MON 1

Lucky: A career in mycology

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I have been lucky to serve as MSA President 2016-2017 and lucky to have a career in mycology. The topic of luck, chance or serendipity in science typically brings some unease to scientists. Darn it, we work hard and deserve our success. Well yes, indeed, but we also benefit tremendously from the opportunities afforded to us by our upbringing, education, and societal context. Reflecting on the topic of luck in my career, I discuss the major influences that got me where I am today. First, the Mycological Society of America has an 85-year history of career opportunities in mycology and I invite you to make it your "luck" to be active in our society. Second, I grew up a little bit wild and that lucky experience suggests to me that nature inspires much of what I do. Third, by the luck of coming to UGA for a Master's degree, I got into mycology and never left. Finally, the greatest luck of all has been the people who love what they do and are willing to share it with me. Perhaps by threading these themes of "luck" through my career as a mycologist, I will encourage you to take advantage of all the luck you have in your careers and as members of the MSA.

MON 2

Thelephoralean ectomycorrhizal fungi may drive early seedling survival in a Neotropical monodominant tree

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From 2003–2017 we quantified seedfall, seedling establishment and survival of the ectomycorrhizal (ECM) caesalpinioid monodominant rainforest tree *Dicymbe corymbosa* in Guyana. *Dicymbe corymbosa* exhibited only two years of high seed-based reproduction (“masting”) during the fifteen year period. Ectomycorrhiza-facilitated establishment of shade tolerant seedlings following masting may contribute to persistent monodominance of *D. corymbosa*. Establishment and survival of seedling cohorts was monitored from 2003-2017. Ectomycorrhization of a large sample of 2016 seedlings was quantified at 2 weeks, 6 months, and 12 months of age. Ectomycorrhizal fungi of seedlings were identified by morphotyping and DNA sequencing. During the 2003 and 2016 mast years ectomycorrhization was rapid on newly germinated seeds. In 2016, species of *Tomentella* (Thelephorales) dominated early seedling colonization (82.4 % at two weeks of age; n = 210 seedlings) and continued to be the most prevalent ECM fungi on surviving seedlings up to 12 months of age. The mast seeding pattern and massive reproductive resource investment of *D. corymbosa* yields seedling cohorts capable of persisting for decadal time scales. While ECM fungi drive mineral nutrient recycling in adult trees, they may also enable seedling survival by quickly establishing ECM networks. *Tomentella* species dominate the seedlings and are abundant on adult trees. While over 200 species of ECM fungi have been documented in *Dicymbe* forests, *Tomentella* species may play a disproportionate role in ecological functioning of host trees in all age classes. The significance of aerial *Tomentella* ectomycorrhizas will be discussed.

MON 3

Community assembly of seedling-colonizing ectomycorrhizal fungi in a neotropical monodominant tree

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Seedling establishment and survival of ectomycorrhizal (ECM) tree species may be influenced by their ECM fungal symbionts. In particular, the community composition of ECM fungi may be important, given that fungal species have varying capabilities of exploring soil and protecting host roots from soil pathogens. We explored changes in the ECM fungal community over time in a population of even-aged seedlings of the tropical monodominant tree *Dicymbe corymbosa* in Guyana. Seedlings (n = 210 per sampling event) were collected at ~2 weeks, six months, and 12 months of age following a July 2016 mast seeding event. Root tips were observed with a dissecting microscope in the field to isolate distinct ECM morphotypes. The percentage of fine roots colonized by ECM fungi was estimated for each seedling. Root tips were also collected from 30 nearby adult *D. corymbosa* trees to allow comparison with seedling ECM fungal communities. Individual ECM morphotypes were Sanger sequenced at the ITS region, the fungal barcoding locus. Bulk samples of the seedlings at each time point, as well as the adults, were sequenced at the ITS locus on an Illumina platform. Ectomycorrhization occurs quickly after seedling establishment, colonizing 26–50% of the roots at ~2 weeks of age, and increases substantially at 6 months of age. Changes in ECM fungal assemblage and phylogenetic diversity on developing seedlings will be discussed. This study will reveal those ECM fungal species colonizing seedlings and their relationship to mycobionts associated with sympatric conspecific adults.

MON 4

Development and decline dynamics of two ectomycorrhizal fungal mat communities in response to a reciprocal soil transfer experiment in old-growth Douglas-fir forests

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Ectomycorrhizal fungi (EmF) form symbioses with trees and profoundly influence forest ecology. Certain EmF form specialized hyphal profusions (mats) which alter soil biogeochemistry, contribute to microbial biomass/respiration, and support unique fungal communities. *Piloderma* and *Ramaria* are dominant mat-forming fungi of old-growth Douglas-fir forests in the Pacific Northwest, stratifying in organic and upper mineral soil, respectively. Their importance to forest ecosystem processes has driven the need to better understand associated fungal communities, particularly development (birth) and decline (death) dynamics. A reciprocal soil transplant experiment was established where *Piloderma*, *Ramaria*, and non-mat soils underwent birth (non-mat into mat), death (mat into non-mat), disturbance control, and non-manipulated treatments. After 51 months, EmF root-tips and soil fungi were sequenced. Results revealed differential EmF mat persistence. In the mineral horizon, originally-unique *Ramaria* communities were no different from non-mat soils, while *Ramaria* was notably missing; this supports the ephemeral nature of *Ramaria* mats. In the organic horizon, *Piloderma* mat communities persisted and remained distinct from non-mat soils. Strong development of *Piloderma* mat communities in birth treatments occurred, making them indistinguishable from *Piloderma* mats. Death treatments were dissimilar to *Piloderma* mats and contained fungal communities similar to non-mat soils, dominated by saprotrophs. To compliment *Piloderma*, *Russula* was a robust indicator of non-mat soils; there was strong evidence for competitive exclusion of *Russula* in *Piloderma* mats. This work contributes to the body of knowledge regarding complex community dynamics of EmF mats. The occurrence and distinct fungal taxa of *Piloderma* mats suggests large-scale spatial differences in ecological function.

MON 5

Ectomycorrhizal community dynamics of Pinaceae invasions in Patagonian *Nothofagus* forests

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Nothofagus species are the only widespread ectomycorrhizal (ECM) host trees native to Southern South America (SSA). Invasion of ECM Pinaceae that are native to Western North America is a growing problem in the area and represents a threat to the biological diversity and stability of *Nothofagus* forests. Recent research has demonstrated that Pinaceae invasions in SSA are facilitated by a community of exotic co-invasive ECM fungi. Given the evolutionary isolation of *Nothofagus* species and their associated ECM fungi in SSA, the introduction of invasive ECM taxa may have unpredictable effects upon the structure and composition of native *Nothofagus* ECM fungal communities. To address this concern, we sequenced the ITS1 region of all fungi in the rhizosphere of *Nothofagus antarctica* and *Nothofagus dombeyi* within invaded sites and along a spatial gradient extending into adjacent *Nothofagus* stands without Pinaceae. The native fungal community of the *Nothofagus* rhizosphere was dominated in all treatments by non-mycorrhizal *Mortierella* species and while the prevalence of these species is unaffected by invasion of *Pseudotsuga menziesii*, they show reduced abundance where *Nothofagus antarctica* is invaded by *Pinus contorta*. Invasion of both *Pseudotsuga menziesii* and *Pinus contorta* into *Nothofagus* stands alters native ECM community composition and *Pinus contorta* also reduces native *Nothofagus antarctica* ECM species richness. This study presents the first metagenomic data that details the response of native *Nothofagus* ECM fungal communities in SSA to co-invasion of Pinaceae trees and their fungal symbionts.

MON 6

Fungi and ecotourism: high macrofungi richness in tourism concession in the Peruvian Amazon

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The southern Amazon of Peru is known for their high biodiversity, part of which is protected inside national parks. However, other areas near reserves are concessionated for touristic activities, which require an evaluation of the impact. As part of a project of recording the biological diversity in the tourism concession of Refugio Amazonas-Rainforest Expeditions (Madre de Dios, Peru) we register the macrofungi richness. The intense search was performed in February 2016 and March 2017 during the rainy season. We collected 91 species, 10 Ascomycota and 81 Basidiomycota, most of them of ligneous habit. We recorded 28 families, of which Marasmiaceae, Polyporaceae, Agaricaceae, Meripilaceae, Mycenaceae and Xylariaceae represent the 59% of the total richness. *Marasmius* is the richest genus with 17 species followed by *Rigidoporus* with 7 species. We compared our results with other studies in the area and observed a clear relation between the disturbance level and the macrofungi richness, with 31 species in average in highly disturbed areas and 85 species in the low disturbed areas (El Manu National Park and our study area). In total the region presents 199 species, 74 of them are exclusive of our study area. The results show the touristic activity carried with responsibility protects a high macrofungi diversity equivalent to the registered in national parks.

MON 7

The chaos after the storm: fungal community composition shifts in response to simulated hurricane disturbance

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Hurricanes alter ecosystem diversity and nutrient cycling in tropical forests where studies of the impact of hurricanes on the soil and leaf litter microbes are limited. We analyzed soil and leaf litter microbial

communities from a simulated hurricane experiment in El Yunque, Puerto Rico. Two treatments were applied: control and trim plus debris. Soil and leaf samples were collected before treatment and for a year after treatment from November 2014 to December 2015. DNA was extracted using MoBio Power Soil DNA Kit and ITS fungal rDNA was amplified using ITS1-F and ITS2 primers for Illumina sequencing. The abundant fungal divisions were Ascomycota (53%) Basidiomycota (32%) and Zygomycota (5.5%). Other divisions comprised less than 1%. Differences in relative abundance of fungal divisions between control and experimental conditions were significant for Chytridiomycota, Basidiomycota, and Ascomycota. Soil and leaf litter fungal communities shifted significantly in the trim plus debris treatment. Fungal communities changed significantly over time for leaf litter but not soil. The dominant families in leaves in both control and trim were Amphisphaeriaceae, Herpotrichiellaceae Marasmiaceae, and Teratosphaeriaceae. Nectriaceae increased in abundance with trimming in leaves while Agaricaceae and Clavariaceae decreased. The dominant families in soil in both control and trim were Archaeorhizomycetaceae, Clavariaceae, Mortierellaceae and Trichosporonaceae. Psathyrellaceae and Xylariaceae increased in abundance with trimming in soil. For both soil and leaves, most of the sequences are unidentifiable. Neither the soil nor leaf litter fungal communities had recovered from trimming after one year.

MON 8

Survey of *Geosmithia* species in the southeast United States

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Geosmithia (Hypocreales) is a widespread and common but little-studied genus of fungi that are mostly associated with bark-dwelling insects. The genus includes a pathogenic species, *G. morbida*, which is a contributing agent in the thousand cankers disease (TCD) of *Juglans* spp. To contribute to the understanding of the origin of the disease, we are studying three questions: (1) what is the diversity of native *Geosmithia* species in the South Eastern USA? (2) what is the specificity between the fungus, the vector beetles and the tree hosts? and (3) is *G. morbida* is invasive in the South East, or native but overlooked? To survey the *Geosmithia* species in their environment, bark beetle specimens and tree branches infested by beetles are collected. Tree species related to *Juglans* spp. and tree species prevalent in the southeast are targeted. Based on our first surveys, neither *G. morbida* or the walnut twig beetle (WTB, *Pityophthorus juglandis*) were discovered in Florida. Nine different *Geosmithia* spp., including five new species and three new to the North America, were recovered from eight different tree hosts. The species of *G. pallida* complex are the most frequently encountered species, followed by *Geosmithia* sp12. The absence of *G. morbida* and *P. juglandis* in this region may be a result of the rarity of their primary host tree. This study reveals that *Geosmithia* species are diverse and ubiquitous in the Southeastern United States.

MON 9

Quantifying temporal and spatial variability in fungivory by eastern chipmunks (*Tamias striatus*)

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Eastern chipmunks (*Tamias striatus*) are fungivorous in the summer, although the type and amount of fungi consumed may change both temporally and spatially. Understanding variation in fungal consumption is important because fungivory promotes dispersal of mycorrhizal spores in forests. We quantified diets of eastern chipmunks in the White Mountains of New Hampshire during the summer of 2014 to determine 1) if fungivory varied temporally, among forest types, or relative to truffle abundance

and 2) whether different methods to quantify diet estimated comparable levels of fungivory. We used scat microscopy to determine spore loads of mycorrhizal taxa and carbon and nitrogen stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$) of both hair and scat to quantify bulk fungal contribution to the diet. Based on microscopy, fungal richness in scat increased from June to August, with eastern chipmunks consuming 28 taxa from at least 13 genera. Isotopic analysis of hair suggested that fungi composed nearly 35% of the summer diet and isotopic analysis of scat indicated that the fungal contribution to bulk diet increased from about 20% in June to nearly 50% in August. Finally, all three analyses suggested that fungal consumption was similar across forest types despite nearly 10 times more truffle availability in softwood forest than hardwood forest. Based on the diversity and amount of fungi consumed and their occurrence in both hardwood and softwood forests, eastern chipmunks may be especially important as dispersers of mycorrhizal spores across forest gradients.

MON 10

Fungal mating system transitions driven by chromosomal translocations involving intercentromeric recombination

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Closely related fungi exhibit tetrapolar, pseudobipolar, or bipolar mating systems, suggesting frequent mating system transitions. However, how these transitions occurred was unknown. Here, we compared the genomes of two closely related species: *Cryptococcus neoformans*, a major human fungal pathogen with bipolar mating-type, and *Cryptococcus amylolentus*, which is non-pathongenic with tetrapolar mating-type. Specifically, we first sequenced, assembled, and annotated the genomes of two *C. amylolentus* isolates, CBS6039 and CBS6273, which are sexual and interfertile. We also identified and characterized the *C. amylolentus* centromeres using bioinformatics and ChIP-seq analyses. By comparing these *C. amylolentus* genomes to those of *C. neoformans*, we show the contiguous *MAT* locus in the bipolar *C. neoformans* is a fusion product of the two unlinked *MAT* loci in the tetrapolar *C. amylolentus*. Additionally, both species have regional centromeres enriched with species-specific transposable elements shared among centromeres, and genome comparisons reveal these centromeres are involved in ectopic intercentromeric recombination resulting in dramatic genome reorganization. Taken together, as well as recent findings of the MAT loci organizations in other related basidiomycetous species, we propose a model in which evolution of the bipolar mating system was initiated by an ectopic recombination event mediated by repetitive centromeric DNA elements shared between chromosomes, and subsequent chromosomal rearrangements established the complete linkage between the two *MAT* loci to form the single contiguous *MAT* locus that is now extant in the pathogenic *Cryptococcus* species.

MON 11

Extensive copy number variation in fermentation-related genes among *Saccharomyces cerevisiae* wine strains

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Due to the importance of *Saccharomyces cerevisiae* in wine-making, the genomic variation of wine yeast strains has been extensively studied. One of the major insights stemming from these studies is that wine yeast strains harbor low levels of genetic diversity in the form of single nucleotide polymorphisms (SNPs).

Genomic structural variants, such as copy number (CN) variants, are another major type of variation segregating in natural populations. To test whether genetic diversity in CN variation is also low across wine yeast strains, we examined genome-wide levels of CN variation in 132 whole-genome sequences of S. cerevisiae wine strains. We found an average of 97.8 CN variable regions (CNVRs) affecting ~4% of the genome per strain. Using two different measures of CN diversity, we found that gene families involved in fermentation-related processes such as copper resistance (CUP), flocculation (FLO), and glucose metabolism (HXT), as well as the SNO gene family whose members are expressed before or during the diauxic shift showed substantial CN diversity across the 132 strains examined. Importantly, these same gene families have been shown, through comparative transcriptomic and functional assays, to be associated with adaptation to the wine fermentation environment. Our results suggest that CN variation is a substantial contributor to the genomic diversity of wine yeast strains and identify several candidate loci whose levels of CN variation may affect the adaptation and performance of wine yeast strains during fermentation.

MON 12

Rewiring of the gene expression network controlled by a key regulator of fungal development impacts secondary metabolism

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The formation of asexual spores (known as conidia in *Aspergillus* and other related species) is a key factor contributing to the fecundity and fitness of many fungi. Properly assembled conidia allow fungi to survive stressful conditions and disperse to new ecological niches. Conidiogenesis is controlled by a complex developmental gene regulatory network (GRN) that interacts with a variety of other networks, including the GRN governing secondary metabolism. To gain insight into the GRN controlling fungal conidiogenesis, we dissected the portion of the network downstream of a highly-conserved regulator of conidial maturation (*wetA*) in three *Aspergillus* species that span the diversity of the genus: the genetic model *A. nidulans*, the human pathogen *A. fumigatus*, and the plant pathogen *A. flavus*. Transcriptome profiling of the *wetA* null mutant and wild-type conidia showed that the WetA-associated GRN contained approximately the same number of genes, but was highly divergent across the three species. Specifically, WetA was found to regulate genes that have predicted functions enriched in secondary metabolism, asexual sporulation, and chitin metabolic processes in *A. flavus* and *A. fumigatus*. In contrast, WetA in *A. nidulans* regulates genes that have predicted functions enriched in transmembrane transport and gene expression. This divergence in regulatory networks is surprising given that many of the phenotypic functions of *wetA* relating to spore maturation are conserved in all three species. Ongoing work is focused on ascertaining the molecular mechanisms by which WetA regulates conidiogenesis and the evolution of conidial phenotypic diversity in filamentous fungi.

MON 13

Widespread adenine N6-methylation of active genes in fungi

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N6-methyldeoxyadenine (6mA) is a noncanonical DNA base modification present at low levels in plant and animal genomes, but its prevalence and association with genome function in other eukaryotic lineages remains poorly understood. Here we report that abundant 6mA is associated with transcriptionally active genes in early-diverging fungal lineages. Using single-molecule long-read sequencing of 16 diverse fungal genomes, we observed that up to 2.8% of all adenines were methylated in early-diverging fungi, far exceeding levels observed in other eukaryotes and more derived fungi. 6mA occurred symmetrically at ApT dinucleotides and was concentrated in dense methylated adenine clusters surrounding the transcriptional start sites of expressed genes; its distribution was inversely correlated with that of 5-methylcytosine. Our results show a striking contrast in the genomic distributions of 6mA and 5-methylcytosine and reinforce a distinct role for 6mA as a gene-expression-associated epigenomic mark in eukaryotes.

MON 14

Fungal gene clusters adapted to degrade plant secondary metabolites

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Eukaryotic genomes display remarkable variation in terms of their gene organization. While much of this diversity is likely to result from non-adaptive evolution, differences attributable to natural selection remain largely unexplored in fungi. Plant-produced secondary metabolites (SMs) mediate critical ecological interactions between plants and fungi, including the inhibition of saprotrophs and defense against pathogens. Here, we propose that selection by plant SMs has resulted in the formation and maintenance of gene clusters encoding degradative metabolic processes that may promote fitness in certain plant-associated niches. We identified hundreds of clusters predicted to be involved in plant SM degradation with distributions that deviate from null models of genome evolution. We show that particular clusters are overrepresented in specific plant-associated lifestyles, most notably plant pathogens, and identify conserved combinations of clusters that occur in disparate fungal genomes. In order to determine whether metabolic pathways encoded by different clusters are adapted to specific plant SMs, we investigated the function and evolution of a group of clusters predicted to encode the degradation of stilbenes, a class of fungitoxic plant SMs. Results from enzymatic assays and phylogenetic analyses suggest that distinct combinations of genes, but not novel protein functions, are associated with ecological transitions at the species level. Our work demonstrates that congruence of gene organization over small spatial scales in divergent fungi is associated with similarities in ecological lifestyle, and further suggests that specific types of degradative gene clusters may play a role in the assembly of fungal communities on living and decaying plant tissues.

MON 15

Comparative genomics of secondary metabolism in insect and nematode pathogens

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We investigate the evolution of secondary metabolite genes and clusters across a diverse group of insect and nematode pathogens across Hypocreales. We explore both broad-scale evolutionary processes leading to diversification of secondary metabolism across the order as well as case studies of closely

related fungi in this group displaying differences in virulence and specialization on distinct hosts. Using PacBio technology to sequence and assemble near chromosomal level assemblies of six strains of *Tolypocladium inflatum*, we characterize evolutionary genetic mechanisms contributing to intraspecific variation and cryptic diversity of genes and clusters encoding the synthesis of fungal secondary metabolites, including polyketides, nonribosomal peptides, terpenes, and alkaloids. Similarly, examination of draft genomes of ten diverse strains of the wide host-range insect pathogen and endophyte *Beauveria bassiana* and several outgroup *Beauveria* species (*B. brongniartii, B. asiatica, B. australis)* has revealed differences in secondary metabolite gene content across strains that correlates with virulence on insects. Differential expression of metabolite cluster genes in plant and insect infection assays examines the potential role(s) of specific metabolites in the colonization and pathogenesis of insects. The results shed light on the relative importance of transposition, selection, duplication/deletion, recombination, and horizontal transfer for the evolution of fungal metabolite clusters and illuminate how secondary metabolites may shape the interaction of these fungi with insect and nematode hosts.

MON 16

Evolutionary expansion of the cytoskeletal septin proteins predates diversification in fungal morphology

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Fungi are a diverse set of organisms with body plans ranging from unicellular yeasts to multicellular mycelia. In Fungi, indeterminate growth is inferred to have evolved on several separate occasions. The cytoskeletal septin protein family has many roles, being required for budding in yeast and controlling hyphal morphology in Ascomycetes. Septins are shared with Fungi and Animals, but Fungi contain several unique septin groups. We sought to assess the presence of septin gene expansions in fungal evolution and assess whether these patterns can explain morphological transitions. We investigated this with a phylogenetic study, taking advantage of recently sequenced genomes. Predicted septins were identified using PSI-BLAST as well as HMMer, and analyzed with maximum likelihood as well as Bayesian phylogenetic methods. By analyzing and comparing the three dimensional folding of septin proteins from Fungi and other Opisthokonts, we identified potentially interacting residues between septin monomers. The earliest septin divergences were ancient and fungi share an ancestral duplication in Group 1 septins with Animals. All septin groups were present before zoosporic phyla diverged. Subsequent changes in fungal morphology show no obvious correlation with septin duplications. Using protein modelling, we identified key residues involved in the septin-septin interactions that likely contribute to quaternary structures that have cytoskeletal functions. We found a difference in the fungal-specific Group 3 septins that may be connected to their role as capping proteins. While septins are now intricately tied to fungal morphology, the presence of septins groups predated the emergence of multicellularity and the diversification of fungal forms.

MON 17

Ultrastructural evidence of *Rozella allomycis'* phagocytosis of host cytoplasm

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With the revelation from molecular phylogenetics that *Rozella* was not a Chytridiomycete, but rather a member of a clade (= Opisthosporidia) sister to the traditional Fungi, interest has grown in what *Rozella* could disclose about the evolution of fungi and possible divergence from Protista. One key question in exploring protistan and fungal relationships of this endoparasite is: What is the mode of nutrition of *Rozella*? To explore this question, we have characterized the ultrastructure of the host-endoparasite interface between *Rozella allomycis* and its host *Allomyces anomalus*. Endoparasite and host

mitochondria are clearly distinctive because mitochondria of the endoparasite have fewer cristae and a more diffuse matrix than do mitochondria of the host. Surrounding the plasmodium of the endoparasite, there is a host cisterna. Thus, the host-endoparasite interface consists of three membranes, interpreted as endoparasite plasma membrane (one membrane) and host cisterna (two membranes). Host mitochondria cluster and align at the surface of the cisterna, forming a layer. As the endoparasite's plasmodia expand within the host, phagocytic vacuoles appear within the endoparasite. The phagocytic vacuole has three-membrane layers, which is lined with host-type mitochondria, and contains cellular material including host-type nuclei. This topology is consistent with arrangement of organelles if the endoparasite phagocytizes host cytoplasm. It also explains why there is no remaining host cytoplasm when sporangial plasmodia discharge zoospores. Thus, in contrast to osmotrophic nutrition of traditional fungi, *Rozella's* nutrition is, at least in part, phagotrophic.

MON 18

Next-Generation sequencing of fungal viromes reveals cryptic mycoviral diversity

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Persistent viral infection is believed to be widespread in fungi, and yet little is known about the frequency of mycoviral infection or diversity of mycoviruses within a fungus. We developed a next-generation sequencing pipeline using the PacBio platform to assess the "virome" within individual fungal isolates. This approach allows us to screen individuals for persistent RNA virus infection and results in viral genomic sequences, thereby linking novel viruses to their hosts. By this approach novel viruses have been identified in fungi spanning five phyla, for which two previously had no viral sequence data. Despite a conservative screening process, an emergent finding from this exploration of fungal viromes is a high level of coinfection whereby infection by a single virus seems to be the exception rather than the rule. By linking novel mycoviral diversity directly to their hosts, we hope to contribute to the growing understanding of the significance of the virome in fungal ecology.

MON 19

Phylogenomic resolution of of early diverging fungal lineages

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Whole genome and transcriptome sequencing has enabled new approaches to comparative biology and systematics of fungi. The Zygolife project and the 1000 fungal genomes (1KFG) and have emphasized sampling of genomes across the zygomycete and chytrid lineages. These data enable examination of conserved or changing gene content, gene organization along chromosomes, and transposable element proliferation. Methods to extract conserved, phylogenetically informative marker genes have been developed using the 1KFG genome dataset (http://github.com/1KFG) to produce a set more than 400 hundred protein coding genes as conserved phylogenetic markers. These markers have been applied to datasets including completely assembled, low coverage genome and transcriptome datasets. One study

has focused on 60 Mortierellomycotina “light coverage genomes” at 5-10x coverage to assess recovery of new phylogenetic clades. These genomes have been used to test the limits of how low genome coverage is possible to still robustly resolve the phylogenetic relationships and evaluate recovery of ITS and rRNA genes from these whole genome shotgun approaches. These phylogenomic approaches have also been used to resolve phylogeny of arbuscular mycorrhizal fungi from single cell transcriptome data and to a dataset of more than 150 Mucoromycota and Zoopagomycota and 25 chytrid genomes to resolve relationships of early branching fungi. We have used whole genome data to focus on placement of *Basidiobolus* lineage within the Zoopagomycota which has been difficult to resolve. Using individual gene trees we are identifying conflicting phylogenetic signals that suggest complex evolutionary histories within these early diverging lineages.

MON 20

Phylogenomics of Zoopagomycota

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With the aid of phylogenomics, the paraphyletic zygomycetes have been segregated into the Mucoromycota and the Zoopagomycota. Many members of Mucoromycota are culturable, and this has allowed for many taxa within this group to be sequenced. In contrast, the Zoopagomycota contains few culturable members, and there are few genomes representing this group. Using single cell genomic techniques, we have sequenced the genomes of four predatory taxa, *Acaulopage tetraceros*, *Stylopage hadra*, *Zoophagus insidians*, and *Zoopage* sp., and the endoparasite *Cochlonema* sp. We use these taxa to update previous phylogenies of the group; in particular, we examine the placement of Zoophagus insidians and the evolution of predation and parasitism within the group.

MON 21

Molecular phylogenetic assessment of the miniature mycoparasite genus *Piptocephalis* (Zoopagomycota)

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The subphylum Zoopagomycotina (Zoopagomycota) is among the earliest diverging lineages of zygomycetes and includes diverse species of mycoparasites and microscopic parasites of small animals (e.g. nematodes, rotifers, amoebae). Despite being among the earliest lineages to adapt a non-flagellated, filamentous growth form, many of the taxa remain understudied and incompletely characterized. One common and diverse group of Zoopagomycotina is the mycoparasitic, haustoria-forming genus Piptocephalis. Most *Piptocephalis* species parasitize widespread saprobic zygomycetes in the Mucoromycotina and Mortierellomycotina, but at least one *Piptocephalis* species grows with an ascomycete host (*Penicillium*). Co-cultures of *Piptocephalis* and their hosts are relatively easy to isolate from soil and dung samples across the globe. Despite the fact that *Piptocephalis* is an apparently cosmopolitan genus with approximately 40 described species, there are no modern taxonomic or molecular phylogenetic treatments of this group. Minimal sequence data are available for *Piptocephalis* species and relatively little is known about the true diversity or biogeography of the genus. Likewise, representation of the genus in environmental sequencing surveys is limited, possibly due to methodological difficulties in sequencing the ITS region. This study constitutes the first attempt to phylogenetically characterize members of the genus *Piptocephalis*. Specifically, the aims of this study are: 1) use molecular data to determine the major lineages and estimate the molecular diversity of *Piptocephalis* and 2) test the monophyly of species to evaluate the utility of a morphological species concept for species identification and description. Here we present our preliminary molecular phylogenetic results and initial assessment of morphological character congruence.

MON 22

Wrestling with the unculturable and the unsequenceable: Taxonomy and phylogeny of three genera of sporodochial hyphomycetes

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Although cryptic and hidden biodiversity is exciting, some uncultured and unsequenced fungi are conspicuous and well-known to mycologists with hand lenses. *Bactridium* species have striking yellow sporodochia on decayed wood, with multi-celled conidia that can be seen with the naked eye. We have been unable to culture our common local species *B. ellisii* but DNA extractions from the large conidia eventually yielded rDNA sequences similar to unpublished sequences of a cultured Japanese species. *Bactridium* is closely related to *Scutellinia* (Pyronemataceae), discomycetes that are also reportedly difficult to culture, but there is insufficient data to determine if they are sister groups or an anamorph-teleomorph pair. Macroscopically similar sporodochia are produced by *Sphaerosporium lignatile*, which we have also failed to culture. rDNA sequences obtained directly from its large, round conidia suggest an affinity with *Tarzetta* (also Pyronemataceae). *Hormomyces aurantiacus*, on the basis of co-occurrence sometimes considered the anamorph of *Tremella mesenterica*, produces spreading, fuchsia-colored, waxy sporodochia with densely compacted branching chains of orange conidia. It cultures easily and 28S rDNA sequences suggest a relationship with Tulasnellaceae, consistent with its *Epulorhiza*-like morphology. Despite many attempts, we were unable to obtain usable ITS sequence from our cultures. In this time of unifying anamorph and teleomorph classification into a single name system, such known but poorly-documented classical genera present a challenge when they endanger more recently described, but arguably better-known names.

MON 23

What lies beneath? Fungal diversity at the bottom of the Great Lakes.

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Fungi are diverse organisms found in nearly every global environment as key component in nutrient cycling and decomposition. To date, most fungal diversity has been documented from terrestrial habitats leaving aquatic habitats comparatively unexplored. Even less is known about fungi inhabiting freshwater lakes, particularly from benthic zones, suggesting that lakes may serve as untapped resources for fungal biodiversity. The goal of this study was to inventory the benthic fungal communities of two North American Laurentian Great Lakes (Lake Michigan, and Lake Superior) and examine if these lakes harbor unique fungal taxa. Benthic sediment and water samples for this project were collected at various depths (50m-273m) during the summers of 2014, 2015 and 2016 using a Ponar dredge. This study employed both culture-dependent and culture-independent environmental sequencing techniques to obtain a more complete snapshot of the fungal community. Our research provides three major findings: the benthic zone of Great Lakes harbor a diverse group of fungi (~425 taxa), community analysis suggests fungal communities in the Great Lakes vary across depths, and utilizing both culture-dependent and culture-independent techniques in parallel provide a more complete inventory.

MON 24

Do endophytic fungal OTUs equate with species? Does it matter?

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Diverse but undescribed species of *Alternaria* are frequently cultured from plants as endophytes, the asymptomatic symbionts living within plant tissues. Understanding the ecological functions of these *Alternaria* endophytes is problematic because ecologists usually generate OTUs from a single barcode sequencing locus, whereas species resolution within *Alternaria* often requires sequencing of multiple loci. I sought to determine if single locus OTUs are sufficient for understanding the ecology of these endophytes for cases in which OTUs do not correspond to species, or the single locus gene tree does not agree with the species tree. Using 1000 *Alternaria* isolates recovered from a single species of prairie legume, I mapped ITS sequences of my isolates onto single and multilocus alignments with the T-BAS phylogenetic toolkit.

MON 25

Exploitation of an ancient fungal-insect symbiosis: *Escovopsis*, a pathogen of fungus-growing ant agriculture

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Fungus-growing ants, a group of over 200 ecologically distinct species, have cultivated basidiomycete fungi for approximately 50 million years. The specialized ascomycete pathogen Escovopsis attacks and consumes that ants' fungal cultivar. At the broad scale, Escovopsis strains are specialized; in in vitro bioassays Escovopsis strains typically can attack strains of the cultivated fungus from which they are isolated in nature as well as closely related strains, but they are actively inhibited by other cultivated fungal strains. These properties are consistent with phylogenetic and population genetic patterns, suggesting host fidelity at the broad scale of host species with little specificity on within species host genotypes. Sequencing and annotation of the first Escovopsis genome reveals that this pathogen has a small size and reduced gene content relative to close relatives that do not exhibit such host specialization. The pathogen, however, has retained functions necessary for attacking and consuming its hosts, including genes necessary for utilizing the carbohydrates most common in its host fungi. The small pathogen genome size and diversity across this ancient host-pathogen system opens the possibility to utilize population genomics to explore the molecular underpinnings of the evolution of pathogen specificity at multiple scales.

MON 26

Passalidae (Coleoptera): Beetles that eat decaying wood

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Fungi are important in forest ecosystems because they degrade coarse woody debris efficiently. In addition to wood-decaying basidiomycetes, other organisms, including insects (e.g., Coleoptera, Passalidae), spend their entire lives ingesting dead wood. About 500 species of passalids are ubiquitous in fallen hardwoods in the Earth's warmer climates. Our work has focused on Odontotaenius disjunctus in eastern North American hardwood forests, but collections from several habitats and geographical regions, including Panama, Guatemala, Thailand, and tropical Australia, showed that certain yeasts consistently occur in the gut of passalids. The gut is divided into four morphologically and physiologically distinct regions, each with characteristic microbial populations. A hallmark of the passalid gut yeasts (e.g., Scheffersomyces and Spathaspora clades) is the rare yeast attribute of xylose-fermention. D-xylose, a backbone molecule of the hemicellulose component of plant cell walls, is one of the most abundant

renewable carbon resources on Earth. Members of other yeast clades (e.g., Sugiyamaella and Trichosporon) also inhabit the passalid gut, and these yeasts assimilate, but do not ferment, xylose. Interactions among the yeasts, other microbes, and insects are not well understood. Our results suggest that colonization by xylose-fermenting yeasts contributes to the extraction of nutrients from decaying wood, but the holdfast attachment and extreme posterior gut position colonized by Scheffersomyces stipitis indicate that this yeast may have evolved as the primary beneficiary of the association. Determining the basis of the interactions is complicated by the presence of gut bacteria with many similar physiological properties

MON 27

Global diversity and fidelity of *Fusarium* symbionts among *Euwallacea* ambrosia beetles

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Euwallacea ambrosia beetles vector members of the ambrosia *Fusarium* clade (AFC), a monophyletic group within the *Fusarium solani* species complex. Several *Euwallacea-Fusarium* consortia have been introduced into the U.S. and have caused varying degrees of damage to orchard, landscape, and forest trees. Recently, PCR multiplexes were developed to discriminate closely related AFC symbionts present in the U.S. Such methods have opened the door for widespread molecular surveillance. This includes testing whether fusaria differ between the native / invaded ranges of these beetles. To this end, 52 fusaria recovered from 5 *Euwallacea* spp. within their native range in China including Taiwan, South Korea, and Vietnam as well as 200 fusaria from 2 *Euwallacea* spp. already present in the U.S. were subjected to multiplex PCR assays. Results confirmed fidelity between *E. validus* and AF-4 in South Korea and the U.S. However, *E. interjectus* from two locations in the U.S. three locations in China including Taiwan all had unique fungal lineages within the AFC. In Taiwan, *E. interjectus* is associated with AF-12, the known symbiont of *Euwallacea* sp. #5 from San Diego, CA whereas in the Eastern U.S., it is associated with AF-3. Fusaria from the other locations likely represent novel lineages. *E. denticulus,* from one location in China, are associated with AF-6, one of two known symbionts of *Euwallacea* sp. #2 from Dade Co., FL. Together these results support fungal infidelity among closely related *Euwallacea* beetles.

MON 28

The hunt for nefarious symbioses in a complex world - experimental, molecular, and statistical perspectives of bark beetles and fungi

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More than 3,500 species of bark and ambrosia beetles maintain nutritional symbioses with fungi. A few of these symbioses have decimated local ecologies and economies as beetles carrying pathogenic fungi invade naive ecosystems. Efficiently characterizing these symbiotic associations could allow researchers to identify pathogenic threats before invasion, and prevent future losses. However, distinguishing these symbioses from incidental associations is a major challenge because they are enmeshed within the complex fungal communities of decaying trees. Fortunately, modern molecular sampling and statistical tools can help us meet this challenge. We use exclusion experiments, culture methods, and meta-barcode amplicon sequencing of DNA and RNA to uncover the full breadth of beetle-associated fungal

communities in standing pine logs of the Southeastern US. Results demonstrate that beetles cause several-fold increases in fungal diversity, particularly Ophiostomatales and Saccharomycetales. These effects track beetle density, decreasing from bottoms to tops of logs, and could have implications for biomass decomposition. Simultaneously, pre-invasion assessments of Asian pine-infesting beetles use contemporary permutations-based statistical analyses to distinguish consistent from coincidental associations, which then informs targeted pathogenicity assessments of potentially invasive taxa. These assessments uncover many facultative associations, demonstrating that each beetle vectors diverse fungal symbionts, and many fungal symbionts are vectored by multiple beetles. Our results reveal an unprecedented breadth in the fungal symbioses of bark beetles and suggest a previously under-appreciated role in fungal community dynamics of decaying forest biomass. Increasingly affordable and widely available molecular sampling and statistical tools continue to accelerate discoveries which could prevent future invasion crises.

MON 29

Ambrosia beetle-fungus symbiosis: Significance and opportunities in controlling invasive *Xylosandrus* spp.

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Ambrosia beetles are wood boring insects that tunnel through sapwood, forming galleries where they culture fungi for food. Most ambrosia beetles attack dying trees, but some attack apparently healthy trees outside of their native range. Ambrosia beetles *Xylosandrus crassiusculus* and *X. germanus*, both native to Asia, are now considered among the most important invasive pests in orchards and nurseries in the US. Both have a wide host range and are difficult to control because of their cryptic habits. The use of microbial control agents may prove effective by targeting both foundresses and their brood inside tree galleries: entomopathogenic fungi could be used to target foundresses, the only stage found outside host trees, and mycoparasitic fungi used to target their fungal symbiont. Since most ambrosia beetles feed solely on their symbionts, suppressing the growth of these fungi will deny developing brood food for survival and limit beetle population increase. Our laboratory and field studies showed that both beetles are susceptible to entomopathogenic fungi *Beauveria bassiana* and *Metarhizium brunneum*. Further, infected females died prior to egg laying or after producing only a small brood, some of which had up to 100% mortality from fungal infection. The use of mycoparasitic fungus *Trichoderma harzianum* resulted in galleries with sparse or no symbiont growth, many of which had few or no brood present. These results show the potential of microbial control fungi in controlling ambrosia beetle populations either directly by killing foundresses and reducing brood production or indirectly by suppressing symbiont growth in their galleries.

MON 30

Evolutionary history of ambrosia beetle symbiosis in the Ceratocystidaceae

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Both native and invasive ambrosia beetles employ a unique symbiosis with fungi, but the history of this symbiosis is unclear. Ambrosia beetles are mostly derived from phloem-feeding bark beetles, but ambrosia beetles farm and feed on fungi in sapwood. They carry their cultivated fungi in specialized organs called mycangia, which vary in size and location. Ambrosia beetles are polyphyletic, and each mycangial type stems from a separate evolutionary event. Ambrosia fungi are also polyphyletic. Most obligate ambrosia fungi are in the genus *Raffaelea* (Ophiostomatales), many species of which are shared among lineages of beetles with relatively small mycangia. We studied lineages within four ambrosia

beetle tribes with four different types of large, complex mycangia and found that each is associated with non-pathogenic members of the Ceratocystidaceae (Microascales), a family of mostly plant pathogens. Phylogenetic analyses revealed that the four mycangial types carry five genera of fungal symbionts (*Ambrosiella*, *Phialophoropsis*, *Meredithiella*, and two undescribed genera from two geographic clades of *Scolytoplatypus*). Each of the five fungal genera appear obligately linked to one of the four mycangial types, suggesting co-adaptation events. Molecular clock estimates suggest that two or three early domestication events up to 50 Mya ago may have been followed by horizontal transfer of Ceratocystidaceae to later-evolving ambrosia beetle tribes. Although fungal genus and mycangial type are tightly linked, the associations are not strictly species-specific because sympatric beetle species with the same mycangial type may share fungal symbionts.

MON 31

***Mortierella elongata* root endophyte promotes flowering within the *Calibrachoa* floriculture system.**

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The saprobic fungi *Atractiella rhizophila* and *Mortierella elongata* isolated as endophytes from *Populus deltoides* roots increases seedling growth of corn, red oak and tomato in pasteurized sand and untreated field soil. A greenhouse experiment was conducted to examine the potential utility of *A. rhizophila* and *M. elongata* for promoting growth of the solanaceous floriculture plant *Calibrachoa*. Seedlings of calibrachoa (cv. 'Kabloom Deep Blue') were transplanted into potting media amended with 1, 2 or 5% (v/v) of millet colonized with either *A. rhizophila* or *M. elongata*. Plants were assessed for flower production, leaf area (cm^2), and above/below ground biomass at 24, 24, and 70 days after transplanting. *M. elongata* isolate 93+ significantly increased (P= 0.0071) the number of flowers produced across inoculum amendment volumes compared to the non-inoculated millet controls. We examined effects of treatment by inoculum amendment volume due to a significant treatment by volume interaction. *M. elongata* isolate 93+ significantly increased leaf area (*P*= 0.0088) at 1% v/v compared to the non-inoculated 1% millet control. However, there was no significant difference in above and below ground biomass between treatments. Overall, plants grown in potting media amended at 1 or 2% v/v had significantly greater flower numbers, leaf area and total biomass compared to 5% v/v across treatments. Our results suggest that *M. elongata* 93+ promotes flower production and foliage growth. This experiment is currently being repeated and an additional experiment is in progress to understand the role of iron as a possible mechanism for promoting flowering.

MON 32

Species composition and abundance of endorrhizal fungi in *Carex pensylvanica* (Cyperaceae) from Wisconsin sand prairies

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Wisconsin sand prairies are rare habitats characterized by sandy soils and sparse vegetation. Previous studies indicate that arbuscular mycorrhizae positively influence plant growth in soils with high sand content; however, *Carex pensylvanica*, the most abundant sedge in Wisconsin sand prairies, has generally been considered facultatively mycorrhizal with low colonization frequency. To better understand plant-fungal associations that may promote *C. pensylvanica* colonization in sand prairies, we characterized the diversity of endorrhizal fungi using culture-based and molecular approaches, as well as microscopy. Plants were collected in pairs along sand prairie/oak barren ecotones. Culturing data revealed 70 morphotypes of fungi, while Illlumina sequencing of roots showed 362 OTUs, the most common species being Acephala harenae nom. prov. Cohabitation of dark septate endophytes, arbuscular mycorrhizal fungi, and ectomycorrhizae was determined within ~1cm root sections using light microscopy and Illumina sequencing. *Tomentella ferruginea*, *Russula*, and *Laccaria* were present in all

samples sequenced. Ascomycota consisted mainly of Helotiales. There was no significant difference in environmental factors or fungal community structure between tree and no tree sites. Soil data showed that pH and organic matter correlate with fungal community structure, the cause of which is unclear. To-date, this is the most in-depth survey of root-associated fungi in any *Carex* species. Results provide insights into the diversity of fungi associated with sedges and the soil factors affecting fungal colonization in plants in sand prairie habitats.

MON 33

Geographic distance and host influence grass root fungal endophytic distribution

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Grasses harbor important fungal symbionts that are beneficial for survival and adaptation to stress. These fungi include root endophytes that may be important for the establishment and expansion of grasslands worldwide. However, the distribution of these endophytes and their interactions with host plants remain poorly understood, especially the effects of environmental conditions and host specificity on the fungal community composition and their function. We sampled six native grass species across 23 sites spanning three replicate latitudinal gradients within the US. Fungal endophytes were isolated from surface-sterilized roots and ITS rDNA sequencing was used to identify the acquired isolates. In total, we isolated and sequenced 1033 fungi. Phylum Ascomycota and orders Hypocreales and Pleosporales strongly dominated the communities. Although fungal communities varied among the sites, environmental gradients and host specificity only marginally affected the distribution of the most common fungal endophytes. We identified five dominant taxa *(Fusarium chlamydosporum complex, Fusarium incarnatum-equiseti complex, Periconia, Lasiodiplodia,* and *Darksidea)* that had low specificity across the host species or along latitudinal gradients. Dominant fungi in the collection were tested in seed germination experiments using *Bouteloua gracilis* to evaluate their effects on plant growth. Preliminary results suggest growth-promoting ability for some fungi, including dark septate endophytes whereas others were pathogenic. In addition to their ubiquitous distribution, this variation in their effects on plants may significantly affect plant responses to climate change.

MON 34

Endophytic fungi associated with *Populu*s roots

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Populus is emerging as an important model tree genetic system for studies aimed at understanding forest ecosystems and the interactions of these with the associated microbiota. *Populus* species are known to establish associations with arbuscular and ectomycorrhizal fungi which vary depending on the host species. Recent studies have unlocked a great diversity of fungal endophytes in *Populus*, associated with different plant tissues. The ecological and physiological roles of fungal endophytes in the Populus-microbe interaction have not been fully characterized. We describe a novel approach using multilocus sequence typing (MLST) approach using PacBio and the downstream analysis to genotype individuals in single sequencing run, providing enough loci to characterize a species complex. This approach was applied to *Ilyonectria* complex, an endophyte present in cottonwood (*Populus trichocarpa* and *Populus deltoides*), but also associated with black-foot disease on grapevines. The methodology could be applied to study the phylogenetics and systematics of other fungal groups. In addition, genomes of Populus root-

associated fungal endophytes are being sequenced. The data extracted from these genomes provides insight into the lifestyle strategies of various endophyte species, and provides a framework for metatranscriptomic approaches to understand the role of endophytic fungi.

MON 35

Effects of analytical parameter settings on estimating patterns in diversity of tropical leaf-associated fungi

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High-throughput DNA sequencing makes it possible to characterize cryptic communities of fungi with enhanced resolution, but can introduce artefactual species due to sequencing errors and/or choice of analytical parameters. Previous analyses of leaf samples from Moorea, French Polynesia using low-throughput (clone library) DNA sequencing revealed several biologically interesting patterns that were not observed in a subsequent preliminary analysis of a high-throughput Illumina dataset. We conducted sensitivity analyses of important analytical parameters to determine whether this observed contradiction results from (1) 'false positive' patterns due to insufficient sampling in the low-throughput data; (2) 'false negatives' when real patterns are obscured by artefactual noise in the high-throughput data; or (3) patterns that differ between species, thus appearing chaotic in aggregate. Our results suggest that artefactual noise was the primary cause of discrepancies between the low- and high-throughput conclusions, but that pre-processing rather than analytical filtering steps were the most critical control point.

MON 36

Community structure and diversity of foliar fungal endophytes along an ecological staircase

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Fungal endophytes living inside plants are one of the most species rich and phylogenetically diverse fungal community assemblages. The community structure, species richness and abundance of foliar fungal endophytes have been shown to depend on host taxa and climate, but there is relatively little known how they change with nutrient levels in the habitat and with plant health, which have been drastically changing with human activities. Here we used high-throughput sequencing of marker genes to explore the foliar fungal endophyte communities within *Pinus muricata* and *Vaccinium ovatum* leaves across the Jug Handle Ecological Staircase, consisting of five marine terraces uplifted between 100 and 500 thousand years ago. Essential nutrients, such as nitrogen and phosphorous, decrease in older terraces, leading to ‘pygmy’ plants with higher levels of tannin and polyphenol. We took advantage of the natural nutrient gradient across the staircases to see if nutrient levels in leaves predictably increase fungal species richness, which is a commonly observed trend for plant species diversity. Despite strong compositional differences across terraces for both host species, nutrient levels did not lead to predictable shifts in alpha diversity. Alpha diversity of FFE increased from non-pygmy to pygmy terraces for the *Vaccinium* hosts but not for *Pinus* hosts. Overlapping fungal OTUs between terraces and plant hosts reveal how geography and local environmental variables influence the endophyte community structure and diversity. Understanding the factors driving fungal endophyte beta and alpha diversity yields insights into mechanisms underlying their high species diversity.

MON 37

Fungal Pharmacy: Using *Metarhizium* and fungal extracts for honey bee health

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Metarhizium brunneum, a common soil-borne entomopathogenic fungi, and extracts of *Fomes fomentarius* and *Ganoderma resinaceum* var. *resinaceum* were evaluated as potential biological control stratagies against Varroa destructor, a devastating honey bee ectoparasitic mite, and viruses vectored by varroa. Although previous studies show Metarhizium can infect and kill varroa without harming the honey bee, virulence varies between species, strains, and application methods. Field trials conducted in 2016 tested the efficacy of a non-conidiating and conidating strain of *M. brunneum* against varroa. Varroa fall onto sticky boards was collected every 48 hours, counted, and plated onto water agar. The non-conidiating strain had no effect on varroa population numbers, whereas the conidiating strain caused a significant increase in varroa mite mortality compared to control hives. Peak varroa mortality occurred 5-7 days post treatment, with a decline in mortality starting at day 9; there is a loss of conidia viability at bee hive temperatures (35 ºC). Varroa is a vector of many honey bee viruses. Mycelium extracts were assessed for use as an antiviral treatment against Deformed Wing Virus (DWV) and Lake Sinai Virus (LSV). Honey bees were fed 2L of a 1% mycelium extract (*F. fomentarius* or *G. resinaceum* var. *resinaceum*) at day 1 and day 15 of the experiment. Viral levels were evaluated using qRT-PCR. DWV viral levels were reduced 12 and 11-fold and LSV viral levels were reduced 14 and over 10,000-fold using F. fomentarius and *G. resinaceum* var. *resinaceum* extracts, respectively.

MON 38

Arsenic hyperaccumulation in *Cyanoboletus pulverulentus*

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Cyanoboletus pulverulentus is an edible ectomycorrhizal mushroom found to hyperaccumulate arsenic. 39 individual collections of fruit-bodies from continental Europe, Madeira Island, and North America were analyzed for total arsenic content by ICPMS. Arsenic concentrations varied in a wide range of 2.4-1,300 mg/kg (in dry weight). All tested collections originated from unpolluted areas and arsenic in fruit-bodies was correlated neither with total nor mobile arsenic in underlying soils. Within the fruit-bodies of two tested samples, around 80 % of arsenic was accumulated in the hymenium. No correlation between arsenic concentration and fruit-body weight was observed. Around 80 % of the arsenic was extractable with pure water. In the extracts, dimethylarsinic acid (DMA) was the only arsenic species that could be detected, besides some traces of methylarsonic acid (less than 0.1 % of the extracted arsenic). DMA has a very low acute toxicity but it is classified as carcinogen; possible health risk for consumers is yet to be calculated. ITS rDNA sequencing revealed that the analyzed American collection (Mushroom Observer ID 245588) is significantly different from the European ones (85.5 % similarity) and thus does not represent the genuine *C. pulverulentus* but a distinct species.

MON 39

Genetic diversity of *Candida* in the healthy human gut, and interactions with a foodborne yeast

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Candida yeasts are the most commonly reported fungi in the healthy human gut, where they are present as commensals in most people at most times. While it is common to observe a single species or strain dominating the gut mycobiome, multiple *Candida* species, or multiple strains of the same species, may coexist. Mycobiome sequencing data suggests an inverse correlation between gut *Candida* and *Debaryomyces hansenii*, a yeast prevalent in cheeses and fermented meats, and approximately half of *D. hansenii* isolates from cheese tested exhibit killer activity against *C. albicans* and *C. tropicalis in vitro.* We report on the MLST profiles of *Candida* isolated from fecal samples of six volunteers over several timepoints. We further report on the interactions between resident *Candida* and *D. hansenii* which these volunteers consumed on naturally colonized cheese during the course of this study.

MON 40

The population genomics of copy number variation in the opportunistic fungal pathogen *Aspergillus fumigatus*

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Copy number variants (CNVs) are fragments of DNA (≥ 100 bp) that are present at different copy number between individuals. In fungi, CNVs remain an understudied source of genetic variation, yet CNVs have been associated with host specificity, fungicide resistance, and degree of virulence. *Aspergillus fumigatus* is an opportunistic human pathogen responsible for a variety of potentially lethal infections in immunodeficiency individuals. We analyzed population and individual patterns of CNV across 43 *A. fumigatus* isolates from 3 populations using publicly available whole-genome sequence data. Through the CNV analysis we identified 75 genes and 830 genes duplicated and deleted in at least 1 isolate, respectively. Meanwhile, 65 CNVs are identified overlapping 26 genes that showed highly differentiated copy number between populations. Lastly, within populations, we also observed large-scale CNVs that overlap genes between individuals. Our results suggest that CNVs provide a cryptic source of genetic variation that can affect gene dosage and phenotype, even between genetically similar individuals.

MON 41

Impacts of weatherization on indoor fungal communities

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This study examined how weatherization and housing ventilation systems impact fungal microbial communities indoors. Weatherization (air-sealing) measures are intended to reduce energy use, but they may alter indoor microbial ecology through alteration of ventilation patterns and indoor environmental conditions. We evaluated a broad cohort of single-family detached dwellings in Portland, OR, to characterize climatic heterogeneity during two seasons of climate extremes (summer and winter). We quantified airborne microbial communities and traditional indicators of air quality using paired indoor/outdoor sampling at residential dwellings before and after weatherization of the building envelope. Health and behavior surveys were sent to participants before and after weatherization to understand how

human interaction with weatherization and changing air composition (in terms of microbial ecology and air quality) impacted residential health. Preliminary results indicate that while there is variation of the indoor fungal communities with some measures of IAQ, there is not, however, an apparent gross effect of weatherization on indoor fungal communities. We find strong correlations between indoor and outdoor fungi, with most indoor community members sourced from outside the home. However, we see strong enrichments for certain taxa (e.g., *Trametes versicolor*) and exclusion of others: the indoor communities are compositionally and structurally distinct from outdoor communities in predictable ways. Additionally, we see strong seasonal effects on both indoor and outdoor fungal communities. Analysis incorporating the health and behavioral survey data is ongoing.

MON 42

Membrane damage-responsive biosensors for the discovery of antimicrobials from Alberta environmental fungal isolates

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Antibiotic resistance in bacterial pathogens is a threat to medical treatment of infections. Conventional methods for antimicrobial screening rely on methods to detect direct antimicrobial killing. However, this approach lacks the sensitivity to detect sub-lethal bioactive molecules. We developed biosensors in *Pseudomonas aeruginosa* that produce light from transcriptional *lux* fusions in response to compounds that damage the outer membrane. Sub-lethal exposure to antimicrobial peptides, the antibiotic cycloserine, and cation chelators induces expression of *arnC::lux* (*PA3553*) and *speE2::lux* (*PA4774*). These genes encode outer surface modifications that protect *P. aeruginosa* from exposure to membrane-damaging compounds. We used high throughput screening to test the cell-free culture supernatants from a panel of fungal species isolated in Alberta. Preliminary results showed a significant induction of both strains of *lux* biosensors in 23 of 29 fungal species screened. Due to the significant amount of biosensor induction from *Lenzites betulina*, *Haploporus odorus*, *Ganoderma applanation*, and *Lentinula edodes*, an 8-week time course of experiments was performed to observe optimal biosensor induction in response to fungal supernatants. Proteins were concentrated from supernatant, at optimal time points, and fractionated with fast protein liquid chromatography (FPLC), using size exclusion chromatography columns. Preliminary mass spectrometry indicates the presence of histones, a known class of antimicrobial peptides, in an active fraction. Additional active fractions identified are under further study. In summary, we developed a rapid and sensitive approach to detect antimicrobials from fungi that target the Gram-negative outer membrane. Further identification of the specific antimicrobial compounds is expected to identify novel antibiotics.

TUES 1

Fungal communities in soybean cyst nematode-infested soils

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The soybean cyst nematode (SCN) causes $1.5 billion in annual soybean yield losses in the U.S. While crop rotation provides some control of SCN, current research is focused on developing biocontrol agents to more effectively combat this plant pathogen. To identify potential fungal biocontrol agents of SCN, ITS1 amplicon sequencing was used to analyze fungal communities in bulk soils, rhizosphere soils, and roots in soybeans under annual rotation and 1, 3, 5, and 34 years of continuous monoculture in a randomized complete block long-term rotation experiment at the University of Minnesota Southern Research and Outreach Center. Sequencing was performed on the Illumina MiSeq 250 platform, and sequence data were assembled into contigs, filtered, and trimmed using the bioinformatics package, mothur. OTU clustering was performed with USearch in QIIME, using the UNITE database as a reference to assign taxonomy to OTUs. Sequence counts for each OTU were converted to relative abundances and square root transformed. ANOVA and Tukey's HSD were used to identify taxa and guilds of nematophagous fungi that increased in relative abundance over successive years of soybean monoculture in bulk soil, rhizosphere soil, and roots. Correlation tests between SCN density and the relative abundance of nematophagous taxa or guilds were also performed. Results showed that SCN-antagonistic fungi belonging to different nematophagous guilds increase in relative abundance in different ecological compartments with increasing SCN density over continuous soybean monoculture. These results suggest that biocontrol of SCN may be more effective if it incorporates fungi from multiple nematophagous guilds.

TUES 2

Diversity and function of temperate bog and stream fungi

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Current concepts in community level ecosystem function suggest that many related species are functionally redundant, certain species are essential for stable community processes, and that the magnitude of ecological processes is a consequence of functional complementarity. Unfortunately, the assessment of environmental function at the community level does not provide information on which species are present, which species are functionally redundant or complementary, or the phylogenetic relationships with respect to species distribution and function. This research examines freshwater bog and stream fungi, providing the opportunity to compare species distribution and functional roles across contrasting aquatic environments. To capture a diverse group of fungi, this study focused on three sites from each of two contrasting freshwater habitats in Pennsylvania and Wisconsin. Fungal isolates for this project were obtained from submerged detritus or substrates on or beneath the streambed. Isolate identity was determined through ITS sequence match using BLASTn against the NCBI database. Qualitative and quantitative assays were used to determine isolate function. Preliminary analysis suggested that habitat and collection time were important main affects in which species were isolated and correspondence analysis suggested that the isolated communities from each habitat were different. Preliminary analysis of enzymes involved in the breakdown of detritus have demonstrated that: 1) many aquatic fungal isolates produce the same plant degrading enzymes, 2) some isolates have a greater magnitude in function, and 3) some isolates perform one environmental function well but may require the presence of other species to persist within the environment.

TUES 3

The roles of endolithic fungi in bioerosion and disease in marine ecosystems: general concepts and specific roles of *Aspergillus sydowii* in causing disease in reef corals

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Endolithic fungi penetrate calcareous substrates formed by living organisms, cause significant bioerosion and are involved in diseases of many host animals in marine ecosystems. A theoretical interactive model for the ecology reef-building corals includes five principle partners that exist in a dynamic equilibrium: polyps of a colonial coelenterate, endosymbiotic zooxanthellae, endolithic algae that penetrate coral skeletons, endolithic fungi (that attack the endolithic algae, the zooxanthellae and the polyps) and prokaryotic and eukaryotic microorganisms which live in the coral mucus. Endolithic fungi are important components of the marine calcium carbonate cycle because they actively contribute to the biodegradation of shells of dead animals composed of calcium carbonate and calcareous geological substrates. They have been implicated as a causative agent of shell diseases in live corals. Opportunist marine fungal pathogens, such as *A. sydowii*, are endoliths, are ubiquitous in the open oceans, intertidal zones, and marine sediments, infect animals which live in these ecosystems and produce toxins which inhibit photosynthesis in coral zooxanthellae. The prevalence of these infections have increased in frequency and severity in recent decades.

TUES 4

Fungal diversity and biogeography in the forest soil of the Republic of Korea

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Fungi play an important role in the forest soil as decomposers and symbionts. Traditionally, fungal diversity was assessed by fruiting bodies or culture dependent methods. However, recent studies using NGS have revealed higher diversity than expected. In the Republic of Korea, a total of 3,664 species (4 phyla, 19 classes, 70 orders, 215 families, 853 genera) have been recorded to date. However, most studies were based on traditional methods, which suggest that a significant amount of the fungal diversity of Korea remains undiscovered. In this study, we conducted a survey of fungal diversity in the forest soil across South Korea using Illumina Miseq platform. Next, we analyzed biogeographic patterns associated with environmental factors. Of 93 samples, we found 4,000 OTUs (species level) belong to 5 phyla, 24 classes, 82 orders, 170 families, and 357 genera. *Russula* and *Amanita* were dominant among the symbiotroph, while *Mortierella* and *Umbelopsis* were dominant in the saprotroph. In addition, there was a large number of unrecorded species among some genera, which may reflect the undiscovered fungal diversity of Korea. The biogeographic analysis of environmental factors (e.g. vegetation and geographic coordinates) revealed associations of spatial patterns within the fungal community. Considering the predicted environmental shifts associated with climate change, geographical pattern of fungal communities are difficult to predict, but likely to change significantly. Therefore, the environmental components that may impact fungal diversity can be investigated using NGS as well as traditional methods in order to understand forest ecosystems and to conserve the fungal community of Korea.

TUES 5

The pan core, and dispensable genome of the Neocallimastigomycota

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Members of the anaerobic gut fungi (AGF) were originally discovered in sheep, then subsequently observed in rumen, hindgut, and feces of ruminant and non-ruminant herbivorous mammals and reptilian herbivores. AGF belong to a distinct phylum lineage (Neocallimastigomycota), play an important role in plant biomass degradation in many herbivores, and represent the only. Overall research progress on AGF has been sparse due to their perceived fastidious nature, lack of reliable storage procedures, and frequent occurrence of senescence in AGF strains. Sequencing of AGF genomes has also been hampered by their extremely high AT content and the proliferation of intergenic repeats in their genomes. Analysis of AGF genomes could provide multiple insights regarding their extensive lignocellulosic capabilities, evolutionary history, patterns of horizontal gene transfer, and effect of sequestration in the herbivorous gut on their genomes architecture. Here we present our progress in sequencing 18 transcriptomes and 8 genomes belonging to 8 different genera within this group, as well as efforts to delineate the core, pan, and dispensiple genome components within the Neocallimastigomycota.

TUES 6

Seasonality drives arbuscular mycorrhizal fungal diversity in Mexican dry seasonal tropical forests

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Considerable gaps remain in our understanding of arbuscular mycorrhizal fungal (AMF) diversity and community ecology in most ecosystems. These gaps are especially large in tropical systems, where few studies on AMF ecology have been conducted. To address this knowledge gap, we have been documenting AMF community diversity and structure in three dry seasonal tropical forest sites in Mexico using AMF barcoding primers NS31 and AML2 adapted for custom dual-indexed Illumina sequencing. In each site, we collected soil and root samples under 25 individual trees and across two consecutive wet-dry seasonal cycles. We analyzed AMF diversity and the relationship between seasonality, soil nutrient levels, and AMF communities in soils and roots using a custom QIIME pipeline. Our analyses showed that: AMF taxonomic richness was significantly higher in soil than root communities; AMF taxonomic richness was higher in the dry than wet seasons; and significant shifts in community composition occurred between seasons. These seasonal shifts were correlated with soil nutrient levels, whereby the lowest AMF richness (wet season) occurred when soils contained the highest levels of NO_3, NH_4, and P. Our results agree with the general consensus that seasonality is an important driver of AMF community composition, and that AMF diversity is negatively correlated with nutrient availability. That AMF diversity is higher in the dry than wet season, however, conflicts with general patterns in temperate systems, and leads to questions about AMF community assembly and functioning, and how AMF communities might respond to future climate change in these systems.

TUES 7

Intraspecific competition between amphibian-killing chytrid strains on a model frog host

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Geographic invasion, and subsequent competition between disease strains may be a key driver of evolution in pathogen species. Ecological theory predicts that direct competition between closely related

disease strains in overlapping hosts will result in only the most virulent strain persisting. Despite its evolutionary implications, this hypothesis remains untested for the vast majority of pathogens. Here, we experimentally investigate the *in-vivo* competitive differences between two highly divergent lineages of the amphibian-killing chytrid fungus (*Batrachochytrium dendrobatidis*, *Bd*). These divergent *Bd* lineages are hypothesized to have diverged in allopatry but recently been brought back into secondary contact by human introduction. Prior studies suggest that a panzootically-distributed, global lineage of *Bd* was recently introduced into southern Brazil, and is competitively excluding endemic lineages in the southern Atlantic Forest. To test for differences in fitness under competition, we performed coinfection studies between invasive versus endemic Brazilian *Bd* strains on a model host frog (*Hymenocirus curitpes*). We tracked zoospore production of each strain over the course of the coinfection experiment with a chip-based digital PCR (dPCR) assay. Our results show that a small proportion of high-virulence strains within the expanding panzootic swarm drive a competitive advantage during the early stages of infection. We describe the application of a novel molecular resource (dPCR) to quantify rare, strain-specific alleles within a mixed fungal population. Finally, we provide new evidence that competitive pressure resulting from the human movement of fungal pathogens can be a force shaping pathogen genetics and virulence evolution.

TUES 8

Unraveling the core mechanisms of *Suillus-Pinus* symbiosis using integrated omics

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Despite the importance of ectomycorrhizal fungi (EMF) to forest health, we know little about mechanisms by which EMF associate and communicate with their plant hosts. We are using the *Pinus-Suillus* EMF symbiosis as a model for study of host-specific interactions and their effects on C/N/P fluxes in forest soils. Here, we applied integrated multiple 'omics approaches to characterize sets of interacting genes between compatible *Suillus-Pinus* pairings (*S. spraguei* x *P. strobus*; *S. decipiens* x *P. taeda*) versus incompatible pairings (*S. spraguei* x *P. taeda*; *S. decipiens* x *P. strobus*). Combined 'omics approaches include de novo fungal genome sequencing and assembly (JGI), metatranscriptomics (JGI) and proteome/metabolome profiling (by EMSL) to identify genes/transcripts/proteins/metabolites. Using time-course studies, genes and gene products involved in early and late stages of fungal-plant communication and nutrient reallocation were identified. Coordinated processes between *Suillus* and their host plants that we highlighted include sets of effector-receptors that are required for symbiotic initiation, development or maintenance. For example, signal transduction components whose transcription changed early during symbiotic initiation include fungal small secretory proteins(SSPs), heterotrimeric G-protein signaling and plant LRR-receptor-kinases. This signal manipulation could precede substantial transcriptional reprogramming involving other sets of fungal SSPs and plant cysteine-rich receptor kinases that are involved in symbiotic maintenance. Integration of omic data confirms fructose metabolites to be the major class of plant carbon relocated to the fungal symbiont followed by conversion to mannitol, trehalose and arabinitol. The chemical shift between symbiotic partners in response to host compatibility and symbiotic efficiency will be discussed.

TUES 9

Mating system and mating gene evolution in *Suillus brevipes*

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Sexual reproduction in fungi is controlled by MAT loci that define different mating types. MAT loci of basidiomycetes are characterized by a high level of polymorphism. The high diversity of mating alleles has attracted much attention, and is explained by strong negative frequency dependent selection in which rare alleles have a selective advantage over popular alleles which have lower fitness. Under this scenario, multiple alleles of MAT loci are predicted to have an extended coalescence time relative to other neutral loci. Previously, mating systems and allele number in basidiomycetes are inferred by pairing of single-basidiospore isolates. In this study, we employed genomic shotgun sequencing data to recover haplotypes of the HD MAT locus from populations of the bolete mushroom *Suillus brevipes* in two stuctured populations in California. The HD MAT loci of *S. brevipes* only contain a pair of homeodomain encoding HD protein. De novo assembly of shotgun sequence data shows 32 distinct alleles among 25 dikaryotic isolates, where heterozygotes in both HD1 and HD2 are consistently found. Comparison of different haplotypes shows that the same HD1 allele always coexists with the same HD2; multipartite linkages are not observed. Our results confirm the high mating type diversity under balancing selection and restricted recombination within the MAT region. Population genetic analysis suggests a distinct mating allele composition for each population, consistent with restricted gene flow between these populations. Phylogenetic incongruence between HD1 and HD2 phylogenies surprisingly implies that recombination also contributes to the generation of MAT allele diversity.

TUES 10

You can't hide your lichenize: Infidelity in the *Leptogium cyanescens* species complex and its associated *Nostoc*

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Symbiosis, in which two or more organisms share scarce resources, is a ubiquitous but poorly understood phenomenon. We hypothesize that lichen species that reproduce asexually will exhibit high specificity because both partners will be co-inherited in vegetative propagules (isidia). In contrast, sexually reproducing lichens should exhibit lower specificity because ascospores contain only the fungus so the symbiosis must be reestablished each generation. We utilized the common lichen *Leptogium cyanescens* sensu lato to assess the degree to which fungal host phylogeny predicts photobiont (*Nostoc* cyanobacteria) phylogeny. We sequenced three genes from the mycobionts (MCM7, RPB1, RPB2) and three from the photobionts (nifV1, rblcX, rpoc2). Within the *Leptogium cyanescens* complex we found four mycobiont clades and two photobiont clades. Three mycobiont species (species B, C, D) formed a clade and associated exclusively with one Nostoc clade, suggesting that the mycobiont speciation occurred without photobiont speciation. The fourth mycobiont (species A) associated only with the second clade of *Nostoc* - an example of high specificity. AMOVA partitioned by mycobiont versus locality showed that, amongst three of the fungal species, the photobiont population structure is best explained by locality. We also detected sexual reproduction within two *Leptogium* species, indicating that ascospores are produced and may provide opportunities to associate with new *Nostoc* genotypes. One *Leptogium* species was specifically associated with one photobiont clade whereas the other three fungal species associated with multiple clades. These findings suggest the importance of wide sampling within a species complex to better understand patterns of symbiotic association.

TUES 11

Decomposition gene loss patterns in the transition from saprotrophy to the ectomycorrhizal habit within the order Russulales

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Russulaceae is a diverse family including the genera *Russula, Lactarius, Lactifluus*, and *Multifurca* and is one of the most widespread and species rich ectomyocrrhizal (ECM) lineages. In a recent collaborative effort, we sequenced 9 genomes and transcriptomes of representative groups across Russulaceae, including the closely related saprotrophic outgroup *Gloeopeniophorella*. We present here a comparative study of genomes across the order Russulales to investigate i) to what extent genes involved in plant biopolymer degradation can be maintained within a single, diverse, ECM lineage and ii) to compare functional diversity within and between functional groups of this ecologically important order, specifically focused on the species' ability to scavenge nutrients from recalcitrant organic matter. Preliminary evidence suggests that members of Russulaceae, though mutualists, have retained a restricted set of genes coding for lignin peroxidases and copper oxidoreductases from their saprotrophic ancestor. In some cases, expansions in these gene families indicate neofunctionalization and suggest the potential for functional niches.

TUES 12

Testing the secotioid syndrome hypothesis across multiple environmental variables: a case study using a global-scale phylogeny of *Cortinarius*

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Sequestrate fungi do not forcibly discharge their spores. They evolved from gilled taxa in many different lineages. Harry Thiers presented the Secotioid Syndrome Hypothesis in 1986 in which the sequestrate state is an adaptation to living in arid habitats, where the lack of moisture limits opportunities for aboveground fruiting body development and spore discharge. Bougher and Lebel hypothesized that there may be an equal but opposing selection pressure to protect the spore-bearing surface from excessively moist conditions. We test these hypotheses in the globally distributed genus *Cortinarius* using both temperate and tropical taxa. We correlate mean annual temperature, mean annual precipitation, and seasonality with the state of the fruiting body (sequestrate vs gilled). We put forward the hypothesis that not all sequestrate species evolved in arid habitats and that some are simply a result of one or several loss-of-function mutations.

TUES 13

Whole genome DNA-methylation (methylome) patterning changes during heterokaryosis in Agaricomycetes

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DNA methylation of cytosines, a well-known form of 'epigenetic' modification, has been shown to be important in such diverse processes as the formation of human cancers, development in multicellular eukaryotes, and the silencing of transposons and repetitive elements in plants, animals, and fungi. Despite the importance and apparent conservation of DNA methylation across diverse clades of eukaryotes, we still lack a basic understanding of its roles in the mushroom-forming fungi of the Agaricomycetes. While it has been shown that DNA methylation in CpG (5' Cà G 3') contexts is important

for the silencing of repetitive DNA elements in fungi, we lack a comprehensive understanding of DNA methylation at the whole genome level in the Basidiomycota. In particular, we know little of how whole genome DNA methylation ("methylome") patterning differs during different life-stages within a species. Using whole-genome bisulfite sequencing (WGBS), we have generated genome-wide methylation profiles of two haploid homokaryotic isolates of five taxa (*Coprinopsis cinerea, Heterobasidion irregulare, Wolfiporia cocos, Coprinellus disseminatus* and *Cyathus stercoreus)* along with a mated heterokaryon for each strain. Here, we report that there is variation of methylation patterning both between homokaryotic isolates and during the transition from homokaryon to heterokaryon. Further, we show that methylation of gene-bodies is occurring in some species and discuss categories of genes that show differential methylation patterning during heterokaryosis.

TUES 14

Fungal terrestrialization: challenges, consequences and scenarios for the colonization of land

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The occurrence and diversification of Fungi in early terrestrial ecosystems has received substantial attention, with a breadth of scenarios elaborating the ecological pathway(s) Fungi employed to conquer the terrestrial realm. These proposals, however, generally pre-date a modern understanding of phylogenetic relationships and the temporal framework within which expansion into terrestrial habitats occurred, thereby complicating their interpretation. Here we evaluate these terrestrialization scenarios, and emphasize the challenges encountered in this transition, and the mechanism by which Fungi have adapted to survive in terrestrial ecosystems.

TUES 15

Fungal Morphology: Principles and Problems

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Fungi grow in a staggering array of shapes and sizes, from microscopic unicellular yeasts to macroscopic multicellular mycelia. Despite this diversity, the same components shape all fungi: the cytoskeleton, the secretory pathway, and the cell wall. These components are combined, regulated, and coordinated by nuclear and circadian cycles to allow proper development and function. Recent key findings in fungal morphology and outstanding research questions will be highlighted.

TUES 16

Investigation of fungal dimorphism in Ustilaginomycotina

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Dimorphism is a phenomenon whereby a fungus can grow as both yeasts and as hyphae. The two different growth forms can be reversibly shifted depending on environmental conditions such as nutrient deprivation, temperature, pH or presence of certain compounds from a host. Many pathogens rely on signals from their hosts to initiate dimorphic switching. Temperature seems to be a common cue for

several dimorphic human pathogens. However, no well-established common signal has been identified that dimorphic plant pathogens utilize for the switching process. Smut fungi are an artificial group of dimorphic plant pathogens most of which phylogenetically belong to Ustilaginomycotina. The growth form in smut fungi is primarily based on nuclear status and mating process, which involve the MAPK pathway as a major signaling cascade. Recent studies have shown that lipid compounds can trigger filamentous growth in the model smut species *Ustilago maydis*, presumably through activation of the PKA pathway. Other than the smut fungi, Ustilaginomycotina also comprise non-smut phytopathogens, animal-associated fungi and saprotrophic fungi. These display a variety of growth forms ranging from yeasts or hyphae to dimorphic. A question of what factors affect which type of growth form is displayed remains poorly elucidated. Herein, through investigation on exemplars from several lineages—Ustilaginales, Violaceomycetales, Microstromatales, Exobasidiales and Entylomatales—we will present preliminary results of ongoing studies on fungal dimorphism in Ustilaginomycotina using physiological and genomic approaches.

TUES 17

Hyphal Tip Characteristics of *Conidiobolus coronatus* (Zoopagomycota, Entomophthorales)

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Characteristics of hyphal structure and growth can provide insights into mechanisms of polarized growth and support investigations of fungal phylogeny. To resolve evolutionary relationships of the zygomycetes, we have used comparative bio-imaging methods (light and transmission electron microscopy; LM and TEM, respectively) to describe selected subcellular characters of hyphal tips of *Conidiobolus coronatus*. We show that growing hyphae of *C. coronatus* contain Spitzenkörper (Spk). Spk are most commonly present in hyphae of the Dikarya, and rarely reported in zygomycete hyphae, which possess an apical vesicle crescent (AVC). Descriptions of additional subcellular characters (e.g., mitotic-phase spindle pole bodies, cytoplasmic behavior, organelle structure) are also addressed. Implications of these findings will be discussed in regard to hyphal tip growth and fungal phylogeny.

TUES 18

Identifying endocytic cargo associated with hyphal growth in *Aspergillus nidulans*

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Understanding the mechanisms of fungal growth is one of the oldest and most fundamental objectives in mycology. Filamentous fungi uniquely produce polarized cells called hyphae. Polarization of hyphae is dependent on a balance between endocytosis and exocytosis that may be maintained through apical recycling. This balance likely involves the Spitzenkörper, a secretory structure that is found only in growing hyphae, and a sub-apical collar that is enriched for endocytosis. Here, a bioinformatics approach was used to identify all *Aspergillus nidulans* proteins that contain a NPFxD motif, which was previously established in *Saccharomyces cerevisiae* to mark proteins for endocytosis. The long-term goal of this project is to examine the predicted endocytic association and function of these NPFxD motif-containing proteins during hyphal growth using fluorescent markers and live-cell imaging. Here, proteins were prioritized based on predicted gene ontologies and the recognized functions of orthologs in other model fungi. Many of these proteins have previously been shown to be involved in cell development and regulation of polar cellular morphology in budding and fission yeasts. TaoA, EcoA, SypA, and CrnA all contain this motif and localize to one of three regions associated with hyphal growth in A. nidulans. Mutants in these genes varied in their ability to establish or maintain polarity suggesting that these proteins could be cargo for endocytosis.

TUES 19

Understanding the role of septin AspD in the early vegetative growth of *Aspergillus nidulans*

Ilkay Dorter, Michelle Momany
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Basic research on septin dynamics in the model organism *Aspergillus nidulans* helps us better understand the cellular and molecular mechanisms of these cytoskeletal elements and can help develop new therapeutic approaches against diseases. Under the right conditions *A. nidulans* spores emerge a germ tube to explore new growth medium. Thereby fungal hyphal tips grow into the food substrate forming a hyphal network with evenly spaced lateral branches. This basic process requires a fine and precise coordination of biochemical and cellular processes. We performed single deletions of the genes encoding for the core septins AspA-D. In the absence of AspA, AspB and AspC we could observe an abnormal increase of lateral branches, which is also known as hyperbranching. The knock-out of the fourth core septin AspD did not result in obvious phenotypic changes whereas fluorescence microscopy revealed abnormal nuclear structures that worsened with each mitotic division. In contrast to WT the average distance between two neighboring nuclei was greatly reduced in the Δ***aspD*** background, whereas the nuclei themselves were slightly elongated. Time-lapse analyses revealed AspD-GFP septin bars locating between the two newly divided nuclei supporting the idea that septin AspD might play a role after mitosis. On a colony level all of the ΔaspD mutants showed changes in conidiospore density and color, known as sectoring phenotype. This might indicate chromosome missegregation.

TUES 20

Genomic editing of *Neurospora crassa* as a tool for studying circadian oscillator synchronization

Brooke Hull[1], Jia Hwei Cheong[2], Michael Judge[1], Zhaojie Deng[2], Carmen Rodriguez[1], James Griffith[1], Leidong Mao[2], Jonathan Arnold[1]
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Circadian rhythms are a well-characterized emergent property of the organism as a whole in *Neurospora crassa* with known responses to external factors, such as temperature and light, but the effect of intercellular communication on this system is not understood. Our group has recently demonstrated synchronicity of cells over time in interactive cell populations, but not in those which are physically barred from cell-to-cell interaction. We therefore hypothesize cells can communicate circadian time to each other, resulting in synchronization of cell clock phase. To measure directly the synchronicity of cells over time we have engineered a second construct with yellow fluorescence. *Venus*, a yellow fluorescent protein, was introduced into the genome in codon optimized form under the control of the promoter of the *clock controlled gene 2* using CRISPR Cas9 guided homologous recombination. When used in tandem with an existing red fluorescence construct, this new strain allows visualization and direct study of circadian synchronicity in *N. crassa* on both a single cell and on a population scale.

TUES 21

Diffuse symbioses: Competition, coevolution, and disease suppression in soil microbiomes

Linda Kinkel
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Microbes and plants exist within complex networks of interacting plant and microbial species. Our work explores the roles of plant community diversity, plant host, and fungal and bacterial species interactions in determining the pathogen-suppressive potential and composition of soil microbiomes, and the

consequences for plant productivity. Unraveling the complex interactions among plants and soil microbiomes can suggest novel insights for active management of soil microbes to support plant productivity. Our results show that rhizosphere *Streptomyces* associated with the same plant host are significantly more pathogen-suppressive when the host grew in monoculture vs. within a high-diversity plant community. In contrast, populations of *Streptomyces* in the rhizosphere of plant hosts growing in high-diversity communities are more niche-differentiated than populations associated with the same host in monoculture. These data suggest that plant community diversity plays a critical role in determining the likelihood of antagonistic arms race coevolution vs. niche differentiation among sympatric soil populations, with significant implications for plant disease suppression. *Fusarium* populations also show evidence of coevolutionary interactions with *Streptomyces*. *Fusarium* are significantly better at inhibiting sympatric than allopatric populations of *Streptomyces*, and inhibition is positively correlated with niche overlap between sympatric, but not allopatric, *Fusarium* and *Streptomyces*. This work illustrates how diffuse networks of species interactions over diverse spatial scales contribute to determining the antagonistic potential of indigenous soil microbes, and suggests specific management approaches targeting species interactions may offer potential for sustainable disease control.

TUES 22

Harnessing fungi to improve agriculture

Jason Wallace
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All land plants live in association with fungi, including many commensals, some beneficial species, and some pathogens. Although pathogens have gotten the most attention in agriculture, work is underway to harness beneficial fungi to improve crop sustainability and production. To achieve these goals, basic research needs to be translated to in-field results that are both reliable and economical. I outline some of the steps that will be required to move laboratory result into the field, including the development of model systems, in-field trials at both small and large scales, and commercialization of promising candidates. I will also discuss several existing systems where fungi have already been commercialized to benefit agriculture, along with the need for independent verification of product claims. There is very large interest and potential benefit from being able to understanding and manipulating fungi in agronomic systems. It will take cooperation from both public and private entities to harness these organisms to improve agriculture.

TUES 23

The effects of root-associated fungi on range grass performance and community stability

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Perennial grasses such as Blue and Black Grama are key to preserving healthy rangelands in the Great Plains of North America. Yet, we have just begun to investigate the role of root endophytic fungi in maintaining natural grasslands, and little is known about pairwise fungi-plant interaction outcomes in this system. In a field experiment, we directly assessed the role of fungal-mediated plant-soil feedbacks on the performance of focal grass species, as well as its role in maintaining stability between the two grass species. From the field experiment, we conducted a wide survey of Blue and Black Grama root-associated fungi using culturing and next-generation sequencing methods. Finally, we investigated the effect of root fungal endophyte colonization on performance of focal grass species at different watering levels using ten fungal strains from the survey. In the field, we found that negative fungal-mediated plant-soil feedbacks were associated with patches that showed high community stability through time. This suggested that plant-soil feedbacks, and particularly those mediated by fungi, could be important in maintaining the stability of rangelands. We found Blue and Black Grama to host diverse fungal communities in their roots, which we were able to manipulate successfully in the field feedback experiment. In the greenhouse, we found that effects of fungal inoculation were context- and host-

dependent. For example, under drought conditions a *Chaetomium* strain increased Blue Grama growth, whereas a *Monosporascus* strain had adverse effects on grama grass root architecture.

TUES 24

What's up with *Monosporascus*?

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Although species of *Monosporascus* are best known as root pathogens of cucurbits in agricultural settings, members of the genus are common root endophytes in arid environments. In central New Mexico, isolates have been obtained from the roots of grasses, shrubs, trees and herbaceous plants. In root endophyte surveys, ribosomal ITS sequences from species of *Monosporascus* often comprise the most abundant OTUs from certain plants. We are employing comparative studies to determine whether endophytic strains of *Monosporascus* species are pathogenic on agriculturally important cucurbits or, instead, pathogenic strains represent lineages distinct from endophytes. Laboratory experiments point to possible life-cycle differences between described species and isolates from New Mexico. In contrast with the original homothallic *M. cannonballus* strains that were identified as pathogens, sexual reproduction has not been observed among any of the New Mexico isolates. On the other hand, preliminary characterization of the genomes of 10 isolates indicates that some strains identified as endophytes are closely related to pathogenic strains. The genomic studies also demonstrate that the genus belongs to the Xylariales, not the Sordariales where it has been placed, and that the genomes of members of the genus are approximately twice the size of those typical for Sordariomycetes. Sexual reproduction remains enigmatic, in part because none of the genomes possess homologs of any of the three genes associated with mating type A (Mat 1-1) in other heterothallic and homothallic filamentous Ascomycota.

TUES 25

Development and applications of the EntomopathogenID MLSA database for use in agricultural systems.

Christopher Dunlap
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The current study reports the development and application of a publicly accessible, curated database of Hypocrealean entomopathogenic fungi sequence data. The goal was to provide a platform for users to easily access sequence data from reference strains. The database can be used to accurately identify unknown entomopathogenic fungi based on sequence data for a variety of phylogenetically informative loci. The database provides full multi-locus sequence alignment capabilities. The initial release contains data compiled for 528 strains covering the phylogenetic diversity of three important entomopathogenic taxonomic families: Clavicipitaceae, Cordycipitaceae, and Ophiocordycipitaceae. Furthermore, the EntomopathogenID can be expanded to other fungal clades that cause important diseases to beneficial and pest arthropods, thus allowing storage of limitless number of specimens and enabling isolate characterization or even evolutionary or functional analyses. In addition to taxonomic and phylogenetic analysis, the database provides a platform to initiate translational research of these organisms in agroecosystems. One example of this type of research application is using the database to identify DNA targets for selective markers for a group of strains. The utility of the database should continue to grow as more Hypocrealean genomes become available.

TUES 26

Harnessing pathogen antagonists for crop improvement

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Endophytic fungi can reduce plant disease severity by interacting antagonistically with pathogens and/or by priming plant defense against pathogens. Harnessing these beneficial fungi in agriculture may provide a more sustainable approach to disease management than traditional practices. However, the integration of pathogen antagonists into crop improvement is limited by our poor understanding of the relationship between plant genotypes and microbiomes. In other words, it is not clear whether we can selectively breed for beneficial plant-microbial interactions. I will address this question by discussing ongoing efforts in my lab to understand the relationship between plant genotypic variation and endophtye-pathogen interactions. Across different crops (poplar, maize), we have found evidence that plant genotypic variation strongly impacts foliar fungal community structure. Moreover, in some cases pathogen antagonism by fungal leaf endophytes varies among host plant genotypes. Our ongoing efforts utilize GWAS and germplasm from real breeding programs to further understand how plant genotype affects endophyte communities and pathogen antagonism.

POSTER 1

Volatile oxylipins alter growth and development of three Penicillium species

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The volatile organic compounds (VOCs) 1-octanol, 3-octanone and 1-octen-3-ol are 8-carbon oxylipins that function as fungal signaling molecules known to prevent spore germination and/or stimulate conidiation in some species. We are studying the effects of these compounds on Penicillium expansum, Penicillium sclerotiorum and Penicillium solitum. We exposed spores and nascent colonies to the oxylipins in the gas phase at 10-fold serial concentrations ranging from 0.3 to 300 µM. Despite the similar structures of the VOCs and the relatedness of the Penicillium species, the compounds had different effects on different species. At 300 µM, 1-octanol and 1-octen-3-ol inhibited spore germination for all species. 300 µM 3-octanone only inhibited spore germination of P. sclerotiorum. Germination inhibition by 1-octen-3-ol and 3-octanone were reversible whereas 1-octanol appeared to be lethal to spores. For P. sclerotiorum, the abundance of synnemata was visually lessened by higher concentrations of the VOCs. Usually, 3-octanone was the least growth-inhibitory compound tested. As an exception, the growth of nascent P. sclerotiorum colonies was slowed more by 300 µM 1-octen-3-ol and 3-octanone than 1-octanol. The VOCs also affected the severity of disease symptoms on apple infected with P. expansum or P. solitum. At different concentrations, the VOCs significantly reduced or did not affect virulence of P. expansum. For P. solitum, 3 µM of the VOCs significantly increased symptom severity. We are continuing to catalog the effects of the volatile oxylipins and to identify gene candidates that may be involved in the differing results.

POSTER 2

Applied Mycology in the curriculum: Teaching the practice of idea 'pitching' with fungi

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At the University of Minnesota, mycology has been a visible and viable area of growth. It is a great time to be in Minnesota if you like fungus. Most of our course offerings, however, cover fungal basics, and application-focused mycological coursework has been thin. In Fall 2016, I taught a course that, I think, pushes fungi into the applied curriculum arena: Applied Mycology: Making use of Fungi. This course had 11 graduate and undergraduate students, and feedback was generally positive (and abundant!). Having 11 students was a comfortable way to kick off a course that I hope has a bright future. The design was not to do a survey of fungal applications (e.g. blue cheese, blue jeans). Instead, I configured the course to challenge students to use basic research articles as their motivation to ‘pitch' application ideas. We called these ‘App Pitches.' As an example, we studied the optogenetics control mechanisms of Neurospora crassa's molecular clock, developed by Louis Larrondo and others. Then, we investigated one of his application ideas for transforming and controlling flocculation in yeasts, allowing control over an important separations step when scaling up fermentation in industry. Over the course of the semester, we read 7 peer-reviewed journal articles, and students wrote App Pitches based on these basic science findings. This forced the students to repeatedly practice pitching application ideas, and this practice of ‘writing to convince' will serve these students going forward. I believe will also help safeguard the health (and wealth) of mycology.

POSTER 3

How can glycosyl hydrolases and Fenton reactions co-exist in early decay in brown-rot fungi

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Brown rot fungi are recognized for their non-enzymatic depolymerization mechanism in the incipient stages of wood decay, in which they use Reactive Oxygen Radicals (ROS) for unspecific oxidative cleavage. Hydroxyl radical (•OH), generated from Fenton reactants Fe2+ and H2O2, was proposed as an important source of these ROS. By using model brown rot fungus Postia placenta, we recent revealed that the transcription of several Glycoside Hydrolases (GH, e.g., GH28 pectinase) and ROS were co-regulated at early decay steps (Zhang et al. 2016. doi: 10.1073/pnas.1608454113). This finding raised important questions about the ability of these enzymes to co-exist in an oxidative and potentially denaturing environment. To confirm the above, we are exploring at higher resolution the direct co-localization of the early-upregulated GHs and the Fenton reagents that drive the radical production. Specifically, a decay experiment in a soil-block system with wood wafers was set to observe a directional growth that allows thin sectioning and analysis of different decay stages. Then, the wood sections from early to late decay were extracted with either acetate buffer or methanol:chloroform (1:2), for enzymatic assays or Fenton reagents detection [e.g., Fe(II), H2O2] respectively. Also, the in situ localization of these agents were confirmed by immune hybridization. In this way, we will establish that GHs could survive in the oxidative environment by co-distribution at early brown rot to synergistically function in plant cell wall decomposition.

POSTER 4

Hyphal Network Formation in *Neurospora crassa*

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We present a novel growth phenomenon in *Neurospora crassa* (*N. crassa*) identified using microfluidic technologies*. N. crassa* cells form a complex web-like network through hyphal extension, branching, and fusion. Our preliminary data indicate that after this filamentous network has been established, bursts of tree-like structures build upon these pre-existing network tracks. These “trees” grow rapidly, branch highly, and remain localized to particular segments of the network. These tree-like structures and their underlying filamentous tracks have not yet been documented in the literature. The goal of this work is to use microfluidic technology as a tool for uncovering the genetic mechanisms dictating formation of these tree-like structures following filamentous network formation in *N. crassa*. This work will provide insights into cell-cell communication, social behavior, and response to glucose availability through “foraging.”

We predict that these structures arise from clonal cell populations. To test this hypothesis, we will combine two populations of *N. crassa* cells in the microfluidic device: cells with *Venus* and *mCherry* fluorescent reporters attached to the promoter of *ccg-2. Venus* and *mCherry* cells will both be inserted into the microfluidic device with three days to grow. We predict that each individual tree structure will contain cells expressing only one reporter, suggesting a clonal population. Additionally, we predict that these tree structures may be related to post-translational modifications. We will test this by exposing *N. crassa* cells to cyclohexamide, an inhibitor of protein synthesis. If these structures are dependent upon post-translational modifications as we propose, cyclohexamide will inhibit their growth.

POSTER 5

Polycomb Repressive Complex 2 in *Neurospora crassa*: The hunt for regulators of repressive chromatin architecture

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Our group is interested in identifying the mechanisms that govern the establishment and maintenance of silent chromatin in the filamentous fungus *Neurospora crassa*. The Polycomb Repressive Complex 2 catalyzes the methylation of Lysine 27 on Histone 3 (H3K27me2/3). Polycomb group proteins assemble

specialized repressive chromatin domains that are critical for proper gene regulation in plants, animals, and some fungi. The specific mechanisms of how Polycomb Repressive Complex 2 target domains are established and maintained are poorly understood. We are analyzing the control and function of repressive chromatin domains using a combination of genetics, proteomics, and genomics. We have identified three new mutants that have significant depletion of H3K27me2/3 throughout most of the genome and we will summarize our findings toward the characterization of these mutants.

POSTER 6

Development of an RNA interference (RNAi) gene knockdown protocol in the anaerobic gut fungus *Pecoramyces ruminantium* strain C1A.

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Anaerobic gut fungi (AGF) reside in rumen, hindgut, and feces of ruminant and non-ruminant herbivorous mammals and reptilian herbivores. No gene insertion, deletion, silencing, or mutation protocols are currently available for AGF, rendering gene-targeted molecular biological manipulations unfeasible. Here, we developed and optimized an RNA interference (RNAi)-based protocol for targeted gene silencing in AGF *Pecoramyces ruminantium* strain C1A. C1A genomic analysis identified dicer (I and II) and argonaute homologues. Dicer is required for dsRNA cleaving into short interfering RNAs, and activation of RNA-induced silencing complex (RISC), where argonaute acts as the catalytic endonuclease. Competency of C1A germinating spores for RNA uptake was confirmed using fluorescent probes. Application of synthetic siRNA targeting D-lactate dehydrogenase (D-*LDH*) gene resulted in marked gene silencing; as evident by significantly lower levels of 1)D-*LDH* transcription, 2)D-LDH specific activity in intracellular protein extracts, and 3)D-Lactate concentrations in supernatant from siRNA-treated cultures. Optimal experimental protocols involved adding 20-75nM siRNA to germinating spores 15-min before transferring to fresh medium, resulting in 2-4 folds reduction in transcriptional activity, 60% reduction in specific enzymatic activities, and 50-67% reduction in D-Lactate concentrations. Finally, comparative transcriptomic analysis of wild type versus siRNA-treated cultures demonstrated that the observed reduction in D-LDH transcription was associated with additional changes in transcriptional levels of multiple central glycolytic and fermentative enzymes involved in sugar metabolism in strain C1A; suggesting that C1A rewires its central metabolic pathways in response to D-LDH-silencing. This study represents one of few protocols for gene manipulation in the fastidious, strictly anaerobic Neocallimastigomycota.

POSTER 7

Differences of hypsiziprenol homologues in *Hypsizygus marmoreus* strains: metabolomic approach

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Two strains of beech mushroom are commercially available in Korea. One is brown and the other white. The scientific name is *Hypsizygus marmoreus*, and it belongs to Lyophyllaceae, In addition to the color, there has been reported taste difference. For elucidate the difference of the quantity of the anticancer metabolites hypsiziprenols, we performed metabolome profiling analyses by GC-MS and LC-MS. Hypsiziprenols were found significantly more in caps than in stipe part, the isomers A10 and A11 were dominant in brown strains. The consumer preference is white, which also lacks bitter taste. The discrepancy should be overcome by breeding to make white + higher hypsiziprenols content. The differences of some amino acids and organic acids levels were also elucidated. There also found

correlation betwwen some amino acids - valine, leucine, serine, and threonine - levels and hypsiziprenol contents.

POSTER 8

Internuclear transport of histone H1 within cellular compartments

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Histone H1 is an evolutionarily conserved linker histone protein that functions in arranging and stabilizing chromatin structure and is frequently fused to a fluorescent partner to track nuclei in live cells. In time-lapse analyses, we observed stochastic exchange of photo-activated Dendra2-histone H1 protein between nuclei within the same cellular compartment. We also observed mixing of histone proteins between nuclei in a heterokaryon derived from fusion of strains carrying histone H1-RFP or H1-GFP. Subsequent analysis of the resulting uninucleate conidia containing both RFP- and GFP-labeled histone H1 proteins showed only parental genotypes, ruling out recombination. These data together suggest that the linker histone H1 protein is transported between nuclei.

POSTER 9

Review and revision of the nomenclature system for *MAT* genes in the Pezizomycotina

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Taxa in the Kingdom Fungi display an exceptionally high diversity of sexual reproduction strategies. In the sub-phylum Pezizomycotina (Ascomycetes), sexual reproduction is controlled by genes present at the mating-type locus. Although some of these genes are conserved, even among distantly related species, several mating-type genes show a lineage-specific distribution. To facilitate the study of these genes, a nomenclature system for naming these genes was developed in 2000. However, the rapid increase in the number of described mating-type genes (largely because of whole genome sequencing) has resulted in many examples where mating-type genes have been erroneously named. This can be attributed to factors such as low sequence similarity among homologs, the misidentification of genes in public sequence repositories and misinterpretation of the rules for naming these genes. In this study, we addressed these problems by undertaking a systematic review of all described mating-type genes from species in the Pezizomycotina. Our results showed that 24 distinct mating-type genes have been described using only 15 gene names. To address this discrepancy, we have amended the currently used nomenclature system and have provided recommendations for changes to the current names of many of these genes. The overall outcome of this revision brings the total number of unique mating-type genes to 20. This study is presented as a review and will provide clear guidelines for naming mating-type genes in future studies.

POSTER 10

Genome sequencing reveals a heterothallic mating system in the *Eucalyptus* pathogen *Chrysoporthe austroafricana*

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Chrysoporthe species are fungal pathogens of *Myrtaceae* and *Melastomataceae* in sub-tropical regions of the world. *Chrysoporthe austroafricana* is native to South Africa where it is considered a threat to commercial plantations of *Eucalyptus* and the native *Syzygium* species. Homothallism has been proposed as the mating system of this fungus based on field observations and population genetic studies. To test this hypothesis the *MAT1* locus was identified and characterised from the whole genome sequence of two isolates of *C. austroafricana*. Additionally, the *MAT1* locus was also characterised in the closely related *C. cubensis* and *C. deuterocubensis*, which also cause canker disease on *Eucalyptus* species. A putative *MAT1-1* idiomorph was identified in one isolate of *C. austroafricana* while a putative *MAT1-2* idiomorph containing a truncated *MAT1-1-1* was identified in the other isolate. The presence of a single idiomorph in either isolate of *C. austroafricana* suggests that this fungus is heterothallic. Frequencies of *MAT1-1* and *MAT1-2* range from 1:1 to non-proportional in isolates from populations from southern Africa. In contrast, the closely related species *C. cubensis* and *C. deuterocubensis* seem to be homothallic, since the *MAT1* locus contained all the expected *MAT1* genes necessary for this reproductive strategy.

POSTER 11

Putting the natural diversity of fire-adapted wood-degrading fungi to work in thermal biomass conversion schemes

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Efforts to convert plant biomass into fuels and other bio-based products are increasingly focusing on thermal methods. These methods offer several key advantages over enzymatic deconstruction routes, including being ‘agnostic' to the type of biomass being treated. Heat-modified residues, however, still require enzymatic processing, and current enzyme ‘cocktails' are not optimized to these tasks. Our goal is to identify and validate novel biomanufacturing enzymes from a logical organism source - fire-adapted microbes. Fungi are perhaps the most well-studied examples of fire-adapted microbes, and an outstanding example is *Neurospora crassa*. This Ascomycete fungus has been co-opted by those studying the gene-for-enzyme theory as a model system for genetic recombination, using its easily-counted melanized spores. This fungus has also been a key model system for studying circadian rhythms, tracking daily sporulation ‘rings' not controlled by light. *Neurospora* has become an enzyme toolkit for studying its habits out of the context of its natural niche on fire-killed plant biomass. This essentially leaves a treasure trove of genetics tools disconnected to a key trait of the fungus, and the gains in unlocking this system in context of thermal deconstruction routes look very promising. There are also other fungal genera (e.g. *Gloeophyllum*, *Schizophyllum*, *Antrodia*) associated with fire, many of which have newly-annotated genomes in the Joint Genome Institute portal, and elsewhere. Tapping into these fire-adapted microbial systems may reveal genes with more relevance to thermal deconstruction processes and with more potential for tailoring to biomanufacturing processes ‘downstream.'

POSTER 12

Systems biology of circadian clock synchronization in *Neurospora crassa*.

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The circadian clock is a widely conserved emergent property driving daily rhythms across multiple levels of biological organization, with oscillations emanating from core transcription-translation feedback loops which then exert control over downstream pathways. In turn, multiple external factors may influence the clock and allow for re-synchronization with external cues, or compensation for changes in temperature and nutrient availability. We have recently found that transcriptional clock/oscillator phases in single cells

of the clock model Neurospora crassa synchronize over time, but only if they are in the same microenvironment. We hypothesize an extracellular chemical communication mechanism to explain synchronization. To explore the nature of this mechanism and the underlying gene-metabolite network, we are using a combination of untargeted NMR metabolomics, clock activity-guided fractionation, and genetic knockout mutants to screen for extracellular molecules and genetic components that may allow clocks to interact. Identifying pathways at the intersection of these approaches will further enable targeted MS experiments and transcript analyses. Preliminary NMR data on nonpolar exometabolites has already revealed circadian features, suggesting interactions of this sort occur in *Neurospora*. This experiment is being repeated with more replicates, clock mutants, and broader chemical diversity. Our approach will also allow us to explore broader properties of the N. crassa extracellular metabolome in the future. Moreover, this work offers fundamental insights about the control and multilevel properties of a pervasive systems behavior in a model organism with biotechnological relevance.

POSTER 13

The Mycological Society of America Student Section

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The Mycological Society of America Student Section is a student-run group within MSA which aims to facilitate communication among all students of the society, provide opportunities for students to network with other individuals in their own research fields and beyond, and connect student members of MSA with scientists performing cutting edge mycological research. As such, the Student Section has the potential to inspire future collaborations. Our activities and events reflect these goals. For example, the Student Section organized the symposium "Fungal functional traits in a changing world" at MSA 2014, to discuss the evolution of selected traits and how key attributes of fungal taxa influence their environment and stress response; and provinding an opportunity for communication between members of the Student Section and the leaders in this field. For MSA 2016, a Professional Development Workshop was planned to address the question, ‘How can you prepare the academic job application for a tenure track position in the sciences?' Panel speakers included researchers at various stages in their career from both small liberal art colleges and research institutions. This workshop had the purpose of providing student section members with adequate tools for successful professional development in academia. The Student Section has also continued to publish student spotlights highlighting the research of students that have received awards from MSA; and spotlights on mycology clubs have been posted on our website. The Student Section is open and inclusive, welcoming the participation of graduate students, postdoctoral researchers, and faculty in building and pioneering this group.

POSTER 14

Functional characterization of AMT and MEP proteins from the model slime mold *Dictyostelium discoideum*

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AMT/MEP/Rh genes encode ammonium transporters. The evolutionary history of AMT/MEP/Rh genes in the fungi is particularly complicated, characterized by multiple horizontal gene transfer events, gene family expansions and contractions, and gene losses. Phylogenetic analyses consistently demonstrate that fungal AMT/MEP/Rh transporters cluster into two clades within the MEP subfamily of transporters, while no fungal sequences from any of the hundreds of published fungal genomes have been found in the AMT clade. By contrast, animals have AMT and Rh proteins, but not MEP proteins. It would appear that the fungal and the animal branches of the opisthokonts each have lost different subfamilies of AMT/MEP/Rh transporters during their evolutionary history. It is possible that the AMTs and MEPs have different transport mechanisms and substrates, leading to their differential retention. Here, we examine the function of the AMT and MEP proteins in an earlier diverging group, the slime molds. Slime molds such as the model organism *Dictyostelium discoideum* are some of the few organisms to have AMT, MEP, and Rh genes represented in their genomes. Three ammonium transporter genes, AmtA, AmtB, and AmtC, were cloned from *D. discoideum*. We will demonstrate their ammonium transport function by complementation of an ammonium transporter mutant of *Saccharomyces cerevisiae*. In addition, we will use expression in *Xenopus* oocytes and electrophysiology to characterize these transporters in detail.

POSTER 15

The domestication of humans by yeast

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Saccharomyces cerevisiae, or brewer's yeast, has been used by humans for thousands of years, possibly before the invention of written language. Ancient Egyptian hieroglyphs have depicted the production of bread and fermented beverages, which were common in most households. This creature unknown to mankind was cared for by humans for generations, with brewers passing on yeast with each new brew and providing the fungus with the sugars necessary to create the magical liquid that people craved. The process of fermentation was poorly understood for millennia, relying mostly on "wild yeast" contaminating malted barley, or passing on yeast cakes. Even the German beer purity law, Reinheitsgesbot, did not originally include yeast. Only through trial and error did brewers of antiquity discover how to appease this fungal god. This sugar loving fungus, which provided humankind with beer and wine, was not discovered until after the invention of the microscope, and only after careful experimentation was it finally proven to be the cause of fermentation. After it was discovered that yeast was responsible for the magic of fermentation, people were able to change their practices to better appease the yeast to produce better beer. Since the discovery of brewer's yeast other species, such as *Saccharomyces pastorianus* and *Brettanomyces* sp., have also been shown to be involved in the creation of specific styles that each require their own care. This educational poster will provide insight into the history of yeast and how these organisms have driven the development of agriculture, technology, chemistry, and microbiology.

POSTER 16

Field trial - estimating phosphorus uptake and translocation by arbuscular mycorrhizal fungi in surface root mats

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Tropical trees often depend on arbuscular mycorrhizal (AM) fungi for phosphorus uptake. AM fungi play a major role in P uptake by foraging for P and delivering it to the root's cortical cells. Current forest productivity models are based on climate and nitrogen, but not phosphorus availability, causing the models to fail in tropical forests. Our goal was to correlate phosphorus uptake with AM hyphal lengths in surface root mats as a means of quantifying translocation. We used zero tension lysimeters for mass balance, and also tested PRS anion exchange membranes for measuring P-flux in the litter-layer. We applied a non-radioactive P solution (KH_2PO_4) to 24 intact root mats, added a rain shield, and harvested

them after 1-, 4-, and 8-day post-treatment. Anion exchange membranes yielded highly variable results, but the mass balance approach using zero tension lysimeters was promising. Phosphorus uptake was successfully measured in 9 lysimeters, and more P was measured after the incubation in 14 lysimeters, compared to before the incubation. This occurred when the initial litter samples collected next to the root mat were less decomposed than in the mat, thus underestimating the initial P content of mats. Although mean amount of P-uptake decreased over time, the strongest relationship between P-uptake and AM hyphal length occurred at 4 days post-treatment (R^2=0.33). A future trial using an improved lysimeter, live AMF analysis (PLFA), and initial litter P samples collected within the mats may yield better results while still avoiding the use of ^{32}P tracer in the field.

POSTER 17

The cutaneous microbiome of North American salamanders affects pathogenicity of chytrid fungi

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The deadly chytrid fungi *Batrachochytrium dendrobatidis (Bd)* and *B. salamandrivorans (Bsal)* have caused significant amphibian population declines worldwide. The search for fungal inhibitors has focused on the resident bacterial community found on amphibian skin. Several studies have found that the amphibian skin microbiome actively inhibits the spread of pathogens, including *Bd*. However, little is known about the structure and immune function of the salamander microbiome, and few effective probiotic treatments have been developed. The objectives of this study were to (1) use high-throughput DNA sequencing to characterize structure of the skin microbiome, (2) isolate cutaneous bacteria from skin swabs, and (3) identify bacterial isolates that inhibit Bd. During spring (May 2016) and late summer (July 2016), plethodontid salamanders were captured from nine sites in Tennessee, and skin swab samples were obtained. Swabs from 11 salamanders were streaked onto R2A agar plates and checked for microbial growth. A total of 98 bacterial colonies were isolated and grown in pure culture. Thus far, thirteen isolates have been challenged against *Bd* on 1% tryptone agar plates. All grew in the presence of *Bd*, but none formed measurable zones of inhibition. These isolates have been discounted as candidate probiotics, but others are currently being screened and are expected to inhibit fungal growth. Additionally, high-throughput DNA sequencing techniques on the Illumina MiSeq platform, and bioinformatics analyses in mothur and QIIME, will help define the composition and structure of the resident skin microbial community across salamander taxa and habitat types.

POSTER 18

Identification of probiotic bacteria with antifungal activity in the cutaneous microbiome of endangered Tennessee bats

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Since its introduction in 2006 into the USA, *Pseudogymnoascus destructans* (*Pd*), the fungal agent of white-nose syndrome (WNS), has rapidly spread killing millions of bats. *Pd* infects bats in caves during their hibernation period, disrupting physiological processes and causing increased arousals from hibernation which consume energy reserves, eventually starving the bat to death. WNS has negatively impacted most bat species found in the Eastern United States, including three federally listed species.

Treatment options for bats infected with *Pd* currently include anti-fungal chemicals, volatile compounds, and naturally occurring antifungal probiotic bacteria. The main objective of this research is to observe spatiotemporal variation in the cutaneous microbiome of bats and its relationship with resistant and susceptible populations of bat species across three different physiogeographic zones of Tennessee. We will isolate resident skin microflora that have probiotic antifungal activity against *Pd* as tentative biocontrol treatments. To date, 121 swabs from 7 bat species have been collected from 21 caves in Tennessee. We have isolated 25 bacterial strains with anti-*Pd* activity that produce both volatile organic compounds and diffusible antifungal metabolites. Identification of the bioactive compound is in progress. We are currently assembling mock bacterial communities to determine if there are any synergistic and additive effects of the microbiome at inhibiting fungal growth. Results will also emphasize spatiotemporal differences in the bat skin and cave microbiome.

POSTER 19

Marine fungi and enzyme activity associated with sailfin sandfish egg masses in Korea

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Aggregation of decaying egg masses of sailfin sandfish along the East coast of Korea are a major environmental problem with concurrent negative economic consequences. In order to discover the potential marine fungi and ameliorate decaying egg masses, we investigate the diversity and community structure of marine fungi from these egg masses and tested for their extracellular cellulase activity (endoglucanase and β-glucosidase) and extracellular protease activity (gelatinase and caseinase). A total of 1,108 strains of 184 species were isolated, and 122 species were identified. *Paradendryphiella salina* was the most dominant species, followed by *Penicillium crustosum, Penicillium aurantioviolaceum, Penicillium steckii*, and *Cladosporium cladosporioides*. The fungal community displayed a significant degree of variation relative to both egg mass color and geographic location. While many of the species exhibited endoglucanase, β-glucosidase, and/or gelatinase activity, caseinase activity was observed in only a few genera, notably *Aspergillus*, *Cladosporium*, and *Penicillium*. Our study suggests that enzyme activity of marine fungi may play an important role in marine nutrient recycling and thus may have the potential for industrial applications directed toward the solution of these kinds of environmental problems.

POSTER 20

Yeast diversity in an urban stream and its impact on mosquito populations

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The study of microbial ecology in freshwater ecosystems and their interactions with other biota is becoming increasingly important. Mosquitoes are widely distributed in many ecosystems and some are important vectors for many human pathogens. Mosquito interactions with microorganisms seem to increase their adaptive success but most studies have focused on bacteria. The objective of this study was to characterize potential interactions between mosquito and fungal populations in an urban stream. Fungal communities were characterized using cultured-based methods and DNA sequencing. Fungal traps containing apples, pears, and cherries were placed in an urban stream in Macomb, Illinois. Dilutions (10-1-10-5) were plated on four types of media (MEA, EYSA, YG, SDA) and incubated at 25° C. Two hundred and thirty fungal isolates were cultured. We isolated eight classes of fungi and 11 orders. *Saccharomyces* (70%) was the most frequent fungal class represented by seven genera (*Meyerozyma, Candida, Geotrichum, Pichia, Kazachstania, Cyberlindnera,* and *Cystofilobasidium*). Some of these genera have also been reported as common isolates of mosquito larva. Yeast identified as the same

species using ITS rDNA showed wide variation in morphology and color. Both native mosquito (*Culex* spp., *Aedes* spp.) and invasive species (*Aedes japonicus*, *Aedes albopictus*) were identified; an increased abundance of invasive species was observed over the last three years. Yeast bioassays will be conducted to determine potential mosquito-fungal interactions. The nature of the interactions between mosquitos and yeasts and their effects on the abundance of native versus invasive populations remains mostly unknown.

POSTER 21

Examining arbuscular mycorrhizal fungi in *Spartina patens* and *Spartina alterniflora* in the Minas Basin, Nova Scotia

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Saltmarshes are one of the most productive ecosystems globally, providing critical nursery and refuge habitat for fish, invertebrates and birds. As well, saltmarshes play a role in storm buffering and coastal shoreline stabilization. Unfortunately, saltmarshes are in decline worldwide due to a variety of anthropogenic and natural causes. Beneficial root-associated fungi are known to colonize over 80% of land plants, but are understudied in intertidal zones. We examined arbuscular mycorrhizal fungi (AMF) in the roots of two dominant saltmarsh grasses, *Spartina patens* and *Spartina alterniflora* (Poaceae) in the Minas Basin, Nova Scotia over the 2016 growing season. AMF root colonization was determined using ink and vinegar staining and microscopy. DNA was extracted from the *Spartina* roots and subjected to a nested PCR to amplify the fungal ITS barcoding regions of the rDNA, purified through agarose gel extraction and re-amplified using a single general fungal primer set for sequencing. *Spartina alterniflora* had 9% AMF root colonization, while *S. patens* had 68%. DNA barcoding identified one AMF species, *Funneliformis geosporum* (Glomeraceae) from roots of both *Spartina species*. Our data will aid in the conservation and restoration of coastal saltmarshes. Knowing the strength of the mutualism and understanding the AMF species involved will help with the production of local AMF inoculants to aid in *Spartina* re-establishment in Nova Scotia.

POSTER 22

Land management, mycorrhizal diversity, and soil carbon sequestration

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Recently, there has been a paradigm shift in our understanding of the factors that control long-term storage of carbon in soils. Recalcitrance of plant residues was initially thought to determine the storage of carbon in soil. However, the importance of soil aggregates and the role of microbial residues in storing carbon is increasingly recognized. In addition, the amount of mycorrhizal fungi relative to other fungal guilds has been correlated with the long-term storage of carbon in soil. Thus, forest management strategies that promote mycorrhizal fungi abundance and diversity may increase soil carbon sequestration rates. To investigate how forest management strategies influence fungal diversity, abundance, and soil carbon sequestration, we compared soils from red pine (*Pinus resinosa)* plantations, red pine old growth stands, and northern hardwood stands of three different timber extraction intensities using estimates of fungal diversity and soil nutrient composition. Across sites, soil carbon stocks were greater in soils with greater chitin concentrations and ectomycorrhizal diversity. Carbon storage was greatest in red pine plantations, indicating that pine plantations may be a suitable management strategy for soil carbon storage. In northern hardwood stands, the fungal community was a strong predictor for carbon storage and ectomycorrhizal diversity was lower in stands with high rates of timber extraction. Together, these results show that fungal communities of forest soil are both correlated with the degree of management and carbon storage through an as yet unclear mechanism.

POSTER 23

Exploring the relationship between *Morchella americana* and tree roots in Pennsylvania

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Morchella ascocarps are frequently observed in the northeastern United States associated with dead and dying elm trees and with stands of ash. This observation gives rise to the hypothesis that these species of *Morchella* exist in mycorrhizal or other types of relationship with roots of these trees. Literature reports of apparent mycorrhizal associations between *Morchella* and tree species provide impetus to explore these relationships. We are testing this hypothesis by documenting the relationship in nature, and by attempting to recreate it in culture. Maps of fruit bodies relative to trees were made in three locations in the spring of 2014, 2015, and 2016. *Morchella* ascocarps were located near elms in two locations, and near ash in one location, however other tree species were present at these sites. The internal transcribed spacer sequence from ITS4 and ITS5 primer amplicons of 14 collected fruit bodies all indicated *Morchella americana* consistent with morphological observations. Ascospore cultures were obtained and used to produce mycelium in liquid culture to inoculate elm and ash seedlings. A slurry of mycelium was applied to the surface of a low-nutrient growth medium containing *Fraxinus americana* or *Ulmus americana* seedlings. After four weeks of growth, seedlings were photographed, and root sections harvested for analysis. We observed mycelial growth from surface sterilized roots of both tree species which were sequenced to confirm *M. americana*.

POSTER 24

Using reverse ecology to elucidate cryptic ecological niches

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The genus *Amanita* is an emerging model used to understand the ecology and evolutionary biology of ectomycorrhizal symbioses. The symbiosis appears to have evolved exactly once within *Amanita*; derived species are ECM while basal species are assumed to be saprotrophic. However, one basal species is enigmatic: *A. inopinata* is basal in the phylogeny, but appears to lack many of the genes enabling decomposition. In contrast to other *Amanita* species, mycologists have a poor understanding of its natural history, reflective of a larger problem: the ecology of many species are poorly understood, even when we have genomes. So, **what is the ecology of *A. inopinata:* ECM, SAP, or something else?** To date, my laboratory has sequenced the genomes of eight *Amanita* species, and an outgroup (a total of 5 ECM, 3 SAP, and *A. inopinata*). Because so many resources are available, *Amanita* emerges as an ideal test case to develop a “reverse ecology” approach and optimize tools to annotate/identify the functions of the genes within a genome. With the available *Amanita* genomes, I can parse genes which are exclusively associated with ECM or SAP species, to determine the function of a genome and relate that to how the organism could function in an ecosystem. I am currently using gene ontology, dN/dS changes, and protein families to identify niche indicators. I will then identify the ecological niche of *A. inopinata* by comparing its genome to closely related ECM and SAP *Amanita* species, and thus provide a test of the reverse ecology approach.

POSTER 25

Effect of novel endophytic fungal species on plant growth effect of novel endophytic fungal species on plant growth

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Most plants in natural ecosystems have symbiotic relationships with fungi. In stressful conditions these symbiotic relationships are important for adaptation and survival. Fungal species in the order Pleosporales and other orders have been shown to provide thermotolerance and drought resistance to plants. In this study we characterized novel fungal species and determined the effect of different isolates belonging to *Culvularia,* novel Pleosporales and Sebacinales on plant growth at room temperature and under various stressful conditions. Fungi were isolated from roots of different types of grasses across the United States and characterized using ITS, LSU and SSU sequencing. In addition, we conducted *in vitro* germination experiments using *Bouteloua gracilis* and maize. At room temperature, several isolates of *Culvularia* improved stem and root growth and under heat stress these isolates improved plant thermotolerance. Additional experiments will be conducted to characterize these novel taxa.

POSTER 26

Diversity and keratin degrading ability of fungi from Canadian High Arctic bird feathers

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We present the first records of fungi associated with bird feathers from the Canadian High Arctic. Twenty species of fungi were isolated from feathers of both seabirds and sea ducks collected in Nunavut and Newfoundland, Canada. Host bird species included the ground-nesting Common Eider (*Somateria mollissima*) and King Eider (*S. spectabilis*), and the cliff-nesting Black-legged Kittiwake (*Rissa tridactyla*), Northern Fulmar (*Fulmarus glacialis*), Glaucous Gull (*Larus hyperboreus*), and Thick-billed Murre (*Uria lomvia*). Fungal isolates were ITS DNA barcoded and screened for the ability to degrade keratin using a keratin azure assay. Fourteen ascomycete and six basidiomycete fungi were identified. Twenty-one % of ascomycetes displayed keratinolytic activity (the ability to produce a keratinase enzyme in the presence of a keratin substrate), which is a known pathogenicity factor for fungi. Known ecologies of fungal isolates are further reviewed.

POSTER 27

Cultivable fungal communities associated to biological soil crusts in a fog oasis of the Peruvian desert

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Biological soil crusts (BSC) are essential components of arid ecosystems and remains poorly studied with respect to their fungal diversity. We examined the differences between fungal communities associated to BSC at Lomas de Lachay, a fog oasis in the Peruvian coastal desert which interacts with surrounding flora and fauna, and superficial soil with vegetation (SSV). Five SSV and BSC samples were taken from a 100 m transect, additionally, soil moisture and pH were analyzed. Soil moisture and pH were higher in SSV than in BSC. A total 75 isolates from 29 species belonging to Zygomycetes (3 species) and Ascomycetes (26 species), were isolated using the dilution plate technique. The most common isolated genera from SSV were *Penicillium* (9 species) and *Aspergillus* (3 species) while for BSC were *Aspergillus*

(6 species), *Penicillium* (4 species) and *Fusarium* (3 species). Likewise, melanin-containing microfungi species were higher in BSC (33%) compared to SSV (15%). Shannon-Wiener diversity index did not show significant differences among sites; however a NMDS analysis showed clearly two different fungal communities directly influenced by soil moisture and pH. These results suggest that differences in microfungal community composition between SSV and BSC, such as the significantly lower percentage of thermotolerant and UV-resistant species and the higher abundance of cellulose degrading species in SSV were caused by the presence of vegetation. Plants protect soil surface from desiccation and increase of humidity during seasonal fog allows the dominance of species with high growth rates such as *Penicillium*, *Aspergillus* and *Fusarium* in BSC.

POSTER 28

The role of rhizosphere and endophytic fungal volatiles on plant growth

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Fungi produce volatile organic compounds (VOC) that can play significant roles on seed germination and plant growth. The objectives of this project were to evaluate the effects of fungal VOCs on the growth of a dominant arid grass, *Bouteloua gracilis* and to determine their role on the control of seed-pathogenic fungi through fungal-fungal bioassays. Rhizosphere and endophytic fungal isolates were obtained in North American grasslands and identified using molecular methods. Seeds were surface sterilized and placed on moist paper towels in sealed containers with the different fungi. Plant responses to the VOCs are being evaluated under different conditions including variations of temperature and media type. Selected taxa for the experiments included *Chaeotimium, Cladosporium, Coniochaeta, Curvularia, Embellisia,* and *Lecythophora*. Fungal VOCs showed diverse effects on plant growth ranging from negative to positive effects on stem length and number of roots. Additional tests with different grass species will be conducted to determine potential connections between growth stimulation and the control of seed-borne pathogens through fungal VOCs.

POSTER 29

Fungi of the Midwest Driftless Region

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Southwestern Wisconsin was unaffected by the glacial drifts that ended some 10,000 years ago, and is now referred to as the driftless area. This area is known for the forested hillsides of limestone-based soils with deep valleys, called coulees. These ridges and coulees offer relicts of forests, prairies, wetlands and grasslands that house a diverse array of organisms. A 20-year survey of three older growth forests found approximately 1200 species of macrofungi that include some species with disjunct distributions. Hixon Forest is dominated by hillsides of oak/hickory a couple miles inland from the Mississippi river. In this most studied area, we have identified 598 total species of fungi, with 339 specific to that site. Perrot State Park along the Mississippi is also dominated with hillsides and lowlands that contain mostly, oak and hickory, but also sandy scrub oak. Perrot had 471 species with 224 being unique to this area. Chestnut Hills is one of the largest stands of American Chestnuts, dating from the early 1900s when 11 trees were planted; now more than 2,500 chestnut trees flourish. However, at the peak of this stand there were over 6000 trees greater than 5” dbh. A total of 538 fungal species have been surveyed within this stand, with 304 being found only with this area. The total overlap within the three sites was just 303/1200 species. Some relict species have been collected (e.g., *Exsudoporus (Boletus) frostii*), as well as unusually high population densities of some fungi considered to be rear elsewhere.

POSTER 30

Migration versus mutualism: Can the small-ranged endemic plant *Rhododendron catawabiense* form specialized ericoid mycorrhizae with soil fungi north of its native range?

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The mutualistic interactions of plants with below-ground soil biota, such as mycorrhizal fungi, are crucial for many species' performance and local distribution patterns. Such specialized mutualistic relationships are also of concern for rare or range-restricted plant species in the face of anthropogenic climate change, because it remains unknown if they will be able to successfully colonize new regions where co-adapted mutualistic partners from their native range might be absent. In this study, we investigated the ecological interactions of a small-ranged endemic plant, *Rhododendron catawbiense* (Ericaceae), with soil biota from sites in the Northeast US, 800-1000 km beyond its native range. To test this interaction, we inoculated 30 experimental mesocosms with organic layer material from the bases of two widespread, Northeast native *Rhododendron* species. Soil in half of the mesocosms was sterilized to eliminate fungi and other soil biota. Fifty seeds were sown into each mesocosm, and seed germination, seedling growth rate, and colonization of roots by ericoid mycorrhizae (EMF) were compared. Seeds germinated at a significantly higher rate on inoculated compared to sterilized soils. Harvested and stained root samples revealed that many seedlings on the inoculated soil had successfully partnered with EMF, despite the inoculum being sourced from habitats far beyond the native range. This result is important, as several recent studies have otherwise shown high degrees of local co-adaptation between plants and mycorrhizal fungi. The presence of other *Rhododendron* and Ericaceae plant species in new regions, and their associated EMF communities, might facilitate colonization by migrating species.

POSTER 31

Seed associated fungi and their roles on plant growth in grasses

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Microorganisms are known to form symbiotic relationships with plants. One example of these symbiotic associations include grass species and their fungal endophytes. The main objective of this experiment was to identify seed-associated fungal endophytes from five different species of grasses (*Bouteloua gracilis, Bo. eriopoda, Buchloe dactyloides*, *Schizachyrium scoparium,* and *Eragrostic curvula*. Seeds were tested using germination and viability assays. The seeds were surface sterilized and plated on malt extract agar media to isolate fungi. Cultures were sequenced using the ITS rDNA region. Germination rates ranged from 14 to 84%. Out of the five different species of grasses, fungal isolation rates varied from 0 to 100%. *Eragrostic curvula* and *Schizachyrium scoparium* showed the lowest rates of fungal endophytes while *Buchloe dactyloides* presented the highest fungal colonization rates. The dominant phylum isolated was Ascomycota, with the majority of the fungi belonging to the order Pleosporales. Many fungi isolated were commonly reported as plant pathogens. We isolated different fungal communities from the seeds covered by lemma and palea with respect to endophytic taxa inside the seeds. The roles of these fungi on seed viability and plant survival will be tested using germination experiments.

POSTER 32

Common cutaneous bacteria isolated from snake skin inhibit *Ophidiomyces ophiodiicola*, the causitive agent of snake fungal disease

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Snake fungal disease (SFD), caused by infection with *Ophidiomyces ophiodiicola* (Oo), has been linked to recent population declines of snake species. The cutaneous microbiome is known to be the first line of pathogen defense in many vertebrate species; however, very little is known about symbiotic microbial associations in snakes. The reptilian skin microbiome may protect against SFD by outcompeting Oo for space, producing antifungal metabolites, and/or stabilizing the microbial community and increasing innate defensive immunity. Identification of beneficial bacterial species and their effects on pathogen defense may aid in future conservation management plans. The objectives of this project were to 1) better define host specificity of the pathogen through culture-dependent and –independent diagnostic techniques, 2) isolate and identify resident skin microflora from two snake species, and 3) determine if resident bacteria possess antifungal activity when challenged against Oo in vitro. Thirteen snakes were captured across three states: Tennessee, Arkansas, and Alabama. Oo infection was confirmed using real-time quantitative PCR (qPCR) and histology in one black racer (*Coluber constrictor*). Oo was also detected via qPCR in three timber rattlesnakes (*Crotalus horridus*). From all 13 host snakes, a total of 58 bacterial colonies were isolated from skin swabs, genotyped, and challenged against Oo. Of these, 14 inhibited Oo growth. The present study sheds light on the innate immune function of the culturable snake cutaneous microbiome and the resident probiotic members which play a role in fighting an emergent disease in both infected and uninfected hosts.

POSTER 33

Assessment of mycobiome variation across geography in the predatory snail genus *Conus* using museum preserved specimens.

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This project seeks to use the extensive collections of a hyper-diverse, predatory genus of marine snails, *Conus*, at the University of Michigan Museum of Zoology to fill a gap in our understanding of the fungi that associate with mollusks and how the mycobiome (fungal community) varies across geographic space, phylogenetic diversity, and ecological niches of the hosts. Several species of *Conus*, have near global distributions and are particularly well represented in the collections, yet we have no knowledge of whether the mycobiome of such animals will be driven by their geographic location or their phylogenetic relationships. To determine mycobiome compositions and determine if microbiomes can be assessed from museum preserved specimens, we dissected the intestines and digestive gland tissues from more than 30 *Conus* spp. from over 20 different countries, extracted DNA, and used fungal-specific and bacterial specific amplicon-based high throughput sequencing of the ribosomal DNA region. First, we identify which fungi are commonly and uniquely associated with the digestive tracts of *Conus* spp., all of which are dominated by *Malassezia* spp. We find little support for a correlation between geography and fungal community structure, and discuss techniques for targeted sequencing of preserved museum specimens for studies.

POSTER 34

Fungal and bacterial communities of individual rhizosphere aggregates across an extreme soil chemistry gradient

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This project explores the interacting influence of edaphic factors and spatial scale in structuring fungal and bacterial communities in soils surrounding *Quercus agrifolia* (Coast Live Oak) roots. Microbial communities of individual rhizosphere aggregates in soils with differing parent materials were characterized using high-throughput sequencing (Illumina MiSeq). Aggregate communities were analyzed at the level of individual trees, tree stands (4 trees per stand), and in three divergent soil types across a landscape. Physical and chemical characteristics of soils were measured for correlation with patterns of microbial alpha- and beta-diversity. We outline two major findings: first, our results suggest that sampling at a small scale (individual soil aggregates) provides greater power in defining the ecological roles of uncultured microbes. Second, we describe a number of possible interactions (antagonistic and/or mutualistic) between members of each domain, both cultured and uncultured. These were especially prevalent in the rhizosphere of oaks growing in or near serpentinitic soils, suggesting that cross-domain mutualisms may be more prevalent than previously thought. These mutualisms may play an important role in extending the niche space of plants, fungi, and bacteria in soils with harsh physical or chemical conditions. Further work will verify the prevalence of these mutualisms across different soil types in different climates, and suggest a more pedology-focused approach to survey and experimentation with soil microbial communities.

POSTER 35

Selecting fungal indicator species in tropical soils

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Indicator species are those that occur in specific habitat types or at specific time points, and are therefore considered as better ecological indicators of environmental changes than generalist species. Detecting indicator species becomes critical in tropical regions such as the Derived Savannas (DS) of the Caribbean Coast of Colombia (South America), where state governments require tools to better assess the present condition of soils in heavily deforested areas. Using taxonomic and abundance data derived from analysis of ribosomal ITS sequences, we applied a combination of indicator species analysis (IndVal index) and ranking of NMDS scores to determine if common agricultural practices have rapid effects on soil communities in DS. Burning and complete removal of vegetation did not have strong short-term effects on the fungal community followed through alternating dry and wet seasons, a result that supports the hypothesis of a highly resistant and resilient fungal community inhabiting highly perturbed soils in this savanna. We also found that only six of the 71 most abundant species could be considered seasonal or temporal indicators of the fungal community. Most of the indicator species had higher relative abundance toward the end of the study, after a period of high precipitation and vegetation recovery. Additional work will be required to determine whether certain species or groups of species can be used as indicators of long-term soil degradation.

POSTER 36

Ectomycorrhizal fungal communities associated with *Oreomunnea mexicana* show high beta diversity at a regional scale in Central America

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Recent studies of the ectomycorrhizal (EM) tree *Oreomunnea mexicana* (Juglandaceae) in Panama indicate that this species dominates some tropical montane forests and is symbiotically associated with a

unique community of EM fungi. *Oreomunnea* forms monodominant forests and it is distributed from Mexico to Panama in tropical montane forests between 1000 - 1900 m.a.s.l. To elucidate the effect of geographic location, soil fertility, precipitation, temperature, and host abundance on the ectomycorrhizal fungal communities associated with *Oreomunnea* we collected fruiting bodies and root tip samples from six localities (three in Panama and three in Mexico). At each locality fungal fruiting bodies were preserved and ITS sequences were generated for molecular identification. In addition EM roots were sampled from 60 *Oreomunnea* trees (40 trees in Mexico and 20 in Panama) and the fungal communities were assessed based on ITS1 sequencing using the Illumina platform. From a total of 874 mushroom specimens sequenced, preliminary results suggest a high diversity of ectomycorrhizal fungi with approximately 360 OTUs. From that total, only 17 OTUs were shared between sites in Mexico and Panama. Similarly, the Illumina results including all fungal species reveal a high turnover of root associated fungal species between the two sampled regions. These results are consistent with the high beta diversity found at local scales in the EM fungal communities associated with *Oreomunnea* in sites with contrasting soil fertility in Panama.

POSTER 37

Seeking synergy: Co-inoculation of a brown and white rot fungus on diesel-contaminated soil

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Several fungal species have shown potential for mycoremediation of petroleum products in soil, but their efficacy varies widely in the presence of other fungi or bacteria. As a result, robust competitors like cord-forming basidiomycetes are prime candidates for mycoremediation of non-sterile soils. Previous studies examined interspecific interactions between white rot cord-formers in non-sterile soil, but none have examined interactions between cord-formers with differing modes of metabolism. The brown rot *Fibroporia vaillantii* and the white rot *Stropharia rugosoannulata* have both been found to degrade PAHs in soil, a group of hydrocarbons found in diesel that can have long-lasting negative effects following a terrestrial spill. The different digestive enzymes produced by white rot and brown rot fungi may contribute to a more complete breakdown of diesel by targeting different fractions of this chemically complex pollutant. However, any synergistic effects for mycoremediation resulting from niche partitioning rely on the ability of these species to persist together as they compete for territory. To evaluate interaction outcomes, we established wood block inocula on trays with a layer of sterile or non-sterile topsoil, with or without the addition of diesel contamination, and monitored species interactions on the soil surface. We report our preliminary findings on interaction outcomes, and discuss the implications for mycoremediation strategies.

POSTER 38

Conceptualizing gut fungi beyond their natural tract by seeking them along other tracks

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We have been conducting field and lab-based studies on larval mosquitoes and their gut fungi (Trichomycetes) for the last couple years at select locations in Idaho. Our first field season, Spring through Fall of 2015, led us to seek pools and other lentic habitats, that had been connected during high water events to more permanent flowing systems. Also, during the 2016 field season, as we began to focus on the actual presence, nearby range and dispersal of the gut fungi we were finding, we also sought candidate aquatic stages (larvae) that inhabited specific aquatic zones of nearby lotic systems. Specifically, we were curious if other hosts might be present and serve as reservoirs of *Zancudomyces culisetae*, and other Harpellales, along the creek/stream gradient. This fungal species is widespread in mosquitoes but other dipteran families are known to harbor it as well. Additionally, might there be a pattern with spring zones (rheocrene) versus splash zones etc. with regard to possible reservoirs and hosts of *Z. culiset*ae. Using morphology alone, challenges arise with the distance between such zones.

Ultimately, we are also interested in the development of genetic/molecular techniques to trace the dispersal and transmission of spores between these highly specialized zones. Candidate host probing and environmental sampling will present major advances in the study of these symbiotic fungi.

POSTER 39

Friend or foe? Symbiotic fungi and a moss

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Fungi are an integral part of everyday life. These diverse eukaryote microbes are used in a variety of ways from pharmaceuticals to agriculture and are of great ecological importance. From plant fungal mutualist, such as mycorrhizae to fungal pathogens that potentially harm human health, fungal symbionts are important as they form close associations with their host. Fungal endophytes are considered commensal if they benefit from the symbiotic relationship while having a neutral effect on its host. My study of the *Daldinia loculata* endophyte, a symbiont living within a plant, has shown that different strains of this fungal species may have effects on a plant host from parasitism to beneficial mutualism. Do strains affect their moss hosts' growth differently? Or does it depend on the moss host?

POSTER 40

Acute and subacute toxcity of *Detarium senegalensis* seed oil extract on wistar albino rat

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Medicinal plant is a therapeutic resource used by traditional population of the African continent specifically for healthcare and which may also serve as precursors for the synthesis of useful drugs (Sofowora, 1993). Also, the World Health Organization (W.H.O 2001), defined a medicinal plant as any herbal preparation produced by subjecting plant materials to extraction, purification, concentration or other physical or biological process which may be produced for immediate consumption or as a a basis for herbal products. The term herbal drug determines the part/parts of a plant used for preparing medicines. The seed from the tropical plant *D. senegalensis* was gotten at oyingbo market area of lagos state, Nigeria. *D. senegalensis* is a small tree up to 10 m tall, It is confined to drier regions of west Africa. It is typically a species of dry savanna (Leung et al.,1968). The seed from the plant is called ofo and was authenticated by Prof. A.A Adekunle of the Department of Botany, University of Lagos. The seed material were dried at ambient temperature between 30-40^{o}C in an oven for five days and powdered to coarsed particles. 900grams of the seed material was extracted n-hexane using hydrodistillation method. Non of the animals used in this study dies and so therefore the LD_{50} could not be calculated meaning that the extract is safe for consumption. The effect of the extract on hematological parameters are shown in (Table 4) The haemoglobin, white blood cells and packed cell volume increased in treated animals compared to the control.

POSTER 41

The potential of fungal mycelium in methane capture

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Filamentous fungi produce networks of hyphae to form mycelia, and these web-like mycelia are often coated in a slime layer that is hydrophobic on its outer surface. This is attributable to a cysteine-rich amphiphilic protein, hydrophobin that embedded in a mucilaginous matrix. Hydrophobin helps fungal

mycelia and spores cope with desiccation stress and it reduces surface tension that can otherwise inhibit aerial growth. For bioremediation, hydrophobin-rich fungi provide an 'added bonus' by improving capture and dissolution of hydrophobic compounds. In our past work, we have shown that fungal inoculations can significantly boost bioremediation rates, even for compounds that the fungus cannot degrade (e.g. methane). Hydrophobic compounds that dissolve into this slime layer, as part of a biofilm, become bioavailable to other microbes (e.g. methanotrophs) living in the biofilm with fungi. This is true for a range of hydrophobic pollutants, including dioxins, chlorinated dibenzofurans, polychlorinated biphenyls (PCBs), and polyaromatic hydrocarbons (PAHs), and this fungal capture effect has been shown in both aqueous- and gas-phase applications. Despite this potential, however, bioremediation research has focused primarily on pollutant metabolism, not bioavailability, and we see a potential to utilize fungal mycelium in these capture improvements as 'low-hanging fruit'.

POSTER 42

Hidden in plain sight: Heterogeneity in asexual spores of *Aspergillus fumigatus*.

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Aspergillus fumigatus spores are found ubiquitously in the environment. The asexual clonal spores (conidia) produced in the environment are inhaled where they can germinate and cause high mortality rates in immunocompromised patients. Germination of conidia is the most crucial step in the development of aspergillosis. Given that conidia are produced in a variety of environments, we tested whether sporulation conditions impact the ability of conidia to break dormancy and grow. Spores from a single colony were bulked on complete media and cultured with environmentally- and medically-relevant stress conditions. Spores from each condition were collected and transferred to all other conditions. Germination and growth kinetics were analyzed for 25,000 conidia from each condition swap experiment using flow cytometry. We found that clonal populations of conidia are heterogeneous for germination and growth phenotypes and the stress increases this phenotypic heterogeneity .

POSTER 43

A phylogeographic study of species from *Aspergillus* section *Flavi*

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Aflatoxins produced by several species in *Aspergillus* section *Flavi* are a significant problem in agriculture and a continuous threat to human health. To provide insights into the biology and global population structure of species in section *Flavi*, a total of 1,304 isolates were sampled across six species (*A. flavus*, *A. parasiticus*, *A. nomius*, *A. caelatus*, *A. tamarii* and *A. alliaceus*) from single fields in major peanut-growing regions in Georgia (USA), Australia, Argentina, India and Benin (Africa), as well as a population of *A. oryzae* from Japan. We inferred maximum likelihood phylogenies for six loci, both combined and separately, including two aflatoxin cluster regions (*aflM/alfN* and *aflW/aflX*) and four non-cluster regions (*amdS*, *trpC*, *mfs* and *MAT*), to investigate barriers to gene flow. We also employed principal component analyses to identify clusters and their associations with six different categories (geography, species, precipitation, temperature, aflatoxin chemotype profile and mating type). With the exception of *A. flavus* S populations in Benin we found no evidence of geographic structure. Populations of *A. flavus* S in Benin were genetically distinct from all other section *Flavi* species for the loci examined, which suggests reduced gene flow and genetic isolation. Evidence of trans-speciation within two non-cluster regions, whereby *A. flavus* S_{BG} strains from Australia share haplotypes with either *A. flavus* or *A. parasiticus*, was observed. Finally, we provide evidence that the amount of precipitation, more than temperature, appears to influence the frequency and distribution of aflatoxin producing and non-producing species.

POSTER 44

The mating-type locus of *Phialocephala scopiformis* DAOMC 229536 confirms ancient homothallism both within the family Vibrisseaceae, and prior to the *Phialocephala fortinii* s.l. - *Acephala applanata* species complex division

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We describe the complete mating-type (MAT) locus for *Phialocephala scopiformis* DAOMC 229536, a basal species within the Vibrisseaceae (Ascomycota). This spruce needle endophyte is of interest due its production of the important anti-insectan rugulosin. Using comparative genomics, we provide some of the first insights into the genome structure and gene inventory of non-clavicipitalean endophytes. Sequence was obtained through shotgun sequencing of the entire *P. scopiformis* genome, and the MAT locus was then determined by comparing this genomic sequence to known MAT loci within the *Phialocephala fortinii* s.l. - *Acephala applanata* species complex. We tested the relative levels of sequence conservation for MAT genes within the Vibrisseaceae (n = 10), as well as within the Helotiales (n = 27). Our results show: (1) a homothallic gene arrangement for *P. scopiformis* [MAT1-1-1, MAT1-2-1, and MAT1-1-3 genes are present], (2) that homothallism is ancestral within the Vibrisseaceae, (3) that *P. scopiformis* contains a unique SAM-Mtase gene proximal to its MAT locus, while also lacking an sla2 gene, and (4) that MAT1-1-1 is the more useful molecular marker amongst the MAT genes for phylogenetic reconstructions aimed at tracking evolutionary shifts in reproductive strategy and/or MAT loci gene composition within the Helotiales.

POSTER 45

Plant cell-wall decomposition mechanisms in litter-decomposing Agaricales inferred from genome sequencing data.

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Soils contain enormous amounts of organic carbon that plays important role as a nutrient source and water storage in terrestrial ecosystems. The organic carbon in soils is the result of two major processes; the gradual decomposition of plant-organic matter and the accumulation of microbial-activity products e.g. metabolites, secreted proteins or cell-wall fragments. The decomposition of plant organic matter in soils contributes to the recycling of nutrients and the release of carbon dioxide to the atmosphere. Fungi play a pivotal role in this process and soils harbor high fungal diversity from all major groups of fungi. Among mushroom-forming fungi, Agaricales is the most species-rich order, representing a group of fungi that have very successfully occupied the soil habitat either as free-living litter decomposers or as ectomycorrhizal symbionts. The mechanisms that litter decomposers in Agaricales employ to break down plant organic matter are not well understood. Here, we examine the decomposition mechanisms of litter decomposers in Agaricales based on genomic data generated by PacBio sequencing. We ask questions about the diversity and number of genes found in those species in relation to the degradation of lignin, cellulose and hemicellulose. Furthermore, we compare their gene content with other litter decomposers in Agaricales and white-rot species from several orders in an attempt to explore the evolutionary mechanisms that allowed Agaricales to make the transition from wood to soil habitats.

POSTER 46

Contribution of multiple horizontal gene transfer to ectomycorrhizal niche transition in *Amanita*

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New gene acquisition may be critical for the adaptation of fungi to novel niches. Horizontal gene transfer is an efficient mechanism used by fungi to acquire functional, yet novel genes. Previous studies have shown that phytopathogenic fungi use horizontal gene transfer genes for the infection, digestion and manipulation of novel hosts. This raises the intriguing possibility that horizontal gene transfer also plays a role in the origin of ectomycorrhizal niches. A carbohydrate esterase family has been reported as horizontally transferred from bacteria to some ectomycorrhizal Amanitas, but because other ectomycorrhizal Amanitas lack these genes, the genes are unlikely to be required for the ectomycorrhizal niche. To discover whether any horizontal gene transfer event was crucial for the transition from saprotrophy to symbiosis among *Amanita*, an MCL algorithm was used to identify the homologous genes which are present in only and all of the three ectomycorrhizal *Amanita* genomes we have sequenced, among genomes of five Amanitas and one *Volvariella*. These 108 homologous gene families were then used as a query for blasting against a curated database of 631 fungal, 1153 bacterial and 87 plant genomes. Phylogenetic trees of protein sequences were built to identify inconsistencies between gene and species trees, the key to identifying horizontal gene transfer events. Seven gene families emerge as plausible candidates for HGT from Ascomycetes and one from Zygomycetes. Constraint analysis will be done to evaluate the likelihood of HGT events. In addition, dN/dS ratios will also be calculated to test for positive selection on these genes.

POSTER 47

Quantifying incidents of Horizontal gene transfer within the genomes of the Anaerobic gut Fungi (Neocallimastigomycota)

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Horizontal gene transfer (HGT) has been shown to play an important role in shaping the metabolic potential and genomic landscape of multiple eukaryotes, including fungi. The anaerobic gut fungi (AGF, Neocallimastigomycota) reside in the anaerobic, eutrophic, and prokaryotes-dominated herbivorous gut; and such proximity is conducive for the occurrence of inter-domain HGT during the course of its evolution. Here, we assessed the patterns and determinants of HGT in 18 transcriptomes and 8 genomic assemblies that represent five different AGF genera. Incidents of HGT were prevalent within the AGF CAZyome, with HGT accounting totally or partially of 34 out of 50 GH families analyzed. The high transcriptional levels and occurrence of gene duplication in HGT-acquired domains suggest their importance as an integral part of the lignocellulosic machinery in AGF. The most common bacterial donors were members of the gram- positive phylum Firmicutes, specifically members of the families Clostridiaceae and Ruminococcaceae, incidences of HGT from other phyla e.g. Fibrobacter were also identified. Patterns of HGT acquisition were remarkably similar across all examined AGF genera; suggesting the occurrence of the absolute majority of such events prior to genus level diversification. Finally, the noted absence of ubiquitous fungal GHs e.g. GH7 and GH61 domains across all examined datasets suggests the simultaneous occurrence of gene loss and gene acquisition as adaptive mechanisms during Neocallimastigomycota evolution. The results suggest that while HGT played an important role in imparting a wide range of lignocellulosic capabilities on the AGF, its role in genus level diversification appears to be limited.

POSTER 48

Phylogenomics and divergence time estimation of the anaerobic gut fungi (Neocallimastigomycota)

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Anaerobic gut fungi (AGF) refer to the group of micro-fungi exclusively live in the gastrointestinal tract of herbivores (i.e. Buffalo, Cow, Elephant, Horse, Sheep etc.). The AGF in the gut serve a critical role in the

plant biomass degradation and fermentation in the anaerobic environment, thus important to their animal hosts. Phylogenetically, AGF represent a distinct lineage (Neocallimastigomycota) within the zoosporic fungi of the Chytridiomycota phylum. Earlier investigation reveals that AGF genomes have extremely low GC content (17%) and evidence of horizontal genes acquisition from bacterial. However, the evolutionary history and divergence time of the AGF are still unknown. We have sequenced 21 transcriptomes and two genomes of AGF taxa and performed a phylogenomic analysis using ~420 conserved orthologous markers with the PHYling pipeline. Both maximum likelihood and Bayesian phylogenetic methods are used to reconstruct the AGF phylogenomic tree with protein and coding sequences. Divergence time of the AGF lineages was estimated with Bayesian Evolutionary Analysis Sampling Trees (BEAST) using a calibration point of the emergence of Chytridiomycota based on other kingdom-wide fungal dating analyses. Preliminary results indicate that *Anaeromyces, Orpinomyces*, and *Pecoramyces* are monophyletic, while *Piromyces* and *Neocallimastix* are paraphyletic. The AGF as a monophyletic clade is recently emerged (~78 Ma), which corresponds well with evolution of herbivory in Mammals (72-100 Ma).

POSTER 49

Population variation in post-harvest rot *Rhizopus stolonifer*

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Globally postharvest diseases contributes to one third of food losses. *Rhizopus stolonifer*, a Mucoromycota fungus, causes postharvest soft rot in fruits and vegetables. Control is typically focused on quick harvesting, packing at cool temperatures combined with treatment of fungicides. However, many fungicides are not approved for direct use on fruits and understanding mechanisms of resistance development is limited. We have phenotyped 130 geographically and substrate diverse R. stolonifer strains and sequenced the genome of half of these. Strains have been cultured from California and Florida strawberries, from almond hulls from California orchards, and obtained from culture stocks from the USDA-NRRL collection. Fungicide resistance varies among isolates with reduced sensitivity to Fludioxonil in some strains. Linear growth rates in race tubes at 12C, 23C, and 30C show significant differences among strains that originate from varied climates or isolation substrates. Whole genome sequencing is being performed on 60 strains from this collection and analysis of patterns of genetic variation was performed to test for evidence of population structure and demography. Preliminary data from a geographically diverse subset of 12 samples identified more than ~250,000 SNPs across the 38 Mb genome. Variants were analyzed to scan for highly diverse gene loci, evidence of directional selection, or insertion/deletions of transposable elements. The strains group into 3 main clades, but no phylogeographic pattern has emerged yet. Further sequencing will test robustness of these potential sub-populations, examine genotype and phenotype correlations, and identify genetic loci with signatures of rapid evolutionary change.

POSTER 50

Antimicrobial activity of *Brassica rapa* nectar lipid transfer protein

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Antimicrobial peptides (AMPs) provide an ancient, innate immunity conserved in all multicellular organisms. In plants, there are several large families of AMPs defined by sequence similarity. The nonspecific lipid transfer protein (LTP) family is defined by a conserved signature of eight cysteines and has a compact structure with a lipid-binding hydrophobic cavity. The antimicrobial activity of LTPs varies greatly among plant species. An LTP from *Brassica rapa* (variety R-o-18) nectar was tested for antimicrobial activity. In a 96-well microplate, each well contained half strength potato dextrose broth, approximately 2000 spores, and concentrations of LTP peptide up to 300 µg/mL in a total volume of 100

µL. After 48 hours of incubation at 25 °C in the dark, absorbance of the wells was measured at 595 nm on a microplate reader to quantify the inhibition of fungal growth. The amount of LTP needed to inhibit growth of pathogen strains by 50% (IC_{50}) was calculated. This *Brassica* LTP was most effective against *Trichoderma* and *Bipolaris oryzae* with IC_{50} values of 0.78 µM and 1.71 µM, respectively. Additionally, both *Colletotrichum trifolii* and *Alternaria solani* had IC_{50} values of less than 4.0 µM. The activity of this *Brassica* LTP at such low biological values indicates that it is a potent defense protein. These results suggest that transgenic expression of antimicrobial LTPs has the potential to lead to improved broad-spectrum disease resistance.

POSTER 51

Understanding the biology and ecology of natural fungal antagonists of Soybean Cyst Nematodes for biological control

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A good biological control agent must not only be able to affect the pathogen in vitro, but must also establish, survive, and thrive in the environment where it needs to effect biocontrol. The present study used both morphological characteristics and ITS sequence for identifying the SCN cyst mycobiome from a long-term soybean-corn crop rotation experiment. Thus far, research on SCN cyst mycobiome has strictly based on morphology over a single season. In this study, fungi isolated from approximately 5000 cysts were collected over three growing seasons. Those genera most commonly associated with nematode cysts and eggs were tested for their parasitism on SCN cysts and eggs, and for their ability to prevent egg hatch. The main genera found were primarily in Hypocreales, including *Fusarium, Dactylonectria, Cylindrocarpon, Clonostachys,* and *Mariannaea* as well the Chaetothyriomycete *Exophiala* and the Dothidiomycete *Leptosphaeria*. Different crop rotation sequences had no significant effect on the community composition of the fungal community associated with cysts. Egg parasitism was scored using the egg parasitic index (EPI) on a scale of 1 to 10 based on the percentage of eggs colonised. One *Fusarium equiseti* strain and one *Metacordyceps chlamydosporia* strain consistently showed an average EPI of 8.5 each. Eggs were hatched in cell free supernatant of these fungi and several isolates also inhibited egg hatching. Future directions include studying chemical compounds involved in SCN egg-hatch inhibition, investigating the ability of these fungi to colonize different soil types and establish without fungistasis, and testing candidate biocontrol agents in greenhouse trails.

POSTER 52

Species composition of root-feeding beetle associated *Leptographium* and *Grosmannia* blue-stain fungi in loblolly pine stands in Georgia

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Loblolly pine (*Pinus taeda* L.), the most commercially significant tree species in the southeastern United States is experiencing relatively higher levels of mortality around the Fall-line and Upper coastal plain regions in Alabama and Georgia. Root-feeding beetles (e.g., *Hylastes* and *Hylobius* spp.) and their Ophiostomatoid fungal obligates (e.g., *Leptographium* and *Grosmannia* spp.) have been associated with areas of dieback; however, the actual species composition of the fungal complex associated with these beetles, and in particular their role in loblolly pine mortality, is yet to be established. Our research objectives are as follows: 1) to assess the diversity and composition of the Ophiostomatoid fungal complex associated with these root-feeding taxa in loblolly pine stands in Georgia; and 2) to analyze whether pathogen pressure and species composition varies in stands with various management practices and environmental conditions. Root-feeding beetles will be collected in loblolly pine stands with differing management histories, such as controlled burning, and across a multi-seasonal gradient. First, a subset

of beetles will be used to isolate and identify associated Ophiostomatoid fungi based on morphological and molecular features. Then, fungal DNA will be extracted directly from the remaining adult beetles and species-specific PCR primers will be developed to determine the incidence of each of the identified fungal species. Results from this study will assist in better understanding of the role of *Leptographium* and *Grosmannia* fungi in the dieback of loblolly pine, and their implications for sustainable forest management practices in the southeastern U.S.

POSTER 53

The interaction between laurel wilt pathogen and the plant host in plant leaves

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Laurel wilt is a devastating disease of Lauraceae trees. The causal pathogen is the fungus *Raffaelea lauricola*, transmitted by redbay ambrosia beetle, *Xyleborus glabratus*. Since 2003, laurel wilt has almost killed all the redbay (*Persea borbonia*) trees in Southeast of United States. In 2012, an outbreak on Avocado (*P. americana* Miller) was detected. As a typical vascular disease, symptoms include the discolored and dark streaking sapwood, wilt stems and leaves, defoliation and finally death of the whole tree. It has been reported that the gels and tyloses in the xylem were related to symptom development. However, the propagation and movement of fungal pathogen inside trees has not been well investigated. It was observed that less than 1% of the Xylem lumena of avocado, swamp bay and camphortree were occupied with a GFP labelled strain of *R. lauricola*. Whether the fungal pathogen is propagated and accumulated in tree leaves is unknown. Therefore *R. lauricola* strain will be qualified using both conventional population assay and qRT-PCR analysis at series of time points after artificial inoculation. At the same time, strain of *R. lauricola* will be inoculated on tree leaves to assay whether the fungal pathogen can be translocated to the entire tree and further cause wilt. This will help to understand host tree response to fungal pathogen and the mechanisms of laurel wilt disease symptom development and finally facilitate the development of durable control strategies for laurel wilt disease.

POSTER 54

Development of a LAMP-based assay for rapid in-field detection of *Raffaelea lauricola*, the causal agent of laurel wilt disease

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Laurel wilt is a rapidly spreading disease that is devastating lauraceous plant species in the southeastern United States, including redbay, sassafras, and avocado. It is caused by Raffaelea lauricola, an invasive fungus vectored by the redbay ambrosia beetle. Reliable and rapid early detection of the pathogen is essential in slowing the spread of the disease, and a key part of an integrated pest management system. We aim to develop a loop mediated isothermal amplification (LAMP)-based assay to detect the pathogen directly in the field at the earliest stages of infection. The assay will enable forest health monitoring agencies and avocado growers to diagnose the disease timely and independently, without having to rely on external laboratories, which will overall reduce costs and allow for faster response time. Two pathogen specific primer sets were designed on a microsatellite region unique to R. lauricola and the β-tubulin gene. Both sets were tested on several isolates of *Raffaelea* species and have thus far shown amplification specific to Raffaelea lauricola only. Further testing for specificity and sensitivity with pure fungal DNA is being conducted before the assay is optimized for use on portable devices with crude DNA

extracts. Finally, the efficiency and accuracy of the assay will be evaluated under field conditions before distribution to and training of forest health personnel. Successful development and implementation of a LAMP-based assay to detect *Raffaelea lauricola* in the field will facilitate effective early detection and assist in management of the disease.

POSTER 55

Resistance response to Fusarium Head Scab in barley

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Fusarium graminearum is a necrotrophic fungal plant pathogen and the primary causal agent of Fusarium Head Blight (FHB) on wheat and barley, which reduces quality and quantity of grain yields. FHB is partially controlled by fungicides, with no strong resistance available in host crops. Barley has a moderate resistance response where *F. graminearum* cannot spread from individual infection sites. This resistance response differs in two-row vs six-row barley, which differ in arrangement of florets and trichome morphology. Previous work has shown an accumulation of plant defense compounds (cellulose and lignin) at trichomes on inoculated barley florets, with greater numbers of focal accumulations on two-row barley varieties with small, domed trichomes. Near isogenic lines (NILS) of barley with loci for two - or six - row trichome characteristics are being studied for focal accumulation. The NILs will allow us to elucidate the importance of trichome morphology in resistance responses.
For biotrophic fungal diseases, barley varieties are available with partial and complete resistance to powdery mildew, which show increased susceptibility to FHB. We hypothesize that the defense compound accumulation seen in trichomes is decreased in the powdery mildew resistant lines, allowing *F. graminearum* to penetrate barley florets more readily. Preliminary data shows fewer incidences of focal accumulation in the completely resistant variety when compared to the partially resistant variety. With further work, we will be able to determine if *F. graminearum* is able to penetrate the plant cells in the more and less resistant varieties of barley.

POSTER 56

A preliminary assessment of potential *Armillaria* spp. distributions in western Oregon, western Washington, and Alaska using bioclimatic modeling.

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Armillaria species are key components of forest ecosystems throughout most regions of western North America. Their ecological roles range from beneficial saprobes to damaging root pathogens, and their impacts vary with environment and host. Under climate change, the impact of pathogenic species within these regions is predicted to increase, which could result in increased tree mortality, growth loss, and hazard trees that threaten public safety. In 2016, a collaborative project was initiated to survey of *Armillaria* spp. distributions in western Oregon, western Washington, and Alaska. Methods and preliminary results of the 2016 and 2017 (ongoing) field surveys/collections will be presented. *Armillaria* isolates derived from collaborative surveys will be identified using DNA-based methods (e.g., translation elongation factor-1α gene sequence). DNA-based identification and 19 location-specific climatic variables will be used to develop models to predict areas suitable for the occurrence of *Armillaria* spp. Preliminary

predictions of geographic distributions of suitable habitat for *Armillaria* under current and predicted future climates will be presented, based on Maximum entropy distribution models (MaxEnt). MaxEnt are used because of their ability to produce statistically robust models using limited occurrence-only data. This information will contribute to habitat-specific management strategies for reducing impacts and increasing the benefits of these ecologically important fungal species.

POSTER 57

Combatting Fusarium Basal Rot of Onion in the Annapolis Valley, Nova Scotia, Canada

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The fungal onion pathogen *Fusarium oxysporum* f. sp. cepae (FOC) has caused significant crop loss in the Annapolis Valley, Nova Scotia, at an estimated annual cost of $600 000. Current control strategies have not reduced symptoms, so we propose an integrated approach that includes identification of the pathogen in the soil prior to planting through the design of a qPCR assay, and the development of a fungal biological control treatment. As this local system has not previously been researched, preliminary work has been undertaken to (1) identify local FOC strains and potential fungal biocontrol agents using DNA barcoding methods, (2) determine the virulence of FOC in a greenhouse bulb onion bioassay, and (3) test potential biocontrol fungi in dual culture trials. More than 40 fungal species have been isolated from onion field soil, including six *Trichoderma* species, three of which have shown biocontrol potential against FOC in dual culture trials. A comprehensive, effective control strategy is essential to prevent the collapse of the Nova Scotia bulb onion industry due to FOC infection.

POSTER 58

Fungal disease protection in rice (*Oryza sativa*) seedlings by growth promoting seed-associated endophytic bacteria from invasive *Phragmites australis*

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Non-cultivated plants carry endophytes that may be used to enhance deveolopment and disease resistance of crops. During seedling establishment, rice may be infected by fungal pathogens. Species of *Fusarium* and *Pythium* cause rice seed rot during germination. *Fusarium* blight in rice seedlings is common and affects seedling development. In this study we screened ten endophytic bacteria isolated from seeds of invassive *Phragmites australis* by inoculating onto rice and Bermuda grass (*Cynodon dactylon*) seeds to evaluate plant growth promotion and protection from *Fusarium oxysporum*. We found that three bacteria, including *Pseudomonas fluorescence*-SLB4, *Pseudomonas* sp.-SLB6 and *Pseudomonas* sp.-SY1 promoted seedling development, including enhancement of root and shoot growth, and modulation of root hair formation in rice and Bermuda grass. Bacteria were positive for phosphate solubilization. *Pseudomonas* sp. (SY1) protected rice and Bermuda grass seedlings from *Fusarium* infection. In co-culture experiments, strain SY1 inhibited fungal pathogens with 85.71 % growth inhibition of *F. oxysporum*, 86.33 % growth inhibition of *Curvularia* sp. and 82.14 % growth inhibition of *Alternaria* sp. Seedlings of Bermuda grass and rice treated with bacteria were found much less infected by *F. oxysporum* in comparison to non-treated controls. Bacteria appeared to actively degrade fungal mycelia. Metabolite products of strain SY1 were also found to inhibit fungal growth on nutrient media. *Pseudomonas* sp. (SY1) was found to produce inhibitory volatiles. MALDI-TOF analysis revealed that SY1 produces antifungal lipopeptides of the fengycin family. Antifungal activity of SY1 could be due to production volatiles and antifungal lipopeptides.

POSTER 59

Hyperparasites attacking rust fungi: Species and distribution

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Rust fungi are one of the most serious plant parasites causing disease in a wide range of hosts. They are mainly controlled by fungicides. However, the application of hyperparasites as potential biological control agents is becoming a promising field in applied biological research. For example, the genus *Sphaerellopsis* is considered a potential biological control fungus because it attacks a wide host range among the rusts, but information related to this hyperparasite is incomplete. This study focused on the geographic distribution and the genetic variation of hyperparasites of rust fungi species from around the world based on the herbarium specimens in the Arthur Fungarium. Three thousand randomly selected rust-infected leaf samples were examined using a stereomicroscope. Samples with visible hyperparasitic pycnidia were isolated for DNA extraction. General and newly designed *Sphaerellopsis*-specific primers were used to amplify the internal transcribed spacer (ITS) region of the fungus. Two different hyperparasitic species were identified: *Sphaerellopsis paraphysata* and *Eudarluca caricis*. Hyperparasites were found on 249 rust fungus samples. Within these, nine rust genera and 131 rust species are new records as hosts of hyperparasites. Geographic data are also increased as we recorded hyperparasites in 19 countries where it was not previously reported. The majority of infections were found attacking the uredinial stage of the host. Finding new rust species attacked by hyperparasites raise the potential that these have biological control properties.

POSTER 60

Evidence and consequence of a highly adapted clonal haplotype within the Australian *Ascochyta rabiei* population

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Australia is currently the world's leading exporter of chickpeas. However, the prosperous industry is being severely threatened by an *Ascochyta* blight caused by the fungal pathogen *Ascochyta rabiei*. One mating type gene has been successfully identified in the Australian *Ascochyta rabiei* population, inferring the population is genotypically narrow. Although the *Ascochyta* mating gene pool is limited, a large diversity of aggressiveness exists. Here, quasi-hierarchical sampling was used to select 598 isolates from major Australian chickpea growing regions and commonly grown host genotypes between 2013 and 2015. Through short sequence repeat (SSR) genotyping, 66 haplotypes were identified with an overall low gene diversity (Hexp = 0.066) and genotypic diversity (D = 0.57). Nearly 75% of the examined isolates were of a single dominant haplotype (ARH01), indicating that the fungus is widely adapted to the unique agro-geographical environments of all chickpea growing regions of Australia. Disease screening identified 17% of the isolates were highly aggressive. Approximately 66% of the isolates collected from the popular grown host genotype, Genesis090 (coined "resistant" during the time of collection), belonged to the ARH01 haplotype. Of these isolates, 46% were highly aggressive, potentially indicating adaptation of the population on this host. The most aggressive isolates that belong to widely adapted haplotypes such as ARH01 and are detected on common cultivars are of highest risk to the Australian chickpea industry. These should be monitored for in association with newly released cultivars and used for future resistance breeding strategies.

POSTER 61

Screening of *Balansia epichloe*-infected grass dpecies for in situ ergot alkaloids using laser ablation electrospray ionization-mass spectrometry

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The *Balansia* are clavicipitaceous symbiotic species associated with various species of tropical grasses. Laboratory culture procedures established that grasses in tall fescue pastures are often infected with conspecific *Balansia* species that produced ergot alkaloids. However, any effects of hosts on the qualitative accumulation pattern by each *Balansia* species are unknown. A method eliminating extensive sample preparations including the lengthy fermentations, extractions, and chromatographic analyses is needed to screen naturally endophytic infected pasture grass species for their ergot alkaloid content. Laser ablation electrospray ionization (LAESI) mass spectrometry is a high-throughput procedure capable of the *in situ* detection of picogram levels of metabolites in plant tissue. LAESI procedure was used to determine the *in situ* chemical analyses of ergot alkaloids produced by grasses infected with the same species in efforts to determine host influence on ergot alkaloid production compared to laboratory culture. *Balansia epichloe* symbiotic with *Sporobolus poiretii* (smut grass) is the reference for the laboratory production of ergot alkaloids, whose alkaloids spectra were reporter earlier. Other *B. epichloe*-infected grasses collected from this same location were used to determine the *in situ* occurrence of ergot alkaloids. The grass species associated with *B. epichloe* included in this study were smut grass, lacegrass (*Eragrostis capillaries,* a new host), and lovegrass (*Eragrostis hirsuta*), all maintained under unheated greenhouse cultivation. These grasses were examined by LAESI for chanoclavine, ergonovine, agroclavine, and ergonovinine reported to occur in laboratory cultural studies of strains isolated from the reference symbiotum *B. epichloe-S. poiretii.*

POSTER 62

Haploid cells of *Ustilago maydis* form filaments on mature leaves that grow directional towards and enter into stomatal openings.

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The smut fungus *Ustilago maydis* is known to infect elongating portions of its maize host as a dikaryon. Immature leaves and silks are easily infected using combined compatible haploid sporidia as inoculum, and microscopic observations have shown that the haploid cells fuse and form a dikaryotic filament that infects via an appressorium. Inoculation of older plant parts does not result in tumor formation or other macroscopic signs of infection. Inoculation using diploid teliospores is generally unsuccessful, which is a little surprising given that this is the stage thought to overwinter in plant debris to produce inoculum for subsequent years. We have shown that haploid cells can survive and reproduce by budding in soil, thus potentially providing a source of haploid inoculum that might be carried on plant surfaces as the plant grows. In investigating how fungal cells might survive on leaf surfaces, we found that haploid cells produced filaments that grew directionally toward guard cells and entered mature leaves through stomatal openings. This directional growth did not require the mating pheromone receptor (Pra) as haploid cells where *pra* was deleted behaved similarly. A solo-pathogenic haploid strain (SG200) was also found to form filaments that grew into stomatal openings on mature leaves. However, it formed appresoria at the stomatal opening unlike the other haploid strains. The directional filamentous growth exhibited by wild-type haploid cells towards stomatal openings is unexpected given the known infection process, and its role in the infection process remains unclear.

POSTER 63

Two novel strains of *Bacillus* with strong antifungal properties

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Two strains of *Bacillus* with antifungal properties have been isolated from 1-scrapings from an apartment air vent (HU-Biol-I), and 2 (TU-4) from a potato dextrose agar (PDA) plate exposed overnight in a classroom. The former becomes dark gray to black after several days' culture on PDA at 26C. The latter becomes tan-colored under similar cultural conditions. To ascertain their antifungal properties 3-day-old median streaks and 3 spot inoculations per plate of each strain were made. The fungi challenged included *Alternaria solani, Fusarium oxysporum, Mucor* sp*., Rhizopus stolonifer, Penicillium* sp. *Aspergillus niger, Sordaria* sp. *Aureobasidium* sp*., Chaetomium* sp. *and Ophiostoma ulmi. Penicillium sp.* was not inhibited by either strain. Inhibition zones were broader between cultures of strain TU-4 when compared with strain HU-Biol-1. Further evidence of the antifungal properties of these bacterial strains was obtained with spore germination tests. Spores of *Alternaria, Ulocladium, Fusarium and Sordaria* were placed in 0.1 ml drops of sterile culture filtrates from 3-day-old potato dextrose broth PDB of each strain. As controls similar tests were made using sterile PDB. During a period of 24 hours only germ vesicles formed in some spores of each of the test fungi whereas prominent hyphal growth was present in the controls. The identities of the strains nor their antifungal components have not been conclusively determined.

POSTER 64

Occurrence of Leaf Blotch on oats vaused by *Drechslera avenae* in Korea

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In January 2017, black spot was observed on grains of oat (*Avena sativa* L.) harvested in a farmhouse in Jeongeup and the symptom appeared as darkening of their superficial tissues. Out of 100 oat grains investigated, 45 grains were infected by *Drechslera* spp. All selected *Drechslera* isolates were identified as *Drechslera avenae* (Teleomorph *Pyrenophora chaetomioides*) based on their morphological and cultural characteristics. The result of conventional identification was ascertained by aligning complete internal transcribed spacer (ITS) rDNA regions and glyceraldehyde 3-phosphate dehydrogenase (GPDH) gene sequences of *Drechslera* isolates. A phylogenetic tree derived from the GPDH sequences showed that Korean isolates of *D. avenae* comprises four distinct groups. In the pathogenicity test, the fungus was pathogenic to leaves and grains of oats. Leaf symptoms at the early stages of disease development included small, dark-brown or black colored spots. As the disease progressed, the spots were enlarged as oblong to elongate, reddish brown lesions with yellow halos and eventually dried out. Oat heads were also infected and diseased spikelet turned brown. This is the first report that *Drechslera avenae* causes leaf blotch on oats in Korea.

POSTER 65

The decline of *Araucaria humboldtensis*, an iconic conifer from New Caledonia

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Araucaria humboldtensis is a threatened conifer endemic to New Caledonia, which is a Pacific island known for its unique endemic flora. New Caledonia is considered one of the smallest biodiversity hotspots in the world. *Araucaria humboldtensis is* found growing in Southern New Caledonia and grow at altitudes of ca. 800 to 1600 m on ultramalfic substrate. Over the last several decades, there have been observations of a general decline in populations of *A. humboldtensis*, which is manifested by massive resin exudation, branch and twig dieback, and eventual mortality. The observed symptoms are typical of a fungal canker disease, but no pathogen has been identified as a primary causal agent. The objectives of this work are to i) identify primary causal agents of the decline symptoms, ii) elucidate the etiology of this potential disease, and iii) preserve unique genotypes of *A. humboldtensis*. From a preliminary survey from Mt. Humboldt in December 2014, *Fusarium oxysporum, Fusarium solani* and *Chalara* sp., which are known plant pathogens in other pathosystems, were isolated from bleeding cankers of several trees. Pathogenicity tests are needed to confirm if these isolated fungi are aggressive pathogens of *A. humboldtensis*. To understand the etiology of this decline, transects will be established among five populations where the health of the trees will be monitored over time and symptomatic tissues will be sampled for associated fungi. Lastly, we plan to genotype and propagate individuals from all known populations. This work will support conservation efforts by identifying potential tolerant populations of *A. humboldtensis.*

POSTER 66

Fungal colonization and *Fusarium* diversity across *Vanilla* cultivation systems

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Vanilla is an orchid of economic importance; native to Mexico but widely cultivated in tropical regions. Root-associated and mycorrhizal fungi were studied in four species of *Vanilla* (*V. planifolia, V. pompona, V. insignis, V. rayada*) using microscopy, cultures, and direct sequencing of peloton structures. Fungal isolates were obtained from surface-sterilized plant material and soil; identified using ITS nrDNA sequencing. Samples were collected from plants in different agrosystems located at Totonacapan (Puebla and Veracruz, Mexico), including traditional and shade house systems with dead, alive, and concrete tutors. Microscopy showed higher peloton colonization in systems that use alive tutors (host trees) in comparison with roots collected from dead tutors. Fungi identified directly from pelotons included *Scleroderma aerolatum*, a common ectomycorrhizal fungus not yet reported as a mycorrhizal symbiont in orchids. Common plant pathogens, including *Fusarium* and *Pyrenophora seminiperda*, were also detected in sites with low colonization rates and more degraded pelotons. Culturing yielded a total of 383 sequences, with 47% identified as *Fusarium* mainly recovered from roots (111 isolates). Out of the *Fusarium* isolates, 73% were isolated from *V. planifolia*. Other commonly cultured genera include *Penicillium, Trichoderma*, and *Aspergillus*. Sequences for the TEF-1α and RPB2 regions were obtained from representative *Fusarium* isolates. The *Fusarium* isolates obtained belong to the *F. solani, F. incarnatum-equiseti*, and *F. oxysporum* species complexes. This research reports for the first time the potential colonization of *Vanilla* by *Scleroderma* as a putative orchid mycorrhizal symbiont and provides a more detailed study of several *Fusarium* species in *V. planifolia*.

POSTER 67

***Cercospora* community composition associated with Cercospora leaf blight changes across developmental stages and is geographically dependent**

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Cercospora kikuchii has been considered the causal agent of Cercospora leaf blight (CLB) and purple seed stain (PSS) on soybean. Modern phylogenetic studies, however, have suggested the presence of four lineages associated with CLB and PSS, two of which have been reported from US soybean populations. We set out to investigate the sources of inoculum for the species associated with CLB and PSS in the US by sequencing calmodulin for 182 *Cercospora* isolates collected from commercial seed prior to planting, symptomatic leaves, and harvested seed. *Cercospora cf. flagellaris* accounted for 71% of the isolates, while *C. sigesbeckiae* (24%) and *C. kikuchii* (4%) accounted for a smaller proportion of the community. *Cercospora cf. flagellaris* increased in frequency from planted seed (50%) to blighted leaves (81.8%) and harvested seed (80.7%). *Cercospora sigesbeckiae* decreased in frequency from planted seed (38.3%) to leaves (13.6%) and harvested seed (19.3%). *Cercospora kikuchii* decreased in frequency from 10% on planted seed to 4.5% on leaves and was absent on harvested seed. However, the community composition on planted seed appears to be geographically dependent. The proportion of *Cercospora cf.* flagellaris (21%) on seed lots originating from Tennessee was significantly lower ($p < 0.01$) than from Arkansas seed lots (60.5%). Not only is this the first phylogenetic confirmation of *C. kikuchii* associated with CLB and PSS in North America, but also suggests that previous observations of site by year variation in disease severity may be due to the geographic origin of the seed.

POSTER 68

Crop rotation shifts the microbial communities in the cysts of soybean cyst nematode

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The soybean cyst nematode (SCN) is a major pathogen of soybean that decreases soybean yield both through direct infection of roots and by vectoring other microbial diseases of soybean. There is great need for development of effective and environmentally sustainable management strategies for the SCN, but development of effective biocontrol is hampered by a lack of knowledge of nematode control microorganisms. The goal of this research is to characterize key genetic, functional and taxonomic groups of fungi colonizing nematode cysts under different crop rotation systems. The research utilizes a long-term crop rotation experiment of corn and soybean that includes annual rotation, 5-year rotation, and continuous monoculture. Fifty intact cysts of SCN from each plot were collected at planting, midseason and harvest in 2015 and the fungal communities were investigated by metabarcoding of the fungal ITS1 region. Additionally, 100 cysts from all the research plots were mixed and DNA was extracted for shotgun metagenomics sequencing. The fungal community composition of first year soybean and soybean monoculture was distinguished from other rotation treatments. Potential biological agents were shifted by different years of soybean-corn rotation. *Exophiala* sp. and *Clonostachys* sp. had greater relative abundance in fifth-year soybean than first-year soybean, while Pochonia sp. had higher abundance in soybean monoculture than second-year soybean. Fungi and bacteria frequently isolated from cysts were detected by shotgun metagenomics. Our results suggest that soybean-corn rotation shifted the fungal community colonizing cysts of SCN and that some nematode biocontrol fungi were reduced when soybean was rotated with corn.

POSTER 69

FvSTUA is a key regulator of development, fumonisin production, and virulence in *Fusarium verticillioides*

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Fusarium verticillioides is one of the most important pathogens of maize, producing fumonisin mycotoxins during infection. Ingestion of fumonisin-contaminated corn causes fatal toxicity in livestock and is associated with specific human cancers, neural tube birth defects, and growth stunting in children.

FvSTUA is an APSES class transcription factor, with homologous proteins regulating crucial developmental processes in fungi species such as sporulation, virulence and toxin synthesis among others. Our objective was to investigate FvSTUA's role in virulence and fumonisin production and development in *F. verticillioides* via functional and transcriptomal analysis of Δ*FvstuA* mutants. The mutants generated via *Agrobacterium*-mediated transformation of *F. verticillioides* with an OSCAR deletion construct, have stunted aerial hyphae, reduced hydrophobicity, and reduced macro- and micro-conidiation. Analysis of fumonisin levels in GYAM shows reduced fumonisin production by Δ*FvstuA* mutants (≥ 100-fold). Additionally, maize seedlings inoculated with Δ*FvstuA* mutants showed reduced disease when compared to seedlings inoculated with wild type. Furthermore, the role of FvSTUA as a transcription factor was corroborated by the observed nuclear localization of a FvSTUA-tdTomato fusion protein in *F. verticillioides*. Ongoing analysis of deletion mutants in genes highly differentially expressed in Δ*FvstuA* mutants will explore regulation by FvSTUA on processes including hyphal growth, cell differentiation, sexual differentiation, and cell wall assembly of ascospores. Planned generation of a chemically inducible promoter-driven FvSTUA together with RNASeq experiments will provide temporal information on the cascade of FvSTUA functions.

POSTER 70

Diversity of ascomycete fungal pathogens on *Theobroma cacao* L. in Merida state, Venezuela

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Venezuela has been home to Cacao trees for more than 400 years. Yet, very little is known about the fungi populations that are involved on these diseases, and especially, in the small cacao plantations distributed in Merida state, Venezuela. Therefore, the goal of this work was to identify fungal pathogens associated with various diseases in cacao trees plantations such as die-back, sudden death cacao trees and anthracnose on fruits. Samples were collected and transported to the phytopathology laboratory of the School of Forestry Engineering, University of Los Andes (ULA) Venezuela. Samples were cut (±5 mm2 sections) from the margin of healthy and diseased tissues. These tissues were surface-disinfected for 30 s in 70% ethanol followed by 60 s in 0.5% sodium hypochlorite, washed three times with sterilized water for 60 s, dried with sterilized filter paper, plated onto 2% malt extract agar and incubated at 25°C for 7 days or until mycelia were observed. Fruits with anthracnose were initially checked for the presence of fruiting bodies (ascomata and/or conidiomata) and conidia. Fungal mycelium was sub-cultured onto MEA. Single spore isolations were made and hyphal tipping methods were performed to obtain pure cultures. Through morphological descriptions, we identified five fungal genera associated with these diseases, including: *Lasiodiplodia* spp., *Neofusicoccum* spp., *Cylindrocladium* and *Fusarium* spp. isolated from stems and branches; *Colletotrichum* spp., *Neofusicoccum* spp. and *Fusarium* spp. from fruit. Future work will include molecular characterization of these isolate to determine fungal species identified with these diseases on cacao.

POSTER 71

Examination of the fungal populations responsible for spoilage of processed tomatoes in Indiana

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The USA is the second worldwide producer of tomatoes generating $2 billion in profit last year and Indiana is the second major US producer of this crop. Spoilage by fungi are a leading cause of loss of produce. Objectives of this study were to determine (1) possible spoilage fungi present within the microbiome of tomato, and (2) determine potential points of introduction of spoilage Fungi during tomato harvesting and/or processing. We sampled four fields in Indiana from which Roma tomatoes and soil samples were collected in duplicate during three consecutive harvesting periods. In addition, 50 mL water samples from five post-harvesting transporting belts were also collected. We isolated the mycobiome of

all samples using culturable (classic microbiology) and non-culture dependent (next-generation sequencing, NGS) methods. For culturable fungi, we isolated into pure culture 43 fungal species which were identified using the broadly recognized ITS barcode for Fungi. For total community analyses, we used the ITS1 locus sequenced on a MiSeq Illumina platform. Several well-known spoilage fungi such as *Didymella rosea, Geotrichum silvicola* and *Hanseniaspora uvarum* were abundantly isolated from both tomato and water samples. Preliminary results of NGS, however, indicate that the highest concentration of potential food spoilage fungi are in the water from the transport belts. This information will help to reformulate growth, sanitation and monitoring procedures to reduce the occurrence of spoilage fungi in final products.

POSTER 72

Boletus rubricitrinus* belongs in *Pulchroboletus

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Macrofungi taxonomy, traditionally based on morphological traits such as pileus color, hymenophore features, stipe decorations, and growth habit, has been extensively rearranged with modern DNA-based phylogenetic tools. To increase the understanding of macrofungi diversity in Florida, we are sequencing fungal specimens housed at the University of South Florida Herbarium. ITS sequences indicate *Boletus rubricitrinus* is closely related to the recently constructed genus *Pulchroboletus*. Unknown bolete sequences from Eastern USA to Mexico have shown to be closely related to *Pulchroboletus*, indicating the *Pulchroboletus* clade may have a more widespread distribution than previously determined.

POSTER 73

***Laccaria* in Southeast Asia: taxonomic and systematic diversity from a biogeographically important region.**

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The ectomycorrhizal fungal genus *Laccaria* is a model for understanding the ecology of ectomycorrhizal associations. Recently the systematic and biogeographic history of the genus has been thoroughly described. This history details a southern hemisphere origin in Australasia prior to dispersal and diversification in the northern hemisphere. Southeast Asia was a likely corridor for the transition of the genus into northern hemisphere Laurasia. This study documents and describes the taxonomic and systematic diversity of *Laccaria* species from Southeast Asia, primarily from Thailand. Molecular phylogenic analysis uses a combination of ITS, 28S, RPB2 and ef1a nucleotide sequences to apply the Genealogical Concordance Phylogenetic Species Recognition (GCPSR) concept. The results of GCPSR are used to delimit *Laccaria* species and identify specimens to describe the macro- and micro-morphological features associated with those species. To date, the analysis recognizes as many as seven phylogenetic species in Southeast Asia, with potential ECM hosts from the Dipterocarpaceae, *Castanopsis* (Fagaceae), and *Pinus*.

POSTER 74

Thelephoraceae of the Andean forests in Patagonia.

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Representatives of the family Thelephoraceae have not been studied in depth in Andean forests due to their inconspicuous fruiting bodies of relatively low abundance. Nothofagaceae-dominated ecosystems constitute one of the most extensive ectomycorrhizal forest types in the southern hemisphere. Growing evidence suggests that many Thelephoraceae species are important components of the soil biota and are common ectomycorrhizal symbionts over wide areas of Nothofagaceae forests. As a result of an extensive sampling effort in the Nothofagaceae forests of Patagonia in South America we have documented several morphologically unique species with ITS sequences that do not match previously described taxa or environmental sequences from ectomycorrhizal roots. Here we provide an overview of Thelephoraceae diversity in the Nothofagaceae forests of Patagonia based both on morphological studies of basidiomata and phylogenetic analysis of ITS sequences from basidiomata and ectomycorrhizal root tips. Our preliminary results based on field observations and herbarium specimens indicate that species diversity and abundance are higher at lower latitudes in Patagonia. Molecular and morphological analyses will allow the description of new taxa in the Thelephoraceae, allowing future studies about life cycles and spore dispersal systems of this group of fungi.

POSTER 75

Two new species of *Ruhlandiella* (Pezizaceae) from Nothofagaceae forests in Patagonia

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Ruhlandiella (Pezizaceae) is a genus of exothecial fungi in the order Pezizales. Exothecial fungi are 'inside-out truffles', i.e. their fruit bodies lack a peridium, and are instead covered with a hymenial layer. Like many truffles, *Ruhlandiella* have highly ornamented ascospores and asci that lack an operculum. The genus was first described by Hennings in 1903 based on *Ruhlandiella berolinensis* from the Australian greenhouse in a German botanical garden. *Ruhlandiella berolinensis* was later identified by Warcup and Talbot as an ectomycorrhizal fungus associated with *Eucalyptus* trees. Since then, mycologists have uncovered *Ruhlandiella* species from elsewhere, including Australia, Spain, Italy, and the USA. Currently, there are four recognized species in this genus: *R. berolinensis, R. peregrina, R. reticulatus* and *R. truncatus.* All were found near Eucalyptus or *Acacia* trees of Australasian origin. We discovered several collections of a gelatinous and exothecial fungus in Nothofagaceae forests in South America. These fungi match the general morphology of the genus Ruhlandiella but are distinct from all known species. Morphological and molecular analyses indicated that there are two novel species of Ruhlandilla among our collections. Although the inconspicuous ascocarps of these species are rare, they regularly form mitospore mats directly on soil across Patagonia. The purpose of this study is to describe these species and construct a phylogenic tree of *Ruhlandiella* and related taxa using four informative loci (the rRNA internal transcribed spacer (ITS), the large rRNA subunit (LSU), the second-largest subunit of RNA polymerase II (RPB 2), and the ß-tubulin protein-coding gene).

POSTER 76

Fungal endophytes in bryophytes and pteridophytes

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Bryophytes and pteridophytes represent two early lineages of land plants that have co-evolved with fungi for about 400 million years. There are at least 300 known Ascomycota species associated with bryophytes and all basal lineages of the pteridophytes have been shown to possess fungal endophytes. The goal of this project was to isolate fungal endophytes from bryophytes and evergreen pteridophytes species to determine if they contain novel taxa. Bryophytes and evergreen pteridophytes were collected from Pennsylvania in December 2016. Samples were thoroughly washed to remove debris, rinsed twice with distilled water, and the outer surfaces were sterilized. Surface sterilized tissues were incubated at 14°C on malt extract agar supplemented with chloramphenicol, pure cultures were obtained from colonies growing from the tissues, and the internal transcribed spacer region (ITS1-5.8S-ITS2) was sequenced for species identification based on BLAST results against the NCBI database. We obtained 71 isolates from ten hosts. Our current results indicate that there are many isolates with low identity sequence match to the NCBI database. Interestingly we discovered one aero-aquatic genus *(Pseudaegerita)* and two xylariaceous species *(Daldinia childiae* and *Nemania diffusa)* in addition to two isolates that were not identified despite obtaining a high quality ITS sequence.

POSTER 77

Pathogenic fungi associated with *Camellia sinensis* and allied species

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Camellia Linnaeus (Theaceae) species are of important commercial and ornamental value, especially *C. sinensis* (tea plant). *Camellia* production is heavily affected by a number diseases caused by fungal pathogens, such as anthracnose, gray blight and ring spot. During the past five years, we carried out an investigation of fungi associated with diseases of *C. sinensis* and allied *Camellia* spp. in 42 locations in the main cultivation provinces in China, and 1042 fungal strains were isolated using single spore isolation and tissue isolation methods. ITS analyses of these strains suggested that they belonged to at least 162 taxa in 68 genera, 38 families, 20 orders, and the top five dominant genera were *Colletotrichum* (25.7%), *Diaporthe* (10.5%), *Pestalotiopsis* (10.7%), *Setophoma* (8.3%) and *Cladosporium* (6.6%). Further morphological examinations and multi-locus phylogenetic analyses were employed to identify fungi in the above five genera to species level, which revealed 11 *Colletotrichum* spp., 9 *Diaporthe* spp., 15 *Pestalotiopsis* spp., 7 *Setophoma* spp. and 9 *Cladosporium* spp. associated with plant diseases of *Camellia* spp., including 20 novel species. This study revealed a high proportion of unrecorded and undescribed species on *C. sinensis*, which increased the known species associated with tea plant from 280 to 384 species, a significant improvement of our understanding on the diversity of fungal pathogens on *Camellia* species.

POSTER 78

Post-fire fungi in the Great Smoky Mountains National Park

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The Great Smoky Mountains National Park (GSMNP) is an International Biosphere Reserve that spans more than half a million acres (2200 km^2) between the mountainous borders of eastern Tennessee and western North Carolina. It has been the site of an All Taxa Biodiversity Inventory since 1998. In November 2016, a fire started in the Chimney Tops area and spread northward to Gatlinburg burning over 11,000 acres resulting in regions of lightly to severely burned forest. The goal of our project is to survey post-fire fungi throughout five areas of the Great Smoky Mountains National Park with light, moderate, and severe burn intensities, within cove hardwoods, oak hickory, and xeric pine forest types:

Chimney Tops Nature Loop Trail (lightly burned cove hardwood), Balsam Point Quiet Walkway (lightly burned cove hardwood), Twin Creeks Nature Center (moderately burned oak hickory), Bullhead Trail (moderately burned oak hickory), and Baskins Creek Trail (severely burned xeric pine). Collecting between March and June 2017 yielded several finds of Ascomycota including *Anthracobia macrocystis, A. melanoma, Geopyxis carbonaria, Morchella exuberans, Peziza echinospora, Pyronema domesticum,* and *P. omphalodes.* Several species of Basidiomycota were also observed: *Coprinellus angulatus, Hygrocybe conica, Laccaria bicolor, Mycena galericulata, Pholiota* highlandensis, and *Psathyrella pennata.*

POSTER 79

A new species of *Tricholoma* in the *pardinum* complex from the southern Rocky Mountains

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We are proposing a new species of *Tricholoma* in the *pardinum* complex (*T. smithii* nom prov). *Tricholoma pardinum* and related species are characterized by a robust stature, squamulose pileus surface and microscopically, by the presence of clamp connections. Cheilocystidia are sometimes present. The new species of *Tricholoma* occurs at high elevations under conifers from the Rocky Mountains of Colorado and New Mexico. The fungus differs from *T. pardinum* by the browner coloration to the squamules, compared to the gray squamules of of *pardinum*, and by the presence of pleurocystidia which are lacking in *pardinum*. It differs from *T. venenatum* also by the browner coloration to the squamules, by the presence of hymenial cystidia and by the difference in habitat, with *venenatum* occurring under hardwoods. In addition to morphology, an ITS sequence analysis positions the *smithii* clade as distinct from but close to the North American and European *pardinum* clades. The new species clade differs from both the European and other North American collections by five distinct apomorphies in the ribosomal ITS region. A sixth apomorphy is shared with a one of two haplotypes in a collection from California. The ITS region of the authentic *Tricholoma pardinum* from Europe differs from the *smithii* clade by 1.2% and from North American *pardinum* by 0.92% while the *smithii* clade and NA *T. pardinum* ITS regions differ by 1.07%.

POSTER 80

Phylogenetic analyses and bioclimatic modeling provide insights into the invasive brown root-rot pathogen, *Phellinus noxius*, in eastern Asia, Australia, and Pacific islands

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Phellinus noxious, an invasive pathogen first described in 1932, causes brown root-rot disease on an extremely wide range of hosts, primarily woody plants representing over 200 species from ca. 59 families. This fungal pathogen is widespread globally, and has been reported in many tropical/subtropical areas of Asia, Australia, Central America, Africa, and Oceania, where it can be quite destructive. This pathogen apparently attacks hosts regardless of health condition, and it can survive a decade or more in organic matter after host death. This study examines phylogenetic relationships and predicts suitable climate space for *P. noxius* collected from eastern Asia, Australia, and Pacific islands. DNA sequences of four loci (26S and internal transcribed spacer rDNA, translation elongation factor 1-α, and RNA polymerase II) revealed three major phylogenetic lineages including (i) eastern Asia (Malaysia, Hong Kong, Taiwan, Japan), (ii) Australia and Pacific islands (Guam, Saipan, Pohnpei, Kosrae, Palau, Taiwan, Japan), and (iii) American Samoa. Maximum Entropy Species Distribution Modeling shows potential distribution (areas with suitable climate space) of *P. noxius* and indicates geographic areas that are at risk from this invasive

pathogen, based on known locations of ca. 150 confirmed isolates from eastern Asia, Australia, and Pacific islands. In addition, bioclimatic modeling indicates that phylogenetic groups of *P. noxius* pose distinct invasive treats. Results also provide limited evidence of spread between geographic areas and potential hybridization between different phylogenetic groups. Continued studies are needed to determine relationships of isolates from Central America and Africa.

POSTER 81

A comparison of ectomycorrhizal fungal diversity between monodominant forests in the Neotropics and the Paleotropics

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Compared to temperate and boreal ecosystems, much less is known about the ectomycorrhizal (EM) diversity in tropical rainforests. Long-term (>16 years) EM sporocarp and root tip sampling efforts have elucidated the exceptional diversity of Neotropical EM fungi associated with the tree genus *Dicymbe* (Caesalpinioideae) in monodominant forests in Guyana. A matched sporocarp sampling effort has been initiated in a complementary Paleotropical system composed of monodominant forests of the EM tree *Gilbertiodendron dewevrei* (Caesalpinioideae) in the Guineo-Congolian region of Central Africa. Here we report preliminary comparisons of the species diversity of EM fungi between these regions based on morphology and ITS sequencing. Species diversity in Amanitaceae, Boletaceae, Elaphomycetaceae, Thelephoraceae and Sclerodermataceae is similar between the two regions. In the Russulaceae, species diversity appears to be greater in the *G. dewevrei* forests. However, the starkest differences in species diversity are in the Clavulinaceae and Cantharellaceae. The *Dicymbe* forests harbor a remarkable diversity of Clavulinaceae, with 21 documented species, compared to five species from the *G. dewevrei* forests. Conversely, 22 Cantharellaceae morphospecies are known from the *G. dewevrei* forests (19 *Cantharellus* and three *Craterellus*), compared to eight from the *Dicymbe* forests (one *Cantharellus* and seven *Craterellus*). Further sporocarp sampling and root tip analysis in the *G. dewevrei* forests will allow us to make more robust comparisons of species diversity at different taxonomic levels between these two regions, as well as to test biogeographic hypotheses regarding the origin of tropical EM fungi of the Guiana Shield and Central African regions.

POSTER 82

Teaching Mycology abroad in Ireland

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An introductory mycology course taught as a study abroad in Ireland was developed by instructors at Valdosta State University, Armstrong State University and the University of North Georgia. Ireland was selected because of its showy lichen community, famous breweries, and infamous history as the location of a devastating potato famine in the 1840s, but there are other great reasons to study mycology there. The three-week program includes tours of a mushroom farm, compost facility, microbrewery, fungal herbarium, agricultural research station, and potato famine museums. Students meet with mycologists, lichenologists, and plant pathologists, and search for fungi at various tourist stops, including the grounds of castles, cliffs, and gardens. Two of the three weeks are spent at a university where classroom and laboratory spaces are rented, and buses with drivers are hired for excursions. The program fee is $3000-3200, ~$175/day, and includes airfare, lodging, and most meals. This poster will provide details about the mycology-related experiences in the course, and reflections from instructors and students on student learning and engagement with mycology through the study abroad experience.

POSTER 83

New tropical *Amanita* species from the Guiana Shield and Central Africa

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The primarily ectomycorrhizal (ECM) mushroom genus *Amanita* (Amanitaceae, Agaricales, Basidiomycota) is estimated to number ~1000 species worldwide, ~800 species formally described. Many *Amanita* species have broad distributions in higher latitude forests, while *Amanita* species in the Neo- and Afro-tropics have restricted ranges in lowland rainforests primarily dominated by ECM trees of Fabaceae subfam. Caesalpinioideae ("caesalps"). Our collecting expeditions in rainforests dominated by the ECM caesalps *Dicymbe corymbosa* in Guyana and *Gilbertiodendron dewevrei* in Cameroon indicate that at local spatial scales both regions are diverse for *Amanita*: 25 morphospecies have been recovered from an area of 10 km^2 in Guyana, and 35 from an area of ~3 km^2 in Cameroon. *Amanita* species were collected annually in Guyana from 2000–2017, and in 2014 and 2016 in Cameroon. Collections were compared with published descriptions and herbarium specimens of previously described taxa. This preliminary work has established that numerous *Amanita* morphospecies from Guyana and Cameroon are currently undescribed, morphologically novel, and common in their local habitats. Macro- and micromorphological features have been compiled from multiple collections of each species, and multi-locus DNA sequence data is currently being generated. This project will formally describe or epitypify 3–4 taxa from each region. The description of new *Amanita* species from these regions will enhance our understanding of fungal biodiversity in tropical ecosystems. An overview of the proposed new taxa will be presented.

POSTER 84

Accurate biological source information for data verification and re-use

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The ITS (internal transcribed spacer) RefSeq project (PRJNA177353) aims to provide accurate name - sequence associations and additional information (public specimen sources) to confirm this association by independent evaluation. Since curators at NCBI have started collecting and annotating type material (identifiers that ties formal biological names to physical specimens), the most immediate impact has been improving the accurate identification of genome and barcode data. Unfortunately, the primary sequence records from type material frequently contain only the minimum information with no other metadata beyond strain or isolate identifiers. Although the RefSeq ITS project does add public collection identifiers and verify the specimen - sequence - name triangle, no additional source data is added on a regular basis. Gathering source information from protologues (species descriptions) scattered among several journals, all of which are not easily accessible, is a high curation burden. However, when researchers in the community get involved, it becomes a more feasible task. As an example, a thorough curation of one of the top ranking important fungal genera, namely Trichoderma was recently completed. The effort resulted in several verified data associations beyond name-sequence associations (eg: isolation source, location etc.). We present the outcome of this process and highlight the importance of source information.

POSTER 85

Phylogenetic analysis of white smut fungi (*Entyloma*) on Asteraceae

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Entyloma comprises more than 170 species of smut fungi parasitizing dicotyledonous hosts that are found on all continents except Antarctica. Infection results in the formation of sori embedded in the plant tissue. More than eighty *Entyloma* species are found on Asteraceae, with twenty-seven reported from North America. Previous phylogenetic studies confirmed monophyly of the *Entyloma* species exclusively parasitizing members of the Asterids (including Asteraceae, Apiaceae), and polyphyly of the *Entyloma* species on members of the Asteraceae. The present study aims to clarify the phylogenetics of the *Entyloma* species on Asteraceae with an emphasis on North American taxa. Newly collected specimens from the United States on five different hosts (*Arnica cordifolia, A. discoidea, A. parryi, Packery eurycephala, Symphyotrichum boreale*) were examined and analyzed by morphological methods, and included in the phylogenetic analysis together with sequences obtained from Genbank. The results of the analysis demonstrated that there are three main clades of *Entyloma* on Asteraceae. The first clade consisted of North American specimens from *Arnica* spp. The other two clades included species parasitizing both Asteraceae, and plants from other host families, including several members of Ranunculids and Euasterids. This distribution could be explained by several host shifts. Three species from the United States used in the analysis are described as new, based on host, molecular, and morphological data. The results of this study suggest that there is likely to be considerably more diversity within *Entyloma* than is reflected in the current taxonomy.

POSTER 86

A new ectomycorrhizal *Leotia* species from Panamanian montane forest

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Leotia (Ascomycota, Leotiomycetes) is a globally distributed genus with approximately 45 described species. Persoon first proposed *Leotia* in 1794. Taxonomic work on this genus was primarily done in the late 1800s and early 1900s; the most recent *Leotia* species was added in 1982 by Otani (*L. himalayensis*). Here we discuss *L. chiricana nom. prov.* (Leotiaceae) a new species associated with *Oreomunnea mexicana* (Fagales, Juglandaceae) in monodominant forest at the Fortuna Forest preserve in Chiriquí province, Panama. This species is recognized by the distinctive bright blue color of its capitate, lobate, stipitate ascomata, 5 - 10 mm broad, and its gregarious and cespitose fruiting habit. Phylogenetic analyses using ITS ribosomal DNA and a variable region of the RNA polymerase II (RPB2) gene strongly support a monophyletic *Leotia chiricana nom. prov.* cluster and resolve this new species as the sister lineage to *L. lubrica* group I sensu Zhong and Pfister (2004). Illumina sequence data (ITS2) and stable isotope analysis suggest that *Leotia chiricana nom. prov.* forms mycorrhizal associations with *Oreomunnea mexicana* and that this *Leotia* species is more abundant in soils with high nitrogen availability. The discovery of a new *Leotia* species from Central America suggests that species richness of ectomycorrhizal fungi in the neotropics is greater than previously understood. More intensive mycological exploration, in conjunction with the increased availability of next generation sequencing and isotopic analysis, will facilitate the discovery of new ectomycorrhizal partnerships.

POSTER 87

The Canadian Collection of Fungal Cultures (CCFC): Technological advances and future directions

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The culture collection maintains 16,000 plant pathogens and wood rotting fungal cultures representing approximately 3,000 species. The CCFC is supported by taxonomists with internationally recognized expertise in most major taxonomic groups whose research is mainly concentrated on solving agricultural problems. The collection now serves as a primary Canadian repository for research strains and functions as a gene bank for microbial genetic resources. It provides pure cultures to researchers in agriculture, forestry, medicine, private industry and biotechnology. The methods of long term preservations of cultures by lyophilisation and cryostorage are aimed at longevity and the stabilization of genetic properties. The collection has recently been databased in SeqDB, an application that will provide standards-compliant information management for collection records to DNA sequence workflows. In conjunction with the use of this database, DNA from reference specimens for regulated pests, close relatives, and other agriculturally significant targets will be sequenced . Next-generation sequencing techniques will be developed, and adapted for high throughput, to rapidly produce a large number of sequences per specimen for a large number of species. DNA barcoding will be performed on 16,000 specimens from the CCFC, with the goal of having barcode data available for 100% of living cultures. Partial or full genomes sequences will aslo be obtained for 575 cultures.

POSTER 88

Taxonomic revision in the Cystobasidiomycetes

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The Cystobasidiomycetes is a class in Pucciniomycotina that mostly comprises pink, orange-red or salmon colored yeast-like fungi currently placed in four orders: Cystobasidiales, Erythrobasidiales, Cyphobasidiales and Naohideales. Mycoparasitism has been reported for some genera such as *Cystobasidium*, *Naohidea* and *Occultifur*, while for others the predominant trophic strategy and reproductive biology is still unknown or unclear. Recently, several new species have been isolated and described from habitats ranging from tropical regions to Antarctic environments, many known from a single location or culture. Some species in the genera *Hasegawazyma, Cyrenella*, *Microsporomyces, Symmetrospora,* and *Buckleyzyma* reproduce asexually; while other species in the genera *Bannoa*, *Cystobasidium, Cyphobasidium, Erythrobasidium, Sakaguchia, Occultifur,* and are known to undergo sexual reproduction. By using different set of genes such as SSU, ITS, LSU, *RPB2*, *TEF1* and *CYTB*, the Genealogical concordance phylogenetic species recognition criteria (GCPSR) was implemented to identify independent evolutionary lineages. Based on molecular, morphological and physiological data, two new species in *Buckleyzyma*, three in *Bannoa*, one in *Sakaguchia* and one in *Cystobasidium* are proposed. In addition, an independent divergent lineage sister to *Cystobasidium* was identified and is proposed as a new genus to accommodate three new species. Lastly, the mycoparasitic species *O. internus* has been sequenced. Molecular data indicate that this species is not congeneric with other species described in the genus. Rather it appears to be related to species currently allied in *Microsporomyces* for which mycoparasitism as a trophic strategy has not been reported.

POSTER 89

Isolation and characterization of novel strains of anaerobic gut fungi (*Neocallimastiogmycota*) from the feces and rumen of domesticated and wild ruminants

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The anaerobic gut fungi (AGF) (*Neocallimastigomycota*) are strict anaerobes that represent one of the early diverging fungal phyla. AGF play an important role in plant biomass degradation in the alimentary tract of herbivores. So far, our attempts to gauge the phylogenetic, metabolic, and genomic diversity within the phylum yielded 64 AGF isolates from the feces and rumen of multiple domesticated ruminants and non-ruminants, as well as the rumen and feces of wild barbary (aoudad) sheep (*Ammotragus lervia*). Our isolates capture the *Neocallimastigomycota* inter- and intra-genus level diversities. Classification of the isolates using both microscopic and phylogenetic-based approaches, identified members of the genera *Anaeromyces* (n=16), *Piromyces* (n=16), *Orpinomyces* (n=8), *Neocallimastix* (n=3)*, Caecomyces* (n=4), and the newly proposed genus *Pecoramyces* (n=13). In addition, six strains belonged to a novel genus with polyflagellated-zoospore related to the *Orpinomyces-Neocallimastix* clade, and are currently being characterized. Within existing genera, multiple *Anaeromyces* strains displayed distinct microscopic characteristics (intercalary sporangia and entangled hyphae with appressoria-like structures) and sequence (ITS-1 and LSU) divergence from existing *Anaeromyces* species, justifying the proposition of a new species (*Anaeromyces contortus*). Finally, ITS-1 and LSU sequence data suggest that 14 *Piromyces* isolates belong to at least three new *Piromyces* species*,* and detailed morphological and microscopic characterization of these strains are ongoing. Carbon source used in the enrichment appears to be a selective factor in isolating specific fungal groups (e.g. switch-grass or corn-stover favoring the monocentric genera and cellulose favoring the polycentric ones) suggesting the feasibility of tailoring enrichment conditions to target specific AGF.

POSTER 90

Octaviania purpurea* is purple but is not an *Octaviania

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Octaviania purpurea is a unique, purple-colored truffle species that has been found only a handful of times in the Eastern USA. This truffle was first described by Coker and Couch in their book “The Gasteromycetes of the Eastern United States and Canada” (1928) based on collections from Chapel Hill, North Carolina. *Octaviania purpurea* macroscopically resembles other *Octaviania* species (Boletaceae, Boletales) because it forms hypogeous sequestrate fruiting bodies that have a marbled, dark colored gleba and a peridium that is pale when young but becomes purplish in age or with bruising. However, the microscopic features of *O. purpurea* are unique compared with other *Octaviania* species. Most *Octaviania* species have globose to subglobose spores with clavate basidia that are 2–4 spored. In contrast, *O. purpurea* has subglobose to elongated spores that are often attached to a pedicel and also basidia that are 1-spored and have an unusual elongated shape. We recently encountered fresh specimens from North Carolina that match the described morphology of *Octaviania purpurea*. Phylogenetic analysis based on DNA sequences of *TEF*1, ITS and 28S indicate that *O. purpurea* is not an *Octaviania* but instead represents a unique lineage of Phallales. Our phylogenetic results suggest that a new genus will be required to accommodate *O. purpurea*.

POSTER 91

Exploring the biodiversity of Georgefischeriales in Guyana

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The Guiana Shield contains one of the largest tracts of virgin tropical rainforests in the world and is a hotspot for undescribed fungal diversity. We have cultured numerous isolates of phylloplane yeasts from the Western Pakaraima Mountains in Guyana. This study explores the diversity within one order of these, the Georgefischeriales. Georgefischeriales is a member of Exobasidiomycetes, Ustilaginomycotina. The order comprises smut fungi and yeast-like relatives. Currently, there are ca. 40 described species in Georgefischeriales, belonging to eight genera and four families. Thus far, most species documented in this order have been found in temperate zones. Our study has recovered ca. 60 isolates representing at least three new species of tropical Georgefischeriales. Extensive multi-locus phylogenetic analyses utilizing ribosomal DNA sequences and protein-coding genes show that of these, one appears to be congeneric with *Tilletiaria*. A second appears to be congeneric with *Phragmotaenium*, which is in the same family (Tilletiariaceae) as *Tilletiaria*. The final clade is closely related to *Jamesdicksonia*, a genus in Georgefischeriaceae. Here we present molecular, culture and physiological data for the new species. With about forty species currently documented in this order, these Guyana isolates are examples that the species diversity of this lineage is larger than originally expected.

POSTER 92

Diversity of Chytridiomycota in the sediment surface of three Brazilian reservoirs: Morphological and phylogenetic analysis

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Fungi constitute important and conspicuous components of aquatic microbial communities, but their diversity and functional roles in aquatic food web dynamics and biogeochemistry remain poorly characterized. The Chytridiomycota phylum is represented by a basal lineage of fungi, which produce flagellated spores and occur in different freshwater habitats. The diversity of these fungi in the reservoirs is still poorly investigated, especially in the sediment, which represents an accumulated information of the entire hydrographic basin and its analysis can provide historical information on sediment deposition as well as magnitudes and trends in water-quality constituents such as phosphorus, nitrogen, and some pesticides. Due the importance of these fungi as parasites and saprophytes in the water column of lakes and reservoirs, the aim of this study was to analyze the diversity of these fungi in the sediment surface of three Brazilian reservoirs. During this study, we measured the organic geochemistry of the sediment surface and we found 17 Chytridiomycota species, the most of them representatives of Cladochytriales and Chytridiales. Some of these species were isolated in culture medium and their phylogenetic placement was evaluated through LSU region of rDNA. *Nowakowskiella ramosa* Butler was inserted for the first time in phylogenetic reconstruction besides two potential new species of this genus. This is the first time that diversity of chytrids is analyzed in the sediment surface of Brazilian reservoirs. Financial support: FAPESP/CAPES/CNPq

POSTER 93

A preliminary survey of *Lepiota* sensu stricto of Indiana

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Lepiotaceous fungi have received limited attention in North America outside of California, despite being one of the most ubiquitous decomposers across the continent. This group of fungi includes species currently allied in *Chlorophyllum, Cystolepiota, Lepiota, Leucoagaricus, Leucocoprinus, Macrolepiota*, and *Melanophyllum*. They occur across a range of substrates - most commonly found as soil decomposers, but a number of clades grow directly from decomposing wood. The Central Midwest is home to numerous under-documented and undescribed species of Lepiotaceous fungi. Several of these genera are known to be polyphyletic and the overall relationships of these pale-spored genera within the Agaricaceae is largely unresolved. Here we take a preliminary morphological, molecular, and phylogenetic look at members of *Lepiota* sensu stricto occurring in various ecosystems of Indiana. New voucher specimens have been attained through extensive surveys and through citizen science involvement. Existing herbarium specimens of these groups are also being examined. First documented species occurrence records for Indiana, the United States, and North America are presented and novel species are discussed.

POSTER 94

Classification of *Phyllosticta*-like species from South Africa in Neophyllostictaceae fam. nov. and Phyllostictaceae

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Members of the genus *Phyllosticta* are widespread, which cause plant diseases on a broad range of host. *Phyllosticta* was previously placed in the Botryosphaeriaceae, and recently the family Phyllostictaceae was resurrected to accommodate the monotypic genus Phyllosticta in the Botryosphaeriales. In the present study, we investigated 74 *Phyllosticta*-like isolates from South Africa. A novel lineage was recognised based on the multi-locus phylogeny using sequences of LSU, ITS and *tef1*, which clustered sister to Phyllostictaceae, representing a new family Neophyllostictaceae. *Neophyllosticta* gen. nov., with 3 new species described. This study recognises a total of seven families in Botryosphaeriales, ie., Aplosporellaceae, Botryosphaeriaceae, Melanopsaceae, Neophyllostictaceae, Phyllostictaceae, Planistromellaceae and Saccharataceae. Furthermore, 5 new species of *Phyllosticta* were introduced, based on the combined ITS, *act, gpdh* and *tef1* sequences analyses and morphological differences.

POSTER 95

Overlooked and underfoot: Diversity of bryophilous fungi

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Mosses and liverworts are a dominant component of the understory vegetation in both boreal and alpine habitats. This veritable forest of small plants provides important habitat for a diverse array of fungi that can act as saprophytes, parasites, and symbionts with important roles in carbon and nutrient cycling. Recent research suggests that bryophytes may be hotspots of fungal diversity, with up to 90 different fungal species associating with a single moss shoot. Despite the high diversity of fungi associated with bryophytes they are chronically under-reported due to their small size. A recent inventory of ascomycetes associated with mosses and liverworts in Norway screened more than 1300 bryophyte specimens from herbarium and field collections, yielding more than 800 records of bryophilous fungi. Thirty-five species new to Norway and three species new to science were recorded, more than doubling the number of

bryophilous fungi known from the country. In addition, two species were ‘rediscovered’ that are known only from one or two localities worldwide, and have not been reported in more than 50 years. Detailed mapping and species distribution modeling of specific species demonstrates that most bryophilous fungi are closely associated with their hosts and primarily limited by host distribution and not climatic conditions.

POSTER 96

Recovery of species-rank OTUs of agarics (Agaricomycotina, fungi) in metagenomic datasets based on various nrDNA amplicon lengths and positions

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Agarics (Agaricomycotina) are very diverse and abundant soil fungi in forest and grassland ecosystems. Various next generation sequencing techniques allow sequencing of DNA amplicons of different length. A variety of loci have been used for metabarcoding of fungi in environmental samples, the most frequently used being the ITS2 region of ribosomal DNA (nrDNA) and reference species sequences of this region are the most widely available in public databases. The ITS2 region has some limitations in the quantification of fungal OTUs and taxon recognition due to high intragenomic variability, unequal sequence length and GC content in some taxa. The adjacent LSU (large subunit) rRNA gene is an alternative less frequently used for metagenomics, which does not suffer from some of the problems listed above, and which for several taxa is better covered by reference sequences. In this study, ITS and LSU nrDNA regions of various length used for metagenomics of soil fungi are analysed for their ability to accurately recognize molecular OTUs and compared with results obtained from multi-loci phylogenetic studies. Evolutionary lineages of closely related species of three agaric genera; *Hodophilus* (Clavariaceae), *Dermoloma* (Tricholomataceae) and *Russula* (Russulaceae); are tested.

POSTER 97

Phylogenetic analysis of ITS and TEF-1 vs. SNP datasets in *Lentinula*

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Sequence read archives for 60 *Lentinula* isolates were generated in 2016 by Xiao et al for the purpose of single nucleotide polymorphism (SNP) analysis. Using a variety of bioinformatics tools, the short reads contained within these archives were mapped to known sequences of the ITS (internally transcribed spacer) and TEF-1 (elongation factor) genes derived from other *Lentinula* isolates. These genes are commonly used for phylogenetics in *Lentinula*, and were then used to analyze these 60 samples. The results were compared to previously developed SNP based phylogenies of these isolates, and used in a broader ITS and EF-1 based phylogeny spanning all known species within *Lentinula.* This work aims to explore the correlation between the SNP-based phylogeny and ITS and TEF-1-based phylogenies used in the study of *Lentinula,* and contribute sequences to larger more comprehensive analysis of the genus as a whole.

POSTER 98

Improved taxonomic and geographic circumscription for three agaric species of conservation concern proposed for IUCN Red List inclusion

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In order to assess the conservation status of a species, reasonable estimates of that species' rarity, geographic range, and ecology are necessary. Taxonomic ambiguity, incomplete knowledge of occurrence and geographic range, and other sources of uncertainty result in a lack of the information necessary to assess conservation threat level. The objective of this project is to gather necessary data on three mushroom species proposed as candidates for the IUCN Red List but classified as Data Deficient due to taxonomic or geographic uncertainty. *Laccaria pseudomontana* is known from only three alpine sites in the Colorado Rockies; however, additional specimens could potentially be found in herbarium collections labeled as the widespread, morphologically similar *Laccaria montana*. *Lepiota luteophylla* is known from a threatened California cypress grove and mixed forests in Michigan, raising the question of conspecificity between these widely disjunct populations. *Amanita zayantensis* nom. prov. appears to be restricted to a rare coastal California sand hill habitat, but morphologically resembles the more broadly distributed sand-inhabiting *Amanita baccata*. Micromorphological examinations and nrDNA-ITS sequencing of herbarium specimens of the three target species and aforementioned lookalikes were performed to clarify taxonomic uncertainties and circumscribe geographic distributions. Results and implications for conservation assessment will be discussed.

POSTER 99

Flying salt shakers of death: molecular studies of the cicada pathogen *Massospora*

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Massospora (Entomophthorales) is a fungus that exclusively infects cicadas. *Massospora* was originally described in 1879 from infected periodical cicadas (*Magicicada* spp.) in a population known as Brood II. *Magicicada* nymphs feed on plant roots for up to 17 years before they emerge as adults. This extended life cycle has made it difficult for pathogens to keep up, but *Massospora* co-evolved with its host, resulting in a long dormancy period synchronized with its host. Previous research has resolved species boundaries using morphology, but few have used DNA sequences. In 2016, Brood V cicadas emerged in WV and surrounding states. Over 100 infected cicadas were collected, with additional specimens obtained from various collections that represented other broods. In total, five cicada species were sampled from at least eight broods. At least four fungal genes were sequenced for both sexes of the three cicada species that were present in Brood V (*Magicicada septendecim, M. septendecula*, and *M. cassini*). LSU, SSU, and b-tubulin were sequenced for representative *Massospora*. During efforts to sequence EF-1a, it was discovered that *Massospora* contains an EF-1-like paralog seen in the Entomophthorales and other early-diverging fungal lineages. Single-gene phylogenies revealed that most samples were clonal regardless of brood, and more distantly related to the Entomophthoraceae than previously thought. Based on these results, it's unclear if *Massospora* will retain its current position in the fungal tree of life. Regardless, the evolutionary war of attrition between these cicadas and *Massospora* will continue to play out in backyards and forests around the world.

POSTER 100

An ultrastructural study of spore bodies in Orbiliomycetes

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Spore bodies are membrane bound structural components of ascospores, seen clearly only with the aid of the vital stain cresyl blue in living spores. Most species of *Orbilia* contain a single spore body in each spore, located at the tip, but the number and position may vary in *Hyalorbilia*. Spore bodies may vary in shape depending on species, but they are unique to the Orbiliomycetes. Their composition and function is uncertain, and their origin is disputed, which confusion is due in part to the tiny size. With transmission electron microscopy, we undertook a developmental study of spore bodies in one species of Orbilia, and a comparative study of spore bodies in five species from two phylogenetic clades, and from the related lineage *Hyalorbilia*. The spore body was not discernable until the secondary wall of the spore was in place. It is attached to the primary wall, and excluded from the sporoplasm by the sporoplasmalemma. After release from the ascus, the spore body remains intact until spore swelling, when its appearance changes. The position of the spore body during germination does not coincide with the origin of the germ tube, and in some cases, is opposite the germ tube. The timing and appearance of spore bodies after release from the ascus suggests that they may be involved in a wall expansion function related to spore swelling. In contrast to the various species of *Orbilia* in this study, a connection between spore bodies and the spore wall was not observed in *Hyalorbilia*.

POSTER 101

Community structure of marine ascomycotan fungi in intertidal sandy beaches of two Caribbean islands with contrasting tourism management: Implications for conservation.

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Tropical sandy beaches are among the less studied habitats in the coastal environment, despite their value as buffer zones against the ocean and recreational places. The island systems are usually less complicated than continental ecosystems and therefore allow one to compare the effects of tourism management procedures on microscopic fungal diversity. The microscopic fungi play a key role as saprotrophs in the flow of energy through the food web. The ecological impact of unregulated rise of tourism is the priority issue of the Caribbean islands. The aim of this work was to evaluate diversity and community structure of marine ascomycotan fungi from the intertidal zone in differentially managed sandy beaches of the Caribbean Sea. We collected a total of 500 samples in four sites of Cozumel Island, Mexico and Cayo Largo del Sur Island, Cuba. Diversity and community parameters assessing distinctive traits among systems were estimated using R version 3.2.1. The major findings suggest that Cayo Largo del Sur has a positive tourism management of beaches evidenced by fungal communities composed of a high number of coexisting species, relative abundance and its dominant structure, whereas Cozumel beaches showed an alteration of fungal community composition as a response to anthropogenic stress or environmental constrains due to inadequate tourism management strategies.

POSTER 102

Evolutionary relationships of North American and European species of *Gyromitra*.

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Gyromitra is a genus of macroscopic apothecial ascomycetes collected in spring or fall in temperate and boreal forests throughout the northern hemisphere. Nuclear ribosomal 28S large subunit sequence data from 63 specimens from North America and 43 specimens from Europe were used in maximum-likelihood and Bayesian analyses to reconstruct a phylogeny of *Gyromitra* in the northern hemisphere. *Gyromitra* sensu lato forms a monophyletic group composed of six major clades including Subg. *Discina (G. gigas, G. korfii, G. leucoxantha)*, Subg. *Caroliniana* (*G. ancilis*, *G. brunnea*, *G. caroliniana,*), Subg. *Gyromitra* (*G. ambigua/G. infula, G. esculenta*), Subg. *Melaleucoides* (*G. melaleucoides* and *Hydnotrya*), Subg. *Pseudorhizina* (*G. californica, G. sphaerospora*), and a clade which includes two sequences originally identified as *G. leucoxantha* which are distant from the remainder of the *G. leucoxantha* sequences in Subg. *Discina* and represent an undescribed species. The inability to better resolve taxa in the *G. gigas* and *G. ambigua/G. infula* species complexes warrants a multilocus study of *Gyromitra.*

POSTER 103

Culture free assessment of fungal diversity in Antarctic cryptoendolithic communities

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Endolithic life is one of the most spectacular microbial adaptations to the Antarctic environmental constraints; this borderline life-style is predominant in Continental Antarctica (Nienow et al., 1993) and represents the last chance of survival for microbes in the far extremes of the Continent before extinction. Although endolithic microbial communities are known to host among the most resistant and extreme-adapted fungi (Onofri et al., 2008; 2012), the extent of Antarctic microbial diversity is still unknown at the community level. The rock composition greatly influences community composition. Sandstone represents the best substrate for cryptoendolithic microbial communities supplying protective niches to prokaryotes and eukaryotes and allowing the spreading throughout inland or high altitude locations (Zucconi et al., 2016). In this study, we investigated the distribution and diversity of fungal communities inhabiting sandstone, analyzing rock samples collected from different localities in the Victoria Land, Antarctica, ranging from 1000 to 3300 m a.s.l., using amplicon sequencing targeting the fungal ITS region. Our study showed a clear dominance of a ‘core’ group of fungal taxa consistently present across all the sampled cryptoendolithic communities, regardless of location and altitude, mainly composed by lichen-forming fungi, and a high diversity of unidentified taxa.

WED 1

The cutaneous snake microbiome correlates with *Ophidiomyces ophiodiicola*, the causative agent of snake fungal disease

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The causative agent of snake fungal disease (SFD), *Ophidiomyces ophiodiicola*, is an emerging fungal pathogen threatening North American snake populations. Previous studies have elucidated clinical presentation, but the life history of this species remains largely obfuscated. This study aims to characterize the cutaneous snake microbiome to determine host-microbiome-pathogen effects that result from the presence or absence of *O. ophioodiicola*. We hypothesized that the cutaneous microbiome of snakes differs by species, geographic region, and presence of *O. ophiodiicola*. We also hypothesized that *O. ophiodiicola* persists in the environment and opportunistically infects susceptible snake species. Cutaneous snake swabs (n=116), soil samples (n=40), and water filtration samples (n=20) were collected between late spring and early fall of 2015 and 2016 across seven states in the Southern U.S.; Alabama, Arizona, Arkansas, Florida, Georgia, Tennessee, and Texas. These samples were subsequently subjected to DNA extraction and quantitative PCR to determine the presence/absence and fungal load of *O. ophiodiicola*. Additionally, high-throughput sequencing was utilized to characterize the bacterial microbiome of cutaneous snake swabs (n=83) and environmental samples (n=10). *O. ophiodiicola* was detected in 21 of 116 snake individuals, in two of 40 soil samples, and zero of 20 water filtration samples. PERMANOVA analysis indicates slight statistical differences (Pseudo-FPERMANOVA = 1.9001, $P < 0.05$) between the assemblages of cutaneous bacterial communities where O. ophiodiicola is present rather than absent, and RELATE indicates no relationship ($\rho = 0.049$, $P > 0.05$) between compared resemblance matrices of fungal load and community assemblage.

WED 2

An herbivore's delight: *Guyanagaster necrorhizus* basidiomes are a nitrogen-rich dietary supplement for their wood-feeding termite dispersal agents

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Guyanagaster necrorhizus is a sequestrate fungus closely related to species of *Armillaria* and allies. It is known only from the remote region of the Pakaraima Mountains of Guyana and utilizes wood-feeding termites for dispersal. Like other sequestrate fungi, *G. necrorhizus* basidiomes harbor a bacterial community. We characterized the bacterial communities of *G. necrorhizus* basidiomes at a range of maturities using the Illumina sequencing platform. The bacterial community in *G. necrorhizus*, composed almost entirely of Enterobacteriaceae species, is very similar to those found in the fungal gardens of the fungal-growing ants and termites. In the fungal-growing ants, the bacteria fix nitrogen to augment the nitrogen-deficient diets of those ants. Therefore, we tested *G. necrorhizus* basidiomes, also at a range of maturities, for the presence of an active nitrogenase enzyme—the enzyme produced by bacteria that is responsible for nitrogen fixation—using the acetylene reduction assay. The highest rate of nitrogenase activity, as well as the highest nitrogen content, was found in the most mature *G. necrorhizus* basidiomes—the only stage at which we have observed feeding by termites. In the genome of *G. necrorhizus*, eight copies of the *copper, zinc superoxide dismutase* gene were detected, compared with two in *Armillaria mellea*. This gene codes for an enzyme that is important to the proper functioning of nitrogenase in rhizobium nodules. To perpetuate its dispersal mutualism with wood-feeding termites—organisms also deficient in nitrogen—*G. necrorhizus* rewards them with additional dietary nitrogen generated by nitrogen-fixing bacteria.

WED 3

Symbiotic fungi associated with platypodine ambrosia beetles in the Southeastern USA

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Platypodinae (Coleoptera: Curculionidae) is a peculiar subfamily of weevils that cultivate nutritional fungi in tunnels excavated in dead or dying trees. Four species are native to the southeastern USA: *Euplatypus compositus, Euplatypus parallelus, Oxoplatypus quadridentatus*, and *Myoplatypus flavconis.* Some are minor pests: *O. quadridentatus* is a parasite on oaks, and *E. parallelus* has become an invasive pest in Africa and Southeastern Asia. Interestingly, a tight but unexplored symbiosis occurs between platypodine beetles and ophiostomatoid fungi, primarily within the genus *Raffaelea*. The specific fungal symbionts of the four native Platypodinae beetles remains unknown. We isolated filamentous fungi from all four beetle species (52 individuals) via dilution series from both mycangia and tunnels, and we identified them by a phylogenetic analysis of 28S rDNA. In total, 21 Ophistomatales fungus species were isolated: 13 *Raffaelea*, 2 *Esteya*, 1 *Leptographium*, 1 *Ophistoma*, and 4 *Ceratocysiopsis*. Few *Ambrosiozyma* and *Fusarium* also presented in our isolation. Neither beetle species yielded a unanimous "primary" fungal associate. Instead, several *Raffaelea* strains can be isolated from even the same individual. Thus, the platypodine-fungus association appears to be promiscuous on the species level, while restricted to Ophiostomatales on the genus level. The newly discovered fungal associates, such as some widespread *Ceratocysiopsis* spp. and *Ambrosiozyma* spp., play an unclear ecological role.

WED 4

Elucidating the diversity and population structure of *Fusarium* species associated with mass mortalities in sea turtle nests

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Fungal diseases of wildlife are increasingly common, with devastating consequences for biodiversity and ecosystem health. White nose syndrome and chytridiomycosis are examples of fungal diseases that have taken a major toll on populations of bats and frogs, respectively. *Fusarium keratoplasticum* (Fk) and *Fusarium falciforme* (Ff) have been associated with mass mortalities in the nests of sea turtles. These are common, cosmopolitan species of filamentous fungi that are known opportunistic pathogens of immunosuppressed, and sometimes healthy, humans. Unravelling their genetic diversity and population structure is integral to elucidating the ecology and epidemiology of the fusaria implicated in both clinical and sea turtle egg diseases. Both species show high levels of genetic diversity, and known anthropogenic isolates of Fk are dominated by an expanding clone complex. *Fusarium* isolated from sea turtle eggs may offer a key to understanding the global population biology of these two species. In addition to isolates obtained from all over the world, selective sampling for *Fusarium* was conducted at three nesting sites in Florida. Disease has never been reported as a major cause of mortality in Florida nesting sites. This study aims to determine the diversity of fusaria present at these sites, and compare these populations with those from sites around the world. The results from this research will allow for inferences to be made regarding the epidemiology of *Fusarium* infections in sea turtle eggs and humans, as well as the impact of anthropogenic versus natural environments on population structure.

WED 5

Microbiome diversity of biological soil crusts from Joshua Tree National Park, Granite Mountain, and Kelso Dunes

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Biological soil crusts (biocrusts) contain diverse variety of microbial communities that are essential to desert environments. Bryophytes, lichens, eukaryotic algae, cyanobacteria, bacteria, and fungi combine with soil particles to form different types of biocrusts. Biocrusts are now widely recognized as a living skin of dryland environment, and biocrust research is critical for desert ecosystem protection. Disturbances on biocrust microbial communities are often not visible and rarely quantified. Likewise, the functions of biocrust are poorly characterized. The stability and temporal variations in microbial community composition are also poorly understood. Work to classify biocrusts has been largely focused on external morphology, which may underestimate the functions and diversity of microbial communities. As a result, this project aims to explore the composition of microbial communities and to investigate spatial and temporal patterns on biocrust microbiome. We have used amplicon sequencing of environmental DNA to assess the composition of bacterial and fungal communities. Biocrusts were collected from Joshua Tree National Park, Granite Mountain, and Kelso Dunes in California. Preliminary results showed that major bacterial phyla were mainly Cyanobacteria, Proteobacteria, Actinobacteria, and Acidobacteria. Major fungal phyla were mainly Ascomycota (Dothideomycetes, Eurotiomycetes, and Pezizomycetes) and Basidiomycota (Agaricomycetes and Tremellomycete). Although alpha diversity analysis showed no different species richness between sites, beta diversity analysis reviewed geographical pattern among three sites. We also found correlation between increasing species richness and raining event. Further analysis on core microbiome and also abundant taxa will be determined and used to prioritize culturing efforts to explore functional diversity and their biotic interactions.

WED 6

Uncovering the diversity and function of fungi associated with the fungivorous millipede, *Brachycybe lecontii*

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Brachycybe is a genus of subsocial millipedes in the family Andrognathidae that associate with fungi. The genus arose 50 MYA, and contains eight described species. One of these species, *B. lecontii*, is widespread in the eastern and south-central United States. *Brachycybe* millipedes have been repeatedly, though casually, associated with fungal fruiting bodies (Basidiomycota: Agaricomycetes) underneath rotting logs. However, isolation of Basidiomycotan fungi from the millipedes themselves has contradicted anecdotal observations, and even culture-independent methods have returned a low quantity of DNA from these fungi. Other fungi, including yeasts, ascomycetes, and members of the Mucoromycota are far more abundant including some well conserved fungal orders and taxa. Thus, it is not clear exactly what the relationship is between *Brachycybe* and specific groups of fungi. In this study, we identified and examined over 1000 fungal isolates recovered from *B. lecontii* sampled across 20 locations spanning 7 states. To clarify the functional roles of fungi associated with these millipedes, we resolved their phylogenetic relationships among known relatives, including determining the placement of several putatively novel species. To explore fungal-fungal interactions, we co-inoculated plates with two fungi each and observed colony interactions (*e.g.* inhibition, overgrowth) over time. Additionally, to help clarify

arthropod-fungus interactions, *B. lecontii* and a well-established insect model (*Galleria mellonella*) were challenged with select fungi to assess pathogencity and characterize fungal secondary metabolite production. This research opens up new questions about fungal ecology and diversity, fungal metabolite production, and microbial interactions.

WED 7

Impact of plant genotype and soil origin on fungal-bacterial networks in the *Populus* rhizobiome

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Plants have evolved with belowground microbial symbionts, which constitute the plant rhizobiome. These microbes function in provisioning nutrients and water to their hosts, and aiding in plant immunity. Thus, fungi in the rhizobiome are of interest for understanding how plants adapt to different soil environments and the processes that structure plant-associated microbial communities. In this study we used bioassay experiments to assess the impact of plant genotype and soil origin on the structure of the *Populus* rhizobiome. High throughput amplification and sequencing of 16S, ITS, 28S and 18S rDNA was accomplished with 454 pyrosequencing. Each locus was analyzed independently, and then 16S and ITS datasets were used to assess co-association patterns between fungal and bacterial taxa. Community bipartite fungal-bacterial networks and PERMANOVA results show a significant difference in fungal or bacterial communities by soil origin, but no statistical differences were attributed to plant genotype. Indicator species analysis identified a number of root endophytic fungi and ectomycorrhizal fungi associated with *Populus* in specific soils. Many fungal-bacterial networks that were over-represented in our dataset included fungal members from multiple ecological guilds (e.g. arbuscular mycorrhizal, endophytic, ectomycorrhizal), and many networks included bacterial taxa in the orders Rhizobiales, Chitinophagales, Cytophagales, and Burkholderiales. While some ectomycorrhizal taxa such as *Tuber* and *Tomentella* were shared between networks, many ectomycorrhizal taxa belonged to independent networks. Our results add further evidence of the importance of soil origin in driving community structure in plant roots, and provide hypotheses to test on fungal-bacterial networks in the *Populus* rhizobiome.

WED 8

Fungal microbiomes - understanding the taxonomy and function of bacteria and archaea on fungal sporocarps

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The role of the microbiome in host-environmental relationships has been a major research focus over the last decade. Many studies have recognized the role of microbes, such as bacteria and archaea, in association with fungi in many different ecosystems. Quite surprisingly, fungal sporocarps or fruiting structures have largely been ignored when observing the taxonomic and functional diversity of organismal microbiomes. Here, I present data on the diversity of microorganisms associated with fungal sporocarps and attempt to understand the role in fungal exudates in shaping their microbiome. From initial sequencing experiments, fungal sporocarps appear to be highly enriched in members of the Enterobacteriaceae and Burkholderiaceae relative to their environmental matrices. The role of associates may extra- or endo-hyphal in nature and may be providing key metabolic processes which help these fungi utilize nutrients derived from the environment.

WED 9

Detection of diverse fungi metabolites in fish feeds from Nigeria

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Fish feed is an indispensable necessity for fish farming but prone to contamination from diverse range of microorganisms and their metabolites. In this study, fungi metabolites contamination of locally formulated fish feeds from Southwestern Nigeria were determined.
Ninety-four fish feed samples intended for juvenile *Clarias gariepinus* (Cat fish) were randomly collected from warehouses within Southwestern, Nigeria. The spectrum of fungi metabolites including mycotoxins in the feeds was assessed using a Liquid Chromatography-Tandem Mass Spectrometry (LC-MS/MS).
A total of 84 metabolites from diverse fungi (*Aspergillus, Fusarium, Penicillium, Alternaria, Claviceps* species and other fungi) were found in the fish feeds. Aflatoxin B1, fumonisin B1, zearalenone and deoxynivalenol were detected in 91 (97.9%), 83 (88.3%), 93 (99%) and 82 (87.2%) of the analyzed feeds. Aflatoxin B1 was the most prevalent aflatoxin occurring at concentrations ranging from 0.70 µg/kg - 550.78 µg/kg with mean of 108.2 µg/kg while fumonisin B1 was the most occurring fumonisin found at levels up to 6097.90 µg/kg with mean of1003.5 µg/kg. Total enniatins {A, A1, B, B1}, beauvericin and moniliformin which are new emerging fusarium mycotoxins were quantified at high frequency in 94 (100%), 94 (100%) and 91 (96.8%) of samples respectively. Considering the array and levels of fungi metabolites found in the fish feeds including those with known toxicities, the fish industries in South-western Nigeria may be at risk of economic losses due to mycotoxicoses in the fish species.

WED 10

DNA-barcoding the microcyclic rust species on Veroniceae (Plantaginaceae)

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In 1978, Savile published a review of microcyclic rust fungi attacking Veronicae host plants. He included descriptions of species and sub-species, most often based on specimens held in The National Mycological Herbarium in Ottawa (DAOM), and a discussion of rust-host relationships and evolution. Extensive recent molecular phylogenetic studies now exist for the three main host genera discussed, *Lagotis*, *Veronica* and *Veronicastum*, and multiple subgenera were recognized within the Veronica complex. In contrast, DNA sequences are available for only one of the nine rust species treated by Savile, *Puccinia veronicae-longifoliae*, a species well-known from Europe but only from isolated collections since 2005 in North America (NA). *Puccinia albulensis*, which occurs NA and Europe, is listed by Mexico and Colombia to be of quarantine concern. To generate DNA barcode data for this group of fungi and confirm host-associations, 42 DAOM specimens representing seven rust species treated by Savile were sampled for ITS2/28S sequences, and the 12 associated hosts for rbcL data. The ITS2 sequences were effective for differentiating five taxa: *P. acrophila, P. albulensis* ssp. *albulensis, P. veronicae-longifoliae, P. veronicarum* from NA and *P. veronicarum* from Europe. They failed to differentiate among the two subspecies of *P. rhaetica* and *P. albulenisis* ssp*. cascadensis*. Teliospore ornamentation is the distinguishing morphological character for these three taxa and warrants re-consideration. The rbcL sequences resolved the genus and sub-genus of host species but additional gene regions are needed for species identification.

WED 11

Seeds of antagonism: An ABC transporter and its adjacent transcription factor in *Fusarium verticillioides* are required for pyrrocidine B tolerance

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Fusarium verticillioides (*Fv*) is a prevalent seed-borne maize endophyte capable of causing severe kernel rot and fumonisin mycotoxin contamination. Within maize kernels, *Fv* is primarily confined to the pedicel, while another seed-borne fungal endophyte, *Sarocladium zeae (Sz),* is observed in embryos. *In vitro* competition assays have indicated *Sz* can inhibit the growth of *Fv*. A lactam-containing antibiotic produced by *Sz*, named pyrrocidine B (PB), is associated with antagonism of *Fv* by *Sz*. In order to explore the mechanism of antagonism, RNA-seq experiments were conducted by challenging the *Fv* liquid culture with PB at subinhibitory concentrations to induce transcriptomic changes. Seventeen lactamase domain-containing genes and an additional 10 genes with dramatic induction in PB treatment were selected as targets to generate gene deletion mutants. Phenotypic analyses revealed that deletion of an ABC transporter gene (FVEG_11089) or its adjacent transcription factor (FVEG_11090) caused increased sensitivity of Fv to PB. Quantitative PCR showed the ABC transporter gene was induced 13530-fold in response to PB exposure, and the induction was dependent on the adjacent transcription factor. Hence, we theorize that FVEG_11089 functions in PB resistance by extruding the antibiotic out of the cell, and FVEG_11090 positively regulates induction of FVEG_11089 to a high level in response to PB exposure. The exploration of the antifungal resistance mechanism addresses the competitive relationships of the two maize seed endophytes colonizing the same ecological niche.

WED 12

Super mycovirus donor strains of the chestnut blight fungus permit widespread mycovirus transmission and reduce canker expansion in American Chestnut

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Chestnut blight is a devastating canker disease caused by the fungal pathogen *Cryphonectria parasitica.* Hypovirulence is a biological phenomenon resulting from the infection of *C. parasitica* by a debilitating hypovirus. *Cryphonectria* hypoviruses exhibit an intercellular lifestyle and are only transmissible via hyphal anastomosis between vegetatively compatible strains. Five unlinked allorecognition [vegetative incompatibility (vic)] loci regulate hyphal anastomosis and thus, hypovirus transmission. Recently, a pair of “Super-Donor” (SD) strains were generated through systematic molecular gene disruptions at four of the five vic loci. When used together, these strains exhibit enhanced transmission of hypovirus to virulent strains regardless of compatibility group. Here, we test the efficacy of these SD strains for hypovirus transmission on natural infections of wild American chestnut (*Castanea dentata*) stems. Three plots were designated for each of the following treatments: 1) Super-Donors 2) wildtype-SD strains (no gene disruptions) and 3) water agar control. Each canker was sampled to isolate the infecting strain and resolve its vic genotype. Cankers were systematically treated by inoculating the canker margins using the designated treatment inoculum. Post-treatment canker expansion was significantly reduced for the SD treatment compared to wildtype-SD strains and the negative control. Subsequent canker sampling indicated increased rates of virus transmission for the SD treatment with 16 unique hypovirulent vic genotypes recovered. Together, these results indicate SD strains of C. parasitica facilitate enhanced hypovirus transmission to resident virulent strains resulting in restricted canker expansion on American chestnut under natural field conditions.

WED 13

The OSCAR method of gene deletion in fungi is an effective teaching tool

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For several years we've use the OSCAR (One Step Construction of Agrobacterium-Recombination-ready plasmids) method as a teaching tool with undergraduate directed researchers. The goal of this method is generation of precise gene deletion mutants in fungi. OSCAR has several advantages for use with undergraduates: 1) it is universal in design regardless of target gene sequence; 2) students are able and encouraged to cooperate with one another, although their projects are unique; 3) it is robust with high success rates, rewarding students with accomplishment for their efforts. Each student is assigned unique target gene(s) related to ongoing research interests. Throughout the production of deletion construct and mutants with OSCAR, students are exposed to hypothesis generation and testing, experimental design, genome database manipulations, primer design, PCR, Gateway Technology, gel electrophoresis, sequencing, fungal transformation and genotyping. A recently published video documenting the OSCAR procedure in JoVE is an additional valuable educational resource. The teaching benefits of this approach and examples in the classroom and research lab settings will be discussed.

WED 14

The effect of urea on perithecial development of pathogenic *Colletotrichum* spp. in North Carolina apple orchards

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Glomerella leaf and fruit spot caused by the *Colletotrichum gloeosporioides* (Cg) fungal species complex is an economically important disease of apple resulting in premature defoliation and yield loss. The cultural practice of applying urea to apple leaves at the end of the growing season enhances leaf litter decomposition and reduces ascocarp development in other fungal pathosystems on apple. However, there is no information on how urea influences the developmental biology of Cg. An in vitro experiment conducted in our laboratory suggested that addition of 5% urea to nutrient medium enhanced mycelial biomass and growth, but delayed perithecial development by three weeks. In this study, we examined the effect of urea on perithecial and ascospore development in diseased apple leaves. Leaves of similar physiological age were collected from apple trees in western NC, cut into 2-cm diameter discs, and treated with water (control) or 2.5, 5, or 10% urea. Ten leaf discs were added into six replicate plastic mesh bags per treatment, and placed on the soil surface at a field location in Mills River and Raleigh, NC. Leaf discs were harvested and assessed every 3 weeks for number of perithecia and developmental stage of 50 arbitrarily selected perithecia per treatment. Treatment with urea did not affect the number of perithecia formed. All concentrations of urea delayed rate of perithecial development, though the most effective concentration varied between sites. Regardless of treatment, perithecial maturity is roughly correlated with apple leaf and fruit development.

WED 15

Evidence for sexual reproduction in *Venturia effusa*, causal agent of pecan scab

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Pecan scab caused by *Venturia effusa* is widespread across southwest USA and epidemics can result in catastrophic yield loss. *Venturia effusa* reproduces asexually during the active phase of the disease cycle (spring through summer) with no evidence of a sexual cycle. Yet, genetic diversity among populations of pecan scab suggest *V. effusa* is a sexually reproducing pathogen. Using BLASTX with the mating type loci of *V. inaequalis* (apple scab pathogen) we were able to identify the *mat1-1-1* idiomorph in *V. effusa* isolate 3Des10b genome flanked by two conserved genes encoding a DNA lyase (apnB) and an uncharacterised PH domain-containing protein. Evaluation of 14 isolates collected from different geographic locations and cultivars by PCR showed that 50% contained *mat1-1-1* and the remaining isolates contained *mat1-2-1*. A multiplex PCR assay developed to amplify *tubB*, *mat1-1-1* and *mat1-2-1*, was used to screen 1203 *V. effusa* isolates collected from 13 pecan populations across the southeastern USA. The sampling protocol represented region, orchard, tree and leaflet so the mating type structure at different spatial scales could be assessed. Analysis of this collection revealed the frequency of the mating type idiomorphs is in a 1:1 equilibrium of *MAT1-1:MAT1-2*. In vitro paired matings resulted in the formation of pseudothecia only between isolates of the opposite mating types indicating that *V. effusa* is heterothallic. Identification of the sexual stage in nature will provide improved understanding of the disease epidemiology, pathogen population genetics, and potentially provide insight into novel approaches to manage this disease.

WED 16

The functional diversity of stilbene catabolism clusters in fungi

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Stilbenes, a diverse group of plant-derived aromatic compounds function in induced and constitutive plant defenses against fungi. Recently, gene clusters (GCs) putatively specialized for degradation of stilbenes were identified in phytopathogenic and saprotrophic fungi. We hypothesized that differential composition of GCs is driven by metabolic steps required to degrade the predominant stilbenoids present in different hosts and stages of colonization. To test this hypothesis, we first used stilbene cleavage enzyme [ligno]stilbene 1,2 dioxygenase (SDO) genes as query loci, to detect a large number of diverse stilbene catabolism clusters (SCCs) across a 550-fungal genome database. We then selected 5 SDOs from SCCs of diverse composition for characterization of substrate specificity. Each SDO was heterologously expressed, and cleavage on a panel of stilbenoids by cell-free crude lysate was assessed. Four SDOs cleaved resveratrol and pterostilbene, while 3 cleaved piceatannol and piceid, all of which have a 4`-OH group required for substrate specificity. Interestingly, two SDOs from SCCs with alternate composition identified in milk and dung saprotrophs cleaved isoeugenol, suggesting possible role in lignin degradation. A fifth SDO, from a distinct locus in *Magnaporthe oryzae* was found to cleave trans-β-Apo-8′-carotenal, unlike closely related sequences that are characterized as resveratrol cleavage oxygenase1. An SCC from *Magnaporthe oryzae* was more thoroughly characterized for co-expression and enzymatic activity of three additional clustered genes required for utilization of stilbenoids as carbon source. Heterologous expression of these novel catabolic GCs will allow us to investigate the role of metabolic stress as a driver of gene clustering in fungi.

WED 17

Diversity and community structure of Ectomycorrhizal fungi associated with *Pinus roxburghii* and *P. wallichiana* across the western Himalayan forests of Pakistan.

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Diversity of ECM fungi was investigated both aboveground and belowground associated with *Pinus roxburghii* and *P. wallichiana* growing in pure stands situated in western Himalayan region of Pakistan. We used direct sequencing of Internal Transcribed Spacer region (ITS) of nrDNA for the identification of sporocarps and ECM root tips. We have collected and sequenced 50 sporocarps and 56 operational taxonomic units. The dominant above-ground fungi identified were *Russula* species in association with *Pinus roxburghii* followed by species of *Astraeus* and *Inocybe*. *Inocybe* was the dominant genus associated with *P. wallichiana* followed by species of *Russula* and *Lactarius*. Though there were several ECM genera shared between the two hosts, *Cortinarius* species were exclusively found in association with *P. wallichiana*. Amongst the Operational Taxonomic Units (OTUs), members of the lineage /russula-lactarius were found dominant in association with both host trees. The following are commonly associated below-ground ECM genera with both *Pinus* species: *Amphinema, Inocybe, Lactarius, Russula, Sebacina* and *Tomentella*. In addition to these common taxa, *Cenococcum, Helvellosebacina* and *Gymnomyces* species were specifically found in association with *P. roxburghii* and *Suillus* and *Tuber* species were identified exclusively in association with *P. wallichiana*. Percent of taxa calculated from representative taxonomic groups in the above- and below-ground survies indicate that members of Inocybaceae were dominant aboveground but members of Russulaceae were abundant belowground. The diversity patterns and fungal species composition identified for both host trees suggests that in addition to spatial factors, host species also plays important role in structuring the ECM fungal community.

WED 18

Historical collections in modern perspective: a case study in *Pluteus* (Agaricales, Basidiomycota)

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The taxonomic interpretation of fungal names described around the first half of the 20th century remains a critical problem in moving forward towards a North American Mycoflora. We will present an overview of the 46 species of *Pluteus* described by William Alphonso Murrill from North America and the Caribbean, between 1911 and 1945. The status of 17 of these species has been already evaluated in recent taxonomic studies, using a combination of morphological studies of type/original collections, lecto-, epi- or neotypifications, and molecular phylogenies. We revised the type collections of the remaining 29 species of *Pluteus* described by Murrill and, based on our findings, these are their taxonomic affinities: 2 belong in *Pluteus* section *Pluteus*; 10 in section *Hispidoderma* (6 in the *P. plautus* complex and 4 in the *P. leoninus* complex); 12 in section *Celluloderma* (9 in the species complexes around *P. ephebeus* and *P. hispidulus* and 3 of uncertain placement within the section). Five of the species described by Murrill are better considered doubtful names, as they likely represent species outside *Pluteus* and/or not enough data are available to elucidate their taxonomic placement. We will discuss how to best apply the existing names to the clades recovered in the molecular phylogenies of the genus.

WED 19

Distinguishing the Many "Faces" of *'G. lucidum'* in the Eastern United States: a challenging taxonomic task

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Ganoderma is a large and diverse, globally-distributed genus of basidiomycete wood decay fungi that includes species that cause white rot on a variety of tree species. In addition, practitioners of Eastern traditional medicine have prescribed the use of laccate (varnished or polished) *Ganoderma* species, commonly referred to as "reishi" or "lingzhi," as a preventative anti-inflammatory or immune enhancing treatment. The taxonomy of the laccate *Ganoderma* species is confusing, but we are elucidating evolutionary relationships among taxa via molecular phylogenetic studies. For the past century, many studies of *Ganoderma* have used the name *'G. lucidum'* for any laccate *Ganoderma* species growing on hardwood trees. Similarly, commercially available grow your own "reishi" kits and vitamin supplements produced and marketed as traditional medicine in the United States are sold under the species label *'G. lucidum.*' Molecular studies have established that *G. lucidum sensu stricto* (Curtis) Karst is not native to North America. Our surveys of *Ganoderma* species collected in the Eastern United States have revealed 10 putative native taxa, including: *G. curtisii* (Berk.) Murrill, *G. martinicense* Welti & Court., *G. meredithiae* Adask. & Gilb., *G. ravenelii* Steyaert, *G. sessile* Murrill, *G. tsugae* Murrill, *G. tuberculosum* Murrill, *G. weberianum* (Bres. & Henn.) Steyaert, *G. zonatum* Murrill, and *Tomophagus colossus* (Fr.) Murrill (syn. *G. colossus*). Many of these taxa infect trees and cause root and butt rot. Functional differences (pathogenicity, decay potential, host specificity, etc.) exist among the native North American *Ganoderma* species. Results from investigations to elucidate these differences will be presented.

WED 20

The Diversity of Russulaceae in Korea and fruiting pattern changes associated with climate change

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Russulaceae species are ectomycorrhizal symbionts of plants and play a crucial role in maintaining the biodiversity of forests. Currently there are approximately 1,800 reported species belonging to four genera of Russulaceae worldwide with 112 reported species in three genera in Korea. But significant morphological variation and difficulty in culturing Russulaceae species present serious challenges for accurate classification and identification at the species level. We compared direct sequencing data from fruiting bodies and metabarcoding data from environmental samples. In this study, we used 2,369 samples 35 years and 162 soil samples countrywide during two years for 454-pyrosequencing. When considering OTUs identified at the species level, total 231 OTUs belonging to four genera occurred in fruiting bodies and soil samples. 124 OTUs were found only from specimens while only 33 OTUs were found from soil metabarcoding data. Compared to Korean species, only 31 species were matched. Surprisingly, 26 species were unrecorded species and 141 species were potential new species. Furthermore, three new species within the genus *Multifurca* were discovered in Korea. By thorough analyses of data collection we aim to establish quantitative relationships between climate change and fruiting time in Korea. An analysis of the trends by genus level showed that the fruiting period of *Lactarius* was delayed, *Lactifluus* was accelerated, and *Russula* remained stable. Based on this research, follow-up studies of new species and unrecorded species in Korea will illuminate the current diversity and changing trends of Korean Russulaceae.

WED 21

Taxonomic and genetic diversity are higher than expected in North American species of *Hydnum* (Cantharellales)

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Hydnum is a genus of ectomycorrhizal fungi comprising five morphological species in North America that is harvested and sold in markets worldwide. Commonly known as “hedgehog mushrooms”, they are closely related to another popular wild edible group, the chanterelle mushrooms. Despite this, *Hydnum* has not been closely studied in North America for over 50 years. However, our data indicate the genus is more taxonomically and genetically diverse than anticipated based on morphology alone. We constructed a *Hydnum* phylogeny based on combined ITS and tef1 nucleotide sequences, which reveals 20 clades in North America, 16 of which appear to be endemic. Two of the three species of *Hydnum* originally described from North America, *H. umbilicatum* and *H. albidum*, show higher than expected genetic diversity with cryptic speciation. Type studies and models to test species delimitation will allow for taxonomic revisions of these groups.

WED 22

Distribution of macrofungi and evidence for endemism of species in the Pacific Northwest

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In this study we explore overlap in geographical distribution between macrofungi common in the Pacific Northwest and elsewhere using ITS barcode sequences. This research takes advantage of the more than 1500 new specimens deposited in the UBC Beaty Herbarium since 2010. In our analyses we used 2952 ITS sequences. Over the past year, we sequenced the ribosomal DNA ITS region for 630 UBC specimens and we analyzed these together with ITS data from previous studies on UBC and WTU herbarium specimens. We used clustering software (mothur) and automatic barcode gap discovery (ABGD) to group the barcodes into species hypotheses. We then compared our sequences to available sequences on GenBank and UNITE public databases. UNITE kindly supplied data on specimen geographical origin. We then asked what proportion of the species found in the Pacific Northwest are shared with other parts of the world. For *Inocybe*, *Cortinarius* and *Russula*, 50% or more species hypotheses have only been sampled from the Pacific Northwest. Our analysis documents frequent misapplication of European names to American species and for example, the species commonly called *Amanita pantherina* and *Lactarius deliciosus* in the Pacific Northwest were not conspecific with the taxa originally described in Europe. Proving that any fungi are regional endemics will require improved sampling from around the world. However, we have shown that systematic DNA barcoding of herbarium specimens can improve our understanding of regional diversity and lead to testable predictions about endemism.

WED 23

Molecular phylogenetics coupled with morphological assessment of some mushroom forming fungi of the temperate habitats of Swat Valley

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Swat valley is the floristically rich mountain ecosystem of the eastern Hindu Kush series of Pakistan that is sometimes referred to as Swat Himalayas. The valley provides enormous opportunities by socioeconomic development through multiple uses of the biodiversity found there. The ecosystem services provided are also important. District Swat lies adjacent to the intersection of the world-famous mountain ranges viz. Himalaya, Hindu Kush and Karakoram, which support diverse forest types. We report the first comprehensive account of basidiomycota of the area, particularly the mushroom forming fungi. These were studied morphologically and molecularly. Many interesting taxa are reported by applying; 1) Phylogenetic analyses based on nrDNA ITS sequences, 2) Scanning Electron Microscopy (SEM), and 3) morphological assessment. Phylogenetic reconstruction resolved the taxonomic placement of many questionable taxa. SEM provided a more in-depth insight into the form and extent of spore ornamentation. Ectomycorrhizal fungi such as those in the Russulaceae (*Russula sichuanensis*), Inocybaceae (*Inocybe rimosa*), Amanitaceae (*Amanita flavipes*) and Hymenogastraceae (*Hebeloma theobrominum*) were described in this study.

WED 24

Bottoms Up! A distributed approach to assembling a North American Mycoflora

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Since the 2012 meeting at Yale, much progress has been made in assembling a North American Mycoflora. However, almost none of this progress took the form discussed at that meeting. The Santa Cruz County Mycoflora Project takes a bottom-up, distributed approach to this task. Although there are many inherently challenging aspects of such an endeavor, our method has proved to be nimble, portable, and robust. Lessons learned, mistakes made, and directions for future growth will be discussed; and a brief summary of some of our more fascinating discoveries will be presented.

WED 25

Growth yield and nutritional quality of two oyster mushrooms (*Pleurotus pulmonarius* and *P. ostreatus*)on different substrates supplemented with wheat bran

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Owing to their nutritional and health benefits, the cultivation of *Pleurotus* species continues to receive global attention .This study aims at evaluating the growth, yield and nutritional quality of *Pleurotus pulmonarius* and *P. ostreatus*. Ten grams each of *Pleurotus* species were separately cultivated on 400g sugarcane bagasse and cotton waste, supplemented with wheat bran (0%, 5% 10% 15% 20% w/w) in triplicates and incubated at 28± 2^0C for 35 days. Data were analyzed using ANOVA. *P. ostreatus* cultivated on sugarcane bagasse with 15% wheat bran additives had the highest stipe length stipe and pileus width. Also *P. pulmonarius* had the widest stipe and highest dry matter on cotton waste with 10% wheat bran at flush 2, while *P. ostreatus* had the longest stipe on cotton waste with 10% wheat bran at flush 3. Highest Total biological efficiency for *P. ostreatus* was shown at 15% wheat bran grown on sugar bagasse. The protein contents ranged from 26.60-30.46%. Highest carbohydrate contents were recorded in *P. pulmonarius* and *P. ostreatus* grown on sugarcane bagasse and cotton waste respectively with 10% additive. Generally *P. pulmonarius* cultivated on sugarcane bagasse with wheat bran additives, irrespective of their percentage concentration had better mushroom quality, yields, and biological efficiency, mineral and proximate compositions than *P. ostreatus*. This study will guide mushroom farmers in selecting mushroom species, substrates and supplements for best harvests

WED 26

Mitigating losses: H3K36me3 plays a compensatory role in heterochromatin-deficient mutants of *Neurospora crassa*

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DNA-based processes in eukaryotes are controlled by chromatin modifications that vary in type and location. These modifications regulate transcriptional activity by establishing different types of chromatin domains: transcriptionally silent heterochromatin and transcriptionally active euchromatin. Trimethylation of lysine 36 on histone H3 (H3K36me3) is a repressive chromatin mark that is traditionally associated with transcriptionally active genes. H3K36me3 maintains transcriptional fidelity and prevents large-scale chromatin remodeling in the wake of transcription. We have found that in the filamentous ascomycete *Neurospora crassa*, H3K36me3 plays a compensatory role when silent heterochromatin is lost. This suggests that H3K36me3 plays an additional role in maintaining chromatin stability beyond its previously defined function during transcription, and I will summarize these findings and their larger impacts on chromatin structure and function.

WED 27

FungiDB: An integrated functional genomics database for fungi and oomycetes

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FungiDB (www.fungidb.org) belongs to the family of EuPathDB resources and it is a free online resource for data-mining and functional genomics analysis. FungiDB integrates diverse datasets and provides easy to use tools to mine the underlying datasets or carry out custom dataset analysis in the EuPathDB Galaxy instance. In FungiDB you can explore genomes, annotation, functional data (transcriptomics or proteomics), metabolic pathways and results from genome wide analyses (ie. InterPro scan, transmembrane domain predictions, orthology, etc..). FungiDB contains an expanding number of genomes from oomycetes and fungi, with the latter including genomes of Agaricomycetes, Chytridiomycetes, Eurotiomycetes, Leotiomycetes, Pneumocystidomycetes, Pucciniomycetes, Saccharomycetes, Schizosaccharomycetes, Sordariomycetes, Tremellomycetes, Ustilaginomycetes, and Zygomycetes. The graphical user interface in FungiDB allows users to conduct in silico experiments that leverage the available data. For example, a search in FungiDB can identify all genes in Ustilago maydis that have orthologs in other species and have a predicted signal peptide. FungiDB also supports community-driven genome improvement projects. Images, PubMed records, phenotypes, and other records can be easily added as user comments. User comments become immediately visible to others and are searchable via the text search option. FungiDB users can also privately analyze their own data via the EuPathDB Galaxy instance where all genomes are already preloaded. Results can be easily exported to FungiDB GBrowse via linking out directly from the Galaxy instance. For questions and suggestions email us at help@fungidb.org. Author presents on behalf of the EuPathDB team. FungiDB is supported by NIH HHSN272201400030C and the Welcome Trust grant WT108443MA

WED 28

A rice and maize N-acetylglucosamine transporter essential for early communication and establishment in arbuscular mycorrhizal symbioses

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During Arbuscular Mycorrhiza (AM) symbiosis, the roots of plants and Glomeromycotan fungi engage in a tightly regulated liaison for their mutual benefit. Vital to the association is the initial recognition of both symbionts, mediated primarily by diffusible signals released into the rhizosphere. Previously, we identified the maize no perception 1 (nope1) mutant to be defective in early signaling during arbuscular mycorrhizal symbiosis. Here, we report cloning of ZmNOPE1 on the basis of synteny with rice. NOPE1 encodes a functional homolog of the Candida albicans N-acetylglucosamine (GlcNAc) transporter NGT1, and represents the first plasma membrane GlcNAc transporter identified from plants. In the fungus *Candida albicans*, exposure to GlcNAc activates cell signaling and virulence. Similarly, exposure of the arbuscular mycorrhizal fungus, Rhizophagus irregularis, to wild type rice but not to nope1 mutant root exudates induced transcriptome changes associated with signaling function, suggesting a requirement of NOPE1 function for presymbiotic fungal reprogramming.

WED 29

Comparative genomics reveals that swainsonine is produced by plant symbionts and pathogens of plants, insects and mammals.

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Swainsonine is produced by seed-transmitted symbionts belonging to two orders (Pleosporales and Chaetothyriales), the clover black-patch pathogen, *Slafractonia leguminicola* (Pleosporales), and the plant-symbiotic insect pathogen, *Metarhizium robertsii* (Hypocreales). The alkaloid is derived from pipecolic acid (a proline analog) and mevalonic acid, so we hypothesized involvement of a multifunctional ketide synthase that includes an amino acid adenylylation domain. We conducted genome sequencing and comparative genomic analysis to identify ketide synthase genes that were likely orthologs in known swainsonine-producing fungi. One such gene, *swnK*, was knocked out in *M. robertsii* to give a swainsonine-nonproducing phenotype, then complemented to restore alkaloid production, confirming its role as a swainsonine biosynthesis gene. Clustered with *swnK* were two hydroxylase genes (*swnH*1 and *swnH*2) and two reductase genes (*swnN* and *swnR*) that also appeared to be orthologous between the sequenced genomes. Homology searching revealed orthologous gene clusters in nearly all sequenced *Metarhizium* species, as well as all sequenced members of the Arthrodermataceae (Onygenales). The Arthrodermataceae cause ringworm, athelete's foot, and other skin infections in mammals, including humans, and swainsonine production was confirmed for representatives of almost all sequenced species in that family. These results extended the taxonomic range of swainsonine production in the Pezizomycotina (filamentous Ascomycota), suggested a revised hypothesis for swainsonine biosynthesis, and raised the question whether swainsonine plays roles in pathogenicity to plants, insects, and mammals.

WED 30

Unraveling immunity of early diverging fungi using a microbial bully

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Imaging, culturing, and sequence based approaches have enabled a detailed examination of all members of microbial communities in plant roots, mammalian guts, and even cheese rinds. The balance between neutral and antagonistic interactions may be mediated by the physical structure of chitin and glucan cell walls but may also be controlled by fungal innate immunity. In particular, aseptate filamentous fungi who lack compartmentalized hyphae may have an advantage to actively avoid bacterial infection since once inside a hyphae there may be little means to partition or apototically remove an infected portion of a mycelium. However, little is known about fungal innate immune defenses. Plant immunity has benefited from studies of defense responses elicited by antagonistic bacteria. We have sought to apply the same approach studying the interactions of antagonistic bacteria *Serratia marcescens* (Sm) with a collection of fungi. In particular we have experimentally compared Mucoromycota, Zoopagomycota, and Dikarya fungi responses to challenges of Sm colonization and found a range of behaviors from susceptible to resistant species. In addition, we have observed growth inhibition of these fungi due to the presence of Sm Comparisons of different strains of Sm bacteria also demonstrates a variety of fungal virulence capabilities. Interestingly, production of prodigiosin (widely considered a general antifungal) seems to have little impact on inhibiting early diverging fungi. Genome sequencing of the fungi and Sm bacteria have allowed us to compare the gene content of these strains and suggest potential genetic differences that may contribute to variation in fungal-bacterial interactions.

WED 31

Analysis of the twelfth chromosome of a representative set of species within the *Fusarium fujikuroi* species complex

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Members of the *Fusarium fujikuroi* species complex (FFSC) possess a haploid chromosome number of twelve. The smallest of these is dispensable, displays chromosome length polymorphism and has low sequence conservation. This has led to the hypothesis that it forms part of the so-called accessory genome and that it may encode unique genes involved in niche adaptation to specific environments. The sequences for chromosome 12 from *F. fujikuroi* and *F. temperatum* were used to assemble the corresponding chromosome in three other species (*F. circinatum*, *F. subglutinans* and *F. nygamai*) using sequence and genic similarity approaches. Among the fungi examined, *F. temperatum* had the largest chromosome 12 and *F. fujikuroi* the smallest, being 30% smaller than that of *F. temperatum*. In comparison to the rest of the genome, the gene density on this chromosome was always lower. However, only thirteen of the predicted genes appeared to be shared between the species investigated. Of interest were several carbohydrate active enzymes detected on each chromosome 12 examined, as well as a secondary metabolite cluster in each of *F. temperatum*, *F. subglutinans* and *F. nygamai*. Phylogenetic analyses further showed that the genes of chromosome 12 had diverse and non-orthologous origins, with only a small proportion sharing an evolutionary trajectory similar to those of the species harbouring them. This study has provided valuable information on the flexible nature of this dispensable chromosome and an indication of the biological properties this chromosome potentially confers to the species harbouring it.

WED 32

Rhizoids point the way: Structure and function of actin during morphogenesis in *Chytriomyces hyalinus* (Chytridiomycota) provide insight into the evolution of filamentous growth across fungi.

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Filamentous growth is so crucial to the fungal way of life that it arose multiple times independently in the Fungi. However, the vast majority of Chytridiomycota lack hyphae. Instead, they evolved anucleate rhizoids that anchor reproductive sporangia to their substrates and absorb nutrients. We sought to elucidate the cellular machinery underpinning the evolution of hypha-like growth forms by investigating the structure and function of actin during morphogenesis in *Chytriomyces hyalinus*. Our study is the first to directly examine actin function within Chytridiomycota. In hyphae, actin plaques involved in maintaining cell polarity are highly concentrated in a collar just below the hyphal apex. Therefore, we predicted that actin plaques would be concentrated near the apices of actively growing rhizoids. Furthermore, because actin is required for hyphal growth, we hypothesized that disruption with the actin inhibitor, latrunculin B (latB), would decrease rhizoid and sporangium growth rates. Using fluorescence microscopy, we observed actin stained with rhodamine phalloidin at different stages of thallus maturation in *C. hyalinus*. We then incubated *C. hyalinus* with latB to determine the roles of actin in morphogenesis. Consistent with our predictions, we found actin plaques concentrated at the tips of growing rhizoids. Thalli treated with 0.2 and 0.5 µg/mL latB were smaller and had shorter rhizoids, with fewer branches, than controls. Thus, actin is critical for filamentous growth in hyphae and rhizoids, leading us to infer that ancient fungi, both hyphal and non-hyphal, used actin to create filamentous structures for substrate colonization and nutrient acquisition.

WED 33

Viral hijacking and evolution of the fungal cell cycle control network: the animal-fungal hybrid network of the zoosporic fungus *Spizellomyces*.

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Cells have been dividing in an uninterrupted chain for billions of years. As such the cell cycle control network is arguably one of the most conserved within Eukaryotes. This conservation extends beyond network components to system-level properties which were elucidated in animals and yeasts. The G1/S regulatory network in animals and yeasts is conserved, even though its core transcription factors E2F (animal) and SBF (yeast) do not have a shared molecular ancestor. Using phylogenetic analysis, we showed that the last eukaryotic common ancestor already had G1 regulators similar to animals. In contrast, evolution along the fungal lineage was punctuated by the acquisition and entrainment of the SBF transcription factor, likely of viral origin. We propose that SBF hijacked cell cycle control by activating genes targeted by the ancestral cell cycle regulator E2F. Thus, cell cycle evolution in fungi proceeded through a hybrid network containing both E2F and SBF, which is still maintained in many zoosporic and pre-Dikarya fungi. Consistent with this hypothesis, we show that SBF can regulate promoters with E2F binding sites in budding yeast. More recently, we measured in vivo accessible chromatin and TF footprints associated with proximal cis-regulatory elements using MNase-seq. These predictions are being combined with DNA-binding specificity measured with universal protein binding microarrays of Spizellomyces E2F and SBF to gain insights into the potential regulon of these TFs. The hybrid cell-cycle network in Spizellomyces provides an opportunity to elucidate how fundamental networks that control cellular decisions are rewired through evolutionary time.

WED 34

The Metagenomes of *Endogone* (Mucoromycota) Sporocarps

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Endogone is a genus of Mucoromycota that forms truffle-like sporocarps and includes ectomycorrhizal (ECM) and presumably saprobic species. The ability to form sporocarps and ECM represents independent origins of these traits relative to Dikarya. Species of the genus are also known to associate with primitive land plants and are hypothesized to be some of the first plant-fungal symbioses in terrestrial ecosystems. As such, *Endogone* plays an important role in our understanding of the evolution of multicellularity and plant-fungus associations in Kindgom Fungi. We performed shotgun sequencing of three *Endogone* species from sporocarps collected in four different locations; these included three ECM isolates, *E. lactiflua* Oregon, *E. flammicorona* Michigan and Italy, and one saprobe, *E. pisiformis* Florida. We explored the genome data for contaminants, symbionts and parasites by using a combination of binning methods based on blast, nucleotide-composition, and GC-coverage plot. We identified large number of sequences from Mollicutes-related endobacteria (MRE), which are known from *Endogone*. Genome assemblies of the MREs produced reduced genomes of about 1 Mb. In contrast, *Endogone* has large genomes (~100 -200 Mb), mainly due to the expansion of repetitive elements, which make up ~ 60-70% of the genomes. Genome-scale phylogenetic analyses support the monophyly of the genus and relaxed clock dating methods are consistent with it being younger than Glomeromycotina. Phylogenomic analyses show that *Endogone* species have reduced diversity of Carbohydrate-Active Enzyme (CAZyme) modules. This is consistent with the CAZy diversity for ECM fungi from Dikarya and questions the saprobic designation of *Endogone pisiformis*.

WED 35

Data dumpster diving in the fungal -omics era

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The generation of countless genomes, including nearly 1,000 from fungi, has facilitated much recent advancement in biological research. Projects such as whole genome sequencing, amplicon sequencing, metagenomics and metatranscriptomics yield massive raw data sets of which large portions are discarded. Rather than just be thrown away, these data can be curated and analyzed to enable key novel biological inferences. In this talk, I will discuss methods for assembling and annotating microbial genomes from mixed starting DNA, and for evaluating relative microbial abundance from raw meta-genome sequence data. I will also present approaches to infer copy number for repetitive genomic regions, strategies for assembling polyallelic genomic regions, and novel insights of integrating -omics data sets with wet lab experiments. Potential implications of these insights and predictions based on pilot studies will be discussed.

WED 36

Coevolutionary patterns in ambrosia fungi and beetles revealed from a global survey

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The ambrosia symbiosis is characterized by fungus-farming, a habit that independently evolved at least eleven times within beetles. In the past ten years, ambrosia fungi and their beetle vectors have emerged as damaging plant pathogens. Laurel Wilt, a disease caused by the ambrosia fungus *Raffaelea lauricola*, has been decimating Lauraceous trees in the southeastern United States since it was introduced from Asia in 2002. Although the ambrosia symbiosis contains important invasive and plant-pathogenic species, the symbiosis remains poorly characterized largely due to their impressive diversity. Of more than 3,400 beetle species, fungal symbionts have only been identified from less than a percent of known beetle species. We collected beetle samples across 16 countries and characterized their fungal communities from 10/11 origins of the symbiosis among Scolytine beetles. Fungi were identified using mycangium histology, culturing, and community metabarcoding. Obligate symbionts were inferred based on read abundance from community sequencing, CFU abundance in culturing availability, and presence across all sampled specimens. Several new species and origins of the ambrosia symbiosis are proposed among fungi. Patterns coevolution and symbiont specificity are proposed for each beetle and fungus clade included in the study. These results will help prevent tree disease epidemics by informing government agencies which beetles are capable of carrying plant pathogens, and which may carry previously unknown pathogens.

WED 37

Origin of cave fungi as revealed by biodiversity assay and divergent time analyses

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Karst caves are distinctly characterised by darkness, low temperature, high humidity, and scarcity of organic matter. A number of troglobiont animals had been discovered with their evolution and speciation well investigated. However the biodiversity, origin and evolution of cave fungi remained largely unknown. During years of 2014-2015, we explored the mycobiota in two unnamed Karst caves in Guizhou province, China, and obtained 563 fungal strains. Preliminary ITS analyses of these strains suggested that they belonged to 246 species in 116 genera, including 20 new species, which accounted for 63% of the total number of new fungal species ever described from caves. Although a number of fungi have been recorded from caves, most of which have been previously known from external environments. Whether caves encompass obligate troglobitic fungi is widely debated. In this study, we further inferred the divergence times of these new species, and compared to the cave formation geologic age. The fossil-calibrated molecular clock analysis showed that the divergence time of these suspected troglobitic fungi are between late Miocene (7.2 My for *Metapochonia variabilis*) and late Jurassic (158 My for *Gymnoascus exasperates*). While based on the historical geological movement and the paleoclimate of Guizhou, it was estimated that the development of investigated caves were later than Pliocene period (2.5-5.3 My), similar to other caves worldwide. Our data presented here strongly suggested that new species described from cave are unlikely troglobitic fungi but travelers from other environments. The geographic history of cave appeared to be too short for fungal speciation.

WED 38

Marasas' et al. 1984 toxigenic *Fusarium* Species: Identity and Mycotoxicology revisted

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Fusarium ranks one of the world's most economically destructive and taxonomically challenging genera of mycotoxigenic plant pathogens. This is reflected, in part, by the numerous efforts to catalog its taxonomic diversity and mycotoxin potential over the past half century. Given the significant threat that fusarial toxins pose to agricultural biosecurity, food safety, and plant and animal health, several compendia have attempted to catalog the diversity of toxigenic fusaria and the toxins they produce. Marasas, Nelson & Toussoun's 1984 compendium "Toxigenic *Fusarium* Species: Identity and Mycotoxicology" occupies a special place in the *Fusarium* mycotoxicology literature because the authors tested a number of the strains in this treatise for toxins, and because all of the strains are archived in the South African Agricultural Research Council (ARC; formerly Medical Research Council - MRC) and Fusarium Research Center (FRC) Culture Collections. Given the transformative impact genealogical concordance phylogenetic species recognition (GCPSR)-based studies have had on Fusarium systematics over the past two decades, the present study was initiated to: (i) reassess species identity and phylogenetic diversity of 145 MRC strains via GCPSR, (ii) predict mycotoxin potential of any putatively novel Fusarium species discovered within the MRC collection by mining their whole genomes for biosynthetic pathways that encode mycotoxins, and (iii) test the MRC strains for mycotoxin production in liquid media and/or solid grain cultures using gas chromatography-mass spectrometry and high performance liquid chromatography-mass spectrometry.

WED 39

Genomics of the orchid mycorrhizal symbiosis

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Fungi interact with plants in myriad different ways. One category of interactions, termed mycorrhizal associations, includes fungi that live in the roots of plants and contribute to an "exchange" of nutrients. One such relationship is that between Orchidaceae and fungi in three genera in Agaricomycotina (*Tulasnella* and *Ceratobasidium* in Cantharellales and *Serendipita* in Sebacinales). Orchid seeds rely on carbon resources delivered by the fungus to promote germination and growth. It is unclear if the fungi receive any benefit at this stage in the life cycle. The goal of my PhD is to use genomics approaches to better understand this unique symbiosis. To accomplish this goal, I have a Community Sequencing Project through the Joint Genome Institute to better understand the genomes of various orchid mycorrhizal fungi, their evolutionary relationships to each other, and what genes are expressed solely in the symbiosis. To do this, we are sequencing whole genomes of 15 fungi, shallowly sequencing up to 400 fungal isolates to perform phylogenetic analysis, and performing RNAseq on orchid protocorms (protoseedling structures) infected with mycorrhizal fungi. These various approaches will inform each other and generate hypotheses about the functionality of this unique symbiosis.

WED 40

Phylogenetic relationships of alpha-amanitin producing *Galerina* from British Columbia

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Mushrooms of some species of *Galerina* species equal the most poisonous *Amanita* species in their concentrations of deadly amanitin toxins. Although individual *Galerina* mushrooms are small, eating about 10 would risk delivering a lethal dose of amanitins to a child. Our aims in this research are to combine phylogenetic and biochemical data to establish the identity of toxic members of the difficult and species rich *Galerina* genus. Although it has been suggested that all toxin-producing species form a monophyletic sub-division of *Galerina*, our study will be the first to test this hypothesis. Our results to date illustrate deep problems with species identification in western N. America that need to be resolved before toxin distribution can be understood. Maximum likelihood analysis of ~200 ITS sequences from UBC's herbarium has revealed that *Galerina* specimens deposited under the same name, from the same collector, frequently grouped within different clades. To improve the accuracy of name application within *Galerina* we borrowed and are sequencing the ITS regions from 36 type specimens from A. Smith (MICH). With sequences from additional loci (RPB2, EF-1α and LSU) we will create a multi-locus phylogeny to clarify relationships among clades. Finally, in collaboration with J. Walton, we will perform HPLC/GC-MS analyses of sequenced herbarium material to determine the presence/absence of toxins in these specimens. By mapping the toxin data to the multi-locus phylogeny, we hope to better understand the evolution of amanitin toxins within *Galerina*.

WED 41

Phylogeny of the genus *Crossopsora* (Phakopsoraceae): a first approach.

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The family Phakopsoraceae Cummins & Hirats since 2003 accommodates 12 genera. Among them the tropical genus *Crossopsora* (type species: *C. ziziphi*), established in 1919 with over 20 species presently known. All *Crossopsora* species show columnar telia morphologically similar to those of *Cronartium* species (Cronartiaceae), a genus present in temperate and cold regions. Besides that, different from *Cronartium*, the *Crossopsora* telia are typically originated from old uredinia, and shows basal paraphyses. The uredinia have strong peripheral paraphyses, instead of a pucciniastraceous peridum as present in *Cronartium* species. On the other hand, species belonging in the type-genus *Phakopsora* of the Phakopsoraceae always show immerse sub-epidermal telia showing teliospores disposed in several layers, with *Crossopsora* species well characterized by typically columnar telia. GenBank lacks any Crossopsora DNA sequence, and contains DNA data only for four out of the 12 genera of the Phakopsoraceae. Thus, we run a phylogenetic analysis using LSU and SSU sequences of rDNA of *Crossopsora* species together with DNA sequences available for phakopsoraceous species and other relevant genera. The phylogenetic trees were inferred from Bayesian and Maximum Likelihood analyses. The results showed the three *Crossopsora* species, located in a well-supported clade, clearly segregated from those clades occupied by the Phakopsoraceae and the Cronartiaceae. The analyses clearly characterized the genus *Crossopsora* and suggest future work that may lead to its accommodation in a new family.

WED 42

Imaging and identifying adventitious fungal root associates in canopy soils of old-growth *Acer macrophyllum* trees, located in the Olympic National Park

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The old-growth temperate rainforests of Western Washington are known for their old-growth forests and unique ecosystem processes, including extreme seasonal rainfall regimes. Over time, epiphytic mats form on the branches, and the bottom layer of these mats decompose, forming canopy soil. Some of the old-growth tree species have adapted to the presence of canopy soils by growing adventitious roots into this organic soil horizon. Preliminary DNA and morphological analyses suggest that these canopy roots have adapted to form a diversity of fungal root associates that differ from those found in the forest floor rooting networks. Currently, there is suggestive evidence that adventitious root-tips in canopy soils have formed a fungal mantle, what appears to be a Hartig-net, and also intracellular coils. Preliminary DNA results also return species never reported to associate with *Acer macrophyllum*. We report dark septate endophytes, species that have been reported mycorrhizal with ericoids, and others that have mycorrhizal affinities. Also, several unidentified ectomycorrhizal sequences were returned during preliminary Sanger sequencing. Since the *Acer* genus, including *A. macrophyllum* predominantly associate with glomeromycetes, further imaging and sequencing analyses is being pursued. Currently, we are implementing a protocol for high-throughput fungal community analysis using Oxford's MinIon Nanopore Sequencer, while clearing and staining root-tips for confocal fluorescent microcopy. Confocal scanned images and the first results from high-throughput community analysis using MinIon Nanopore Technology will be reported.

WED 43

Fungal communities as carbon conductors: fungi and the fate of carbon in soils

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The proportion of photosynthetically fixed carbon which is stored in soils over long time periods, and not returned to the atmosphere via respiration, is a significant moderator of atmospheric carbon levels and global climate. The balance between soil carbon storage and mineralization is mediated by micro-organisms, including fungi, which transform plant litter and exudates during decomposition. A relationship between carbon fate in soils and microbial community composition has been regularly postulated and indirectly implied but empirical evidence directly linking the two is lacking. We created decomposition microcosms to show that differences in the composition of naturally occurring microbial communities, in the absence of differences in substrate or environment, can influence carbon fate in soils. Inverse relationships between the quantities of $C0_2$ released to the atmosphere and dissolved organic carbon produced by the microbial communities were observed. This change in the ratio of carbon outputs demonstrated that differences in decomposition outcomes among different communities extend beyond differences in decomposition rates. High throughput sequencing confirmed that community composition was related to carbon outcomes. These results demonstrate that not all soil microbial communities are created equal in terms of soil carbon fates. In addition, we have demonstrated that the fate of carbon in litter already colonized by a microbial community can be altered by an introduced community. Accurately predicting carbon cycling requires an improved understanding of the relationship between microbial community composition and key decomposition functions, and the abiotic drivers of both of these.

WED 44

Characterizing the diversity of lignin-degrading fungi in a dry seasonal tropical forest

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Saprophytic fungi are drivers of litter decomposition and carbon (C) cycling due to their ability to rapidly decompose biopolymers (lignin, cellulose). The importance of saprophytic fungi in C-cycling processes raises the question of how these fungi, and subsequent C fluxes, could become increasingly vulnerable to changes in climate and precipitation. In this study, we used lignin traps to examine fungal degrader community dynamics, including roles of seasonality, in a seasonally dry tropical forest (TDF) in Mexico. Using high-throughput Illumina sequencing of the ITS region, we detected 465 fungal taxa, 100 of which were acknowledged lignin degraders and 38 ectomycorrhizal (ECM) taxa. Measures of diversity did not differ significantly between years and seasons. However, there was a high turnover in community composition from year-to-year because certain taxa were abundant during a single sampling year, e.g., *Microdiplodia* in 2013 and *Gymnopus* in 2015. In addition, unique fungal assemblages were also detected in dry- versus wet-seasons because certain fungi were restricted to the wet or dry season. ECM fungi also showed similar variations in abundances between seasons (Pezizales, dry) and years (Boletales, Pezizales; 2015). Both known lignin degraders and ECM are important in C cycling in TDF, and many of these fungi are known to possess genes encoding for peroxidases and/or laccases. In addition, some of these taxa are known to endure extremely negative soil water potentials. Thus, reductions in rainfall may result in degrader communities comprising primarily dry season fungi, which could influence litter decomposition and C cycling under a changing climate.

WED 45

Mercury content of lichens collected across Nova Scotia, Canada

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Mercury is a global pollutant present in a wide range of ecosystems. Atmospheric transport of elemental mercury gas allows long-range deposition. Quantifying mercury in biological indicator species such as lichens provides information about where mercury pollution may be an issue. Three hundred samples of *Hypogymnia* and *Usnea* lichens were collected from trees throughout mainland Nova Scotia, Canada. Samples were analyzed for total mercury using thermal degradation - atomic absorbance analysis. Selected specimens were also ITS DNA barcoded to confirm morphological identities. Mercury concentrations and sample geolocations were mapped using QGIS 2.12 and ArcGIS 10.4 to produce kernel density analysis hotspot maps. From these maps, areas of higher mercury concentrations and trends across Nova Scotia were detected. The presence of high lichen mercury concentrations in areas with known mercury problems such as Kejimkujik National Park suggests that lichens are useful indicators of regional atmospheric mercury trends.

WED 46

Field inoculations of pecan (*Carya illinoinensis*) seedlings with the edible, native, truffle *Tuber lyonii*

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Humans have tried for centuries to create consistently successful truffle orchards. With the recent aid of DNA sequencing methods, the mutualistic symbiotic relationship between certain fungi and the roots of compatible host trees (ectomycorrhizae) has become better understood and the practical application of this knowledge has spread to the commercial truffle industry. Our research focuses on the pecan (*Carya illinoinensis*) industry and the pecan truffle (*Tuber lyonii*). We document for the first time a successful method for establishing *T. lyonii* on pecan seedlings at two commercial and one experimental nursery in Georgia. We assess the impact of soil fumigation and varying concentrations of truffle inoculum on the ectomycorrhizal community and the downstream abundance of *T. lyonii*. To determine seedling fungal communities we performed ITS1 metagenomic sequencing using the Illumina MiSeq platform. Our inoculation methods were developed for the pecan truffle industry but could provide insight for large-scale cultivation of other gourmet, ectomycorrhizal fungi.

WED 47

Fungi in the wind: A decade-long study of the diversity of fungal spores captured while air sampling the upper atmosphere in Hawai'i

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Many fungi produce spores small enough to enter the upper atmosphere and disperse long distances via global air currents. An active air sampler system was placed above the cloud layer at the Mauna Loa Observatory on the island of Hawai'i, 3397 meters above sea level, and captured all particles smaller than 10 µm on borosilicate glass fiber filters for 13 years. We expected these filters to capture a variety of the small spores floating around the upper atmosphere. Using Illumina targeted amplicon sequencing of the fungal ribosomal internal transcribed spacer (ITS) region, we identified 160 operational taxonomic units (OTUs), representing 139 unique species, from 172 filter samples. Each air filter represents a snapshot of the aerobiota present in the upper atmosphere at the time of collection. The community richness of the filters was low, averaging 35 OTUs (SD = 7.36) on each filter, and showed no significant trends over seasons or the decade-long sampling effort. Similarly, the beta diversity between communities was low, with an average Bray-Curtis dissimilarity of 0.41 (SD = 0.08). Surprisingly, beta diversity showed no trend over the decade-long sampling effort, but we did find significantly increased dissimilarity between filters collected in the first quarter of the year (January, February, and March). Local weather and atmospheric variables were poorly correlated with community composition, however, climate variables from long distance source locations may better explain the community compositions of these potentially long distance dispersing fungi.

WED 48

Post-fire soil fungal communities and ecosystem function in boreal forests

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Fire is the dominant disturbance in boreal forests and climate change is causing increased wildfire activity in the North. Evidence shows this altered fire regime could lead to sustained changes in forest structure from coniferous- to deciduous-dominated systems. Little is known about concurrent changes in soil fungal communities, which can have species-specific effects on plant growth and decomposition, driving plant community structure and nutrient cycling. Heat-resistant fungi (HRF) may become increasingly important for ecosystem processes post-fire and as fires become more severe. However, their identities, abundance, or roles in boreal forests are unknown. A record 3.4Mha of boreal forest burned in wildfires in Canada's Northwest Territories in 2014. In 2015, we investigated post-fire soil fungal communities across a landscape of varying burn severities and forest types to test two hypotheses: (1) HRF are abundant

post-fire and have species-specific effects on seedling growth and litter decomposition; (2) Fire severity is a major driver of soil fungal community structure. Seven taxonomically unique HRF were cultured, which demonstrated critical roles impacting plant growth and decomposition that may impact post-fire forest structure and nutrient cycling, particularly for deciduous tree species. Illumina sequencing of total soil fungal taxa from 49 sites identified 4181 fungal operational taxonomic units (97% similarity, ITS1), including ectomycorrhizas. Microsite characteristics and fire were the main drivers of total soil fungal community composition. Results will be synthesised in the context of post-fire ecosystem function.

WED 49

Assessing the effects of bark and ambrosia beetle colonization: Exclosure experiment reveals a radical alteration of fungal community assembly and the reduced decay of forest biomass

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Bark and ambrosia beetles (Coleoptera: Curculionidae: Platypodinae and Scolytinae) colonize dead or dying trees and inoculate their galleries with the symbiotic fungi on which their progeny will feed. Globally, this phenomenon is consistently observed, but we have yet to elucidate the effects that these beetles have on the entire community of fungi that colonize decaying trees and what effects beetles and their fungi may have on the decay process. Therefore, we conducted a large-scale exclosure experiment to characterize and compare the composition of fungal communities in beetle-colonized and beetle-excluded loblolly pines (*Pinus taeda*) trees in a Southeastern US pine forest. We used quantitative fungal culturing techniques on selective and non-selective media, and rDNA barcode sequence identification (Large Ribosomal Subunit - LSU) to characterize fungal assemblages from experimental logs and dispersing beetles. Here, we reveal unprecedented complexity in the fungal symbioses of bark and ambrosia beetles as they manifest their impressive role in dramatically altering fungal communities. Beetle colonization increased fungal diversity and abundance, particularly among Ophiostomatales fungi, and the strength of these effects was correlated with ambrosia beetle density. Additionally, we uncovered a surprising relationship with wood decay, which decreased with increasing beetle colonization. Our results reveal the comprehensive effects of bark and ambrosia beetles on fungal community assembly and alter our perception of these ubiquitous beetles' natural roles in ecosystems worldwide.

WED 50

Evidence for climate as a driver of genetic divergence in native populations of the Douglas-fir Swiss Needle Cast Fungus *Phaeocryptopus gaeumannii*

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Swiss needle cast (SNC), a Douglas-fir foliage disease caused by *Phaeocryptopus gaeumannii* Rohde (Petrak), has become a serious forest health concern in western North America. Regional variation in the abundance of P. gaeumannii, and resulting disease, is strongly influenced by climate. Initial studies of the population genetics of *P. gaeumannii* revealed the presence of two sympatric lineages of this fungus and suggested that distributions of these cryptic lineages may also be related to SNC severity. This study aims to assess genetic variation along a disease gradient in the western Oregon and Washington Coast Ranges in relation to climate variables that might influence *P. gaeumannii* growth and reproduction. A non-metric multidimensional scaling (NMS) analysis of allele frequencies for 9 SSR loci from 884 *P. gaeumannii* isolates across 23 sites revealed strong spatial genetic differentiation between sites with severe disease near the coast and those with lower disease severity inland. The NMS ordination was then overlaid with vectors representing environmental and geographic variables such that the strength of

the relationships between these variables and the NMS axes could be determined. Spatial allelic variation was strongly correlated with mean winter temperature, mean summer maximum temperature, maximum vapor pressure deficit, and mean dew point temperatures. These variables have been previously identified as determinants of spatial variation in *P. gauemannii* abundance. However, these results further suggest that climatic variation was a potential driver of the divergence of two sympatric *P. gaeumannii* lineages from a native ancestral population.

WED 51

Diversity of *Geosmithia* in the Southeastern United States and their potential threat to native forests stands

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Many new *Geosmithia* taxa species have been described in the last few years, revealing its high diversity and ubiquity. The majority of species have been reported from forested ecosystems in Europe and the western U.S., as well as in close association with bark and subcortical beetles. Although most *Geosmithia* species are non-pathogenic, a few have been recognized as causal agents of diseases in hardwoods. To explore *Geosmithia* diversity and association with potential beetle vectors in Tennessee, we used ethanol traps to sample beetles and culture-based techniques to isolate fungi. To better characterize *Geosmithia* diversity in the southeastern U.S., we included isolates collected in Florida and Georgia acquired through varied sampling techniques. The ITS (Internal Transcribed Spacer) and EF-1 (Elongation Factor alpha) barcode regions were used for fungal identification. Vectors were identified using morphology and the cytochrome-c-oxidase-I (COX1) region. We obtained 57 *Geosmithia* isolates, 43 of which clustered within the "*G. pallida*" species complex and corresponded to previously-reported, but not formally-described species. The remaining 14 isolates were identified as *G. lavendula*, *G. obscura*, *G*. sp. 10 and *G*. sp. 21. Most of the fungal lineages recovered constituted novel reports for the region. Some of our isolates have a close genetic relationship with *Geosmithia* sp. 41; the pathogen causing Foamy Bark Canker disease on coast live oaks in California. In agreement with other lines of research, we did not find signs of vector specificity. Our study revealed an unexplored biodiversity of *Geosmithia* in the southeastern U.S. with potential implications for forest health.

WED 52

Emergence and distribution pattern of a new *Xylaria* parasite of *Chlorocardium* seeds from Guyana.

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Greenheart (*Chlorocardium* spp.) is an important timber species in Guyana that was first commercialized in the late 18th century. Because the seeds are known to contain numerous toxic alkaloids they are largely immune to predation. Moreover, despite more than a decade of silvicultural research with special emphasis on greenheart regeneration, there are no reported cases of seed pathogens of greenheart. In 2011, we observed *Xylaria* stromata fruiting on *Chlorocardium* seeds in the central Guyana. The current study presents results of ongoing surveys of both species of *Chlorocardium* in logged and unlogged mixed greenheart forest throughout its range in central Guyana. We record ca. 80% of greenheart seeds infected with *Xylaria* at all sampled sites. The almost sudden emergence of this fungus is indicative of a novel invasive species that has successfully colonized a new and economically important host. The exact

time of introduction of this fungus is unclear, although our examination of historical records would indicate that it was sometime after 1980 but before 2000. These data and their implications for the future of greenheart production in Guyana will be discussed.

WED 53

Evaluation of *Calonectria pseudonaviculata* microsclerotia survival in compost

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Boxwood blight is a serious fungal disease found in 24 U.S states and Europe. The causal agent of boxwood blight in the U.S. is *Calonectria pseudonaviculata*, whereas *C. henricotiae* causes the disease in Europe. Production of microsclerotia within infected plant material is prolific for both *Calonectria* species. Homeowners or producers may simply compost blighted boxwood plants as a means of disposal. However, it is not known if microsclerotia survive composting. To determine if microsclerotia could survive composting, discreet microsclerotia of *C. pseudonaviculata* were subjected to composting treatments maintained at 40, 50, and 60 °C for 24, 48, and 72 hrs, as compared to heat alone at the same temperatures and durations. Composted microsclerotia exhibited limited survival after 24 hrs at any temperature, and were killed at ≥ 40 °C after 48 hrs. In contrast, microsclerotia consistently survived within heat incubators at 40 °C for all time periods, and were not killed until temperatures reached ≥50 °C for any duration. In conclusion, microsclerotia of *C. pseudonaviculata* are killed more quickly in compost than by heat treatments alone. Well-managed compost may offer a sustainable disposal method for diseased boxwoods.

WED 54

Population biology of the cacao pathogen *Moniliophthora roreri*

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Frosty pod rot disease in cacao, caused by *Moniliophthora roreri*, is one of the major limiting factors to cacao production in Latin America. The pathogen belongs to the Marasmiaceae (Agaricales, Basidiomycota) and has two known mating types. While both mating types are geographically distributed in South America, only one has been found in Central America. No evidence of sexual reproduction has ever been found for this fungus. However, inferences in prior studies may have been skewed by relying on geographically scattered samples rather than true populations. Therefore, in this study we aimed to sample true populations of *M. roreri* in cacao plantations from Ecuador, Peru and Bolivia to analyze potentially hidden genetic structure and diversity of *M. roreri*, and to determine the distribution of mating types within a single plantation. Previously isolated samples from Central America and from the very recently affected Caribbean country Jamaica will be incorporated into this analysis. Inferences about dispersal and population biology of *M. roreri* within this geographic range will be discussed.

WED 55

Host-specialized populations of *Corynespora cassiicola* are causing emerging target spot epidemics in the southeastern U.S.

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Fungal pathogens are causing numerous emerging plant and animal disease worldwide. *Corynespora cassiicola* is a ubiquitous fungus causing outbreaks including target spot of cotton, soybean, and tomato

in the southeastern U.S. Previous studies suggest that populations from cotton, soybean, and tomato in the U.S. are host specific and genetically differentiated based on host of origin. Although variation in aggressiveness to cotton and tomato were observed, no genetic variation was detected within populations sampled from each of these hosts. Our aim was to understand the emergence of the target spot epidemics by developing microsatellite markers for *C. cassiicola* populations to assess genetic variation within each of the populations. Two hundred sixty-five isolates were genotyped with 13 microsatellite markers, and analyzed for genotypic diversity, clonal composition, population structure by host and geography, and recombination events. Genotypic diversity revealed genetic variation within each of the populations collected from different hosts, with the cotton population dominated by clonal genotypes and showing the least diversity. In addition, *C. cassiicola* populations on different host species were genetically distinct and structured based on host species. However, evidence for recombination among *C. cassiicola* populations was not detected suggesting clonality. These results suggest that the cause of the emerging epidemics in the southeastern U.S. is likely due to an introduction of host specialized isolates or the evolution of more aggressive strains on each host. Knowledge on the pathogen population diversity is critical for understanding the genetic basis of disease emergence.

WED 56

Using NGS with Koch's Postulates to discern causal agent(s) of dieback on western hemlock, Southeast Alaska

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Classical and new techniques have been used to identify the cause of a hemlock canker disease in Southeast Alaska. Outbreaks have been detected one or more times per decade since the 1970s. Running diffuse cankers originating on the smallest twigs advance down to major branches causing dieback. In smaller trees (<25cm diameter) in road- and creek-side forests, cankers often advance to the trunk and cause mortality; branch and stem mortality typically reaches a maximum crown height of 12m. From 2012-2016, we isolated numerous potentially pathogenic fungi by classical techniques from discolored cambium margins. Potential pathogens included *Alternaria porri, Collophora* sp., *Coniochaeta/Lecythophora* sp.*, Dermea padi, Discocainia treleasei, Nectria* sp.*, Ophiostoma piceae, Pestalotiopsis* sp., *Pezicula pruinosa, P. aurantiaca*, *Sarea resinae, Sydowia* sp., and *Zalerion arbicola.* In replicated trials, 775 saplings adjacent to infected stands and healthy stands nearby were challenged with inoculation. *Nectria* sp. and *O. piceae* occasionally invaded inoculation controls causing large cankers. Koch's Postulates were completed for the virulent species *D. treleasei* and *Nectria* sp., but isolation frequencies of these species from natural cankers were very low. In further search for a key pathogen, in-field DNA collection from diseased cambium at multiple geographic locations was captured on Whatman FTA® PlantSaver cards. Additionally, DNA was extracted directly from finely-ground cambium with treatment for removal of PCR inhibitors. ITS1 amplicon sequencing with Illumina MiSeq technology and bioinformatic analysis of these samples yielded relatively quantifiable and comprehensive fungal flora of the cankers, and has led to discovery of further species for inoculation studies.

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