) were obtained from herbarium specimens, including representatives of type species for most genera, using rust-specific primers for targeted PCR amplification and Sanger Sequencing. The phylogenetic tree produced monophyletic genus-level clades delimited by Maximum-Likelihood and Bayesian distance-based models. In future studies, this tree could be used to study co-evolution of these families with their hosts as well as expedite identification and characterization as novel invasive pathogens emerge in these families.

POS02-047: ENDOPHYTES OF THE UNIVERSITY OF COLORADO DENVER – MYCO-ED PILOT FALL 2023
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Abstract
Myco-Ed is a novel, ambitious nation-wide Course-Based Undergraduate Research Experience (CURE) in fungal biology and genomics. We implemented a Myco-Ed pilot in our Fall 2023 Fungal Biology course at the University of Colorado (UC) Denver to study endophytic fungi on our campus. We isolated 12 Ascomycota species belonging to seven genera from a range of plants and obtained ITS sequences that we used to refine phylogenetic placement. To test for links between genotypes to phenotypes, we tested for isolate growth rate and zinc tolerance and found variation across fungi, with a Didymellaceae sp. isolate tolerant to 10 mM zinc. Furthermore, 10 of our isolates represented species without reference genomes. Therefore, we prepared tissue from these for whole genome sequencing through the Joint Genome Institute. In addition, we used MycoCosm to identify and annotate mating types and natural products of previous Myco-Ed genomes, Aspergillus fumigatus and Penicillium ribium, both of which were obtained from the UC Denver campus. In summary, the Myco-Ed pilot CURE was a great success in our class! It allowed hands-on research experiences that most of us had not been exposed to, leading to deep personal involvement and empowerment on our ability as researchers.

POS02-048: DIVERSE ARRAY OF FUNGAL ENDOPHYTES FROM LEAVES COLLECTED BY UNDERGRADUATE MYCOLOGY STUDENTS AT GEORGIA SOUTHERN UNIVERSITY
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Abstract
Plant leaves are known to harbor fungal endophytes. These fungi have been found to enhance the host plant’s physiologies as well as produce bioactive chemicals, some of which have medical or antibiotic properties. As a part of the Mycological Curriculum for Education and Discovery (Myco-Ed) program funded by the Joint Genome Institute (JGI), an undergraduate Mycology lab course collected leaf samples from the Armstrong campus of Georgia Southern University in Savannah, GA to search for fungal endophytes. Approximately 16 leaves were collected from 13 different plant families including representatives from both flowering and non-flowering plants. Leaves were cut into six, 2-3 cm pieces, and surface-sterilized in bleach and ethanol. Each leaf piece was plated onto PDA media amended with ampicillin. After 1 week, fungal isolates that grew from leaf cuttings were sub-cultured onto fresh PDA until pure isolates were obtained. DNA was extracted, and the ITS region of each isolate was sequenced. Sequences indicated that the fungal endophytes represented a wide variety of fungal families from the Ascomycota phylum. The ecological niche of many of the isolates collected include saprophytes and plant pathogens. Other isolates are known endophytes like Colletotrichum fioriniae, while others are endophytes known to produce antibiotic chemicals (antivirals, antifungal, insecticides) such as Epicoccum nigrum, Colletotrichum siamense, Nigrospora sphaerica, and Aspergillus nidulans var. dentatus.