**Abstracts for Symposia, Contributed Talks, and Poster Sessions arranged by last name of primary author. Presenting author in \*bold.**

**1. UNITE - Unified system for the DNA based fungal species linked to the classification \*Abarenkov, Kessy** (1), Kõljalg, Urmas (1,2), Nilsson, R. Henrik (3), Taylor, Andy F. S. (4), Larsson, Karl-Hnerik (5), UNITE Community (6) 1.Natural History Museum, University of Tartu, Vanemuise 46, Tartu 51014; 2.Institute of Ecology and Earth Sciences, University of Tartu, Lai 40, Tartu 51005, Estonia; 3.Department of Biological and Environmental Sciences, University of Gothenburg, Box 461, Göteborg SE-40530,Sweden; 4.The James Hutton Institute, Craigiebuckler, Aberdeen, AB15 8QH, UK; 5.Natural History Museum, University of Oslo, P.O. Box 1172 Blindern, Oslo 0318, Norway; 6.https://unite.ut.ee/acknow.php. kessy.abarenkov@ut.ee

formats for downloading and using locally or in a range of applications (e.g. QIIME, Mothur, SCATA). 4. Analysis tools - UNITE provides variety of analysis tools including, for example, massBLASTer for blasting hundreds of sequences in one batch, ITSx for detecting and extracting ITS1 and ITS2 regions of ITS sequences from environmental communities, or ATOSH for assigning your unknown sequences to SHs. 5. Custom search functions and unique views to fungal barcode sequences - these include extended search filters (e.g. source, locality, habitat, traits) for sequences and SHs, interactive maps and graphs, and views to the largest unidentified sequence clusters formed by sequences from multiple independent ecological studies, and for which no metadata currently exists.

*Poster P15*

**2. *Cintractiella* sp., a remarkable new smut fungus parasitic on *Mapania* (Trib. Hypolytreae, Cyperaceae)**Abbasi, Mehrdad(1), **\*Eamvijarn, Amnat**(1,3), Flynn, Tim(2), Wood, Ken(2), Aime, M. Catherine(1) 1.Department of Botany and Plant Pathology, Purdue University, West Lafayette, IN 47907, USA.; 2.National Tropical Botanical Garden, 3530 Papalina Road, Kalaheo, HI, 96741, USA.; 3.Department of Agriculture, Ministry of Agriculture and Cooperatives, 50 Phaholyothin Rd., Ladyao, Chatuchak, Bangkok, 10900, Thailand. aeamvija@purdue.edu

*Cintractiella* is a unique genus among smut fungi. Sori are produced as adventitious gall-like spikelets on vegetative or generative organs of members of Trib. Hypolytreae (subfamily Mapanoideae, Cyperaceae). *Cintractiella lamii* is the only known member of the genus producing its sori on vegetative organ (leaves). The species was described based on a specimen collected from Indonesia about 80 years ago. The type specimen was subsequently lost shortly after publication and all later descriptions of this fungus have been reproduced from the original protologue. No other specimens of *C. lamii* have been reported so far and no other species of the genus *Cintractiella* on vegetative organs of Hypolytreae, have been described. In September 2009 on the volcanic island of Kosrae, located in the eastern Caroline Islands and within the Federated States of Micronesia (5 ̊20’N and 163 ̊0’E), a specimen of *Mapania pacifica* was collected displaying *Cintractiella*-like sori in adventitious spikelets on the host leaves. Sori were hypophyllous, occurring in groups of spikelets composed of olivaceous-brown scale like leaves, 1–1.5 mm wide and up to 6 mm long. Microscopic comparison with the protologue and drawings of the type material of *C. lamii* show several differences in teliospore and sori characters between it and the newly

UNITE (https://unite.ut.ee) providing reference datasets and web based tools for the molecular identification of fungi based on rDNA ITS sequences - the official barcode marker for fungi. Since 2003, when the first version of UNITE was released publicly, the database has transitioned from being online DNA sequence key for ectomycorrhizal fungi with limited geographical scope into a comprehensive reference database covering all fungal taxa known from DNA barcode sequences globally. Current features of UNITE include: 1. UNITE Species Hypotheses (SH) - a unique way how to communicate fungal species using stable identifiers. ITS sequences submitted to UNITE and International Nucleotide Sequence Databases (INSD: GenBank, ENA, DDBJ) are grouped into SHs by following a two-step clustering process, first at the subgeneric/generic level, then at a species level on different distances to the closest SH (e.g. 3%, 2.5%, etc.) All SHs are linked to the Linnaean classification and they have a stable accession code and digital object identifier (doi) making it possible to cite and communicate them in published studies. 2. Tools for the third-party sequence annotation of INSD sequences - used by the UNITE Community to annotate and improve the quality of fungal ITS sequences in INSD. The local copy of INSD dataset is updated on a regular basis. Any third- party annotation added to the INSD dataset (e.g. locality, habitat, source, traits, taxon identifications, and interacting taxa) is made publicly available to the research community through web services and on UNITE homepage. 3. Reference datasets for sequence identification pipelines - UNITE provides reference datasets with annotated sequences and SHs in various

is a

database

collected material on *Mapania*. To our knowledge this represents only the second known collection of any member of *Cintractiella* on vegetative organs of Hypolytreae. Herein we will fully illustrate and discuss this enigmatic genus as well as examine its phylogenetic position in the smut fungi.

*Poster P2*

**4. Myxogeography of Cerrado: A first approach** Agra, Leandro A.N.N., **\*Dianese, J.C.** Universidade de Brasília, Departamento de Fitopatologia, Brasília, 70910-900, Brazil. jcarmine@gmail.com

The Cerrado, a world biodiversity hotspot, is the largest savanna in Western Hemisphere, inserted in the Brazilian territory. Myxomycetes has been studied in Brazil since 1889, however in the Cerrado the first record, *Physarum pusillum*, occurred only in 1965. Major additions consisted of the 1974 survey in the Southern part of the Cerrado (State of São Paulo) by Cavalcanti where 25 species were identified in Pirassununga; and later in 1980 23 species were found in Botucatu by Maimoni-Rodela and Gottsberger. For the next 23 years sporadic records added 37 species. Starting in 2003 a major effort with researchers connected with the UB Mycological Collection, up to 2015 added 286 records to the known myxobiota of the Cerrado. Besides that a total of 57 records were revealed through collections from a Cerrado inserts in the State of Roraima, transition Cerrado/Caatinga in Piauí, Serra do Roncador (Mato Grosso), Anápolis, Silvânia and Pirenópolis (Goiás), completing a total 108 species in the Brazilian Cerrado *sensu* Batalha (2011)[47°22'Nto28°20'S,73°02'Wto40°45' W]. A total of 609 records representing 139 species in 20 localities were used to generate a set of maps revealing a temporal evolution of the detection of the Myxomycota within the Cerrado where six myxogeographic gaps were filled when herbarium data and new field collections were considered. Thirty-two species were recorded for the first time in the Cerrado. Two of them are probable new species; a species belonging to the genus *Diacheopsis* was for the first time found in Brazil; *Cribraria tecta* was for the second time found in the world; three species were new for the Neotropics, four for South America, and two for Brazil. Seven of the 20 localities studied showed only one record suggesting need for more collections; on the other hand, 59 species were found only in one of the 20 localities, a rate that is identical to the plant species considered rare for the Cerrado. *Contributed Talk C18.2*

**5. Exploring ‘dark matter fungi’ using single-cell genomics**

**\*Ahrendt, Steven**(1), Quandt, C. Alisha(3), Ciobanu, Doina(1), Clum, Alicia(1), Salamov, Asaf(1), Cheng, Jan-Fang(1), Woyke, Tanja(1), James, Timothy(3), Grigoriev, Igor V.(1,2)

1.DOE Joint Genome Institute, Walnut Creek, CA, 94598, USA; 2.University of California, Plant and Microbial Biology, Berkeley, CA, 94720, USA; 3.University of Michigan, Ecology and Evolutionary Biology, Ann Arbor, MI, 48109, USA. sahrendt0@gmail.com

Fungi are critical research systems as they impact global carbon cycling and have remarkable potential for sustainable biofuel production processes. Current estimates suggest that under 10% of the estimated 1.5 million species worldwide have been described, and the majority of those described fall within the later branching lineages in the Dikarya. The true extent of the phylogenetic diversity among the early diverging fungal lineages is poorly explored at best. “Dark Matter Fungi” (DMF) is a term used to describe uncultured and understudied fungal diversity, much of which resides in these early diverging lineages. A polyphyletic group of these lineages can be characterized by their aquatic lifestyles facilitated by the presence of a motile, flagellated spore. As such, they are often referred to as “zoosporic fungi” and are ubiquitous in the environment. Additionally, the phylogenetic diversity of these lineages is estimated to rival that of the rest of the fungal kingdom. Traditional high-throughput sequencing is poorly suited for DMF, since it relies on large amounts of DNA extracted from many cells of the same species. Single-cell genomic sequencing, however, aims to use individual cells to reconstruct genomes of uncultivated organisms directly isolated from the environment. Therefore environmental DMF, particularly among the zoosporic fungi, make exceptional targets for single-cell genomic techniques. As much of the current single- cell genomic work focuses on mammalian, bacterial, and archaeal systems, there is a need to develop these protocols for fungi. Primary goals for this research include the development of a standard production workflow for fungal single-cell genomes, and comparative genomic analyses to address questions regarding the evolutionary biology of DMF, including aspects of pathogenicity and phylogenetic diversity within these lineages. *Poster P105*

**6. Phylogenetic species recognition criterion reveals little species diversity in assessment of Indiana’s morphologically diverse morels (*Morchella* spp.)**

**\*Albright, Nicolette**(1), Zaspel, Jennifer M.(2), Aime, M. Catherine(1), Goodwin, Stephen B.(3), Beckerman, Janna L.(1)

1.Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA; 2. Purdue University, Department of Entomology, West Lafayette, IN, 47907, USA; 3. Crop Production and Pest Control Research Unit, U.S. Department of Agriculture- Agriculture Research Service, Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA. nalbrigh@purdue.edu

Characterizing morel (*Morchella* spp.) diversity is challenging due to the limitations in both morphological species recognition (MSR) and single- locus, nuclear ribosomal internal transcribed spacer (ITS) fungal barcoding criteria. In many regions, cryptic species make it impossible to distinguish species limits, while the ITS fungal barcode largely underestimates *Morchella* species diversity. Because of inconsistencies with these methods, the current standard for assessing morel diversity is through phylogenetic species recognition (PSR) criteria of a multilocus molecular data set. To date sixty-five morel species have been phylogenetically resolved worldwide, yet morel species diversity in many locations has not been assessed. Indiana is known for its prolific fruiting and morphologically diverse ascocarps, yet the genetic diversity remains uncharacterized with current species limits and methodologies. To address this, we collected morels from five counties every spring in 2013, 2014, and 2015. Genetic diversity was measured through both single and multilocus phylogenetic species recognition (PSR) criteria of three loci previously used to resolve *Morchella* diversity: elongation factor 1-alpha (EF- 1α), the second largest RNA polymerase subunit (RPB2), and nuclear ribosomal large subunit (LSU) 28s rDNA. Despite tremendous morphological variability in ascocarp size and colorations, over 90% of 144 morels collected were resolved to one phylogenetic species, *Morchella americana.* We still have no MSR matrix to confidently distinguish *Morchella* species in our region. However, PSR criterion using single locus EF-1α expedited the characterization of genetic diversity, as it was the only locus that provided significant bootstrap support to resolve species limits. Our results describe the ascocarp variability within phylogenetic species boundaries of *Morchella* in a region where morel diversity has not been assessed.

*Contributed Talk C10.5*

**7. Fungivorous Hawaiian tree snails destabilize phyllosphere communities: Why it’s not a big deal to poop where you eat \*Amend, Anthony S.**(1), Gaughen, Kapono(1), O’Rorke, Richard(2)

1.University of Hawaii at Manoa, Department of Botany, Honolulu, 96822, USA; 2.Griffith University, Environmental Futures Research Institute, Nathan, QLD 4111, Australia. amend@hawaii.edu

Though grazers have long been recognized as top- down architects of plant communities, animal roles in microbial community assembly are seldom examined. Tree snails, which both skim leaf surfaces and transplant microbes across leaves, could potentially stabilize or destabilize fungal communities over time. In this study we examine the feeding habits of endangered Hawaiian tree snails and conduct an enclosure study to see how these fungivores impact fungal community composition relative to matched control exclosures. Following snail introductions, fungal community composition and changes were determined by Illumina sequencing over the course of six weeks. SEM microscopy was used to quantify phyllosphere biomass. We recorded 3.5 times more fungal hyphae in control exclosures compared to those containing snails. A significant proportion of the initial leaf phyllosphere persisted in the mesocosms over the course of the experiment despite this heavy grazing by snails. Variance in snail-enclosure diversity was significantly higher than control exclosures due to high enrichment in airborne environmental fungi. Our results suggest that snails are weak dispersal vectors, but exert a strong, destabilizing influence on phyllosphere fungal composition. By creating patches of disturbance, snails extend the duration of early, stochastic, assembly processes. *Contributed Talk C13.1*

**8. The genome of an unculturable nematode- destroying fungus and its role in resolving the zygomycete tree of life \*Amses, Kevin R**

University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, MI, 48109, USA. amsesk@umich.edu

Phylogenetic explorations of Zygomycota *s.l.* have consistently shown it to be an artificial assemblage. Although abruptly and convincingly uprooting our historically best estimate of evolutionary relationships within this ubiquitous and diverse group of microscopic Fungi, phylogenetic analyses based mainly on rRNA genes have been unable to resolve a well-supported zygomycete classification below the level of subphylum. To begin to close this knowledge gap, we plan to leverage large genomic data sets toward generating strong phylogenomic hypotheses regarding evolutionary relationships within Zygomycota *s.l*. As a first step we have sequenced the genome of *Stylopage hadra* (Zoopagomycotina), a predatory zygomycete fungus that captures and digests nematodes in natural and

agricultural soils. Like many other taxa in this understudied zygomycete subphylum comprised of obligate parasites of other zygomycetes and small soil animals, establishment of axenic cultures of *S. hadra* has so far proven impossible. To circumvent this major obstacle to its study, we have employed single cell genomic approaches to generate whole genome libraries of this cryptic soil fungus. The *S. hadra* genome and methodologies employed in our approach will be discussed before being applied to the broader goal of synthesizing a strongly supported tree of life for this early diverging lineage of Fungi.

*Contributed Talk C17.4*

**9. Resilience of fungal guilds and nutrient content following *Alliaria petiolata* (garlic mustard) eradication \*Anthony, M.A.**(1)., Frey, S.D.(1), Stinson, K.S.(2), Haines, D.(2), Aylward, J.(2)

Invasive plants can disrupt native soil fungal communities and the nutrient cycling processes fungi mediate. Our earlier work showed that *Alliaria petiolata* [garlic mustard] invasion was associated with reduced fungal beta diversity, including a shift from ectomycorrhizal [EMF] to saprotrophic fungal dominance and enhanced pathogenic fungal diversity. Invaded soils also exhibited lower soil organic C content and greater soil nutrient availability. Currently, there are national campaigns to eradicate *A. petiolata* across North America, but how *A. petiolata* eradication facilitates recovery of degraded soils is unknown. In this study, we tested the resilience of soil fungal communities and nutrient levels to one year of garlic mustard eradication. We compared replicate uninvaded, invaded, and eradicated plots across eight temperate deciduous forests in the Northeastern U.S.A (*n* = 144). Organic horizon and mineral soil samples were collected and characterized for fungal community structure [ITS metabarcoding], fungal biomass [PLFA], nutrient availability [inorganic N and P], and soil C stocks. We found that eradication did not restore soil nutrient or organic C content relative to uninvaded levels. Although fungal beta diversity was lower in the eradicated plots compared to the uninvaded plots, beta diversity was higher in the eradicated plots than the invaded plots. Eradication was also associated with increased relative abundance of EMF fungi, predominantly within the Russulales and Agaricales. Eradicated plots also exhibited lower relative abundance of saprotrophic fungi, primarily within the Mucoromycotina and Agaricomycetes. In contrast, there was sustained accumulation of pathogenic taxa between eradicated and invaded plots compared to uninvaded plots, especially *Ganoderma* and *Cryptococcus* spp. In summary, soil fungi partially recovered from garlic mustard invasion after one year

of eradication, despite sustained alteration to the pathogenic community, soil C content, and nutrient availability. *Symposium S6.3*

**10. Endomycorrhizae on Puertorrican ‘Ají dulce’ (*Capsicum chinense*) and their effects on plant growth**Aponte-López, Carla M., **\*Cafaro, Matías J.** 1.Department of Biology, University of Puerto Rico, Mayagüez Campus, Mayagüez, Puerto Rico, 00680. carla.aponte@upr.edu

*Capsicum chinense* is widely cultivated in the Caribbean region. Most types are pungent, such as 'Scotch Bonnet' and 'Habanero'. In Puerto Rico, non- pungent types called "ají dulce" are consumed as part of the local cuisine. Currently, in commercial agriculture, the use of chemical fertilizers dominates the local market, while biological ones are overlooked. The purpose of this research was to characterize and identify the endomycorrhizae associated with locally grown *C. chinense* in the western area of Puerto Rico. We collected “ají dulce” roots and surrounding soil from plants growing in experimental plots at UPRM. Pland were grown under six treatments using commercial Promix® BX for general purpose, Promix® Mycorrhizae (*Glomus intraradices*), Promix® with 25% soil from the UPRM, greenhouse Promix® with fertilizer, Promix® Mycorrhizae (*Glomus intraradices*) with fertilizer and Promix® with 25% soil from the UPRM greenhouse with fertilizer. Significant differences were obtained when compared using ANOVA, obtaining a p-value <0.0001 between Promix® Mycorrhizae and Promix® BX treatments resulting in greater stem length, fruit and leaves numbers. Furthermore, to calculate the percentage of infection, slides were made utilizing stained roots. Consequently, significant differences were found in at least one of the treatments. DNA extractions and PCR reaction using specific primers for mycorrizhae were performed. Cloning of PCR products for subsequent sequencing is underway. Based on the gel electrophoresis observation for the sets of primers used *Glomus* and *Gigaspora* seem to be present in UPRM soil.

*Poster P73*

**11. Perspectives from leaves and lichens on the scale and distribution of the global endobiome \*Arnold, A. Elizabeth**(1,2), U’Ren, Jana M.(3), Miadlikowska, Jolanta(4), Carbone, Ignazio(5), Huang, Y u-Ling(1), Bowman, Elizabeth A.(1), May, Georgiana(6), Lutzoni, François(4)

1.University of Arizona, School of Plant Sciences, Tucson, AZ, 85721, USA; 2.University of Arizona, Ecology and Evolutionary Biology, Tucson, AZ

85721; 3.University of Arizona, Agricultural and Biosystems Engineering, Tucson, AZ, 85721, USA; 4.Duke University, Department of Biology, Durham, NC, 27708, USA; 5.North Carolina State University, Department of Plant Pathology, Raleigh, NC, 27695, USA; 6.University of Minnesota, Department of Ecology, Evolution, and Behavior, St. Paul, MN, 55108, USA. arnold@ag.arizona.edu

The internal tissues of photosynthetic organisms represent one of the most extensive and biochemically dynamic habitats on earth. In turn these tissues host some of the planet’s most ubiquitous and diverse symbionts, endophytic fungi. By sampling across the green tree of life – from woody angiosperms to the green algae and cyanobacteria that occur in lichen thalli – we have assembled a global collection of endophytes that provides a basis for evaluating the factors shaping this species-rich portion of the ‘global endobiome’ in photosynthetic tissues across diverse spatial scales, hosts, and ecological communities. Here we use newly developed phylogenetic- and biodiversity informatics tools to visualize the relationships of endophytic fungi and ecological metadata in an eco-evolutionary framework. We discuss the factors shaping endophyte distributions at local, regional, and landscape scales, and address gaps in knowledge regarding the complementarity of culture-based and next-generation studies; the taxonomic novelty of fungi obtained in survey efforts, for which only short sequences and/or few to no morphological characters are available; and the relevance of taxonomic vs. functional similarity in community structure. Finally we will describe progress with multilocus- and genomic approaches to interrogate some of the limitations of current methods for understanding the biogeography of endophytic fungi.

*Symposium S11.1*

**12. Following the path of differential expression to natural product discovery in *Tolypocladium inflatum*\*Arvidson, Rheannon**(1), Tehan, Richard(2), Spatafora, Joseph(1), McPhail, Kerry(2), Bushley, Kathryn(3), Gazis, Romina(4), Chaverri, Priscila(5) 1.Oregon State University, Botany and Plant Pathology, Corvallis, OR 97331, USA; 2.Oregon State University, College of Pharmacy, Corvallis, OR 97331, USA; 3.University of Minnesota, Plant Biology, St. Paul, MN 55108, USA; 4.University of Tennessee, Entomology and Plant Pathology, Knoxville, TN, 37996, USA; 5.University of Maryland, Plant Science and Landscape Architecture, College Park, Maryland, 20742, USA. arvidsor@oregonstate.edu

Secondary metabolites of fungi are an important source for industrial and medicinal natural products. Understanding secondary metabolism from a genomic perspective is a key part of natural products discovery. This is particularly important since many gene clusters involved in secondary metabolite synthesis are silent (i.e. not expressed) under standard laboratory conditions. *Tolypocladium inflatum* (Ascomycetes, Hypocreales) is an ideal system for investigating secondary metabolite production. The clinically important immunosuppressant, cyclosporin A, and the gene cluster responsible for its production, was first discovered in *T. inflatum*; however, from genome- based secondary metabolite predictions, we know that many of the secondary metabolite gene clusters in *T. inflatum* are either silent or have not been linked to known metabolites. The environment influences fungal secondary metabolite production and we have taken advantage of this by growing *T. inflatum* on selective media supplemented with different amino acids. This approach was chosen to target the secondary metabolites produced via non-ribosomal peptide synthetase (NRPS) pathways, specifically those involved in peptaibiotic biosynthesis. Expression and production of secondary metabolites were investigated with RNA sequencing and mass spectrometry, respectively. Genomic predictions of secondary metabolite genes in *T. inflatum* were used to guide investigations of secondary metabolite specific changes in gene expression between different growth conditions. Clustering and heat maps of mass spectrometric data were used to identify differences in secondary metabolite production between growth conditions. This combination of approaches effectively reveals variations in secondary metabolite production between different growth conditions. An application of this approach to identify peptaibiotics in *T. inflatum* will be presented. *Contributed Talk C2.3*

**13. Progress towards genetic transformation in a Blastocladiomycete fungus \*Auxier, Benjamin**, Berbee, Mary University of British Columbia, Botany, Vancouver, V5Z 1L9, Canada. ben.auxier@mail.ubc.ca

The recent explosion of sequenced fungal genomes has led to an increased recognition of the diversity in the genetic makeup of Fungi. Analysis of this genomic data is revealing patterns of evolutionary change such as expansions of gene families involved in morphogenesis or encoding carbohydrate active enzymes. A limitation to these comparative genomic studies with early-diverging fungi is the inability to use standard molecular biology techniques to verify the results. Without techniques such as fluorescent tagging, knockout mutants, and heterologous

expression, the inferences that can be made with comparative genomics are restricted to analysis of sequence homology and computational protein predictions. To address this limitation, I have been pursuing a reliable transformation system in the Blastocladiomycete fungus *Blastocladiella emersonii* using *Agrobacterium tumifasciens*-mediated transformation, as has been previously been reported. As an initial step towards this goal, I am using the filamentous ascomycete *Grosmannia clavigera* as a positive control to confirm the components of the plasmids to be used in the transformation system. For these transformations, I am inserting the DNA for the Lifeact peptide, which allows visualization of the actin network, initially in *Grosmannia* and eventually in *Blastocladiella*. The visualization of the actin network will allow for critical comparisons between an early- diverging fungus and the better studied fungi in Dikarya. In the future a transformation system in early-diverging fungi would allow for detailed molecular investigation of the divergent processes in these interesting fungi.

*Contributed Talk C11.3*

**14. Substrate use of saprophytic and pathogenic ophiostomatoid fungi associated with an indigenous South African plant genus \*Aylward, Janneke**(1), Steenkamp, Emma T.(2), Dreyer, Léanne L.(1), Roets, Francois(3), Wingfield, Brenda D.(4), Wingfield, Michael J.(2)

1.Department of Botany and Zoology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa; 2.Department of Microbiology and Plant Pathology, University of Pretoria, Pretoria 0002, South Africa; 3.Department of Conservation Ecology and Entomology, Stellenbosch University, Private Bag X1, Matieland 7602, South Africa; 4. Department of Genetics, University of Pretoria, Pretoria 0002, South Africa. janneke@sun.ac.za

*Knoxdaviesia* species associated with *Protea* trees occupy a specialist niche, growing on decaying flowers in seed cones. The saprophytic association of these ophiostomatoid fungi with indigenous plants is a sharp contrast to the pathogenicity often encountered in their sister family. *Ceratocystis albifundus* is the causal agent of *Acacia mearnsii* wattle wilt, but has been isolated from wounded stems of native South African plants, including *Protea*. Both *Knoxdaviesia* and *Ceratocystis* are vectored by arthropods, yet the two occupy distinctly different niches. The aim of this study was to investigate the basis for pathogenic wound-association versus saprophytic life in seed cones. We hypothesise that carbon resource utilization capacity plays a role in the host exclusivity of *Protea*- associated *Knoxdaviesia* species and the wide host range ability of *C. albifundus*. Substrate use in these

two environments was investigated by integrating phenome and whole-genome data from two *Knoxdaviesia* species and *C. albifundus*. Contrary to expectations, results indicate that *C. albifundus* uses less than half the carbon sources used by *Knoxdaviesia*. We speculate that the nutrient stability in wounds and the continual resource depletion in decaying seed cones may have respectively influenced the loss and maintenance of carbon metabolism genes. *Contributed Talk C13.8*

**15. Examining phylogenetic signal in a suite of novel intergenic sequence markers for *Colletotrichum* systematics**Baer, Caroline(1), Veloso, Josiene S.(1, 2), Hutchins, Haley(1), Câmara, Marcos P.S.(2), Rehner, Stephen A.(3), **\*Doyle, Vinson P.**(1)

1.Department of Plant Pathology and Crop Physiology, Louisiana State University AgCenter, Baton Rouge, LA 70803; 2.Departamento de Agronomia, Universidade Federal Rural de Pernambuco, Recife, 52171-900, Pernambuco, Brazil; 3.Systematic Mycology and Microbiology Lab, USDA-ARS, Beltsville, MD 20705. vdoyle@agcenter.lsu.edu

An important limiting factor for advancing understanding of *Colletotrichum* biology is the ability to reliably delimit species and infer the species tree in the presence of topological heterogeneity among individual gene trees. To understand the role of incomplete lineage sorting and hybridization in generating topological conflict while delimiting species, genes with strong phylogenetic signal are needed. Here we report on new intergenic (IGS) loci with strong phylogenetic signal identified using whole genome sequence data from representative species within the *C. gloeosporioides* species complex. Using a high quality assembly and gene annotations of a single genome, we located intron/exon and genic/intergenic boundaries and extracted syntenic regions from assemblies of related species. These regions were aligned, filtered, and ranked according to several metrics, including IGS length, number of variable characters, the proportion of indels, and uncorrected p-distance, to assess their utility for phylogenetic analysis. We selected thirty candidate markers deemed eligible by these criteria from the list of nearly 2800 IGS regions. After testing the amplification success of these markers in representative isolates within the *C. gloeosporioides* species complex we selected 11 for sequencing isolates spanning the diversity of the *C. gloeosporioides* species complex. These markers were compared with the most informative of the commonly used markers for *Colletotrichum* systematics with respect to phylogenetic informativeness, topological

information content (entropy), and site-specific likelihood support for existing phylogenetic hypotheses to estimate their utility for addressing species delimitation issues within the *C.*

*gloeosporioides* species complex. The informative markers will be useful for screening large collections of isolates for genetic diversity and incorporating into multilocus targeted amplicon sequencing or sequence capture studies.

most

*Poster P102*

**16. Grinding up the coffee rust genus: Molecular phylogenetics of *Hemileia*\*Bailey, Jordan**(1), Aime, Mary Catherine(2), Castlebury, Lisa(1)

The genus *Hemileia* Berk. & Broome was established in 1869 in response to the new ‘coffee leaf rust’ disease progressing through the coffee plantations of Sri Lanka. *Hemileia vastatrix*, the causal pathogen, devastated plantations and continues to be the most important disease of coffee in the world today. While extensive research has been performed on control and management of the disease as well as morphology, cytology and infection studies of *H. vastatrix*, little has been done taxonomically with the genus, which now contains ca. 50 species. Classification of *Hemileia* has been difficult and despite over 100 years of research spermagonia and aecia have not been observed for any member of the genus. However, basidiospores are unable to reinfect the primary host, indicating that these species are most likely heteroecious. *Hemileia* was considered *incertae sedis* until 2003 when, based on morphology, Cummins and Hiratsuka placed it in the Chaconiaceae, a heterogeneous assemblage of mostly tropical rusts that do not undergo teliospore dormancy. Subsequent studies based on molecular characters have alternatively placed *Hemileia* within the Mikronegeriaceae, a family of macrocyclic heteroecious rust fungi. In this study, we used

*Poster P96*

**17. Reinvestigating the disease ecology of *Rhizoctonia* fungi associated with vascular streak dieback disease of cacao in The Phillipines.** Balidion, Johnny F.(1), Budot, Bernard O.(1), **\*Cubeta, Marc A.**(2)

1.Department of Plant Pathology,

2.Department of Entomology and Plant Pathology, Center For Integrated Fungal Research, North Carolina State University, Raleigh, NC, USA.

Vascular streak dieback disease of cacao is caused by at least three genetically divergent lineages of *Ceratobasidium* in the Rhizoctonia species complex that include *C. cornigerum* (anastomosis groups (AG) AG-A and AG-G) and *C. theobromae* based on multilocus DNA sequence analysis. This study was initiated to determine the prevalence of these species of *Ceratobasidium* in diseased cacao tissues obtained from the province of Palawan and the southern Philippine provinces of Mindanao where cacao has been intensively cultivated for decades. Pure culutres of *C. cornigerum* were obtained and maintained on corticium culture medium. However, the near-obligate nature of *C. theobromae* created challenges for isolating and establishing pure cultures of this organism. Furthemore, the probability of isolating *C. theobromae* was limitted by the presence of the faster growing fungi *Colletotrichum gloeosporoioides*, *Fusarium equiseti* and *Lasiodiplodia theobromae* in cacao tissue. An *in planta* PCR-based assay that deployed the use of specific primers (Than\_ITS1/Than\_ITS2) was developed and used to detect *C. theobromae* from asymptomatic and symptomatic cacao tissue. The conserved primers ITS5/ITS4 and TUB1/TUB2 primers that amplify fungal and cacao DNA, respectively, were used as internal controls. Results suggest that detection sensitivity is influenced by the level of cacao inhibitors in the DNA template used. DNA extracted from cacao tissue with commercial kits provided more consistent amplification of *C. theobromae* compared to traditional precipitation-based extraction protocols and may be more suitable for routine early disease detection and indexing in seedling nurseries and production areas. Management approaches that provide early detection of these pathogens in susceptible plant host species not exhibiting signs and/or symptoms could potentially limit introduction of infected plant material into cacao production areas, minimizing possibilities of disease outbreaks in the future. *Contributed Talk C8.3*

Biodiversity Division, Crop Protection Cluster, Biological Science Building, University of the

Pest Biology and

 

Phillipines, Los Banos, Laguna, Philippines;



fbalidion@up.edu.ph

 

|  |
| --- |
| 1.USDA ARS Systematic Mycology & Microbiology |
| Lab, Beltsville, MD 20705; 2.Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907. Jordan.Bailey@USDA.ARS.gov |

herbarium material from the U.S. National Fungus Collections and Purdue’s Arthur Fungarium to sequence the 18S and partial 28S rDNA regions for species of *Hemileia* and related anamorphs. Maximum likelihood and Bayesian inference are used and we present the first findings on the phylogenetic relationships of species of *Hemileia* which includes the confirmation for inclusion of several anamorphic

species.

**18. An overview of the genus *Lactarius* (Russulales) in the Greater Yellowstone Ecosystem \*Barge, Edward**, Cripps, Cathy L. Montana State University, Plant Science and Plant Pathology Department, Bozeman, MT 59717, USA. ebarge9@gmail.com

The Greater Yellowstone Ecosystem (GYE), located in the Central Rocky Mountains of western North America, is one of the largest nearly intact temperate-zone ecosystems on Earth. Here, *Lactarius* is an important component of ectomycorrhizal communities in many habitat types, from low elevation riparian areas to high elevation conifer forests and alpine tundra. Molecular phylogenetic analyses of ITS and *RPB2* gene sequences along with detailed morphological examination confirm at least 21 *Lactarius* species and varieties, as well as two unresolved species groups in the GYE. Six species are reported from the GYE for the first time, and nearly every major ectomycorrhizal host plant in the GYE appears to have at least one *Lactarius* species associated with it. Broad intercontinental distributions are suggested for alpine *Salix* and *Betula* associates, and for certain subalpine *Picea* and aspen (*Populus* spp.) associates. Some species appear to be restricted to western North America with *Pinus, Pseudotsuga* or *Abies*. The distribution and/or host affinities of others is not clear due in part to ambiguous host assignment, taxonomic problems or the relative rarity with which they have been reported. Further sampling, sequencing of additional loci, and examination and sequencing of a relevant selection of Hesler & Smith’s North American type material in comparison to European material could help resolve some of these issues. The morphology, a molecular phylogeny and a discussion of habitat/host for *Lactarius* species of the GYE will be presented. *Poster P93*

**19. Edible and poisonous mushrooms of British Columbia \*Bazzicalupo, Anna L.**, Berbee, Mary L. University of British Columbia, Botany Department, Vancouver, V6T1Z4, Canada. annabazzicalupo@gmail.com

Mushrooms in BC have been responsible for 96 cases of symptomatic poisoning over the last two years. Even more common have been hospital visits after someone, often a young child, accidentally ate a mushroom. Meanwhile, edibles such as pine mushrooms are valuable BC non-timber forest products and ecologically important mushroom- forming fungi keep forests healthy by providing fertilizer nutrients to trees. In this project, we will develop a barcode DNA sequence identification database, to systematically barcode mushroom

specimens, prioritizing toxic or edible species. Species of mushrooms that are more commonly involved in poisoning are often poorly characterized. Preliminary data on species of *Amanita pantherina* or *Inocybe mixtilis*, show that specimens identified as those taxa belong to different lineages. While expert amateurs from NAMA and other local mushroom groups are the ones who are asked to identify mushrooms involved in poisonings and are familiar with those taxa, there is an inherent lack of knowledge in the literature about the actual species found in the Pacific Northwest region. We chose 960 UBC specimens belonging to genera known or suspected to be poisonous and common edibles. We plan to sequence the ITS regions to start a reference pool of specimens that can be used to delimit species in the genera, to compare specimens from poisoning cases. The species delimitation will allow us to recover general habitat and fruiting times of the species by matching them with herbarium-label data. Undergraduate students at UBC were able to gain research experience by collecting specimens of common edible and poisonous mushrooms, extract DNA and sequence the ITS barcode regions from those collections. The proposed database of mushrooms will assist food protection programs in creating guidelines and education for wild mushrooms harvest, sale and purchase. Information about the exact species will inform on toxicity and treatment options, particularly with mushrooms implicated in delayed onset syndromes. Identification and matching with specimens previously collected in BC will bring together information on known seasonality, habitat and distribution of the species, leading to better predictions about where mushroom poisonings are likely to occur.

*Poster P24*

**20. Effects of host genetics and immunity on the amphibian skin microbiome \*Belasen, Anat M.**, James, Timothy Y. University of Michigan Department of Ecology and Evolutionary Biology, 830 North University Avenue, Ann Arbor, MI 48109. abelasen@umich.edu

Emerging infectious disease is a major threat to biodiversity and human health. In recent years, the microbiome has been recognized as a potential mediator in host-pathogen interactions, but the relationships between intrinsic host characteristics, microbiome diversity, and disease susceptibility are not well-understood. In this study, we examine the effects of long-term fragmentation on host genetics, microbiome diversity, and pathogen diversity in an endemic Brazilian frog. Brazil is a hotspot for Batrachochytrium dendrobatidis (Bd), the fungal pathogen associated with recent dramatic amphibian declines. Although our study populations appear to be

little impacted by Bd, host genetics may be influencing microbiome differences. Notably, several potential pathogens (including fungi, stramenopiles, and alveolates) appear to be elevated in populations with low overall genetic diversity and lower diversity at a locus important for immune function. Our results suggest that intrinsic host factors may be responsible for microbiome shifts associated with altered infection susceptibility.

*Contributed Talk C1.4*

**21. Genetic differentiation and hierarchical structure of two divergent populations of *Phaeocryptopus gaeumannii* in the Pacific Northwest**

**\*Bennett, Patrick I.**, Stone, Jeffrey K. Oregon State University, Department of Botany and Plant Pathology, Corvallis, Oregon 97331-2902 USA. bennetpa@oregonstate.edu

*Phaeocryptopus gaeumannii,* a common foliage parasite that co-occurs with its host Douglas-fir (*Pseudotsuga menziesii*) throughout western N. America, presents a unique opportunity to investigate sympatric speciation in natural populations of a plant pathogenic fungus. Where it is abundant, the fungus causes Swiss needle cast, a premature loss of foliage leading to growth reduction, but it is also common as an inconspicuous inhabitant of needles throughout most of the range of Douglas-fir. Previous studies have identified two distinct lineages of this fungus in the western United States. The objective of this study was to compare the distributions of these lineages and population differentiation in relation to disease severity. Multilocus microsatellite genotypes were analyzed from 862 isolates collected from Douglas-fir foliage in Oregon and Washington. Significant subpopulation structure and genetic differentiation were detected at various scales, including regional populations, sampling sites, trees within sampling sites, and individual needles. Population differentiation was assessed by K-means clustering combined with bootstrapped UPGMA dendrograms, and PhiPT was calculated from a hierarchical analysis of molecular variance (AMOV A). Discriminant analysis of principal components (DAPC) was used to determine differentiation among individual sampling sites. The genetic differentiation observed between lineages at the regional scale is consistent with reproductive isolation, suggesting that these populations are diverging. Finer-resolution analyses using genomic data such as SNPs could provide a more thorough understanding of the mechanisms underlying these evolutionary processes. *Contributed Talk C3.1*

**23. Preferential allocation, physio-evolutionary feedbacks, and predicted strengths of the mycorrhizal mutualism with environmental change \*Bever, James D.**

University of Kansas.Department of Ecology and Evolutionary Biology and The Kansas Biological Survey, Lawrence, KS, 66045. jbever@ku.edu

The common occurrence of mutualistic interactions between plants and root symbionts is problematic. As the delivery of benefit to hosts involves costs to symbionts, symbionts that provide reduced benefit to their host are expected to increase in frequency. The spread of non-beneficial symbionts can be limited by plant preferential allocation to the most efficient symbiont and this preferential allocation can promote the evolution of mutualism even when the cost to the symbiont is very large. Moreover, the physiological plasticity of preferential allocation likely

**22. The impacts of fungal interaction on the decomposition of two wood substrates \*Betts, Henry**George Washington University, Biology Department, Washington DC, 20052, United States. hhbetts@gwu.edu

Fungi are responsible for the majority of wood decomposition in temperate forests. The rate of wood decomposition is dependent on both the community of fungi that inhabit the wood and the substrate in which it is growing. Wood secondary chemistry can inhibit fungal growth and wood decomposition through high lignin content and antimicrobial properties. The species interactions within the substrate influence the respiration rates and total hyphal growth of a focal species. Little is known about this interaction between varying wood secondary chemistry and the total mass loss of the wood as two species of fungi interact and compete on it. We designed an experiment to investigate the difference in growth of four fungal species pairs commonly found fruiting together in mid Atlantic forests across two species of wood with high and low levels of secondary chemistry. We measured CO2 respiration, hyphal growth rate, and total wood mass lost in microcosms inoculated with each species alone and in pairs. As expected, microcosms with species pairs showed greater respiration than single species. However, greater respiration rates were observed on*Quercus veluntina*, the wood substrate with greater secondary chemistry, opposing our hypothesis that less secondary chemistry would provide an easier substrate for the fungi to grow on. Further research on the specific enzymatic activity of the fungi as they interact is needed to understand the variations in fungal growth and their interaction with the substrate.

*Poster P49*

leads to coexistence of beneficial and non-beneficial symbionts. Physiological plasticity of preferential allocation also forms a basis for prediction of shifts of strengths of mutualism with changing environment. For arbuscular mycorrhizal fungi, which facilitate plant uptake of phosphorus, we demonstrate that the strength of preferential allocation declines with increasing levels of soil phosphorus and with declining light resources. I construct a general model of the interactive feedbacks of host preferential allocation and the dynamics of root symbiont populations to generate predictions of patterns of efficiency of nutritional mutualisms. For arbuscular mycorrhizal fungi, the model predicts greater phosphorus transfer per unit carbon invested in these fungi with decreasing levels of soil phosphorus and with increasing levels of atmospheric CO2. Both of these patterns have been observed in laboratory and field studies. By connecting physiological plasticity in plant allocation to population processes that govern mutualism stability, this framework advances our understanding of the stability of mutualism and their likely responses to anthropogenic perturbations.

*Symposium S6.2*

**24. Comparative biogeography of lodgepole pine- associated ectomycorrhizal fungal communities in the native and invaded range \*Boaz, Briana**

University of California, Berkeley, Integrative Biology, Berkeley, CA 94720, USA.

*,*

The provenance for the majority of New Zealand plantation lodgepole pines (

absence of compatible ECM fungi is considered a substantial barrier to pine invasion. Lodgepole pines that have escaped from New Zealand timber plantations do not form symbioses with native ECM species. Although unknown, it is likely that lodgepole pines and their specialist ECM fungi from western US have been co- dispersed through the timber industry on a global scale, which could significantly determine the dispersal and distribution of this invasive species

locally and worldwide.

*Poster P56*

**25. Big fungal data: Addressing global change questions in fungal ecology and biogeography with assembled pan-European datasets \*Boddy, Lynne**(1), Kauserud, Håvard(2), Andrew, Carrie(2) and the ClimFun team

1.Cardiff University, School of Biosciences, Cardiff CF10 3AX, UK; 2.University of Oslo, Department of Biology, NO-0316 Oslo, Norway. BoddyL@cf.ac.uk

Species occurrence data are becoming increasingly available for analysis through field mycology, citizen science projects, and digitization of fungarium records. We have assembled a pan- European meta-database of observational fungal fruit body records which we are using to address ecological, biogeographical and phenological questions relating to global change. Initially over 7.3 million unique species records, spanning nine countries, were processed and assembled into 6 million usable records of more than 10,000 species. Unsurprisingly, time of fruiting varies geographically. Fruiting phenolgy is changing: typically, the average fruiting season is extending, though for some species it is contracting. Different species and functional groups behave differently: fungi ectomycorrhizal on deciduous trees tend to fruit later now than in the past; saprotrophs are more variable though most have an extended fruiting season. Some species now fruit both in spring and in autumn, and spring fruiting is getting earlier. Ranges of species are also likely to be shifting with changing climate.

*Contributed Talk C6.2*

**26. Reorganization of the endoplasmic reticulum of *Fusarium graminearum* during trichothecene mycotoxin induction.**Boenisch, Marike J.(1) Broz, Karen L.(2), **\*Kistler, H. Corby(2**)

1.Department of Agronomy and Plant Genetics, University of Minnesota, St. Paul, MN USA; 2.USDA ARS Cereal Disease Laboratory, St. Paul, MN 55108, USA. hckist@umn.edu

The ascomycete fungus *Fusarium graminearum* causes disease on wheat and barley and contaminates

communities are likely important in determining the potential range of this invader, and may be predicted by Island Biogeography Theory. The research objectives are to (1) compare ECM communities associated with lodgepole pine in the western US native and New Zealand invaded ranges; (2) determine whether Island Biogeography Theory can describe ECM dispersal and distribution patterns; (3) determine the spatiotemporal and environmental gradients structuring these ECM communities; and (4) predict

the consequences for future plant invasions.

beboaz@berkeley.edu

Lodgepole pine (*Pinus contorta*)

ectomycorrhizal (ECM) tree

western North America, is one of the most widely planted tree species in the world. It is one of the most aggressive and ecologically damaging invasive plants in the southern hemisphere,where it has been extensively cultivated in timber plantations and has frequently escaped into adjacent plant

an obligately

with a native range in



communities.



*contorta*) is the western coastal United States. Lodgepole pine-associated ECM communities

*P. contorta var.*

 

show high host specificity, and the



The dispersal and distribution



patterns of lodgepole pine-associated ECM



grains with trichothecene mycotoxins making them unfit for human consumption. Using fluorescence tagged proteins and the fluorescent dye ER-Tracker Blue-White DPX, we discovered that three enzymes, catalyzing early and late steps in trichothecene biosynthesis, hydroxymethylglutaryl CoA reductase (Hmr1p), trichodiene oxygenase (Tri4p), and calonectrin oxygenase (Tri1p), co-localize with each other under toxin inducing conditions *in vitro* and *in planta* at the endoplasmic reticulum (ER). Applying super resolution microscopy, we determined that the ER organization shifts from being highly reticulate under non-toxin inducing conditions to being tubular and exhibiting pronounced perinuclear ER upon toxin induction. The reorganization of the ER upon toxin induction was further confirmed by observing similar fluorescence patterns with the native ER resident protein Sec22p of *F. graminearum* tagged with GFP (green fluorescent protein), as well as with GFP containing the ER-retrieval sequence HDEL. High pressure freezing and freeze substitution for TEM (transmission electron microscopy) revealed the ultrastructure of ER membranes in toxin producing and non-toxin producing cells. Different types of proliferations of the smooth ER, including lamellar stacks of perinuclear ER membranes as well as lamellar stacks of peripheral ER membranes and concentric stacks were observed in cells grown under toxin producing conditions. Visualizing nuclei of a histone H4p::GFP/Tri4p::RFP doubly tagged strain under toxin induction supported that trichothecene biosynthesis is localized at both smooth perinuclear ER and peripheral ER. As a consequence, trichothecene biosynthesis appears to be localized at particular regions of the smooth ER. Subcellular changes which occur during trichothecene production *in vitro* and *in planta* might facilitate toxin biosynthesis and self-protection of the fungus.

*Poster P122*

**27. Strong evidence for plant-based choice and rewards in the ectomycorrhizal symbiosis \*Bogar, Laura**(1), Peay, Kabir(1), Kornfeld, Ari(2), Huggins, Julia(3), Hortal, Sara(4), Anderson, Ian(4), Kennedy, Peter(3)

1.Stanford University, Department of Biology, Stanford, 94305, USA; 2.Carnegie Institution, Department of Global Ecology, Stanford, 94305, USA; 3.University of Minnesota, College of Biological Sciences, Saint Paul, 55108, USA; 4.University of Western Sydney, Hawkesbury Institute for the Environment, Richmond, 2753, Australia. lbogar@stanford.edu

In arbuscular mycorrhizal and legume-rhizobia interactions, plants can respond to both the potential and realized quality of potential symbionts: prior to

interacting, by interpreting microbial signals, and after interacting, by rewarding cooperative microbial behaviors. In the ectomycorrhizal symbiosis, however, it is not know if the same mechanisms operate. We performed two separate experiments examining the influence of identity-based microbial signals (pre- interaction partner discrimination) and the performance of fungal symbionts (post-interaction rewards) on symbiotic outcomes in interactions between ectomycorrhizal fungi in the genus *Suillus* and Pinaceae host plants. The first experiment challenged *Larix occidentalis* seedlings with three different *Suillus* species of apparently similar symbiotic qualities, and found that both the timing and extent of colonization – measures of pre-interaction discrimination – varied with the identity of the fungi present and with fungal competitive context, suggesting that plants can discriminate among partners based on identity signals even before the symbiosis begins. In the second experiment, we manipulated fungal partner quality and used 13CO2 enrichment to examine post-interaction rewards. Using a split root system, we measured differences in *Pinus muricata* carbon allocation to genetically identical *Suillus brevipes* isolates differing only in their N supply, simulating differences in fungal partner quality. We found that symbiotic ectomycorrhizal13 roots with higher nitrogen content received more C from the plant, demonstrating that the plant host can differentially reward more cooperative partners. Our results indicate that ectomycorrhizal host plants have fine-tuned abilities to discriminate among fungal partners based both on identity and quality, which may help explain the global diversity, success, and stability of this mutualistic interaction over the last hundred million years.

*Contributed Talk C19.1*

**28. Identification of polarity-defective mutants in**

***Aspergillus nidulans***

**\*Bomer, Brigitte**; Gwinn, Jesse; Shaw, Brian D. Texas A&M University, Department of Plant Pathology and Microbiology, College Station, Texas, 77840- 2132, USA. bbomer2@tamu.edu

Cell polarity is a fundamental process necessary for growth and development. Polarized growth is required for disease initiation in many pathogenic systems, such as filamentous fungi. Filamentous fungi concentrate the addition of new cell wall material at the apex. The amenable genetics of Aspergillus nidulans, as well as the prevalence of apical extension make it an ideal model for studying polar growth. The work described here was designed to identify genes involved in polar growth. A collection of temperature- sensitive (TS) A. nidulans mutants was screened for deficiencies in polarity. A series of temperature-shift

experiments revealed that the isolated mutants, C47 and M5, were aberrant in polarity establishment and maintenance when grown at restrictive temperature (42oC). To identify the gene responsible for the TS phenotype, complementation using a genomic library, constructed in the autonomously replicating vector pRG3-AMA1, fully restored wild-type (WT) growth and allowed for isolation of the plasmid containing the complementing gene. Progress toward identifying the function of the complementing genes will be discussed. We hypothesize that the gene contained in the genomic insert found in the complementing plasmid plays an important role in polarity establishment during isotropic growth and polarity maintenance during hyphal extension.

*Poster P118*

**29. Neighbor effects on plant microbiomes \*Bonito, Gregory**(1), Benucci, Gian Maria Niccolò(1) Hameed,Khalid(2), Schadt, Christopher W.(3) Vilgalys, Rytas(2) 1.Michigan State University, Department of Plants, Soil and Microbial Sciences, East Lansing, MI 48824, USA; 2.Duke University, Biology Department, Durham, NC 27708, USA; 3.Oak Ridge National Laboratory, Oak Ridge TN, USA. bonito@msu.edu

Fungi and bacteria that directly associate with plants are known as the plant microbiome. There is renewed interest in characterizing the structure and dynamics of these microbial communities given their presumed role in plant health, disease and local adaptation. While plant microbiomes have been shown to be structured by geography and host, and mycorrhizal networks are known to link forest trees through belowground carbon flow, the impact of neighboring plants on each others belowground microbiome are still not clear. Thus, we designed a series of trap-plant experiments in which pairs of conspecific and heterospecific plants were grown together in a common soil to determine neighbor effects on the plant microbiome. We used combinations of *Populus deltoides, P. trichocarpa, Pinus taeda* and *Quercus alba* in these experiment and assessed rhizobiome community structure with high throughput MiSeq amplicon sequencing of the ITS and 16S rDNA. In agreement with previous studies we found that root fungal and bacterial communities were structured by plant host. However, plants grown alongside heterospecific hosts differed from those of plants grown with conspecific hosts, and that the shift in community structure was dependent on the species of neighboring plant. For instance, *P. trichocarpa* increased fungal diversity on pine roots but decrease diversity on oak. These results highlight the impact of neighbor effects on the assembly and function of plant microbiomes.

*Contributed Talk C20.3*

**30. Arsenic in macrofungi: Diversity of species \*Borovička, Jan**(1,2), Braeuer, Simone(3), Kameník, Jan(1), Goessler, Walter(3) 1.Nuclear Physics Institute, The Czech Academy of Sciences, Hlavní 130, 25068 Řež, Czech Republic; 2.Institute of Geology, The Czech Academy of Sciences, Rozvojová 269, 16500 Prague 6, Czech Republic; 3.Institute of Chemistry, University of Graz, Universitätsplatz 1, 8010 Graz, Austria. bore.bor@gmail.com

Arsenic is an element with varying toxic properties known to accumulate in macrofungal fruit- bodies. In most macrofungi from pristine sites common content of arsenic does not exceed 1 mg kg-1 (dry biomass). However, our screening of arsenic concentrations in nearly 1,000 samples of European macrofungi has revealed remarkable accumulation of this element. In some species, arsenic concentrations may reach up to thousands of mg kg-1. The highest concentrations were determined in ectomycorrhizal Basidiomycetes (Boletus s.l., Cortinarius, Hebeloma, Inocybe, Russula, and Thelephora) and two Ascomycetes (Sarcosphaera and Elaphomyces). Interestingly, arsenic concentrations up to hundreds of mg kg-1 were detected in many Alnus-associated symbiotic fungi, e.g. Cortinarius alnetorum and several Alnicola species. Furthermore, arsenic levels in macrofungi from sites with arsenic-rich soils were significantly elevated. In some species, high As contents were correlated with high zinc concentrations (up to ~1000 mg kg-1). Preliminary screening of the arsenic species in fungal biomass has revealed a variety of compounds. Inorganic arsenic was the major constituent of all analyzed Alnicola species. In most other macrofungi organic arsenic compounds such as methylarsonic acid, dimethylarsinic acid, arsenobetaine, arsenocholine, and trimethylarsine oxide were dominating. Several minor arsenic compounds are yet to be identified.

*Poster P71*

**31. Two distinct new species of *Phytophthora*, taxon mugwort and taxon juncus, isolated from restored California ecosystems \*Bourret, Tyler B.**(1), Mehl, Heather K.(1), Swiecki, Tedmund J.(2), Bernhardt, Elizabeth A.(2), Hillman, Janell M.(3), Rizzo, David M.(1)

1.University of California-Davis, Department of Plant Pathology, Davis, CA, 95616; 2.Phytosphere Research, Vacaville, CA, 95688; 3.Santa Clara Valley Water District, San Jose, CA, 95118. tbbourret@ucdavis.edu

A survey of sites containing plantings of nursery- origin native Californian flora was conducted between

August 2015 and April 2016 in Santa Clara County. *Phytophthora* species were baited with pear fruits and Rhododendron leaves from samples containing soil and root material. More than thirty species of *Phytophthora* were recovered including *P*. taxon mugwort and *P*. taxon juncus from California Mugwort (*Artemisia douglasiana*) and rush (*Juncus* sp.), respectively. Neither *Phytophthora* species could be unambiguously placed into a subgeneric clade based on analysis of the ITS nuclear ribosomal DNA and mitochondrial COXII and mtCOXI barcoding loci, so a multi-locus phylogenetic approach was undertaken using six loci (large subunit rDNA, nuclear beta tubulin, mtCOXII, mtNad9, mtRPS10 and mtSecY) recommended for resolving relationships within the genus. Model and partition schema tests for likelihood-based phylogenetics suggested the implementation of highly parameterized models of molecular evolution; the trees inferred with these schemata appear to resolve the placement of the two novel taxa and also suggest different relationships between some of the subgeneric clades of *Phytophthora*. Morphological features of the novel taxa were studied, highlighting the distinct sporangia of *P*. taxon mugwort. Although the two species were isolated from California and associated with planted native flora, it remains a serious question whether they are native or exotic, with implications both for our understanding of the natural history of *Phytophthora* and the health of California's natural ecosystems. *Poster P62*

1.University of Arizona, School of Plant Sciences, Tucson, AZ, 85721, USA; 2.University of Arizona, Department of Ecology and Evolutionary Biology, Tucson, AZ, 85721, USA. eabowman@email.arizona.edu

Community composition of EMF differed as a function of elevation but composition of FEF did not. Canonical correspondence analysis revealed effects of biotic and abiotic factors relevant to elevation in shaping distributions of EMF (soil chemistry, climate, and plant community composition). *Humaria hemisphaerica* (Pezizomycetes) and *Tomentella* spp. (Agaricomycetes) were significantly associated with high elevation sites, which featured pine- and pine- Douglas fir stands, lower temperatures, higher precipitation, and higher quantities of soil nutrients. *Cenococcum geophilum* (Dothideomycetes), *Tuber separans* (Pezizomycetes), and *Russula* spp. (Agaricomycetes) were significantly associated with low elevation sites, which were warmer, drier, less nutrient-rich, and characterized by pine-oak

woodlands and pine stands.

*Poster P25*

**33. Natural *Saccharomyces* hybrids give clues about fungal domestication \*Boynton, Primrose J.**(1), Nolte, Arne(2), Greig, Duncan(1)

1.Max Planck Institute for Evolutionary Biology, Experimental Evolution Research Group, Plön, 24306, Germany; 2.Carl von Ossietzky University, Institute for Biology and Environmental Sciences, Ecological Genomics Working Group, Oldenburg, 26111, Germany. pboynton@evolbio.mpg.de

The genomes of domesticated fungi often contain evidence of past hybridization and introgression events. We do not yet understand whether human- influenced environments select for introgressed genes, or if humans simply enable hybridization by bringing related species together. We surveyed the genomes of *Saccharomyces* yeast strains isolated in and around a winery in Montalcino, Italy for evidence of hybridization. We assessed the genome diversity of 50 *Saccharomyces* isolates by sequencing RAD-tagged genomic DNA and comparing sequences to the reference genomes of five closely related *Saccharomyces* species. Forty-three of the 50 analyzed genomes showed considerable hybridization, with minority species contributions of at least 3% and as much as 42% of a strain's genome (*e.g.,* one strain, isolated from the soil beneath an oak tree, contained DNA matching 45% of the *S. cerevisiae*, 42% of the *S. kudriavzevii*, and 12% of the *S. paradoxus* reference

Ectomycorrhizal fungi (EMF) increased in abundance with elevation, whereas foliar endophytic fungi (FEF) decreased. Diversity of EMF and FEF did not change



with elevation.

 

provide a simultaneous perspective on EMF and FEF associating with *Pinus ponderosa* in forests of the southwestern US, which are experiencing rapid and

Together these data

 

cascading ecological changes due to a shifting climate.



**32. Ectomycorrhizal and foliar endophytic fungal communities of *Pinus ponderosa* along a spatially**



**constrained elevation gradient**



**\*Bowman, Elizabeth A.**(1), Arnold, A. Elizabeth(1,2)



Understanding factors that influence the distributions of plant-symbiotic fungi is important for projecting species- and community-level responses to climate change. We examined ectomycorrhizal and foliar endophyte communities associated with *Pinus ponderosa* along an elevation and climatic gradient in southeastern Arizona. Sites spanned a distance of 10.1 km and an elevational change of 635 m, corresponding to a difference of 4°C in annual temperature and 15 cm in annual precipitation. We collected roots and needles of 63 mature trees and measured soil chemistry at representative individuals. We sequenced nrITS and, when possible, an adjacent portion of the nrLSU for ectomycorrhizal root tips (459 sequences, 156 OTU) and endophytes (419 sequences, 49 OTU).

genomes). Strains from domesticated environments had less hybridization than strains isolated from neighboring oak trees. On average, oak-associated strains' genomes were composed of 23% minority species DNA, and strains isolated from grape plants, agricultural soil, compost, insect, and fermenting grape must were composed of 5% minority species DNA. Additionally, the majority species in 11 of 14 oak-associated strains was *S. kudriavzevii*, while the majority species strains from all other sources was *S. cerevisiae*. Fermentation vats also lost hybrid isolates with time: strains isolated within the first two weeks of fermentation had more introgressed DNA than strains isolated at the end of fermentation. Domesticated environments appear to select against hybrid genomes, but may select for individual introgressed genes. Ongoing research is investigating the fitness consequences of hybridization in natural and domesticated environments and the genomic patterns of winery hybrids.

*Contributed Talk C14.6*

**34. Plant host and geospatial effects on diversity of leaf-associated fungi in a tropical island ecosystem \*Bradley, Amanda**(1); Garbelotto, Matteo(2), Osmundson, Todd W.(1)

1.University of Wisconsin–La Crosse, Department of Biology, La Crosse, WI, 54601, USA; 2.University of California, Department of Environmental Science, Policy and Management, Berkeley, CA, 94720, USA. bradley.aman@uwlax.edu

Estimating Earth’s biodiversity is a difficult task, considering the many challenges that come with conducting exhaustive surveys of organisms worldwide. Fungal biodiversity estimates often rely on extrapolations from limited amounts of data on plant : fungal richness ratios. Understanding what factors influence the association between plant and fungal diversity is therefore a key component to making more accurate estimates of fungal diversity. We characterized the diversity of leaf-associated fungi on the island of Moorea, French Polynesia across host species and geographic distance by sampling leaf material from every plant located within sampling plots situated throughout the island. Fungal communities were characterized using analyses of Illumina sequence libraries, with plant species confirmed using rbcL DNA barcodes. Patterns of fungal richness and beta diversity will be assessed between plant hosts and levels of geographic distance. *Poster P28*

**35. Continental-level population differentiation and environmental adaptation in *Suillus brevipes* \*Branco, Sara**(1), Taylor, John W.(2), Bruns, Thomas D.(2)

Recent advancements in sequencing technology allowed researchers to better address the patterns and mechanisms involved in microbial environmental adaptation at large spatial scales. Here we investigated the genomic basis of adaptation to climate at the continental scale in *Suillus brevipes*, an ectomycorrhizal fungus symbiotically associated with the roots of pine trees. We used genomic data from 55 individuals from seven locations across North America to perform genome scans to detect signatures of positive selection and assess whether temperature and precipitation were associated with genetic differentiation. We found that *S. brevipes* exhibited overall strong population differentiation, with potential admixture in Canadian populations. This species also displayed genomic signatures of positive selection as well as genomic sites significantly associated with distinct climatic regimes and abiotic environmental parameters. These genomic regions included genes involved in membrane integrity and DNA/RNA processing that most likely play a role in cold stress response. Our study sheds light on large- scale environmental adaptation in fungi by identifying putative adaptive genes and providing a framework to further investigate the genetic basis of fungal adaptation. *Contributed Talk C3.2*

**36. Population genomics can improve our understanding of disease emergence by uncovering genetic variation and adaptation in plant- pathogenic fungi**

**\*Brewer, Marin**(1), Stewart, Jane(2), Sumabat, Leilani(1) 1. University of Georgia, Plant Pathology, Athens, GA 30602 USA; 2. University of Colorado, Bioagricultural Sciences and Pest Management, Fort Collins, CO 80523 USA. mtbrewer@uga.edu

Emerging plant diseases caused by fungi in both natural and agricultural settings have increased due to factors including global movement of plant material, climate change, monoculture, evolution of aggressive genotypes, and host susceptibility. Exobasidium leaf and fruit spot of blueberry, caused by Exobasidium maculosum, is an emerging disease that has rapidly increased in prevalence throughout the southeastern US since 2011. Target spot of cotton, soybean, and tomato, caused by Corynespora cassiicola, a ubiquitous tropical pathogen with a very wide host range, has also emerged recently in the southeastern US. We used molecular systematics, population

1.University of Paris, Sud, Departement Genetique et Ecologie Evolutives, Orsay, 91405 France; 2.University of California, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA.



sara.mayer.branco@gmail.com



genetics, and population genomic approaches, including ddRAD-Seq and whole genome resequencing, to investigate genetic diversity and adaptive regions in the genomes of these fungi to understand the basis of emergence of these two diseases. Results showed that populations of E. maculosum are geographically structured and very diverse, with high levels of diversity distributed across the genome. Rapidly evolving regions of the genome that may underlie adaptation to different geographic regions have been identified. We conclude that the emergence of Exobasidium leaf and fruit spot is not due to a recent introduction, host jump, or the evolution of more aggressive genotypes of E. maculosum, but could be due to an increasing host population or an environmental change. Conversely, C. cassiicola populations are structured by host species, but not geography, and have little to no genetic diversity. Thus, target spot is likely due to host jumps, multiple introductions specialized to different host species, or evolution of aggressive genotypes. Ongoing comparative genomic analyses of isolates from different hosts will shed light on genes that may be involved in adaptation to diverse hosts. These studies reveal how population genomics can be used to understand both the genetic patterns and processes of disease emergence.

*Symposium S8.3*

**37. Wood-rotting basidiomycetes associated with grapevine trunk diseases in Texas \*Brown, Albre**(1), Lawrence, Daniel P.(2), Baumgartner, Kendra(3), Appel, David(1)

1.Texas A&M University, Department of Plant Pathology, College Station, TX, 77843-2132, USA; 2.Department of Plant Pathology, University of California, Davis, CA 95616, USA; 3.United States Department of Agriculture-Agricultural Research Service, Davis, CA USA, 95616. albreabi@gmail.com

The grapevine trunk diseases Esca, Botryosphaeria dieback, Eutypa dieback, and Phomopsis dieback impact vineyards in all major grape-growing regions of the world. The causal pathogens (*Phaeomoniella chlamydospora* and *Phaeoacremonium minimum*, *Neofusicoccum parvum*, *Eutypa lata*, and *Diaporthe ampelina*, respectively) represent five separate orders, spanning three classes of ascomycetes. They cause localized, internal infections after entering the vine via pruning wounds. Typically, multiple pathogens infect a single vine and sometimes even a single wood lesion. Infections by wood-rotting basidiomycetes, which are thought to follow the ascomycetes, cause more extensive decay, although the interactive effects of such mixed infections on expression of trunk-disease symptoms have not been verified. Past reports of basidiomycetes

in Esca-symptomatic vines in Australia, Europe, New Zealand, South Africa, and South America identified species of *Auricularia*, *Fomitiporia*, *Inonotus*, *Phellinus*, *Stereum*, and *Trametes.* There are only two reports of basidiomycetes causing Esca-associated white rot in North America. Observations in 14 Texas vineyards from 2014-2016 revealed the presence of three genera of white-rot fungi, *Tropicoporus*, *Inonotus*, and *Stereum,* all of which are new reports on grapevines in Texas. A majority (146 of 160) of samples revealed a relationship between the presence of the basidiomycetes and Esca symptoms in diseased vines. These observations raise questions concerning the origins and spread of the specific genera of basidiomycetes in Texas vineyards, and their association with trunk pathogens and other diseases. However, it is clear as the vineyards in Texas age, the impacts of trunk diseases are worsening and improved management options are becoming more and more critical.

*Contributed Talk C8.4*

**38. We do not know what we do not know: Elucidating biodiversity, ecosystem processes, and community assembly of fungal wood-decomposing communities in tropical aquatic and marine habitats**

**\*Brown, Shawn P**., Heath, Katy D., Dalling, James W., Ferrer, Astrid 1.University of Illinois at Urbana-Champaign, Department of Plant Biology, Urbana, IL, 61801, USA .spbrown1@illinois.edu

One of the grand challenges of sequence based fungal ecology is to link fungal community composition to community function and ecosystem processes. Here, we focus on tropical aquatic/marine wood decomposing fungi to shed new light on these organisms. We used a multi-faceted approach to query aquatic fungal communities. Through traditional wet- culturing methods, we have established ~400 single spore isolates, many of which are novel. Taxa descriptions are ongoing including traditional morphological as well as sequence based phylogenetic placement using next-generation phylogenetics using Fluidigm Integrated Fluidic Chips (IFC) to simultaneously amplify and sequence phylogenetically informative genes and functional genes to provide rapid placement and functional understanding of previously unknown/poorly known taxa. Additionally, these organisms were tested for the production of functional decomposition enzymes. Further, using culture independent means, fungal, bacterial, and archaeal communities were sequenced directly from decomposing wood across a salinity gradient to understand mechanisms of community filtering. Salinity provides strong community selection

pressures that structures communities but decomposition stage only impacts fungi. There is an apparent disconnect between observed culture based and culture-independent taxon distributions. Fungi are presumed to be the primary wood decomposers, but we demonstrate that many organisms play large roles in aquatic decomposition. Particularly important are syntrophic associations between diazotrophic bacteria and dominant fungal organisms that exchange carbon for nitrogen from the bacteria. This is the first time such an association has been demonstrated for aquatic fungi. Taken together, this project vastly expands our understanding of tropical aquatic and marine fungal distributions and ecosystem processes.

*Symposium S2.3*

**39. Can co-inoculation of brown and white rot fungi increase degradation of crude oil in soils? \*Bruce, Andrea L.**(1), Rolfhus, Kristofer R.(2), Osmundson, Todd W.(1)

1.University of Wisconsin, Department of Biology, La Crosse, WI, 54601, USA; 2.University of Wisconsin, Department of Chemistry and Biochemistry, La Crosse, WI, 54601, USA. bruce.andrea@uwlax.edu

Wood decay fungi are promising candidates for soil remediation due in part to their production of extracellular enzymes. It is well established that the lignolytic enzymes of white rot fungi are able to degrade a wide range of environmental pollutants. Some brown rot fungi have been shown to degrade organic pollutants to a similar extent, likely involving different mechanisms. We hypothesize that white and brown rot fungi may be able to degrade different fractions of complex organic pollutants as they do different fractions of woody substrates to increase bioremediation efficiency. The brown rot fungus *Antrodia vaillantii* and the white rot *Stropharia rugosoannulata* have been found to be good soil colonizers, capable of significant PAH degradation without suppression of indigenous soil microbes known to contribute to bioremediation of petroleum hydrocarbons. We aim to apply the concept of niche partitioning observed in nature to mycoremediation by co-inoculating *A. vaillantii* and *S. rugosoannulata* in crude oil-contaminated soil to examine synergistic degradation effects in non-sterile soil. Experiments will be conducted in soil microcosms at room temperature and sampled every 2 weeks for a total of incubation period of 10 weeks. Petroleum hydrocarbons will be extracted via mechanical shaker and separated by GS-MS to calculate removal ratios per carbon chain length at each sampling. Abundance of each inoculated fungus, relative to the other, will be analyzed using qPCR to assess competitive outcomes. *Poster P74*

**40. Mechanisms of population genomic variation in secondary metabolism \*Bushley, Kathryn E.**(1), Menke, Jon(2), Rehner, Steve(3), Spatafora, Joseph W.(4)

1.University of Minnesota, Plant Biology, Saint Paul, MN 55108; 2.Cargill, Wayzata, MN 55391; 3.Systematic Mycology and Microbiology Laboratory, USDA-ARS, Beltsville, Maryland 20705; 4.Oregon State University, Botany and Plant Pathology, Corvallis, Oregon, 97331. kbushley@umn.edu

We investigate population genomic variation of genes and clusters involved in secondary metabolite biosynthesis in two insect pathogenic fungi, the beetle pathogen *Tolypocladium inflatum* and the wide host- range insect pathogen and biocontrol agent *Beauveria bassiana*. The draft genome sequence of T. inflatum revealed its potential to synthesize a diverse array of secondary metabolites beyond the well-known immunosuppressant drug Cyclosporin A. Using Pac Bio single molecule real time sequencing, we improved the resolution of the sequenced reference strain T. inflatum NRRL 8044 and synthesized genomes of five additional strains isolated from different hosts and environments. Assembly, annotation, and comparative genomic analyses of these strains provides an avenue for investigating evolutionary genetic mechanisms contributing to intraspecific variation in genes and clusters that encode the synthesis of fungal secondary metabolites, including polyketides, nonribosomal peptides, terpenes, and alkaloids. Similarly, draft genomes of ten strains of *B. bassiana* and several outgroup *Beauveria* species (*B. brongniartii, B. asiatica, B. australis*) have been sequenced using Illumina technology to analyze the evolution of metabolite clusters. Differential expression of metabolite cluster genes in plant and insect infection assays examine the role(s) of specific metabolites in the colonization and pathogenesis of plant versus insect hosts. The results of our analysis shed light on the relative importance of transposition, selection, duplication/deletion, recombination, and horizontal transfer in the evolution of fungal metabolite clusters and illuminate how secondary metabolites may shape the interaction of these fungi with distinct hosts. *Contributed Talk C2.2*

**41. A fast and reliable procedure for spore collection from anaerobic fungi: Application for RNA uptake and long-term storage of isolates \*Calkins, Shelby**, Elledge, Nicole, Hanafy, Radwa A., Elshahed, Mostafa S., Youssef, Noha

Oklahoma State University, Department of Microbiology and Molecular Genetics, Stillwater, OK 74078, USA. shelby.s.calkins@gmail.com

Anaerobic gut fungi (AGF) represent a basal fungal lineage (Phylum Neocallimastigomycota) that resides in the rumen and alimentary tracts of herbivores. The AGF reproduce asexually, with a life cycle that involves flagellated zoospores released from zoosporangia followed by encystment, germination, and the subsequent development of rhizomycelia. A fast and reliable approach for AGF spores collection is critical not only for developmental biology studies, but also for molecular biological (e.g. AMT- transformation, RNAi) approaches. Here, we developed and optimized a simple and reliable procedure for the collection of viable, competent, and developmentally synchronized AGF spores under strict anaerobic conditions. The approach involves growing AGF on agar medium in serum bottles under anaerobic conditions, and flooding the observed aerial growth to promote spore release from sporangia into the flooding suspension. The released spores are gently collected using a wide bore sterile needle. Process optimization resulted in the recovery of up to 7X109 spores per serum bottle. Further, the released spores exhibited synchronized development from flagellated spores to encysted spores and finally to germinating spores within 90 minutes from the onset of flooding. At the germinating spore stage, the obtained spores were competent, and readily uptook small interfering RNA (siRNA) oligonucelotides. Finally, using multiple monocentric and polycentric AGF isolates, we demonstrate that AGF grown on agar surface could retain viability for up to 16 weeks at 39oC, and hence this solid surface growth procedure represents a simple, cryopreservative- and freezing temperatures-free approach for AGF storage. *Poster P131*

**42. Focal adhesion genes expression in the anaerobic fungus *Orpinomyces* sp. strain C1A \*Calkins, Shelby**, Elledge, Nicole, Youssef, Noha. Oklahoma State University, Department of Microbiology and Molecular Genetics, Stillwater, OK 74078, USA. shelby.s.calkins@gmail.com

Anaerobic gut fungi (AGF) reside in rumen, hindgut, and feces of ruminant and non-ruminant herbivorous mammals and reptilian herbivores. They constitute a basal fungal lineage with an asexual life cycle involving a swimming zoospore stage that usually germinates into a vegetative hyphal stage upon exposure to solid surfaces or carbon source. Our efforts produced the first published genome of AGF isolate *Orpinomyces* sp. strain C1A, identifying multiple unique genomic features differentiating them from Dikarya fungi. One feature is possession of some genes for focal adhesion (FA), which is completely absent in Dikarya fungi. In this study, we sought to identify the role of FA in C1A. We hypothesized that

FA in C1A might either be functional for 1) adhesion to solid surfaces, 2) during flagellar assembly (zoosporogenesis), or 3) during spore germination. Investigating hypothesis 1, we studied the transcription of talin, vinculin, paxillin, and actinin (genes encoding the scaffolding proteins of focal adhesion), during C1A growth using insoluble substrate (attached) versus soluble substrate (unattached). We show FA genes were transcribed under both growth conditions, suggesting adhesion might not be the physiological function of FA in C1A. Exploring hypotheses 2 and 3, we used our recently published flooding protocol for obtaining swimming spore-only (SS) and germinating spore-only (GS) samples of C1A to measure transcriptional levels of FA genes using qRT-PCR. We show FA genes were transcribed in the SS sample, however transcription was significantly higher in the GS sample; Suggesting a possible role of FA scaffolding proteins during flagellar assembly, and during spore germination. Though these results agree with previous studies showing FA scaffolding proteins associate with basal bodies in ciliated cells and function during ciliary assembly, we show for the first time that FA scaffolding proteins may play an additional role in germ tube growth during germination.

*Poster P130*

**43. Effect of manufacturing processes on fungal colonization and incidence of decay in Irish utility poles \*Cappellazzi, Jed E.**, Morrell Jeffery M.

Oregon State University, Wood Science and Engineering, Corvallis, OR, 97331, USA.

Environment, seasoning, and preservative treatments are major factors driving fungal decay of in-service utility poles. This study investigated the presence of fungi in creosote treated scots pine utility poles from Ireland. Eleven-hundred poles were sampled at five heights from groundline to pole-top. Increment cores were plated on malt benlate agar and unique decay fungi were identified to species-level with Sanger sequencing. Fungal data were combined with environmental and preservative treatment metadata, as well as visible pole decay, to identify wood protection problems. The most common fungal species isolated were *Phlebiopsis gigantea*, *Neolentinus lepideus*, *Sistotrema brinkmannii* and *Stereum sanguniolentum*. Over 50% of poles contained at least one decay fungus. Poles most effected by decay varied by supplier, treatment year and duration of air seasoning. Most isolations occurred in poles treated after 1996, which correlated with changes in pole procurement practices. The relative dominance of *N. lepideus* may be explained by evidence of creosote resistance from this species. Air-

seasoning for longer than 6-months resulted in higher incidence of decay. These data will be used to help guide process-management decisions in climates conducive to fungal decay.

*Poster P80*

**\*Carbone, Ignazio**(1), White, James B.(1), Miadlikowska, Jolanta(2), Arnold, A. Elizabeth(3), Miller, Mark A.(4), Kauff, Frank(5), Schoch, Conrad(6), U'Ren, Jana M.(7), May, Georgiana(8), Lutzoni, François(2)

1.North Carolina State University, Department of Plant Pathology, Raleigh, NC, 27695, USA; 2.Duke University, Department of Biology, Durham, NC, 27708, USA; 3.University of Arizona, School of Plant Sciences, Tucson, AZ, 85721, USA; 4.University of California, San Diego Supercomputer Center, San Diego, La Jolla, California, 92093 USA; 5.University of Giessen, Department of Medicine, Giessen, Germany; 6.National Institutes of Health, National Library of Medicine, National Center for Biotechnology Information, Bethesda, Maryland, 20894 USA; 7.University of Arizona, Agricultural and Biosystems Engineering, Tucson, AZ, 85721, USA; 8.University of Minnesota, Department of Ecology, Evolution, and Behavior, St. Paul, MN, 55108, USA. icarbon@ncsu.edu

High-quality phylogenetic placement of sequence data has the potential to greatly accelerate studies in the diversity, systematics, ecology, and function of diverse groups. We developed the Tree-Based Alignment Selector (T-BAS) toolkit to allow evolutionary placement and visualization of diverse DNA sequences representing unknown taxa within a robust phylogenetic context. In its initial form, T-BAS v1.0 uses a core phylogeny of 979 taxa (including 23 outgroup taxa) representing all 13 classes, 61 orders, 175 families, and 496 genera of the largest subphylum of fungi – Pezizomycotina (Ascomycota) – based on sequence alignments for six loci (5.8S, nrLSU, nrSSU, mtSSU, *RPB*1, *RPB*2). These alignments and the multi-locus phylogeny are curated and will be updated actively as more taxa are sequenced and high quality sequences become available for reference taxa. T- BAS v1.0 has three main uses: (1) Users may download alignments and voucher tables for members of the Pezizomycotina directly from the reference tree, facilitating systematics studies of focal clades. (2) Users may upload sequence files with reads representing unknown taxa and place these on the phylogeny using either BLAST or phylogeny-based approaches, and then use the displayed tree to select

reference taxa to include when downloading alignments. The placement of unknowns can be performed for large numbers of Sanger sequences obtained from fungal cultures and for alignable short reads of environmental amplicons generated with next- generation sequencing (e.g., nrLSU). (3) User- customizable metadata can be visualized on the tree. Overall, T-BAS makes core functions in evolutionary and ecological studies more efficient: the assembly of multi-locus datasets for small and large scale phylogenetic studies, the generation of voucher tables, the placement of novel biodiversity in a phylogenetic context, and the rapid visualization of metadata for evolutionary and ecological inferences.

*Symposium S2.4*

**45. T-BAS: Tree-Based Alignment Selector toolkit for phylogenetic-based placement, alignment downloads, and metadata visualization: An**



**example with the Pezizomycotina tree of life**



**46. Taphrinamycotina/Plant Interactions: *Saitoella complicata* increased growth rate in the presence of *Arabidopsis thaliana*\*Carter-House**, Derreck A., Stajich, Jason E., University of California, Riverside, Department of Plant Pathology and Microbiology, Riverside, CA, 92507 USA; dcart001@ucr.edu

*Saitoella complicata*, a saprophytic yeast fungi, isolated from the Himalayas nearly fifty years ago has recently come under our examination due to its interesting ability to seemingly detect the presence of plants. While looking for changes in cellular morphology while near roots, we noticed that the yeast did not produce hyphae or extracellular appendages as expected, but showed increased growth rates. Saitoella covers the root surface after coming in contact. In an attempt to develop a more quantitative method to measure growth we grew the yeast in liquid media with plants and used spectroscopy to measure optical density over time. After observing that Saitoella grows faster while in the same liquid media as Arabidopsis, we began to explore why. The yeast may be sensing hormone signals produced by the plant, much like many other ectomycorrhizal fungi. Strigolactone is one hormone that has gained popularity lately for its ability to be exuded from the plant roots and be detected by pathogens, parasitic weeds, and symbiotic fungi. We tested this hypothesis by growing the fungi in the presence of stigolactone mutants (*max3-11, max 4-6*). Looking for similar results in close relatives we found that *Schizosaccharomyces pombe* also demonstrates an increased growth rate in the plant- containing liquid media. Pombe, being such a well- studied organism, has an annotated genome and knockouts generated for most of its genes. Many important questions still remain. Why is this saprophyte growing faster with Arabidopsis? What receptors are detecting the plant? Can they be transformed to other yeast or fungi to create symbiotic

relationships that may protect plants from pathogens and benefit the agricultural industry? *Poster P141*



**47. A transcriptomic analysis of the pyrophilous ascomycete *Pyronema omphalodes* in burned soil \*Carver, Akiko**, Bruns, Thomas D. U.C. Berkeley, Plant and Microbial Biology, Berkeley, 94720-3102, USA. aacarver@berkeleydotedu

Post-fire soil systems have significant direct and indirect effects on global carbon storage. Fires result in a large amount of carbon that remains resident on the site as partially pyrolyzed material that has a long residency time and constitutes a significant pool in fire-prone ecosystems. In addition, fire induced hydrophobic soil layers, caused by condensation of pyrolyzed waxes and lipids, increase post-fire erosion and lead to long-term productivity losses. A small set of pyrophilous soil fungi dominate post-fire soils and are likely to be involved with the degradation of these compounds, yet almost nothing is currently known about the metabolic processes these fungi employ. Here we analyze the transcriptome of *Pyronema omphalodes*, a dominant pyrophilous ascomycete, in order to characterize its effect on burned soil. *Poster P45*

**48. 100 year legacy of deforestation and slash burning on soil microbes in Great Lake forests \*Castillo, Buck**(1), Nadelhoffer, Knute(2), Le Moine, James(3), James, Timothy Y.(4)

1.University of Michigan, Ann Arbor, Department of Ecology and Evolutionary Biology, Ann Arbor, 48104, United States. buckcast@umich.edu

Determining how disturbances alter ecosystems and their communities is essential to understanding how the state of the world’s forests will change, and what impact those changes will have on energy balances at a local to global scale. Forest fires are important disturbances that impact microbes directly through heat induced mortality and indirectly when symbiotic relations, nutrient availability, and available carbon sources (energy) are altered. During the late 19th and early 20th century, widespread logging and wildfire across the northeastern United States left a legacy of disturbance throughout northeastern US forest ecosystems. Few studies conducted to date have utilized meta-genomics, enzyme assays and soil physical and chemical properties to gain an in depth picture of microbial community composition and function post disturbance. This research focuses on the effects of slash and burn disturbances on soil microbial communities structure and function. Here we aim to establish data for fire legacies post deforestation in Great Lakes forests by utilizing a 100+ year burn- chronosequence at the University of Michigan

Biological Station (UMBS). Sampling across the already established chronosequence will offer insight into the long-term legacy of disturbances often difficult to obtain by experimental approaches. I will quantify the long term effects of fire on microbial diversity and function by measuring 1) soil physical and chemical properties (C:N) 2) microbial communities through rDNA and reverse transcribed rRNA to determine present and active communities, respectively, and 3) a suite of hydrolytic and oxidative enzymes responsible for soil organic matter decomposition. To examine legacy effects I will identify patterns whereby diversity is altered through time since disturbance, and I hypothesize that diversity and abundance of microbial decomposers and their associated enzymes, and in turn C cycling rates, will increase along with stand age.

*Contributed Talk C20.5*

**49. Potential bioremediation role of fungi associated with red mangroves in Puerto Rico** Castro, Emily Kelly, **\*Cafaro, Matías J.**University of Puerto Rico, Mayagüez, Department of Biology, Mayagüez, PR 00680. matias.cafaro@upr.edu

Mangroves harbor fungi able to synthesize all the necessary enzymes to degrade lignin. Lignolytic enzymes have low substrate specificity, which make them capable of degrading different compounds. Several lignolytic fungi are known to degrade polycyclic aromatic hydrocarbons (PAHs). We studied the capability of selected fungal isolates from red mangrove, *Rhizophora mangle,* to use xenobiotics through the lignin degradation pathway. A total of 20 fungi were isolated including Eurotiales, Hypocreales, Pleosporales and Tritirachiales. Six isolates were selected for experiments using Congo Red and naphthalene as their only carbon and energy source. *Penicillium citrinum* (RmBS 2-1-2) and *Aspergillus caelatus* (IRmPL 5) showed strong ability of using Congo Red, while *Fusarium solani* (RmBS 3) and *Purpureocillium lilacinum* (RmPL 5-1e-2) presented better degradation of naphthalene. Isolates tested positive for laccase, Mn and Li peroxidase activities in the supernatant supporting their potential use as biorremediators.

*Poster P72*

**50. Phylogenomic analyses suggest early origins of major fungal clades and independent diversifications to break down cellulose-rich cell walls**

**\*Chang, Ying**(1), Stajich, Jason(2), Martin, Francis(3), Hainaut, Matthieu(4), Marcet-Houben, Marina (5,6), Gabaldón, Toni(5,6,7), Henrissat, Bernard(4), Spatafora, Joey W .(1)

1.Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR 97331, USA; 2.University of California, Department of Plant Pathology and Microbiology, Riverside, CA 92521, USA; 3.INRA Nancy, 54280 Champenoux, France; 4.Université Aix-Marseille, Architecture et Fonction des Macromolécules Biologiques (AFMB), UMR 7257 CNRS, 13288 Marseille, France; 5.The Barcelona Institute of Science and Technology, Centre for Genomic Regulation (CRG), Barcelona,Spain; 6.Universitat Pompeu Fabra (UPF), Barcelona, Spain; 7.Institució Catalana de Recerca I Estudis Avançats (ICREA), Barcelona, Spain. changyi@science.oregonstate.edu

The vast majority of extant fungi are closely associated with plants or plant material. However, little is known regarding the origin and evolution of this association. We approached these questions by studying the evolutionary patterns of plant-cell-wall- degrading enzymes (PCWDE) across the Kingdom Fungi. We sampled whole genome data from 352 taxa (338 fungi and 14 outgroups). We reconstructed a phylogeny and performed dating analysis based on 434 single-copy proteins. We examined the distribution of 36 PWCDE families across all sampled taxa. We investigated the evolutionary patterns of these enzyme families by reconstructing gene genealogies and reconciling with the species phylogeny. We also explored duplication events based on species overlap algorithm. Our results resolved the common ancestors to the phyla of fungi as being older than land plants and that many fungal PCWDE families also have an ancient origin that predates the origin of land plants. We identified multiple, independent episodes of diversification of PCWDE associated with the origins of several higher fungal taxa. The timing of and the fungal taxa involved in these diversification events suggest that major fungal clades were present in terrestrial environments prior to land plants and that they interacted with early terrestrial life forms that contained cellulose-rich cell walls (e.g., streptophytes, microbial mats). *Contributed Talk C17.2*

**51. Diversity in the Mycological Society of America \*Cheeke, Tanya E.**(1), Branco, Sara(2), Haelewaters, Danny(3), Natvig, Donald O.(4), Maltz, Mia(5), Cantrell Rodriguez, Sharon(6), May, Georgiana(7) 1.Indiana University, Department of Biology, Bloomington, Indiana 47405, USA; 2.Université de Paris-Sud, Departement Genetique et Ecologie Evolutives, Laboratoire Ecologie, Systématique et Evolution, UMR 8079 CNRS-UPS-AgroParisTech, Bâtiment 360, Orsay cedex, 91405 France; 3.Department of Organismic and Evolutionary Biology, Harvard University, 22 Divinity Avenue,

Cambridge, Massachusetts 02138, USA; 4.University of New Mexico, Department of Biology, Albuquerque, NM 87131, USA; 5.University of California-Irvine, Department of Ecology & Evolutionary Biology, Irvine, CA 92697, USA; 6.Universidad del Turabo, Biology Department, PO Box 3030, Gurabo, 00778, Puerto Rico. tcheeke@indiana.edu

Increased awareness of systematic biases across the Sciences, Technology, Engineering and Mathematics (STEM) has fueled calls for action. Unfortunately, the recent report of Branco and Vellinga (give citation) suggests that despite a long history of inclusiveness in The Mycological Society of America (MSA), persistent biases exist. In their 2015 paper, Branco and Vellinga report pronounced gender biases within the MSA, both in serving officers and awards, and that white males dominate the more prestigious society’s positions and awards. Following the publication of this study, MSA created an ad-hoc Diversity Committee with the goal of identifying and implementing specific actions to counteract potential biases pertaining to diversity within the society. To provide data for MSA membership, the Diversity Committee conducted a survey to better understand the demographic makeup of our society. The survey revealed gender equality in younger and less academically advanced categories (students and postdoctoral researchers) and male dominance among the older and more academically advanced categories. The survey also showed that MSA is overwhelmingly white, with female minorities particularly underrepresented. These results reflect known trends across STEM fields. Because only specific actions to counteract diversity biases can make MSA more inclusive, the MSA Diversity Committee is developing a set of best practices to be incorporated into the Manual of Operations. The Diversity Committee itself is made up of male and female MSA members, international members, and Lesbian/Gay/Bi/Trans (LGBT) members from across academic rank (e.g., graduate students, postdocs, professors), reflecting just some of the diversity within the MSA. *Poster P148*

**52. The Mycological Society of America Student Section**Cheeke, Tanya(1), Deaver, Ryan(2), Haelewaters, Danny(3), Nelsen, Donald(4), Romero-Olivares, Adriana(5), Smyth, Christopher(6), \***Torres-Cruz, Terry**(2), Uehling, Jessie(7).

1.Indiana University, Department of Biology, Bloomington, IN, 47405, USA; 2.Western Illinois University, Department of Biological Sciences, Macomb, IL, 61455, USA; 3.Harvard University, Department of Organismic and Evolutionary Biology, Cambridge, MA, 02138, USA; 4.University of

Arkansas, Department of Biological Sciences, Fayetteville, AR, 72701, USA; 5.University of California-Irvine, Department of Ecology and Evolutionary Biology, Irvine, CA, 92697, USA; 6.Pennsylvania State University, Department of Plant Pathology and Environmental Microbiology, University Park, PA 16802, USA; 7.Duke University, University Program for Genetics and Genomics, Durham, NC, 27708, USA. tj-torrescruz@wiu.edu

The Mycological Society of America Student Section is a student-run group within MSA, which aims to (1) facilitate communication among all students of the Society, (2) provide opportunities for students to network with other individuals in their own research fields and beyond, and (3) 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 both the evolution of selected traits and how key attributes of fungal taxa influence their environment and stress response. Functional traits are determinants for where fungi can live, how they evolve, and which other organisms they interact with. Recently, trait databases have been launched to centralize current knowledge on fungal traits, document functional diversity, and improve our understanding of how fungi develop and use functional traits to interact with their rapidly changing environments. Our symposium provided an opportunity for communication between members of the Student Section and the leaders in this field. For MSA 2016, we plan a Professional Development Workshop on Thursday August 11th, 2016. This workshop will address the question, ‘How can you prepare the academic job application for a tenure track position in the sciences?’ Panel speakers will include researchers at various stages in their career ranging from new assistant professors to tenured professors from both small liberal art colleges and research institutions. This workshop intends to provide student section members with adequate tools for successful professional development in academia. The Student Section has also continued to publish student spotlights in Inoculum, highlighting the research of students that have received awards from MSA. Additionally, spotlights on mycology clubs have been posted on the Student Section website. The Student Section is open and inclusive, welcoming the participation of graduate students, postdoctoral researchers, and faculty in building and pioneering this group. We hope you will join us at our future events. *Poster P149*

**53. Mycorrhizal responsiveness differs among native and non-native prairie plants \*Cheeke, Tanya E.**(1), Gurholt, Carli R.(1), Bever, James D.(2).

1.Indiana University, Bloomington, Indiana; 2.University of Kansas, Lawrence, Kansas, USA. tcheeke@indiana.edu

Early successional plants, such as non-native asters and grasses, often colonize disturbed prairies, preventing the establishment of native, late successional species. The reduction of mycorrhizal density with disturbance can confer a competitive advantage to non-native plants if they have low dependency on mycorrhizal fungi compared to native, late successional plant species. To test whether non- native plant species have low growth responses to arbuscular mycorrhizal (AM) fungi compared to early- and late-successional plants, we inoculated six non- native plant species, three early-, and three late- successional species with one of five different AM fungal species isolated from remnant prairies in Indiana, USA. Mycorrhizal responsiveness was calculated as total biomass with AM fungal inoculation / total biomass without AM fungal inoculation. We found that *Schizachyrium scoparium* and *Andropogon gerardii*, both late successional grasses, were very responsive to AM fungi, and grew up to twenty times larger when inoculated with AM fungi than without. Early-successional and non-native grasses had negligible or negative mycorrhizal growth responses. Both native and non-native asters, including *Echinacea pallida*, *Rudbeckia hirta*, dandelion, and chicory, were generally responsive to AM fungi, and grew two to five times larger when inoculated with AM fungi than without. We also saw differences in plant growth among the different fungal treatments. *Entrophospora infrequens* generally improved the growth of late successional native prairie plants while inhibiting the growth of non-native grasses. *Racocetra fulgida*, on the other hand, had a negative effect on growth of both native and non- native plants, regardless of successional stage. This study shows that although inoculating native plants with AM fungi can be important for improving plant growth, plant-fungal specificity is also an important consideration for increasing the success of restoration ecology efforts. *Symposium S7.4*

**54. Metatranscriptomic analysis of the moss *Dicranum scoparium* reveals active fungal communities and functionalities across a senescence gradient**

**\*Chen, Ko-Hsuan**(1), Liao, Hui-Ling(1,3), Arnold, A. Elizabeth(2), Lutzoni, François(1)

(1) Department of Biology, Duke University, Durham, NC, 27708, USA; (2) School of Plant Sciences and Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, AZ, 85721, USA. (3) NFREC, University of Florida, Quincy, FL, 32351, USA. kc178@duke.edu

Mosses are known to be associated with a variety of microorganisms including fungi. However, only a few moss-fungus interactions have been investigated and their symbiotic interactions remain mostly unknown. The moss *Dicranum scoparium* has three main growth stages in an individual plant: 1) a photosynthetic layer at the top of moss mats, 2) a mainly dead layer with minor decomposition in the middle, and 3) a highly decomposed layer in the lower portion of gametophytes. Studying the individual mosses that contain three growth stages provides an opportunity to understand transitions of fungal community composition and function in response to host senescence. The metatranscriptomes of plants, including *D. scoparium*, contain fungal transcripts in addition to expected plant transcripts. By integrating methods ordinarily used for detecting differential gene expression and microbial communities for metatranscriptomics, we show that active fungal communities in *D. scoparium* are structured by the degree of senescence. Overall, Ascomycota are more active in the photosynthetic layer, whereas Basidiomycota are more active in decomposing tissues. Entomophthoromycota, Glomeromycota, Chytridiomycota, Mortierellomycotina and Mucoromycotina were detected with less abundance. Two additional methods (amplicon-sequencing of cDNA and culture-based sampling from surface- sterilized tissues) were compared for community assemblies and OTU clustering. The functions of fungal communities were further investigated with emphasis on the activities of CAZymes and transport of nutrients (carbon, nitrogen and phosphorus). Transcript activity of genes for nutrient transport are enriched toward the bottom layers. Our study demonstrates the utility of metatranscriptomics for studying the taxonomic and functional aspects of complex symbiotic systems and provides insight into the ecology and functional components of bryophyte- fungal interactions. *Contributed Talk C13.3*

**55. *Cronartium* and The International Quarantine \*Chen, Momei**University of California, College of Natural Resources, Berkeley, CA, 94720 momeichen@berkeley.edu

Pine rust causes economically costly disease throughout the Northern Temperate zone, resulting in malformation, reduced vigor, and ultimately death of

pine plantation and nursery pine plants. Pine rusts are heteroecious specific, having coevolved with their hosts. Tree rust have the most complicated lifecycles of the fungal taxa in the ecosystem. The geographic pattern is diverse in North America and East Asia. Chen (2006) recently identified 3 major species (available through CABI): *Cronartium ribicola* parasitized 12 white pine species, and 24 *Ribes* or *Pediculris* in the United States, Canada, China, Japan, South Korea, Pakistan, Ireland, and Switzerland; 27 pine species and 28 *Quercus* species susceptible to *Cronartium quercuum* in North America: United States, Canada and East Asia China, Japan, Korea, Russia. *Cronartium coleosporioides* is known only in USA and Canada with seven pines hosts and a number of Scrophulariaceae alternative hosts. Chen (2004) provides new evidence and theories on pine rust flora. It has been suggested that white pine blister rust was introduced to the US from externally source, but the lineage evidence is lacking. Factors in the invasive forest pathogens infestation and establish always resultant with unbalances ecosystem, poor plantation design, and lack of integrate pest management. An improved phytogeography will depend on information gathered from molecular evolutionary genetics, natural history, population biology, paleontology and speciation analysis as well as improve the control of tree rust spread and International Quarantine on tree host plants.

*Contributed Talk C18.3*

**56. Does elevation affect symbiont network dynamics? A gradient study of foliar fungal endophytes \*Cobian, Gerald M**., Amend, Anthony S.

University of Hawaii at Manoa, Department of Botany, Honolulu, HI 96822, USA. gmcobian@hawaii.edu

Foliar endophytic fungi (FEF) form ubiquitous and intimate symbiotic relationships with every major plant lineage examined. These fungi are not pathogenic and have been show to play important roles in plant biochemistry, water conductance, and heat/drought tolerance. FEF community composition has been shown to be correlated with environment and host identity, but many of the studies showing these correlation have shallow environmental gradients and host differences are usually at the genus level or higher. A study in 2012 on Hawaii Island observed over 4200 FEF operational taxonomic units (OTUs) associated with the foundational species *Metrosideros polymorpha* along a steep elevation and precipitation gradient with very few OTUs shared among sites. To learn more about fungal community dynamics, we aimed to determine whether dispersal or selection assembly processes was more important in shaping



FEF communities. Additionally, we investigated how spatial effects influence FEF community composition. We collected leaves from hosts of varying relatedness along an elevation gradient on Hawaii Island and along an orthogonal transect in which elevation was held constant. Using Illumina sequencing technology, we amplified the fungal ITS region of the rDNA to characterized fungal communities found within the leaves of our host plants. We expect this research will help address questions about how fungal communities are affected by various community assembly processes and serve as base-line data for future research on FEF community assembly.

*Contributed Talk C9.2*

**57. Mechanisms maintaining coexistence among foliar fungal endophytes \*Connor, Elise**(1), Hawkes, Christine V.(2) University of Texas at Austin, Department of Integrative Biology, Austin, TX 78712, USA. eworchel@austin.utexas.edu

Plant leaves are broadly colonized by horizontally transmitted endophytic fungi that can affect plant physiology, growth, and stress responses. Endophyte diversity within a single plant host can be high; for example, native Texas grasses are colonized by an average of 15 endophyte taxa, based on culturing. To better understand how high levels of endophyte diversity are maintained, we examined the role of two coexistence mechanisms, fluctuating environments and niche differentiation, in predicting interactions between endophytes in culture. To test fluctuating environments, we examined 60 endophytes isolated from native Texas grasses for temporal variation in resource consumption, buffered growth, and tradeoffs in stress tolerance and competition. To test niche differentiation, we examined how trait dissimilarity affected competition for 80 pairs of endophytes. Trait similarity was based on ten traits related to growth, resource acquisition, and stress tolerance. We found that dissimilarity in fungal resource use was the best predictor of competitive outcomes among endophytes in culture, supporting fungal coexistence via niche differentiation. Furthermore, within our system only a few endophyte taxa met the conditions required for fluctuating environment to be an important mechanism of coexistence. However, coexistence mechanisms must still be tested in the plant, a more complex environment where multiple forces are likely simultaneously supporting high fungal diversity. Identifying mechanisms that maintain highly diverse endophyte communities provides a powerful theoretical framework for the development and application of endophyte communities composed of taxa with diverse benefits for crop management. *Poster P53*

**58. Fungal community diversity and spatial structure in a Costa Rican rainforest canopy \*Cook, Kelsey**(1), Sharma, Jyotsna(2), Taylor, Andrew D.(3), Taylor, D. Lee(1)

1.University of New Mexico, Department of Biology, Albuquerque, NM, 87131, USA; 2.Texas Tech University, Department of Plant and Soil Science, Lubbock, TX, 79409, USA; 3.University of Hawai’i at Manoa, Honolulu, HI, 96822, USA. kcook2@unm.edu

Despite great advances in plant ecology, we still lack a thorough understanding of how plant species coexist. This is particularly true in hyper-diverse rainforest canopy habitats. The spatial distributions of symbiotic fungi may play an important role in controlling the distributions of plants and allowing them to coexist. Unfortunately, almost nothing is known about the spatial distributions or substrate specificity of canopy fungi. We utilized a metagenomics approach to begin addressing this deficiency. Samples were collected at 135 locations across five tree branches in a riparian *Saurauia montana* forest in Tapanti National Park, Costa Rica. Sampling locations were situated between one centimeter and over seven meters apart to capture community heterogeneity at a variety of spatial scales. Samples were divided into four substrate types: living bryophytes and lichens, dead plant litter, outer tree bark, and wood. To identify fungi, we used the Illumina platform to sequence ITS amplicons. Spatial autocorrelation analysis was used to explore the spatial structure of the fungal community within and between tree branches. Here we discuss our findings on the diversity in the canopy fungi community, and its variation across space and between substrate types. In ongoing research, we are analyzing how distributions of canopy fungi influence the structure of the epiphytic plant community. *Contributed Talk C5.4*

**59. Nitrogen addition alters ectomycorrhizal fungal communities and soil hydrolytic enzyme activities in a tropical montane forest \*Corrales Osorio, Adriana**(1), Turner, Benjamin L.(2), Tedersoo, Leho(3), Anslan Sten(4), Dalling James W.(1)

1.University of Illinois at Urbana-Champaign, Department of Plant Biology, Urbana, IL 61801 USA; 2.Smithsonian Tropical Research Institute, Apartado Postal 0843–03092, Balboa, Ancon, Republic of Panama; 3.Natural History Museum, University of Tartu, Tartu, Estonia; 4.Institute of Ecology and Earth Sciences, University of Tartu, Tartu, Estonia. adricorrales33@gmail.com

In nitrogen (N)-limited temperate forests, a long- term increase in N availability can reduce species

richness and alter the composition of the ectomycorrhizal (EM) fungal community. It has been proposed that differences in the sensitivity to N addition among EM fungi are associated with variation among taxa in fungal strategies of growth, colonization, and nutrient acquisition. Consistent with this, we find that nine years of N addition in a tropical montane forest has significantly changed the species composition of EM fungi associated with *Oreomunnea mexicana* (Juglandaceae). The relative abundance of the EM fungal genera *Laccaria* and *Lactarius* increased with N addition, while the abundance of *Cortinarius* declined. This is consistent with *Laccaria* and *Lactarius* using labile N forms and increasing in abundance under high N availability, and the ability of *Cortinarius* to use organic N forms and to increase under low N conditions. In addition, we find a reduction in soil phosphatase and *N*-acetyl- glucosaminidase activity following N addition potentially linked with a reduction in the abundance of EM fungi, which was reflected in a lower EM colonization of *Oreomunnea* roots. We conclude that a reduction in EM fungal taxa specialized in organic N and phosphorus (P) absorption (e.g., *Cortinarius*) along with a decrease in EM colonization of host plants could cause a decrease in soil enzyme activity that could have feedback effects on key ecosystem processes, including soil carbon storage and the cycling of N and P.

*Contributed Talk C12.3*

**59.1. Harnessing the microbiome for agricultural sustainability in bioenergy-based systems**\*Craven, Kelly D.(1), Ghimire, Sita R.(2), Ray, Prasun(1), Charlton, Nikki D.(1), Chi, Myoung- Hwan(2)

1.The Samuel Roberts Noble Foundation, Plant Biology Division, Ardmore, OK, 73401, USA; 2.International Livestock Research Institute, CGIAR, Nairobi 00100, Kenya. kdcraven@noble.org

Declining reserves of mineral phosphorus and growing economic and environmental costs associated with fertilizer use (and misuse) have necessitated efforts to identify cropping systems and strategies that can be sustained under and low-input strategy. One approach to ameliorate such losses is to utilize microbial symbionts that have evolved to promote plant growth through nutrient and water acquisition as well as reduce plant stress when grown on marginal, low-quality soils. Soils such as these are expected to be tapped to grow cellulosic feedstocks for biofuel production. Here, we describe our efforts to maximize the performance and abiotic stress tolerance of switchgrass, a C4 grass native to the prairies of northern OK, through microbial symbiosis. Strain discovery combined with the implementation of high-

throughput screens for potentially useful traits, have resulted in a manageable number of bacterial and fungal endophytes that we are testing in greenhouse trials. Results to date suggest that both biomass and drought tolerance can be enhanced by a novel type of mycorrhizae and bacteria have been identified that are being tested for phosphorus solubilization, nitrogen fixation and the alleviation of ethylene-induced plant stress.

*Symposium S5.4*

**60. Lessons from the Alpine: Using type specimens, DNA sequences, and detailed morphology for species identification \*Cripps, Cathy L.**(1), Barge, Edward G.(1), Osmundson, Todd W.(2)

1.Plant Science and Plant Pathology, 119 Plant Biosciences Building, Montana State University, Bozeman, MT 59717, USA; 2.Department of Biology, 3034 Cowley Hall, University of Wisconsin, La Crosse, 1725 State Street, La Crosse, WI 54601, USA. ccripps@montana.edu

Sequencing specimen DNA – especially the ITS barcoding region – has taken high priority as the go-to method for species identification in recent years. Detailed morphological study as a companion practice has not kept pace. However, sequence matches to unconfirmed or misidentified collections in sequence databases have significant potential to provide misleading pictures of the ecology, distribution, rarity and endemicity of species. The true basis of a species is the physical Type (when there is one), and although it is not always possible to successfully sequence older Type specimens, such efforts should be given high priority. Here we give examples for ectomycorrhizal fungi (Agaricales and Russulales), primarily from arctic-alpine habitats, where joining detailed morphological study with sequencing of Type specimens or authentic material has helped confirm transcontinental distributions, clarify host associations (including identification of host jumping), and resolve taxonomic tangles. Examples are drawn from species of *Inocybe, Lactarius, Laccaria,* and *Cortinarius*, many of which have Holarctic distributions, particularly in association with hosts in the Salicaceae and Betulaceae. Lessons include studies revealing: little molecular variation for distinguishing closely related species of morphologically distinct *Lactarius* species; the deception of arctic-alpine nano-forms in *Laccaria* and *Cortinarius;* the existence of transcontinental distributions of arctic-alpine, boreal-alpine, subalpine-alpine fungal species; evidence that Type specimens from both sides of the ocean need to be considered; that micromorphology can reveal molecular mistakes; and that host and habitat are

not always constant, but sometimes they are. The interplay of morphology and molecular sequencing can help dispel potential errors in species identification that stem from one data type alone, and this benefit is amplified when Type specimens are employed.

*Contributed Talk C15.1*

**61. The soil mycobiome associated with orchids in Sweden \*Cubeta, Marc A.**(1), Carbone, Ignazio(1), White, James B.(1), Mahmood, Shahid(2), Finlay, Roger D.(2), Stenlid, Jan(2).

1. Department of Plant Pathology, Center For Integrated Fungal Research, North Carolina State University, Raleigh, NC 27606; 2.Department of Forest Mycology and Plant Pathology, Swedish University of Agricultural Sciences, Uppsala. macubeta@ncsu.edu

Rhizoctonia fungi can establish beneficial symbiotic associations with orchids to promote seed germination and seedling growth. In this study, soil samples were collected from eight geographic locations in central Sweden where orchid seedlings of *Cypripedium calceolus*, *Dactylorhiza incarnata*, *D. maculata, Epipactis palustris, Listera ovata* or *Plantathera bifolia* were present. Soil fungal communities were determined with high throughput pyrosequencing of extracted genomic DNA and bioinformatics-based methods using the Sequence Clustering and Analysis of Tagged Amplicons (SCATA) analytical platform. To identify operational taxonomic units (OTUs) and characterize members of the soil fungal community, generated sequences were subjected to RDP classifier using the UNITE fungal ITS reference database. Sequence data were also analyzed with Tree-Based Alignment Selector (T- BAS) toolkit to determine OTU distribution. According to UNITE, fungal taxa in OTUs were distributed as follows; 984 Ascomycota (50%), 643 Basidiomycota (31%), 210 Chytridiomycota (4%), 201 Zygomycota (7%), 184 Glomeromycota (2%), and 58 Rozellomycota (1%). Of the total Ascomycota diversity, Leotiomycetes represented 22%, Sordariomycetes 9%, Saccharomycetes 6%, Dothideomycetes 4%, Eurotiomycetes 3%, Pezizomycetes 2%, and Xylonomycetes 1%. Five of 14 OTUs sampled from all locations were tentatively identified as *Exophiala equina*, *Mortierella amoeboidea*, *Operculomyces laminatus*, *Phoma brasiliensis,* and *Tetracladium furcatum*. Fungal taxa that commonly form symbiotic associations with photosynthetic terrestrial orchids (e.g., *Ceratobasidium*, *Sebacina*, *Thanatephorus*, and *Tulasnella=Epulorhiza*) occurred in low frequency (>0.1%) across all samples, except for *Epulorhiza* sp.

MO41 and two species of *Sebacina* at two locations where seedlings of *C. calceolus* and *L. ovata* occurred, respectively. Research is currently in progress to examine the association of soil chemistry with orchid and fungal taxon distribution.

*Poster P35*

**62. The food spoilage implications and origins of fungi in sea salts \*Daniels, Megan N.**, Hodge, Kathie T. Cornell University, SIPS Plant Pathology and Plant- Microbe Biology. Ithaca, NY , 14853, USA. MND24@Cornell.edu

Sea salts are produced in salterns, natural pools used to progressively concentrate seawater. The diverse fungi found in salterns are adapted to harsh conditions that are similar to those found in some low water activity foods. We asked whether sea salts may be sources of spoilage molds when used as food ingredients. We quantified the viable filamentous fungi in seven commercial sea salts, identified fungal isolates by DNA sequencing, and examined the compositions of fungal communities among salts relative to their origins. We assessed the spoilage risk this ingredient poses by comparing sea salt taxa with known spoilage fungi. Every sea salt contained viable fungi, though there was significant variation in the number of fungi among salts (p=0.021, α=0.05). In total, 85 fungi were isolated across seven genera. Representatives of the most abundant genera, *Aspergillus*, *Cladosporium,* and *Penicillium* were found in every salt. Ordination analysis revealed a common set of taxa, with minor differences in fungal communities between salts originating from the Atlantic and Pacific oceans (ANOSIM R=-0.012, p=0.46). This supports the hypothesis put forth by some researchers that saltern environments select for a core group of taxa, which can be found globally. Many of the sea salt fungi are known inhabitants of solar salterns, suggesting that propagules of saltern fungi remain viable in the finished salt. We concluded that salt destined for the consumer may pose a spoilage risk to some foods, and furthermore, may include dangerous or toxigenic species (e.g. *A. fumigatus, A. niger*). Further study is needed to examine the diversity and ecological roles of these fungi in salterns. Food safety concerns suggest a need to examine the link between salterns and spoiled foods, and to devise methods to reduce fungal inoculum in sea salts. *Poster P84*

**63. Elevated relative humidity may cause indoor bacterial and fungal growth in carpet \*Dannemiller, Karen**(1,2), Weschler, Charles J.(3), Peccia, Jordan(4)

1. Ohio State University, Department of Civil, Environmental and Geodetic Engineering, College of Engineering, Columbus, OH 43210, USA; 2. Ohio State University, Department of Environmental Health Sciences, College of Public Health, Columbus, OH 43210, USA; 3.Rutgers University, Environmental and Occupational Health Sciences Institute, Piscataway, NJ 08854, USA; 4.Yale University, Department of Chemical and Environmental Engineering, New Haven, CT, 06520-8286, USA.

Carpeted flooring is an important source of human exposure to bacteria and fungi due to dust resuspension. Previously identified sources of microbes in carpet include tracked-in soil, settled dust, human shedding, and growth in water damaged areas. However, it is not yet known if microbial growth occurs indoors under normal conditions. The goal of this work is to determine if water absorption from the air provides sufficient moisture for fungal and bacterial growth in carpets. In experimental chambers, we exposed carpet coupons embedded with house dust to controlled relative humidity conditions (50%, 80%, 85%, 90%, 95%, and 100% for one week; 85% and 100% for six weeks) and measured microbial growth using qPCR and DNA sequencing of the 16S (bacteria) and ITS (fungi) regions. The water activity of the carpet samples increased rapidly after 24 hours and stabilized within one week. After one week, fungal growth was observed at ≥80% equilibrium relative humidity (ERH), and bacterial growth was observed only at 100% ERH. During this initial week, the 100% ERH conditions resulted in 27 times increase in fungal concentration and 2.7 times increase in bacterial concentration compared to the starting concentrations. Fungal growth rates after the initial week ranged-1 from -18,500 (±3,050) spore equivalents·day ·mg dust at 85% ERH to 113,000 (±13,700) spore equivalents·day-1·mg dust-1 at 100% ERH. Fungal richness decreased from 847 to 227 operational taxonomic units (OTUs) and dominant genera at elevated relative humidity included *Aspergillus*, *Wallemia*, and *Penicillium*. After one week, there were statistically significant differences at varying ERH levels in fungal (*p*<0.00001) and bacterial communities (*p*<0.00001) based on principal coordinate plots. This work demonstrates that growth significantly impacts microbial communities under normal building conditions at ≥80% relative humidity, and this may be an important additional source of human exposure.

*Symposium S3.2*

**64. Utilizing herbaria to elucidate patterns of microbial diversity in the *Clermontia* (Campanulaceae) phyllosphere across the Hawaiian Islands**

**\*Datlof, Erin M.**, Hayward, Jeremy A., Earl, Kamala, Wade, Rachael M., Amend, Anthony S., Hynson, Nicole A. University of Hawai‘i at Mānoa, Department of Botany, 3190 Maile Way, Room 101, Honolulu, HI 96822, USA. edatlof@hawaii.edu

Herbaria samples are collected and stored throughout the world to document and store the biodiversity of diverse groups of organisms ranging from plants to insects to mammals. However, an additional and unexplored use of herbarium collections is to document the diversity of microorganisms that inhabit specimens such as those in the phyllosphere of plants. Utilizing previously collected specimens and DNA banks to study patterns of microbial diversity could significantly increase our understanding of overall patterns of biodiversity from snapshots in time. Here, we investigated the fungi inhabiting the phyllosphere of an endemic Hawaiian plant genus, *Clermontia* (Campanulaceae). This genus is part of a plant radiation arising from a single common ancestor that arrived in Hawai‘i 13 million years ago, and has diverged into 4 endemic genera and many species across the Hawaiian Islands. From just 20 DNA bank samples, using next generation DNA amplicon sequencing techniques, we uncovered approximately 3,000 fungal operational taxonomic units (OTU’s). This study is the first of its kind to utilize herbaria DNA banks to elucidate historical patterns of fungal diversity. With thousands of herbarium specimens preserved throughout the world microbial biodiversity and patterns are readily available to study.

*Contributed Talk C19.6*

**65. Fungal root-endophytes in *Carex pensylvanica* from sand prairies \*David, Samuel**, Paluch, Elisabeth, Osmundson, Todd, Thomsen, Meredith, Volk, Thomas

1.University of Wisconsin - La Crosse, La Crosse, WI, 54601, USA. david.samu@uwlax.edu

Sand prairies and oak savannahs are both rare and threatened habitats in Wisconsin. *Carex pensylvanica*, a very common understory plant of those habitats, forms relationships with various fungal groups including arbuscular mycorrhizal fungi (AMF) and dark septate endophytes. Dark septate endophytes (DSE) are a morphological group of fungi that grow in the roots of many land plants, especially in abiotically stressed environments. Although generally believed to provide some benefit, the exact role DSE play with their plant host is not well understood. Dark septate endophytes were identified via culturing and DNA sequencing from roots of *Carex pensylvanica* growing under and away from oaks on sand prairie-oak savannah borders. Root sections were also measured for hyphal colonization to compare AMF and DSE in

different soil conditions. Results will provide insight on the fungal species found in *Carex pensylvanica* and how environmental factors influence fungal colonization of roots.

*Poster P55*

**66. Inventory of chytrid diversity using a multiphasic approach \*Davis, William J.**(1), Antonetti, Jonathan(1), Edmonds, Jennifer(1), Fults, Jessica(1), Letcher, Peter M.(1), Picard, Kathryn(2), Powell, Martha J.(1) 1.Department of Biological Sciences, University of Alabama, Tuscaloosa, Alabama 35487 2. Department of Biology, Duke University, Durham, North Carolina, 27708. daviswj@umich.edu

Chytrids are an inconspicuous, microscopic early- diverging lineage of fungi. They are among the “dark matter fungi;” little is known about them relative to what is known about Dikarya fungi. We inventoried the chytrid diversity in two temporary forest ponds using culture-based methods, light microscopy, and next generation sequencing (i.e., Ion Torrent sequencing of barcoded amplicons).Temporary forest ponds are depressions that annually cycle between non-inundated and inundated stages. Little is known about the microbial communities of temporary forest ponds and less is known about the chytrids present. The culture-based methods revealed few chytrid taxa from one of the temporary forest ponds. More chytrid taxa were observed using a combination of light microscopy and molecular techniques than the culture- based method alone. Despite the few taxa found in the culture-based study, two chytrid strains were used to revise a species and describe a new species and a third strain awaits description as a new species. Our work shows that different methods detect a range of chytrid taxa and that a multiphasic approach provides a basis for assessing chytrid diversity.

*Contributed Talk C11.5*

**67. Global diversity of *Gyroporus* (Basidiomycota, Agaricomycetes, Boletales) \*Davoodian, Naveed**(1, 2), Bergemann, Sarah E.(3), Hosaka, Kentaro(4), Smith, Matthew E.(5), Raspé, Olivier(6), Halling, Roy E.(1)

1.New York Botanical Garden, Institute of Systematic Botany, Bronx, NY, 10458, USA; 2.City University of New York – Graduate Center, Program in Biology, New York, NY, 10016, USA; 3.Middle Tennessee State University, Department of Biology, Murfreesboro, TN, 37132, USA; 4.National Museum of Nature and Science, Department of Botany, Tsukuba, Ibaraki, 305-0005, Japan; 5.University of Florida, Department of Plant Pathology, Gainesville, FL, 32611, USA; 6.Botanic Garden Meise,

Department Bryophytes-Thallophytes, Meise, B-1860, Belgium. ndavoodian@nybg.org

*Gyroporus* is a genus of ectomycorrhizal fungi with representatives on every major continent except Antarctica. These fungi form mutualisms with an array of ectotrophic plant species including members of Pinaceae, Fagaceae, Myrtaceae, Betulaceae, and Phyllanthaceae, among others. In addition to functioning as mycorrhizal symbionts in forest ecosystems, *Gyroporus* species are important as wild edible mushrooms. Despite a long history of formal recognition and research, significant details within *Gyroporus* have yet to be uncovered. This is primarily because the diversity of *Gyroporus* is in large part extra-European, composed of geographically widespread species complexes. To address this problem, a combined taxonomic and phylogenetic approach was used to examine species limits and infer relationships within the group. Molecular phylogenetic analyses of the nuclear gene *rpb2* and the mitochondrial gene *atp6* have provided robust insights into infrageneric relationships and species diversity. The monophyly of *Gyroporus* is corroborated, and strongly supported clades are inferred within the genus. These clades are intercontinentally distributed, with significant species-level diversity on continental scales. A number of new *Gyroporus* species have been discovered, particularly in Australia, which has a diverse but poorly described bolete mycota. Our analyses indicate that many *Gyroporus* collections that are similar morphologically represent several distinct species both between and within continents. Though approximately 30 *Gyroporus* species have been published to date, these investigations suggest that the true diversity is likely closer to 80–100 species. Further research on *Gyroporus* will likely reveal a wealth of undescribed biodiversity. *Contributed Talk C18.4*

**68. Fungal conservation in the United States: Current challenges, future solutions \*Davoodian, Naveed**(1, 2), Minter, David W.(3), Castellano, Michael A.(4)

1.New York Botanical Garden, Institute of Systematic Botany, Bronx, NY, 10458, USA; 2.City University of New York – Graduate Center, Program in Biology, New York, NY, 10016, USA; 3.Centre for Agriculture and Biosciences International, Egham, Surrey, TW20 9TY, United Kingdom; 4.USDA Forest Service, Northern Research Station, Corvallis, Oregon, 97331, USA. ndavoodian@nybg.org

Fungal conservation has progressed in recent years. The International Union for Conservation of Nature (the world’s largest conservation NGO) now considers fungi as essential as animals and plants. In the USA, despite significant achievements of a few

mycologists, fungal conservation is still rudimentary, almost entirely limited to scientific work, and often based outside the country. Most mycologists are poorly aware of the need to protect fungi. There are many challenges to surmount before effective fungal conservation will be achieved in the USA. Despite some recent pioneering work in education, the general public and even many science and conservation professionals lack basic understanding of fungi. Social and political awareness of fungal conservation is virtually non-existent in the USA. Worse, there is currently no infrastructure through which this awareness could be developed. The MSA has a Conservation Committee, but is unable to lobby because of its tax status, and NAMA has no formal conservation infrastructure at all. There is no scientific body or group to examine or propose legislation relevant to fungal conservation. There is some, but not enough, translation of relevant data to red-listing initiatives. Red-listing workshops and similar training are currently organized ad hoc by determined individuals who lack formal support. USA conservation NGOs rarely acknowledge the need to protect fungi, probably due to lack of education. Major federal frameworks through which fungi might be protected are compromised by ambiguities in regulatory language and implementation, especially in that they do not satisfactorily distinguish fungi from plants. These are only a handful of the many challenges that mycologists urgently need to address. The time is ripe for the mycological community to clearly outline these problems, identify solutions, and propose action.

*Symposium S9.1*

**69. Turnover of fungal pathogen communities across life history stages of native and exotic grasses in a California grassland \*Daws, S. Caroline**, Mordecai, Erin A.

Stanford University, Department of Biology, Stanford, CA 94305, USA. cdaws@stanford.edu

Fungal pathogens can shape plant communities by influencing recruitment and survival; however, the identities of such fungi are largely unknown in natural grassland ecosystems. Previous research has explored how pathogens influence plant community demographics, but the consequences of wild pathogens on competitive outcomes between co-occurring plants remain unclear. Here, we investigate how fungal pathogens differ between life stages, from seedling to adult, and how these pathogens influence survivorship in a California grassland. In many grasslands, annuals, often exotic, tend to outcompete long-lived, native perennials. Because fungal pathogens can influence both seedling recruitment and adult survival, they may alter competitive outcomes between hosts. We

surveyed pathogen communities and foliar damage on seedlings of three exotic annual grasses and seedlings and adults of two native perennial grasses in the early and late growing season. We identified pathogen communities by culturing from visible lesions and comparing sequences of the ITS region. We compare pathogen communities on annual and perennial seedlings and adults over the growing season and link seedling pathogen damage to survival to understand how fungal pathogens affect fitness. Each of the five focal grass species experienced extensive foliar damage; many of the causative fungal pathogens infected multiple host species, including several fungi from the genus *Pyrenophora.* Given differences in life history, annual plant population growth may be more sensitive to seedling mortality than perennials. These results suggest that turnover in fungal pathogens over the lifetime of a host may alter the structure of California grasslands. Characterizing the identity and lifetime impact of fungal pathogens on individual plants is critical for understanding how pathogens structure natural plant communities.

*Poster P87*

**70. All roads lead to Rome: Distinct patterns of nuclear distribution and cytoskeletal organization underlying the evolution of indeterminate growth in Chytridiomycota**

**\*Dee, Jaclyn M.**(1), Roberson, Robert W.(2), Longcore, Joyce E.(3), Berbee, M.L.(1) 1.University of British Columbia, Botany, Vancouver, BC, V6T-1Z4, Canada; 2.Arizona State University, Life Sciences, Tempe, AZ, 85281, USA; 3.University of Maine, School of Biology and Ecology, Orono, ME, 04469. jaclyn.dee@botany.ubc.ca.

Consider the “humongous fungus”, a subterranean honey mushroom mycelium that has infiltrated an area equivalent to over 1000 football fields. A mechanism for nuclear migration was a prerequisite for the indeterminate hyphal growth that made this astounding feat possible. Indeterminate hyphal growth is often associated with evenly spaced nuclei in Ascomycota, or paired nuclei and clamp formation in Basidiomycota. In comparison to hyphal growth, some chytrid species capable of growing indefinitely have rhizomycelia, which are extensively branched rhizoids, often with intermittent nucleus-containing swellings. We hypothesized that different patterns of nuclear migration would characterize lineages with independent origins of indeterminate growth and are, for the first time, examining nuclear migration patterns in the Chytridiomycota. We used fluorescence microscopy of chemically fixed material to correlate actin organization and nuclear distribution with developmental stages in two genera, from two different orders, that demonstrate indeterminate

growth. The genera examined are phylogenetically nested among other genera with determinate growth. During growth, nuclei in both *Cladochytrium* (Cladochytriales) and *Physocladia* (Chytridiales) migrate from an older to a newer, developing rhizoidal swelling at the colony margin. In *Cladochytrium*, a single nucleus migrates after a single nuclear division, whereas in *Physocladia*, migration of one nucleus, or possibly multiple nuclei, occurs following multiple rounds of nuclear division. Anucleate young swellings contained short fragments of actin. This suggests that although control of nuclear migration is essential for indeterminate growth, alternative patterns and timing of nuclear migration in relation to nuclear division reflect independent evolutionary origins.

*Contributed Talk C11.1*

**71. Geographic and phylogenetic scale of host effects on endophyte community assembly \*DeMers, Mara B.**, May, Georgiana University of Minnesota, Plant Biological Sciences, Saint Paul, MN, 55108-6112, USA. demer013@umn.edu

Although foliar fungal endophytes are found in a wide variety of host plants, species- and population- level effects of the host on endophyte community assembly and endophyte diversity are not well understood. *Dalea purpurea* and *D. candida* (purple and white prairie-clovers) represent a useful system for studying host effects because these plants are closely related and co-occur in many isolated remnant prairie sites across Minnesota. Endophytes were cultured from plants of 12 populations of each *Dalea* species ranging from N43°52' to N47°42' and from W091°55' to W096°28'. Preliminary observation of cultures indicated that darkly pigmented fungi occurred more frequently in southern host populations. Barcode sequencing of the internal transcribed spacer region was used to corroborate this result and facilitate identification of cultured endophytes for further analysis. *Poster P54*

**72. Comparative genetics of spore germination across Sordariomycetes and Dothidiomycetes** DeMiguel Rojas, Cristina(1), Wang, Zheng(2), Cavinder, Brad(1), Townsend, Jeffrey(2), **\*Trail, Frances(1)**

1.Michigan State University, Department of Plant Biology, East Lansing, 48824, USA; 2.Yale University, Departments of Biostatistics and Ecology & Evolutionary Biology, New Haven, 06510, USA. trail@msu.edu

The long-term goal of our research is to identify the genes important to the evolution of spore germination and the diversity of plant penetration

processes across the Ascomycota. To this end we have performed transcriptional profiling of five species of fungal pathogens and one saprotroph at distinct developmental stages on a single defined medium, and on their hosts or natural substrates. The selected stages of conidial germination are: dormancy, polar growth, doubling of the long axis and the initiation of branching on medium; and development of infection structures on hosts (pathogens) or natural substrates (saprotrophs). We hypothesize that a genome-based RNA-seq analysis will reveal a large number of differentially expressed species-specific and infection- specific genes. Gene enrichment analysis and pathway analysis will be presented to further elucidate the divergence of spore germination and plant penetration processes among pathogenic and saprotrophic fungi. *Poster P133*

**73. Fire, fungi, and a changing boreal forest \*DeVan, M. Rae**, Taylor, D. Lee University of New Mexico, Department of Biology, Albuquerque, NM, 87131-0001, USA. raedevan@unm.edu

Mycorrhizal fungi are important drivers of productivity, nutrient cycling, and carbon storage in one of the largest and most influential biomes in the climate system, the boreal forest. Globally, fire severity and frequency have increased in the boreal forests due to warmer and drier conditions associated with climate change. In Interior Alaska, high severity fires have been strongly linked to shifts in canopy dominance from black spruce to deciduous species like paper birch and trembling aspen. Additionally, fire-adapted lodgepole pine is common in plantations across Alaska, and is undergoing a slow post-glacial migration into the region. The combination of changing fire regimes and spread of lodgepole pine has the potential to alter successional trajectories and displace native plant and fungal communities. While there has been a wealth of research investigating the effects of fire or host plant species on mycorrhizal fungal community structure, none thus far have elucidated the interactive effects of fire and host dominance shifts. In this study we address how mycorrhizal fungal communities are affected by the interaction of host species with fire severity. To address these questions, we used Illumina sequencing to characterize the ectomycorrhizal fungal communities on four native species of host seedlings and non-native lodgepole pine that were planted in burn sites of varying severity after the largest fire year on record in Alaska (2004). *Contributed Talk C12.1*

**74. A new *Wallemia* species from South America**

**\*Díaz-Valderrama, Jorge R.**(1), Nguyen, Hai D. T.(2), Aime, M. Catherine(1) 1.Purdue University, Department of Botany and Plant Pathology, West Lafayette IN 47901 USA; 2.Agriculture and Agri-Food, Ottawa Research and Development Centre, Ottawa, Ontario, Canada. jdiazval@purdue.edu

Species of *Wallemia* (Wallemiomycetes, Basidiomycota) are ubiquitous fungi able to thrive in environments with reduced water activity (aw). Historically, the genus has been enigmatic, both in terms of phylogenetic placement as well as its natural environmental niches. To date, seven *Wallemia* species have been described: *W. sebi*, *W. mellicola*, *W. canadensis*, *W. tropicalis, W. muriae*, *W. ichthyophaga* and *W. hederae.* During routine sampling we discovered a new *Wallemia* species from the rooftop of a rural house located in an agronomic field in Lurín-Lima, Peru. Four isolates were collected by exposing 50% glucose-supplemented MYA media to air overnight. We examined the macro- and micro- morphology, growth rate and production of exudates on two basic media (MEA and MYA) containing different amounts of glucose and NaCl (aw values from 1.0091 to 0.8614). We also evaluated the chaotropic and kosmotropic tolerance on media containing MgCl2 and MgSO4 at multiple molar concentrations (aw values from 0.9880 to 0.7877). Finally, we amplified the 18S and ITS rDNA and performed a Bayesian phylogenetic analysis. Isolates are xerophilic and halotolerant, growing faster on glucose-supplemented media (20% and 50% glucose) than on NaCl-supplemented media (10% and 17% NaCl). Isolates also grew on 4M MgSO4 media, a kosmotropic tolerance that has not been observed in other *Wallemia* species that have been tested for this ability. This is the first new species of *Wallemia* to be described from South America and the first association of a *Wallemia* species with a rural agricultural environment on this continent.

*Poster P116*

**75. The use of an automated tool for identifying *MAT* loci and analyzing mating systems across Basidiomycota**

Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN 47907, USA. jdiazval@purdue.edu

**76. The emerging science of linked plant-fungal invasions \*Dickie, Ian A.**1. Lincoln University, Bio-Protection Research Centre, Lincoln, New Zealand. ian.dickie@lincoln.ac.nz

Interactions and links between plants and fungi can drive biological invasions and contribute to or mitigate ecosystem impacts. Most of our knowledge about how linked plant-fungal interactions influence invasion come from case-studies. These case studies have led to a proliferation of proposed hypotheses and mechanisms, often treating pathogens and mutualists as entirely distinct fields of research. This has created unnecessary redundancy and obscured emergent patterns. I will present early results from a New Phytologist sponsored workshop, "The emerging- science of liked plant-fungal invasions", where we worked to integrate these mechanisms, using simplified interaction motifs. These motifs show strong parallels in mutualism and pathogen interactions which have not been fully recognized by the current division between these fields, and suggest possible interactions that remain under-explored as possibilities. I will then discuss a series of case studies

multi-allelic and unlinked *MAT* loci. One of them encodes homeodomain transcription factors (HD) and the other one encodes pheromone precursors and STE3 pheromone receptors. However, during Basidiomycota evolution, multiple transitions from the tetrapolar to the bipolar mating system have occurred. One of the ways for bipolar systems to arise is through chromosomal rearrangement and physical linkage of *MAT* loci. Moreover, a third type of mating system, called pseudo-bipolar has recently been described. Due to initiatives such as the 1000 Fungal Genomes Project led by the Joint Genome Institute, many fungal genomes are now publically available to the mycological community, most of which have yet to be mined for *MAT* data. Therefore, an automated tool able to capture this information would significantly facilitate the study of fungal mating systems. In this poster we present the development of a Python script that identifies *STE3* and *HD* mating genes through a BLAST-based method and the assessment of their linkage to conserved genes around the *MAT* loci. We then provide a comparison of the *MAT* loci arrangement across species of Agaricomycotina, Pucciniomycotina and Ustilaginomycotina. We also identify mating systems based on linkage of both *MAT* loci. Finally, we test the hypothesis that bipolarity derived from tetrapolar mating systems and assess whether physical linkage of *MAT* loci has occurred in

any recently derived lineages.

*Poster P117*

|  |
| --- |
| **\*Díaz-Valderrama, Jorge R.**, Parra, Pedro |
| Pablo, Kijpornyongpan, Teeratas, Aime, M. Catherine |

The mating (*MAT*) loci determine sexual identity and compatibility between fungal individuals. In most fungi, *MAT* is comprised of a single locus, known as a bipolar mating system. Members of Basidiomycota have evolved a more complex and diverse mating system, called tetrapolar, which is governed by two



from New Zealand that explore how these motifs can develop over time with invasion, and some of the determinants of when and where these matter in determining invasion outcomes. In particular, I will explore how introduction reduces the functional diversity of ectomycorrhizal fungal exploration types, and change the fundamental structure of plant-fungal interaction networks. The results suggest that linked plant-fungal invasions are complex but tractable through a combination of a clear hypothetical framework and appropriate analyses.

*Symposium S7.1*

**77. Elucidating the genetic basis for biofuel relevant phenotypes in the yeast *Kluyveromyces marxianus*\*Donnelly, Marie K.**, Yu, Ka Man Jasmine, Baker, Jacob S., Bruns, Thomas D., Taylor, John W. University of California, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA. mariekdonnelly@gmail.com

A chief technical hurdle to industrial cellulosic biofuel production is *Saccharomyces cerevisiae’ s* sensitivity to high temperatures and toxic products of biomass pretreatment and hydrolysis in the fermentation. While much work has been done to engineer suitable industrial strains, a complementary approach is to look for desirable traits in closely related yeasts, such as the thermotolerant yeast, *Kluyveromyces marxianus*. Few strains of *K. marxianus* exist in culture collections, and the extent of natural variation is unknown. To sample the natural variation of *K. marxianus*, we traveled to the sugarcane growing and refining region of Florida and collected sugarcane bagasse from active compost piles where the temperature was between 40 and 50°C. Strains of *K. marxianus* isolated from the compost were grown up in liquid media to assess phenotypic variation within this population. A set of 21 additional strains was provided to us, including a population from Mexico and three culture collection strains. Aerobic growth at various temperatures, with various carbon sources, and in the presence of biomass hydrolysate was measured over 24 hours in a BioscreenC. Genomic DNA was extracted from each individual and sequenced via Illumina HiSeq. Sequence data was analyzed using GATK and revealed 134,892 SNPs across 51 individuals within three populations, Mexico, Florida 1, and Florida 2. Phenotype analysis shows similarly clustered populations, such as Florida strains show higher growth rates at high temperatures than Mexico strains, and the Florida 2 sub population shows higher growth rates on cellobiose. Genome wide association is being used to identify genes underlying these distinct phenotypic differences. More strains of *K. marxianus*

collected from a wider variety of environments could reveal a greater natural diversity of biofuel relevant traits and guide some of the rational engineering of *S. cerevisiae* for industrial biotechnology.

*Symposium S5.2*

**78. Abiotic causes and consequences of coprophilous fungal succession on Tule Elk dung \*Dunkirk, Nora C.**(1), Stajich, Jason E.(2), Peay, Kabir G.(1)

1.Stanford University, Biology Department, Stanford, CA, 94305, USA; 2.University of California Riverside, Department of Plant Pathology & Microbiology, Riverside, CA, 92521. ndunkirk@stanford.edu

Some of the earliest questions in fungal ecology were centered on the ecological mechanisms that drive fungal succession during decomposition. Coprophilous fungi are one of the earliest systems used to study fungal succession, in large part due to their simple community and highly predictable patterns of community development. Despite this, few modern fungal ecology studies have revisited this system using modern molecular tools, despite the potential for insight into ecological mechanisms and the role of fungi in controlling ecosystem processes. We revisited these questions using an experimental decomposition- succession study system developed around coprophilous fungi inhabiting Tule Elk dung at Point Reyes National Seashore, CA. We assessed community composition using 16S and ITS iTag DNA sequencing on an Illumina MiSeq from independent dung pellets harvested at 8 time steps over a 32-day period. To determine the strongest abiotic factors correlated with succession, we measured a range of dung moisture content, lignin, cellulose, total carbon and nitrogen, sugars, protein and time, and quantified their relationship with fungal community composition. This dung fungi model system is being developed to integrate community genomics with the ecological study of fungi and their impacts on ecosystem processes. *Poster P68*

**79. Detecting oomycete communities in nursery irrigation water using the Illumina MiSeq platform \*Eberhart, Joyce**, Funahashi, Fumiaki, Parke, Jennifer. Department of Crop and Soil Science, Oregon State University, Corvallis, OR 97331 USA. joyce.eberhart@oregonstate.edu

Horticultural nurseries are under increasing pressure to reduce, remediate, and recycle irrigation water. A major constraint for reusing irrigation water is contamination by *Phytophthora* and *Pythium* species. Our research monitors oomycete pathogens in water. Vannini et al. developed an ITS6 and ITS7

primer set to amplify oomycetes with the Roche 454. We modified these primers for the Illumina Miseq platform to identify waterborne oomycetes potentially present at low concentrations and to provide a semi- quantitative method to determine the relative frequency of diverse, co-occurring species. We created mock communities composed of 11 *Phytophthora* and *Pythium* species. Extracts diluted to 5 ng/μl DNA were combined in equal amounts and pooled. PCR performed with the pooled samples showed that species mostly had similar abundances. We then pooled these extracts using 20x as much of *Phytophthora syringae*, and found that the number of reads for this species was approximately 16x the average number of reads for the other species. We also separately amplified each species combining the resulting amplicons at 5 ng/μl each. When compared with extracts combined in equal amounts, results were mostly similar. For detection of oomycetes in nursery water, samples were filtered through 5μm filters. DNA was extracted directly from filters. For a subset of the samples, we compared the detection sensitivity for DNA extracted directly from filters with extraction from rhododendron leaf baits. A multivariate plot of oomycete communities from filtered water, baited leaves, and mock community samples showed distinct communities. Illumina sequencing is a sensitive method to detect, identify, and determine the relative abundance of oomycetes from water samples comprised of mixed assemblages of species. Our findings will help nursery managers make effective decisions about water disinfestation strategies, thereby reducing the risk of establishment of plant pathogens. *Poster P78*

**80. Genome assembly of a novel *Entomophthora muscae* isolate*,* a natural pathogen of *Drosophila melanogaster*\*Elya, Carolyn**, Bronski, Michael, Eisen, Michael B. University of California, Molecular and Cell Biology, Berkeley, CA, 94720, USA. elyac@berkeley.edu

The *Entomophthora musace* species complex is a member of the basal fungal phylum Entomophthoramycota and consists of entomopathogenic fungi that infect, behaviorally- manipulate and kill dipteran hosts. Though these fungi have been observed since at least the mid nineteenth century, we have a very poor understanding of their molecular biology. Our lab recently isolated a novel strain of *E. muscae* from Berkeley, CA that is a natural pathogen of Drosophilids, including the model organism *D. melanogaster.* In establishing the *D. melanogaster*-*E. muscae* infection as a laboratory system to study the molecular biological basis of parasitic manipulation, we are sequencing the genome of this isolate. Our data suggest that the genome of *E.*

*muscae* is about 200-times larger than that of *Conidiobolus* coronatus, the only other sequenced representative of Entomophthoramycota. Preliminary analysis has uncovered thousands of copies of retrovirus-like transposons and thousands of copies of a highly-diverged ~700 bp repeat. With continued sequencing and analysis, we aim to achieve an annotated draft assembly of the *E. muscae* genome for use in sequencing experiments and to better understand genome architecture in an ancient fungal lineage.

*Poster P145*

**81. Ectomycorrhizal mutualism and water stress: A transcriptomic view on traits and trade-offs \*Erlandson, Sonya R.**, Peay, Kabir Stanford University, Department of Biology, Stanford, CA, 94305, USA. erlandso@stanford.edu

Changes in water availability, such as drought or flooding, are a common environmental stress with which soil microbes and plants must cope. Ectomycorrhiza can ameliorate drought stress for plants and show varied tolerance to drought stress, but the traits or physiological characteristics important in ectomycorrhizal stress response and trade-offs in fungal physiology are not well characterized at the genetic level. To identify ectomycorrhizal fungal stress response traits and trade-offs between stress response and mutualism function we performed a drought experiment with *Suillus pungens* and Bishop pine. We measured fungal gene expression and pine growth/survival in three soil moisture treatments over two months and an acute 2-week drought stress. We extracted RNA from 36 samples of mycorrhizal roots and soils exposed to either low, moderate or high soil moisture, and from 18 root and soil samples taken at 6 time points during a soil dry-down experiment. Sample cDNA was sequenced on a single HiSeq lane and transcripts are being assembled using the reference genome of *Suillus granulatus*, a close relative of *S. pungens*. We will compare gene expression across soil moisture treatments and compare trends in differential gene expression with pine growth as a measure of mutualism outcome. *Poster P143*

**82. What factors maintain commonness and rarity in tropical forests? \*Faircloth, Brant C.**(1), Gilbert, Gregory S.(2, 3), Glenn, Travis C.(4), Hubbell, Stephen P.(3, 5) 1.Louisiana State University, Department of Biological Sciences and Museum of Natural Science, Baton Rouge, LA, 70806, USA; 2.University of California - Santa Cruz, Environmental Studies Department, Santa Cruz, CA, 95064, USA; 3.Smithsonian Tropical Research Institute, Balboa,

Ancón, Republic of Panama; 4.University of Georgia, Department of Environmental Health Science, Athens, GA, 30602, USAl; 5.University of California – Los Angeles, Department of Ecology and Evolutionary Biology, Los Angeles, CA, 90095, USA. brant@lsu.edu

Tropical forests are incredibly diverse, yet the balance of diversity among tree species is often biased: most tree species are rare, while a very few tree species are incredibly common. Although this pattern occurs worldwide, there are few, well-tested hypotheses explaining the commonness and rarity of tropical forest trees. The goal of our Dimensions of Biodiversity research project is to test the Enemy Susceptibility Hypothesis (ESH) which states that inherent variation in susceptibility to attack by "enemies", such as wood-decay fungi, may help explain why many tree species are rare (those that are more susceptible) whereas few tree species are extremely common (those that are most resistant). We are combining genetic, genomic, and functional assays to explicitly test predictions of the ESH. Preliminary data from non-invasive sonic tomography of living trees in the 50-ha Forest Dynamics Plot on Barro Colorado Island, Panama, support several initial predictions of the ESH: we found that nearly a quarter of all trees show internal decay by the time they reach canopy height, and that the probability of decay increases with tree diameter. We also found that rare species are much more likely than common species to suffer decay. We will discuss these data, as well as additional techniques that we have developed to conduct further strong tests of the ESH, including: (1) improvements we have made for high-throughput sequencing of fungal ITS loci, and (2) new techniques we have developed for universal phylogenomic analyses of fungal lineages. *Symposium S2.2*

*Poster P86*

**84. Austral *Austroboletus*: An update**Fechner, Nigel(1), Bonito, Gregory(2), Lebel, Teresa(3), **\*Halling, Roy E.**(4) 1.Queensland Herbarium, Mt. Coot-tha Road, Toowong, Brisbane, Queensland, Australia; 2.Department of Plant, Soil and Microbial Sciences, Michigan State University, East Lansing, MI 48824 USA; 3.National Herbarium of Victoria, Royal Botanic Gardens, South Yarra, Victoria, Australia; 4.Institute of Systematic Botany, New York Botanical Garden, Bronx, NY 10458 USA. rhalling@nybg.org *Austroboletus* is a well-characterized genus of Boletaceae (Basidiomycotina, Boletales). Ornamented spores with a pinkish vinaceous color in deposit along with an alveolate to heavily reticulated stipe are diagnostic features. The majority of species are found in countries of the western Pacific, both north and south of the equator. There are approximately 15-16 species known from Australia and New Zealand. Exact numbers from New Caledonia, Papua New Guinea, Malaysia, and Indonesia are wanting. Continued field exploration has uncovered further diversity and documented additional distribution patterns. Further, the field work promoted the development of a finer resolution of the diagnostic characters. Molecular phylogenetic analyses have helped to refine species concepts. *Contributed Talk C18.1*

present in populations of *Stipa pulchra* growing in serpentine vs. nonserpentine soils at Jasper Ridge Biological Preserve. For two years, I have surveyed percent leaf infection of plants in these environments and isolated fungal specimens from symptomatic tissue. DNA sequencing shows differences in species makeup and diversity of fungal pathogens. Although fewer culturable fungi were collected in the serpentine grasslands, there was greater diversity within this group of culturable serpentine fungi than within its nonserpentine sister group. Over the coming months, I will add chemical and genetic analyses that should clarify the implications of my data. Comparison of the chemical makeup of *Stipa* leaves from serpentine and nonserpentine sites will aid in our understanding of whether or not soil chemistry affects leaf chemistry and thereby the infectious capabilities of various pathogens. The pairing of DNA sequencing of symptomatic leaf tissue with the isolation of culturable fungi from the same tissue will provide a more holistic picture of the fungal community hosted by infected *Stipa* by providing data about the presence of non- culturable fungi in leaf spots. Ultimately, this project may provide insight into how the “invisible” forces of disease and soil chemistry interact to shape the species

makeup of ecosystems.

**83. Effects of soil chemistry on fungal plant**

**pathogen communities**

**\*Farner, Johannah,** Mordecai, Erin, Spear, Erin,

Daws, Caroline

Stanford University, Department of Biology, Stanford,

94305, USA

.

jfarner@stanford.edu

In California, serpentine grassland ecosystems host native plant species specially evolved to grow in toxic serpentine soils. Disease can drive the species makeup of ecosystems, yet very little is known about pathogens in serpentine grasslands. Working from the hypothesis that serpentine soil’s unique chemistry might influence the ability of fungal pathogens to infect the plants it supports, and thereby the variety and abundance of fungal species found in serpentine vs. nonserpentine grasslands, I have performed a survey-based comparison of the fungal pathogens

**85. Detection of the effects of saprotrophic Agaricales on forest litter dissolved organic matter using Fourier transform infrared spectroscopy \*Floudas, Dimitrios**, Wang, Tao, Tunlid, Anders Lund University, Biology Department, Microbial Ecology Group, Lund, 223-62, Sweden. dimitrios.floudas@biol.lu.se

Litter decomposition plays important role in carbon cycling in terrestrial ecosystems. Through decomposition and assimilation, organic carbon gets incorporated into the microbial biomass, is released to the atmosphere as carbon dioxide and is transformed into other molecules that become part of the soil organic matter. Furthermore, decomposition results into the release of other nutrients, such as nitrogen, which become available for microorganisms and plants. Despite the importance of litter decomposition, we still lack a deeper understanding of the mechanisms involved in this process. Here, we focus on the decomposition activity of litter decomposers in Agaricales. We selected nine species with diverse habitat preferences from the marasmioid, agaricoid and tricholomatoid clades. We grew the strains on dissolved organic matter extracted with hot water from forest litter supplied with glucose. We followed glucose consumption over a period of three, six and nine days. Finally, for each species we have selected a time point, when glucose was largely consumed, and measured the total organic carbon and total nitrogen left in the growth medium. For the same time point, we used Fourier transform infrared spectroscopy to search for changes in the dissolved organic matter e.g. oxidation caused by the litter decomposing fungi. *Poster P47*

**86. Natural production of ECM fungi in west Soudanian woodlands \*Furneaux, Brendan R.**(1), Yorou, Nourou S.(2), Houdanon, Roël(2), Aignon, Hyppolite L.(2), Badou, Akotchayé S.(2), Laourou, Gérard(2), Ryberg, Martin(1)

1.University of Uppsala, Department of Organismal Biology, Uppsala, 75236, Sweden; 2.University of Parakou, Research Unit “Tropical Mycology and Plant-Fungi Interactions”, Laboratory of Ecology, Botany and Plant Biology, Parakou, 03 BP 125, Benin. brendan.furneaux@ebc.uu.se

Wild edible fungi are used as a food source and traded locally in communities in West Africa. The majority of utilized species are ectomycorrhizal, and associate with trees in the families Caesalpiniaceae, Dipterocarpaceae, and Phyllanthaceae. However, little is known scientifically about the factors that control mushroom production in this region, especially in light of climate change. This field study investigates the

natural production of ECM fungi in West Soudanian savannah woodlands in the *Forêt Clasée de l’Ouémé Supérieur* (Upper Oueme River Forest Reserve) in central Benin, West Africa, with special focus on edible species utilized by the local population. Nine 0.25-ha plots dominated by one of three ECM tree species are surveyed for fruitbodies twice weekly during the mushroom season June-October for three years, beginning in 2015. Morphological identification of fruitbodies is supplemented with DNA barcoding using the internally transcribed spacer (ITS) region. In addition, microclimate parameters are recorded at each site using automated dataloggers, and surveys of canopy cover, ground cover, and soil characteristics have been conducted. The first year of the study yielded more than 100kg of mushrooms, including almost 14kg of the two most common edible species, *Amanita masasiensis* and *Lactifluus gymnocarpoides*. Additional ongoing work includes metabarcoding to assess the soil fungal community, population genetics of three edible species, and ethnomycological investigation in the surrounding communities.

*Poster P82*

**88. Macrofungal diversity of Moorea, French Polynesia at biogeographic and community scales. \*Garbelotto, Matteo**(1), Bergemann, Sarah(2), Rasmussen, Rikke(1), Osmundson, Todd(1,3) 1.Department of Environmental Science, Policy & Management, University of California, 137 Mulford Hall, Berkeley, CA, 94720 USA; 2.Department of Biology, Middle Tennessee State University, P.O. Box 60, Murfreesboro, TN, 37132 USA; 3.Department of Biology, University of Wisconsin – La Crosse, 1725 State Street, La Crosse, WI, 54601 USA. matteog@berkley.edu

Oceanic hot spot archipelagos are important systems for studying evolutionary and ecological processes, however, diversity studies of macrofungi in these habitats are extremely few. During the BIOCODE effort, we examined diversity and potential endemicity of macrofungi on the island of Moorea, French Polynesia, using intensive field studies, examination of morphological traits, and DNA sequence data. Diversity and habitat associations were measured using morphological characters and similarity assessment of rDNA ITS sequence data. A total of 553 specimens yielded 203 morphospecies; 440 sequenced specimens yielded a molecular:morphological richness ratio of 1.44:1. Approximately 36.1% of sequences lacked a close (≥ 98%) match in GenBank. Moorea fungi appear to follow a similar biogeographic pattern to that observed for plants and arthropods: predominantly eastward migration from the western Pacific Rim and a lesser

degree of westward migration. Historical processes (geological or associated with early Polynesian migration) appear more dominant than contemporary human-mediated transport in shaping this biota, though the latter can also be observed. Fungal communities are partitioned by vegetation type, with overlap most significantly correlated to geographic and environmental similarity. Sequence and taxonomic studies indicate that endemicity occurs at the island or island group level.

*Contributed Talk C5.6*

**89. Diversity of fungal communities found in thousand cankers disease-associated galleries and lesions \*Gazis, Romina**(1), Poplawski, Laura (1), Boggess, Sarah L(1), Ownley, Bonnie(1), Collins, Tamara(1), Klingeman, William(2), Seybold, Steven(3), Graves, Andrew(4), Trigiano, Robert(1), Hadziabdic, Denita(1)

1.University of Tennessee, Department of Entomology and Plant Pathology, 2505 E. J. Chapman, Dr., 370 Plant Biotechnology Building, Knoxville, TN 37996; 2.University of Tennessee, Department of Plant Sciences, 2431 Joe Johnson Dr., 252 Ellington Plant Sciences Building, Knoxville, TN 37996; 3.USDA Forest Service, Pacific Southwest Research Station, 1731 Research Park Drive, Davis, CA 95618; 4.USDA Forest Service-Forest Health, Southwestern Region, 333 Broadway SE, Albuquerque, NM 87102. rgazisse@utk.edu

Thousand cankers disease (TCD) affects different species of walnut trees (*Juglans*) and has now been reported in several states on both USA coastlines. TCD represents a major threat for the nut and lumber industry, as well as natural stands of walnut trees and the ecosystem services they provide. Galleries created by the insect vector, *Pityophthorus juglandis*, are colonized by *Geosmithia morbida*, the actual causal agent of necrosis. These galleries represent a suitable substrate for the establishment of many other fungal species. It is unknown if other fungal colonizers might act antagonistically towards *G. morbida*, thus representing a potential source of natural enemies that could be developed as biological control agents against TCD. As part of a larger study, in which we are investigating the genetic diversity, dispersal dynamics, and co-evolutionary history of *G. morbida* and *P. juglandis*, we collected non-*Geosmithia* fungi from TCD affected walnut species from California, Tennessee and Utah. Five hundred isolates were obtained from a total of fifteen trees, directly from *Geosmithia*-colonized galleries and from the surrounding necrotic lesions. The objectives of this study were to: (1) characterize the fungal community associated with TCD and (2) develop a pilot study

addressing their antagonistic potential towards *G. morbida*. We found low species diversity in TCD communities with few dominant species, represented by genera commonly reported as secondary or weak plant pathogens. However, we observed significant differences in species composition between samples from the East Coast (CA, UT) and Southeast (TN). *Ophiostoma* (cf. *abietinum*) dominated TCD- communities in samples from CA and UT, while *Trichoderma* (cf. *harzianum*) dominated TCD- communities in TN. *Trichoderma* species are known to have antagonistic interactions with a broad variety of fungal pathogens; therefore, these strains are proposed for further *in-vitro* and *in-planta* testing against TCD.

*Contributed Talk C19.5*

Trichomycetes is a traditional fungal class now recognized as an ecological group of fungi and protists obligately associated with the the digestive tracts of various non-predaceous arthropods. Among candidates, Isopoda is a well recognized host currently known to harbor up to 7 genera of these endobionts. Ecologically and evolutionary they are an interesting host because of varied habitats that include freshwater, marine and terrestrial ecosystems. Some taxa can be easily collected and recognized. A f

We report on gut fungi from collections of terrestrial isopods over the past several years, including *Asellaria, Baltomyces* and *Parataeniella*, in respects to their morphological identification and distribution. There is much to discover in this group which, despite their ease of collection and dissection, are relatively

under-surveyed in the literature.

*Poster P85*

**91. Are more data better for phylogenomics? Contradicting phylogenetic stories told by genome- scale datasets for basal relationships of the Basidiomycota** + + Gerber, Daniel (1), Prasanna, Arun N. (1), Kijpornyongpan Teeratas(2), Aime, M. Catherine(2), \***Nagy, Laszlo G.**(1)

1. Synthetic and Systems Biology Unit, Biological Research Center, HAS, Szeged 6726, Hungary; 2. Purdue University, Department of Botany & Plant

**90. Holy moly roly poly! Exploring endobionts in**



**Isopoda**



**\*Geisler, Mathew**, Hollar, Sierra, McCormick,



Michael, White, Merlin



Boise State University, Department of Biological



Sciences, Boise, ID, 83725-1515, USA.



mathewgeisler@u.boisestate.edu



avorite childhood



isopod, the roly-poly or pill-bug, is an excellent host



of gut fungi, which will be highlighted herein.



Pathology, West Lafayette IN 47901 USA; shared first authors. cortinarius2000@gmail.com

Reconstructing ancient relationships is a challenging task even when using genome-scale phylogenetic datasets. The inference of true relationships can be complicated by systematic patterns not accounted for by current models of evolution. Systematic model misspecification can lead to strongly supported incorrect relationships, which are not alleviated by the addition of more data. Rather, such systematic errors become more pronounced with increasing dataset size. We address this problem by trying to reconstruct the historically recalcitrant relationships between the three Basidiomycota subphyla, the “rusts” and their allies (Pucciniomycotina, Pu), “smuts” and their allies (Ustilaginomycotina, Us) and the “mushroom- forming” fungi and their allies (Agaricomycotina, Ag) as a test case. Previous phylogenomic analyses yielded strongly supported contradicting relationships, placing either rusts or smuts as the sister group of mushroom- forming fungi, or rusts and smuts as a monophyletic clade. We assembled several phylogenomic datasets containing from 314 to 950 single-copy protein families (46.000 to >700.000 amino acid sites) and analyzed them using a range of approaches, including Maximum Likelihood (ML), Bayesian inference and summary-based methods (Astral). The shortest but most conserved datasets consistently recovered the Pucciniomycotina as a sister group to Agaricomycotina, albeit with weak to moderate bootstrap (BS) support (59-71% ML BS), whereas larger but less conserved datasets supported Ustilaginomycotina as the sister to Agaricomycotina with strong support (95-99% ML BS). Gradual removal of the fastest evolving sites from the less conserved datasets decreased BS support for Us+Ag topologies, eventually recovering Pucciniomycotina and Agaricomycotina as sister groups. This suggests that strong support for Us+Ag may be a result of highly variable, noisy sites and focusing datasets to a small but mostly conserved fraction of sites can improve phylogenomic inference. In support of this hypothesis, tree inference under simple (e.g. unpartitioned) models of sequence evolution tend to support Ustilaginomycotina and mushroom-forming fungi as sister groups. Interestingly, methods taking incomplete lineage sorting into account consistently recover smuts and Agaricomycotina as sisters, whereas a gene-content based phylogeny yielded a strongly supported Pu+Ag topology. Although these results are not satisfactory from a biological point of view, they highlight the need for rigorous testing of the phylogenetic signal even in phylogenomic datasets. Our goals include deciphering the historical events causing the observed contradiction between

datasets and inferring a reliable estimate of the relationships between the three Basidiomycota subphyla that help interpreting biological (e.g. ultrastructural) similarities between rusts, smuts, and mushroom-forming fungi.

*Contributed Talk C7.3*

**92. Heart-rot communities in standing trees \*Gilmartin, Emma C.**, Jones, T. Hefin, Boddy, Lynne. Cardiff University, School of Biosciences, Cardiff, CF10 3AX, UK. gilmartinec@cardiff.ac.uk

Fungal decay of the interior of tree trunks and large branches, termed heart-rot, is a natural part of tree ageing. Heart-rot and subsequent hollowing releases nutrients for continued tree growth and is ecologically essential for a range of organisms, including birds, invertebrates and other fungi. However, this habitat is poorly represented as it occurs in old, or veteran, trees that have developed heartwood. This project explores fungal community structure and development in European beech (*Fagus sylvatica*). We have investigated communities in recently fallen trees via traditional culture-based methods, and will use high throughput sequencing of sapwood and heartwood from standing treess to survey unculturable or latently present species. Experiments on wood decay rates and interactions between known heart-rot fungi are also underway. Ultimately, we would like to determine if heart-rot can be induced via inoculation of appropriate fungi into trees with no evidence of decay. This will be tested at southern UK sites with a generation gap between current veteran trees and the younger cohort. *Poster P48*

**\*Glassman, Sydney I.**(1,3), Wang, Ian J.(2), Lubetkin ,Kaitlin C.(3), Bruns, Thomas D.(1,3) 1.University of California, Department of Environmental Science Policy and Management, Berkeley, CA; 2.Environmental Systems, University of California, Merced, CA, USA 95343; 3Department of Plant & Microbial Biology, University of California, Berkeley, CA, USA 94702 sglassman@berkeley.edu

We use a natural experimental system of isolated “tree islands” in Yosemite National Park to test the fundamental question of whether environment or geography primarily structures fungal community composition. This system consists of isolated pairs of two congeneric species of pine trees established at varying distances from each other and the forest edge, allowing us to disentangle the effects of geographic

|  |
| --- |
| **93. Environmental filtering by pH and soil** |
| **nutrient habitat drives community assembly in ectomycorrhizal fungi on subalpine tree islands** |

distance versus host and edaphic environment on associated fungal communities. We detected fungal community composition with Illumina sequencing of ITS amplicons, measured all relevant environmental parameters for each tree island - including tree age, size, and soil nutrient content - and calculated geographic distances of each tree from all others and the nearest forest edge. We applied generalized dissimilarity modeling (GDM), a non-linear form of matrix regression, to test whether total and ectomycorrhizal fungal (EMF) communities were primarily structured by distance decay, host species, or edaphic environmental filtering. Geographic isolation affected total fungal but not EMF beta-diversity, while host tree affected EMF but not total fungal communities. Most strikingly, however, we found that soil environment played a greater role in structuring both fungal communities than either geographic distance or host specificity. In fact, soil environmental variables, especially pH, were the largest contributors to the variance in tree island fungal community composition. This result is particularly surprising for EMF community composition, because host identity has long been expected to be the primary driver of EMF communities. Here, we describe an emerging paradigm of pH as the strongest predictor of both EMF and total fungal community composition.

*Symposium S1.1*

**94. What has happened to the aquatic phycomycetes on the way to the forum? Part I. A brief historical perspective \*Gleason, Frank**(1), Marano, Agostina(2), Lilje, Osu(1), Lange, Lene(3)

1.University of Sydney, School of Life and Environmental Sciencs, Camperdown, 2006, Australia; 2.Instituto de Botânica, Núcleo de Pesquisa em Micologia, São Paulo, SP, CEP 04301-912, Brazil; 3.Technical University of Denmark, Department of Chemical and Biochemical Engineering, Lyngby, 2800 Kgs, Denmark. frankjanet@ozemail.com.au

The aquatic phycomycetes (*sensu* Sparrow) constitutes an ecologically and economically important assemblage of eukaryotic microorganisms which share many morphological traits and ecological functions and interact with each other in the same aquatic ecosystems. The last two decades of research have provided both molecular and structural evidence that the aquatic phycomycetes is a diverse, polyphyletic assemblage of species placed into four unrelated super groups by Bladauf (2008) and therefore not a valid taxonomic entity. Very little research has been conducted with the aquatic phycomycetes for many years, possibly because they were thought to be economically and ecologically unimportant, but this perception has recently changed.

Many of these species have been found to play key roles in biomass conversion in food webs and in the carbon cycle, may harbor enzymes of importance for industrial biomass upgrade and serve as indicator species for eco-tox monitoring. Many species are emerging facultative parasites of economically important hosts. We have renamed this diverse assemblage of aquatic true fungi and fungus-like species the Zoosporic Heterotrophic Aquatic Microorganisms assemblage. The placement of these species into the phylogenetic systems designed by Baldauf (2008) and Ruggiero (2015) is discussed. *Contributed Talk C21.1*

**95. What has happened to the aquatic phycomycetes (sensu Sparrow) on the way to the forum? Part II: Shared properties of fungus and fungus-like groups**

\*Gleason, Frank(1), Lilje, Osu(1), **\*Lange, Lene**(2) 1. University of Sydney, School of Life and Environmental Sciences, Camperdown, 2006, Australia; 2. Technical University of Denmark, Department of Chemical and Biochemical Engineering, Lyngby, 2800 Kgs, Denmark. frankjanet@ozemail.com.au

Some fungus-like species Perkinsozoa, Oomycota, Hyphochytrioomycota, Labyrinthulomycota and Phytomyxea share morphological and ecological characteristics with some species of true fungi (Phylum Chytridiomycota) and with some fungus-like species in the Phyla Aphelidae and Mesomycetozoa. These characteristics include chemotactic, free living zoospores (either uni- or biflagellate), zoosporangia, thick-walled resistant cysts, rhizoid-like structures, hyphal-like structures and cell walls (composed of chitin and /or cellulose microfibrils, either just outside the cell or within alveoli just inside the cell membranes) in several phases of their life cycles. These species also inhabit marine, brackish and freshwater ecosystems in which aquatic zoosporic fungi and fungus-like organisms are found, have similar life cycles, use similar infection strategies and infect some of the same host plants or animals. For example, the heterokont zoospores of some Perkinsozoa species are very similar morphologically to those of some Oomycota species. Many of these species, particularly those within the Oomycota, were once included in the aquatic phycomycetes, an assemblage of microorganisms which Sparrow (1960) considered to be true fungi. However, DNA sequences from ribosomal RNA genes have recently placed the Oomycota into the super group Stramenopilia, separate from true fungi in the super group Opisthokonta, and other fungus-like species of zoosporic microorganisms in different super groups (Baldauf 2008). However, Richards et al.

in the Phyla

(2006) and Richards and Talbot (2007) recently provided strong molecular evidence for the exchange of genes between unrelated groups of eukaryotes in general and specifically the lateral transfer of genes for pathogenicity from the Phylum Ascomycota (super group Opisthokonta) to the Phylum Oomycota (Super group Stramenopilia). These plant pathogenic species have evolved in unrelated phyla.

*Contributed Talk C21.2*

**96. The impact of plant secondary metabolites on the evolution of fungal genome structure \*Gluck-Thaler, Emile**, Slot, Jason The Ohio State University, Department of Plant Pathology, Columbus, 43210, USA. gluckthaler.1@osu.edu

Changes to genome structure often underlie adaptations to specific ecologies in many organisms. In pathogenic bacteria, genes that participate in host colonization are frequently organized into pathogenicity islands and in plants, genes encoding various secondary metabolite biosynthetic pathways are co-localized into gene clusters. In fungi, many genes that encode for secondary metabolite biosynthesis can also be found clustered, but little is known about the extent of clustering of catabolic (i.e., degradative) pathways. Yet catabolism often plays an essential role in the colonization of plant material by saprotrophs and pathogens both in terms of nutrient acquisition and the degradation of defense metabolites. We developed a new cluster discovery pipeline to systematically investigate the incidence of clustering in the genomic neighborhoods of fourteen different ‘anchor’ gene families that participate in the degradation of phenylpropanoids, a diverse group of plant defense compounds. We found that clustering is rampant: anchor genes from eight of these families are part of conserved gene clusters found in diverse fungal species. Clusters from different anchor genes are typically composed of unique sets of metabolic enzymes, transporters and transcription factors, suggesting that there has been repeated selection for clusters that encode diverse pathways for the degradation of phenylpropanoid compounds. Furthermore, the complex distribution of many of these clusters is often best explained by the shared ecology among fungi that possess a given cluster, independent of phylogeny. The clusters identified here and the previously undescribed catabolic pathways they encode may therefore represent important adaptations in the evolution of plant substrate and host specialization in fungi. *Poster P108*

**97. Evaluating the evidence of fungal long distance dispersal**

**\*Golan, Jacob**. University of Wisconsin-Madison, Botany Department, Madison, WI, 53703, USA. jgolan@wisc.edu

Research on the long-distance dispersal (LDD) of fungi faces many challenges due to the rarity and stochasticity of such events, as well as to methodological and theoretical impediments. Inferences based on comparing allele frequencies or gene flow serve to capture rare instances of successful dispersal, but are limited in their ability to describe underlying demographic processes and mechanisms of LDD. In many cases, LDD is defined inconsistently and the basic life history of fungi is neglected. Extreme instances of LDD, such as trans-oceanic dispersal, are poorly corroborated by biological knowledge, raising questions as to how ephemeral propagules remain viable under extended periods of harsh environmental conditions. The integration of ecological, genetic, biophysical, and historical data reveals that Human-mediated LDD is the most prevalent mechanism of recent LDD. The critical importance of LDD in disease epidemics necessitates a better understanding of anthropogenic vectors, of the physical properties of fungi and fungal propagules, and of dispersal models. *Poster P69*

**98. Host diversity increases proportionally to host overlap among mycoheterotrophic plants \*Gomes, Sofia I.F.**(1), Merckx, Vincent S.F.T.(1); Saavedra Serguei(2)

1.Naturalis Biodiversity Center, Understanding Evolution, Leiden, 2333 BE, The Netherlands; 2.Massachusetts Institute of Technology, Department of Civil and Environmental Engineering, MA, 02139- 4307, USA. sofia.fernandesgomes@naturalis.nl

More than 80% of land plants obtain their vital resources through arbuscular mycorrhizal fungi. Generally, this happens in exchange of photosynthetically fixed carbon from the plants to the fungal partner, but occasionally the interaction is mycoheterotrophic, and the carbon flux is inverted. Hence, this mutualistic interaction becomes parasitic. Host specificity is a hallmark of parasite systems, and – as expected – mycoheterotrophic interactions involve narrower lineages of fungal hosts than mutualistic interactions. Thus, the fungal diversity available for mycoheterotrophic plants is restricted. This implies that host diversity and overlap among mycoheterotrophic plants may have important consequences for their coexistence. Yet, little is known about these host patterns. In this study, we shed light on mycoheterotrophic interactions patterns. We used high-throughput DNA sequencing data to investigate the interactions between arbuscular mycorrhizal fungi and mycoheterotrophic plants. We

detected no phylogenetic signal on the number of fungal host nor on the shared fungal hosts among these plants. Interestingly, we found that the phylogenetic diversity of fungal hosts associated with any given group of mycoheterotrophic plants increases proportionally with their overlap in fungal hosts. Furthermore, we show that this symmetry between diversity and overlap is a characteristic of coexisting mycoheterotrophic plants in the field. Importantly, our findings open up a new set of questions of whether host diversity in mycoheterotrophic plants is more strongly modulated by ecological than by evolutionary processes, responding to maximize co-occurrence and avoid competitive exclusion among plants. *Contributed Talk C19.2*

**99. Microfungi diversity isolation from sandy soil of Acapulco touristic beaches \*González María C.**(1), Hanlin Richard T.(2), Glenn Anthony E.(3)

1.Universidad Nacional Autónoma de México Departamento de Botánica, Coyoacán, CDMX 04510, México; 2. University of Georgia Museum of Natural History Annex 4435 Atlanta Highway, Athens GA 30606 USA; 3.USDA, ARS, Toxicology & Mycotoxin Research Unit, Russell Research Center, Athens GA 30604 USA

mcgv@ib.unam.mx Microscopic fungi diversity in marine sandy soil

habitats is associated with key functions of beach ecosystems. There are few reports on their presence in Mexican beaches. Although standard methods to obtain the fungi from soil samples are established, the aim of this pilot study was to test the plating technique using two culture media with a mix of three antibiotics at five different concentrations. The results will permit us to apply a methodology specifically designed for a further project to study the arenicolous fungi from this unique place. Eight beaches in Acapulco de Juárez, State of Guerrero, México, located on the littoral of the Pacific Ocean were studied: Caleta, Tlacopanocha, Hamacas, Hornos, Hornitos, Calinda, Icacos and La Palapa. At intertidal zone of each beach, a sample of sandy soil (200 g) from the surface layer was collected in a Zip lock bag and transported to the laboratory to be processed within 24 h. The soil plating method was applied for qualitative and quantitative isolation of sandy beach mycobiota. One gram of wet sandy soil was put onto a sterile Petri dish and immediately covered with autoclaved Mycosel agar previously cooled to 45 °C. As some fungal development may be influenced or inhibited by the ingredients and antibiotics of this culture medium, V-8 vegetable juice agar, supplemented with different concentrations de penicillin G/streptomycin sulfate/chloramphenicol also was prepared and inoculated using the same

procedure. The media with the sandy soil was shaken gently and solidified. Ten plates of each media were prepared, including positive and negative controls, for each single beach. After 7, 14, 21, 28 d of incubation at 25 °C, the dishes were examined. The colonies obtained were identified based on their macro- and micro-morphological characteristics and their occurrence indicated by: 1) number of fungi obtained in pure culture, 2) number of different colonies divided by the number of Petri dishes prepared, 3) frequency of isolation of fungi (number of fungal colony forming units of a given species divided by the total number of fungi × 100%). Results indicated that the sand beach community is relatively species rich, with representatives of sewage habitats. The optimal concentration of antibiotics to inhibit the growth of bacteria was several times higher than the values established in the literature for the isolation of fungi from sewage. Adequate concentrations of antibiotics will control the growth of rapidly growing fungi and will permit the isolation of other species with slower growth. A total of 46 fungi were isolated. *Acremonium, Aspergillus, Cladosporium*, *Fusarium* were the common genera and *Gymnascella, Malbranchea, Mucor,* the less common. Most of the genera belonged to the *Ascomycota*, with fewer to the *Mucorales*. The Hornos Beach has the highest species richness and the lowest in the adjacent Hornitos Beach. The mycobiota obtained using the two media showed a 98% of dissimilarity. Of the total number of Petri dishes inoculated, 87% were positive for fungal growth.

*Poster P32*

The roots of woody plants are colonized by diverse assemblages of fungal endophytes. They also contain high concentrations of tannins; phenolic secondary defense metabolites that inhibit microbial growth by mechanisms such as protein and metal binding. As fungi show a wide range of tolerance to tannins, we speculated that the fungal endophytes of woody plant roots might be especially tolerant to these compounds. We therefore compared the effect of varying concentrations of condensed and hydrolysable tannins on the growth and enzymatic potentials of fungal endophytes from roots, bark and leaves, as well as wood decay, plant pathogenic and mycorrhizal fungi. Although the majority of fungi tested were strongly inhibited by tannin, the dark septate endophytes (DSE) represented by *Phialocephala fortinii* sensu lato, *P. sphaeroides* and an unidentified

**100. Tannin tolerance in fungal root endophytes**



Griffin, Amanda, **\*Kernaghan, Gavin**



Mount Saint Vincent University, Department of Biology, Halifax NS, B3M 2J6,



Canada. gavin.kernaghan@msvu.ca



*Phialocephala* species, were significantly more tolerant to tannic acid than isolates from any of the other ecological groups, including other root endophytes. The DSEs also retained enzymatic functions and could still degrade pectin in the presence of relatively high levels of tannin. The DSEs also produced polyphenol oxidases (e.g. laccase) that eventually detoxified the tannin by oxidation.

*Poster P52*

**101. NextGen Sequence data and conservation biology: Assessing the distribution of rare fungi \*Griffith, Gareth W.**, Detheridge, Andrew P. Aberystwyth University, IBERS, Cledwyn Building, Aberystwyth SY23 3DD WALES

gwg@aber.ac.uk Hitherto NGS (NextGen Sequencing) approaches

have mostly been used to address fundamental questions in fungal ecology. We have applied these methods in conservation biology, specifically as an alternative to fruitbody surveys when assessing the fungal conservation value of grassland habitats, both as an aid to planning policy and also for provision of legal protection to areas of high biodiversity value. NGS metabarcoding has the main advantages of being rapid, and allowing "out of season" assessment of macrofungal diversity.

Our efforts have focused mainly on the grassland waxcaps (Hygrophoraceae) and corals (Clavariaeceae), with the former having a high profile across Europe for non-specialist conservationists. We developed a metabarcoding approach based on the LSU D1 region, and have supplemented our in-house RDP database with local reference sequences. Comparison with both ITS2 metabarcoding data and fruitbody surveys shows good concordance.

When studying macrofungi believed to be rare or threatened, it is often unknown whether the fungus in question is truly rare or simply form fruitbodies only rarely ('shy'). The examples of *Squamanita paradoxa* (spectacular parasite of *Cystoderma amianthinum*) and *Cryptomyces maximus* (willow blister, only fungus in IUCN top100 threatened species) will be discussed. This work also relies heavily on the contributions by citizen-scientists.

*Symposium S9.4*

**102. Fungal genomics for bioenergy and biotechnology \*Grigoriev, Igor**1.US Department of Energy Joint Genome Institute, Walnut Creek, CA 94598, USA and University of California, Plant and Microbial Biology, Berkeley, CA 94720, USA. ivgrigoriev@lbl.gov

Future energy demands can be addressed by learning from biological processes encoded in living

organisms such as fungi. Genomics is a powerful and quickly evolving tool to understand these processes. The Fungal Genomics Program of the US Department of Energy Joint Genome Institute (JGI) partners with researchers around the world to explore the Kingdom Fungi in several large scale genomics projects.

One of them, the *1000 Fungal Genomes* project, aims at exploring the diversity across the Fungal Tree of Life in order to better understand fungal evolution and to build a catalogue of genes, enzymes, and pathways for biotechnological applications. Embracing such diversity requires further advances in genome sequencing including *single cell genomics* of unculturable fungi or *single molecule sequencing* that delivers better genome assemblies and DNA methylomes, all at once. These advances, in turn, allow decoding genomes of diverse fungi with extreme GC content to explore alternative mechanisms of cellulose degradation or alternative genetic codes for new biotechnological applications. Over 700 fungal genomes integrated in MycoCosm (jgi.doe.gov/fungi) and equipped with comparative genomics tools enable researchers to address a broad spectrum of biological questions and applications for bioenergy and biotechnology.

*Symposium S5.1*

**103. Agricultural and non-cultivated soil fungal diversity across a latitudinal transect in Wisconsin \*Grubisha, Lisa C.**(1), Nellis, Samantha (2), Moyer, Joshua R.(1), Cotty, Peter J.(3)

1.University of Wisconsin–Green Bay, Department of Natural and Applied Sciences, Green Bay, WI, 54311- 7001, USA; 2. University of Wisconsin–Green Bay, Environmental Science and Policy Graduate Program, Green Bay, WI, 54311-7001, USA; 3.United States Department of Agriculture–Agricultural Research Service, University of Arizona, School of Plant Sciences, Tucson, AZ, 85721, USA. grubishl@uwgb.edu

A diverse soil microbial community is important for biogeochemical cycling. Microbial diversity is influenced by plant community diversity. In this study we addressed the question of whether mono-cropped agricultural soil has a less diverse soil fungal community compared to non-cultivated soil. A total of 22 plot soil samples were collected from four regional sites along a latitudinal transect in eastern Wisconsin. Four 15 cm soil cores were collected from each sample plot and pooled in the field. DNA was isolated from the 22 plot samples. PCR was performed using Illumina barcodes and ITS primers for the ITS1 region of the ribosomal DNA repeat. Data will be presented from Illumina MiSeq sequencing of the soil DNA. These results will provide information on how current agricultural practices affect soil fungal biodiversity.



*Poster P36*

**104. *In vivo* inoculation of pecan seedlings with the pecan truffle (*Tuber lyonii*) \*Grupe II, Arthur C.**(1), Mujic, Alija B.(1), Brenneman, Timothy B.(2), Smith, Matthew E.(1) 1.University of Florida, Department of Plant Pathology, Gainesville, 32611, USA; 2.University of Georgia, Department of Plant Pathology, Tifton, GA, 31793, USA. agrupe@ufl.edu

The Pecan, *Carya illinoinensis* (Juglandaceae), is an economically important nut crop in the southeastern USA that also forms ectomycorrhizas. One ectomycorrhizal fungus regularly recovered from commercial pecan orchards is the gourmet Pecan Truffle, *Tuber lyonii* (Ascomycota). While pecan production is already a 600-million dollar industry in the USA, the opportunity for co-cropping both pecans and pecan truffles could allow for even higher profits per acre. Although many members of the Fagales have been successfully inoculated with edible truffles species in a greenhouse setting, there are a lack of field inoculation trials. To assess the ability to successfully inoculate pecan seedlings in outdoor nurseries with *T. lyonii*, we conducted field inoculation tests on seedlings in both fumigated and non-fumigated field soils*.* Aside from our standard inoculation concentration, we also tested various dilutions of it to establish a minimum concentration. In order to determine if field inoculations were successful and to quantify the relative abundance of *T. lyonii* we sampled seedling ectomycorrhizas after one year. The fungal community was assessed via next-generation sequencing of the fungal ITS rDNA. This poster will present the results of year one sampling and will discuss implications for controlled cultivation of pecan truffles. *Poster P81*

**105. Molecular analysis reveals host-associated diversity in a microscopic fungal parasite \*Haelewaters, Danny**(1), Pfister, Donald H.(1) 1.Organismic and Evolutionary Biology, Harvard University, 22 Divinity Avenue, Cambridge MA 02138, USA. dhaelewaters@fas.harvard.edu.

As a practice that started even before Linnaeus’ *Species Plantarum*, many species have been described based on morphological characters. However, it may be reasonable to argue that species delimited for small organisms with global distributions and/or wide host ranges are artifacts of the morphological species criterion. One such organism is *Hesperomyces virescens* (Fungi, Laboulbeniales), which is an ectoparasite of lady beetles (Coleoptera, Coccinellidae). By the morphological species concept, *H. virescens* is a single species with a characteristic

morphology, a global distribution, and a wide host range. Since its description 120 years ago, this parasite has been reported from 31 lady beetle hosts on all continents except Antarctica. Previous research, based on transmission experiments, hints at the existence of different lineages of *H. virescens* and that each of these lineages has a high degree of host specificity. Its wide host range suggests that *H. virescens* could contain many different phylogenetic species, each adapted to individual host species. We combined a morphometric approach with molecular data and found distinct clades of *Hesperomyces virescens*, with each clade corresponding to isolates from a single host species. Additionally, using a molecular clock, we estimated that the *H. virescens* clade started diverging in the Oligocene (about 29 Mya).

*Contributed Talk C4.3*

**106. Antifungal activity of western bat biota against white-nose syndrome \*Hamm, Paris S.(**1), Caimi, Nicole A.(2), Northup, Diana E.(2), Valdez, Ernest W.(3), Buecher, Debbie C.(4), Dunlap, Chris(5), Labeda, David(5), Lueschow, Shiloh(5), Porras-Alfaro, Andrea(2)

1.Western Illinois University, Department of Biological Sciences, Macomb, IL 61455; 2.University of New Mexico, Department of Biology, Albuquerque, New Mexico 87131; 3. U.S. Geological Survey, Fort Collins Science Center; 4.Buecher Biological Consulting, 7050 E. Katchina Court, Tucson, AZ

85715; 5.U.S. Department of . Agriculture, 1815 University St., Peoria, IL 61604 ps-hamm@wiu.edu

N.

White-nose syndrome (WNS), a bat fungal disease caused by the psychrophilic fungus *Pseudogymnoascus destructans*, has been estimated to cause the death of more than six million bats in the eastern U.S. and Canada. Fungal and bacterial surveys have been conducted to explore bats’ natural microbial communities as a possible defense against this pathogen. In this study we evaluate the antifungal potential of naturally occurring Actinobacteria isolated from WNS-free bats from New Mexico and Arizona. Bacteria colonizing bat fur and membranes were isolated from 12 healthy bat species from New Mexico and Arizona, providing approximately 2700 isolates. We have screened over 700 of the 2700 bacterial isolates using a bi-layer method, of which 36 isolates show antifungal activity against *P. destructans*. Fungal inhibitors were cultured from nine different species of bats with representatives from all of the five cave systems or nearby surface habitats sampled. Of the 36 positive Actinobacteria, 32 (89%) were from the genus *Streptomyces*, known for their antibiotic production. Seven of the isolates with antifungal activity against *P. destructans* were identified as novel *Streptomyces* species after morphological and multi-gene

phylogenetic analysis. Our results show that bats in western North America possess bacterial microbiota with the potential to inhibit *P. destructans*. USGS: This information is preliminary and is subject to revision.

*Contributed Talk C1.2*

**107. Phylogenomics and evolutionary history of the Neocallimastigomycota \*Hanafy, Radwa A.**, Elshahed, Mostafa, Youssef, Noha

Department of Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK, 74078 USA. Noha@okstate.edu

The anaerobic gut fungi (phylum *Neocallimastigomycota*) reside in the gastrointestinal tract of mammalian and non-mammalian herbivores, and represent one of the early-diverging fungal phyla. They are characterized by their broad fermentative capabilities, anaerobic physiology, extremely low G+C content, and the presence of a flagellated zoospore stage in their life cycle. As part of a wider effort to resolve the evolutionary origin of the phylum and genera within, we are currently isolating, characterizing, and sequencing the genomes of representatives belonging to each of the known AGF genera. Isolation efforts from the feces of cow, goat, and sheep yielded several AGF isolates (n=22). Classification using microscopic and phylogenetic- based approaches identified 21 isolates as members of the genera *Anaeromyces*, *Neocallimastix*, and *Orpinomyces*, while one isolate, strain S4B, putatively represents a novel genus. Strain S4B is phylogenetically close to members of the Orpinomyces genus but morphologically distinct based on its monocentric thallus and monoflagellated zoospore. Biochemical characterization for strain S4B is underway. Genome and transcriptome sequencing of 13 of the current isolates has started. Genomic analyses will be aimed towards resolving the evolutionary history of the phylum Neocallimastigomycota within the fungal tree of life, and correlating the timing of such event to the evolution of the host, as well as resolving the evolutionary history and diversification of various AGF genera.

*Poster P110*

**108. Transcriptional effects of global warming on**

***Neurospora***

**\*Hann-Soden, Christopher**(1), Romero-Olivares, Adriana L.(2), Montoya, Liliam A.(1), Treseder, Kathleen(2), and Taylor, John W.(1) 1.University of California, Berkeley, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA; 2.University of California, Irvine, Ecology &

Evolutionary Biology, Irvine, CA, 92697-2525, USA. channsoden@berkeley.edu

Models of climate change tip from bad to worse depending on how saprobes respond to warmer temperatures. Arctic soils are te world's largest terrestrial reservoir of carbon and are also subjected to warming at double the average rate. If utilization of this carbon reservoir increases as arctic soils thaw, we can expect a positive feedback cycle on global warming as arctic decomposers release more sequestered carbon. However, we don't know how saprobes might respond to mitigate this effect. If arctic decomposers compensate or perform poorly at high temperature climate change might not be as catastrophic. To understand microbial responses, we are studying the affect of acclimation to warmer temperatures on carbon metabolism. We have measured global transcription and respiration of Neurospora grown at high or low temperatures on sucrose or lignin. By correlating the degree of response to recalcitrant carbon at high or low temperatures to gene expression levels, we are attempting to determine the expression-level underpinnings for how temperature response affects carbon utilization.

*Poster P43*

**109. Large scale sequencing of Dothideomycetes provides insights into genome evolution and adaptation. \*Haridas, Sajeet**(1), Crous, Pedro(2), Binder, Manfred(2), Spatafora, Joseph(3), Grigoriev, Igor V .(1)

1.DOE Joint Genome Institute, Walnut Creek, CA. USA; 2.CBS Fungal Biodiversity Centre, Utrecht, The Netherlands; 3.Oregon State University, Corvallis, OR. USA. sharidas@lbl.gov

Dothideomycetes is the largest and most diverse class of ascomycete fungi with 23 orders 110 families, 1300 genera and over 19,000 known species. The 1000 fungal genomes project aims to fill in gaps in the Fungal Tree of Life by sequencing at least two reference genomes from the more than 500 recognized families of Fungi. As part of this project, we have sequenced 50 Dothideomycetes genomes, and compared them to 40 previously published Dothideomycetes genomes, together encompassing 45 families. We were able to clarify the phylogenetic positions of several species whose origins were unclear in previous morphological and sequence comparison studies. Comparisons of gene content in clades with contrasting lifestyles have uncovered clues to genome evolution and adaptation. *Poster P146*

**110. Fungal community overlap and assemblage mismatch between *Ips typographus* and its phoretic mites \*Harrington, Alison**(1), Linnakoski, Riikka(2,3), Mahilainen, Saila(4), Vanhanen, Henri(5), Eriksson, Miikka(6), Mehtätalo, Lauri(7), Pappinen, Ari(4), Wingfield, Michael J.(3)

1.Thomas J. Watson Fellow, Watson Foundation, New York, NY, USA; 2.Department of Forest Sciences, Faculty of Agriculture and Forestry, University of Helsinki, Finland; 3.Department of Microbiology and Plant Pathology, Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, South Africa; 4.School of Forest Sciences, Faculty of Science and Forestry, University of Eastern Finland; 5.Natural Resources Institute Finland, Joensuu, Finland; 6.School of Applied Educational Science and Teacher Education, Philosophical Faculty, University of Eastern Finland, Joensuu, Finland; 7.School of Computing, University of Eastern Finland, Joensuu, Finland. AHHarrington1@gmail.com

The European spruce bark beetle (*Ips typographus*) is a major agent of forest succession, and carries a diverse suite of yeasts, fungi, and mites that affect beetle fitness and tree host-beetle interaction. Phoretic mites of *I. typographus* are phylogenetically and ecologically diverse, and the nature of interaction between bark beetles and these poorly studied mites ranges from brood parasitism to commensalism depending on species and context. These mites carry their own suite of fungi that is co-dispersed during bark beetle dispersal flights. In this study, we investigated the culturable fungi of *I. typographus* and its phoretic mites with an emphasis on preliminary data from the small subset of beetles carrying mites. Following an *I. typographus* outbreak region in southeastern Finland, 297 adult bark beetles and the 39 phoretic mites present on 19 of these beetles were collected in different seasons, at different beetle life phases, and from different substrates in a wind- damaged spruce forest. Their fungal associates were isolated in culture and individually assigned to genus or species using the ITS region sequences, the megablast algorithm in GenBank with a 98% similarity cutoff, and compiled GenBank species sets aligned in MAFFT. Depending on the season and collection site, mites were found on 2% to 22% of the adult beetles. The average number of isolates was 1.33 per mite and 1.35 per beetle in the complete set of beetles. The average number of isolates per beetle was 0.79 in the subset with mites, but the net isolates per beetle plus its mites was 2.68. There were no OTUs present in the pooled mite community that were not present in the beetles’ pooled total community, but 92.6% of the isolated OTUs from individual mites were not found on their individual host beetle. These

suggest that the presence of mites on beetles has the potential to impact fungal dispersal and alter the fungal communities of their host trees. *Poster P60*

**111. Are sequestrate taxa evolutionary dead-ends? Assessing evolution and diversification of sequestrate *Cortinarius*\*Harrower, Emma**(1), Smith, Matthew E.(2), Mujic, Alija Bajro(2), Truong, Camille(2), Henkel, Terry W.(3), Aime, M. Catherine (4), Clark Ovrebo (5), Matheny, Brandon(1)

1.University of Tennessee Knoxville, Ecology and Evolutionary Biology, Knoxville, 37996, USA; 2.University of Florida, Department of Plant Pathology, Gainesville, Florida, 32611, USA; 3.Humboldt State University, Department of Biological Sciences, Arcata, California, 95521, USA; 4. Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA; 5.University of Central Oklahoma, Department of Biology, Edmond, OK, 73034. eharrowe@vols.utk.edu

*Cortinarius* is the most species-rich genus of Agaricales with some 2000 accepted species, most of which are epigeous and agaricoid in form. Distribution of the genus is largely north and south temperate, although an increasing number of species are known from the tropics. About 90 sequestrate species, however, have been described and are now generally accepted as *Cortinarius*. Sequestrate taxa have an enclosed hymenophore and typically statismosporic basidia, thus having lost their ability to disperse their basidiospores through the air. Most rely on vertebrate- based mycophagy for dispersal. Thiers hypothesized that these evolutionary changes in sequestrate taxa have resulted from selection pressures to avoid a loss of moisture in dry environments. However, Bougher and Lebel hypothesized that there may equally be a selection pressure to protect the hymenophore from excessively moist conditions. Using a global phylogeny of temperate and tropical *Cortinarius* species, we tested whether a correlation exists between the occurrence of sequestrate *Cortinarius* in wet and dry environments. We also used speciation and extinction models to test the hypothesis that sequestrate taxa have higher extinction rates than agaricoid taxa. Finally, the distribution of sequestrate taxa among clades across the *Cortinarius* phylogeny was assessed.

*Contributed Talk C10.3*

**112. Characterization of a fungal-bacterial interaction between a *Coprinellus* species and *Pseudomonas baetica***

**\*Hart, Andrew**, Volk, Thomas, Osmundson, Todd, Bratina, Bonnie University of Wisconsin-La Crosse, Biology Department, 1725 State Street, La Crosse, WI 54601, USA. hart.andr@uwlax.edu

A leading factor in the development of most community associations (e.g. mutualism, parasitism, competition) involves occupying the same niche over long periods of time. As fungi developed the capability to degrade lignin and invade woody material approximately 300 million years ago, they gave certain bacteria the opportunity to colonize and form associations. Fungi and bacteria interact with a wide variety of organisms largely due to their ubiquity and diverse metabolic natures. Until recently, little research has been performed to understand the interactions between fungal and bacterial wood- inhabiting organisms relative to analogous interactions in the soil/rhizosphere. Studies in woody systems have been typically dedicated to specific taxa or groups of related taxa. We are interested in a more broad microbial ecology of woody ecosystems. Our research applies a simple screening model to identify and characterize a novel fungal-bacterial interaction in the context of decaying wood. We have observed a bacterium, identified as *Pseudomonas baetica*, induce a stress response coupled with atypical heliotrope pigment production from a co-existing *Coprinellus* species. By characterizing the interaction between the wood-inhabiting *Coprinellus* and *P. baetica*, we can start developing a more comprehensive understanding of wood ecology. In culture the *Coprinellus* pigment is restricted to submerged hyphae, occasionally depositing on the bacterial streak, but never seen in the medium. Characterization includes cultural techniques, thin layer chromatography, light and atomic microscopy, minimum inhibitory concentration, and mass spectrometry. As we have mined soil interactions for useful secondary metabolites, it is only logical to employ competitive assays in order to induce potential production of novel secondary metabolites. Environmental research such as this will help gain an understanding of wood ecology.

*Poster P46*

**113. Effects of fuels treatments of ponderosa pine (*Pinus ponderosa*) in the blue mountains of eastern Oregon: A mycorrhiza perspective \*Hart, Benjamin**(1), Smith, Jane E.(2), Luoma, Daniel L.(1)

1.Oregon State University, Department of Forest Ecosystems and Society, Corvallis, OR 97330 USA; 2.USDA Forest Service, Pacific Northwest Research Station, Corvallis, OR 97330 USA. ben.hart@oregonstate.edu

Severe wildfires are an increasing risk as the western United States becomes hotter and dryer for longer periods annually due to the changing climate. Reduction of historically uncharacteristic woody fuels that drive large, severe forest fires is an increasing priority for forest managers. Traditionally, fuel reduction has been achieved with mechanized thinning for removing over-crowded trees and low-intensity prescribed fire to reduce woody fuels near the forest floor. However, the long-term impact of these fuel reduction treatments is poorly understood with respect to ectomycorrhizal fungi (EMF). We quantified EMF biodiversity and abundance associated with ponderosa pine (*Pinus ponderosa*) in four randomly assigned replications of restoration treatments (thinned, burned, thinned and burned, and untreated), applied over a decade ago in the Blue Mountains of Oregon. The belowground community composition and structure of EMF at the site were characterized using molecular methods. Results indicate that species richness and abundance were similar across treatment types, and that fire effects on community composition were smaller than anticipated. Our results provide evidence that a 10+ year interval allows EMF to disseminate and re-colonize areas from which they have been removed or reduced by disturbance treatments. Knowledge of the long-term impacts of forest restoration treatments on EMF will aid in understanding the outcomes of management designed to produce stands with large-tree retention and low fuel loads. *Contributed Talk C20.2*

**114. Application of the mycobiome requires an ecological understanding of plant-fungal interactions \*Hawkes, Christine V .**(1), Giauque, Hannah(1), Worchel, Elise(2), Sandy, Moriah(1)

University of Texas at Austin, Department of Integrative Biology, Austin, TX 78712, USA, chawkes@austin.utexas.edu

Plant-associated fungi can mediate how plants perceive and respond to the environment, which is particularly relevant for coping with environmental stress. Yet much of our understanding of fungal- mediated effects is piecemeal. Here we argue that to harness the mycobiome as a practical tool will require (1) the development of a predictive, mechanistic framework for the outcome of plant-fungal interactions, (2) the ability to scale that predictive framework to multiple interacting microbes simultaneously occupying the plant host, and (3) a focus on underlying mechanisms, such as plant genes and fungal metabolites, that can be used for tool development independent of the fungi per se. We apply this multi-faceted framework to the widespread,

horizontally-transmitted, foliar fungal endophytes and their role in plant drought tolerance. The mycobiome represents an innovative plant management strategy with the potential for rapid, scalable benefits, but these will only be fully realized if we can gain a systems- level mechanistic understanding of their interactions with the plant.

*Symposium S5.3*

**115. Hyperdiversity of ectomycorrhizal fungal sporocarps in monodominant *Gilbertiodendron dewevrei* (Caesalpinioideae) forests of Cameroon, and delimitation of a new *Armillaria* lineage.**

2.Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA; 3.Royal Botanic Gardens, Kew, Comparative Plant and Fungal Biology, Richmond, Surrey TW9 3DS, UK; 3.United States Department of Agriculture, Forest Service, Northern Research Station, Corvallis, OR, 97331, USA; 5.University of Tennessee, Department of Ecology and Evolutionary Biology, Knoxville, TN, 37996, USA. twh5@humboldt.edu

Here we report preliminary investigations on the species diversity of ectomycorrhizal (EM) and armillarioid fungi in monodominant *Gilbertiodendron dewevrei* forests in the Guineo-Congolian region of Central Africa. In an effort to build a specimen and sequence database to test biogeographical hypotheses regarding tropical EM fungi of the Guiana Shield and Central African regions, a collecting expedition was mounted to the Dja Biosphere Reserve of Cameroon from Aug–Oct 2014. In two months of collecting within three 1-hectare plots and the immediate surrounding area, 208 distinct ECM fungal morphospecies were described and vouchered. At the family level, Russulaceae, Boletaceae, Amanitaceae, Cantharellaceae, and Inocybaceae were collectively most dominant, accounting for 87% of the EM species recovered. *Russula* was the most species-rich genus at 52 species, followed by *Amanita* (31), *Cantharellus* (19), *Lactarius* and *Lactifluus* (14), *Tylopilus* (13), and *Inocybe* and *Auritella* (11). Taxonomic highlights include three new species of *Elaphomyces* constituting the first records for this genus from native ecosystems in the African continent. Two new species were discovered in the poorly known agaric genus *Auritella* (Inocybaceae), raising the number of *Auritella* species to 15 worldwide. Among the non-EM fungi, a new genus was delimited from African *Armillaria* species, including a new Cameroonian species to be described. Molecular phylogenetic analysis indicated that the new

armillarioid lineage is sister to the sequestrate genus *Guyanagaster* from the Guiana Shield, and that together they represent the most ancient group in the greater *Armillaria* lineage, suggesting a trans- continental biogeographic relationship.

*Poster P21*

**116. Isotopic patterns in ectomycorrhizal fungi reflect fertilization, taxon-specific effects, and composition \*Hobbie, Erik A.(**1), Hasselquist, Niles(2), Chen, Janet(3)

1.Earth Systems Research Center, University of New Hampshire, Durham, New Hampshire, 03833, USA; 2.Department of Forest Ecology and Management, Swedish University of Agricultural Sciences (SLU), Umeå, 90183, Sweden; 3.International Atomic Energy Association, Vienna, Austria. Erik.Hobbie@unh.edu

Nitrogen and carbon isotope patterns in ectomycorrhizal fungi were assessed in two long- running nitrogen addition experiments (Norrliden and Rosinedalsheden) in conifer-dominated stands in central Sweden. Fungal δ15N (adj. r2 = 0.698) was primarily influenced by genus and species (94% of variance). Control samples from Norrliden averaged 1.9‰ higher than those from Rosinedalsheden. Surprisingly, treatments did not significantly affect fungal δ15N, suggesting that system losses of N with fertilization had similar δ15N to losses without fertilization. In contrast, soil δ15N was higher than controls in N2 (2460 kg/ha total N added) and N3 (2070 kg/ha total N added) treatments at Norrliden and in high-N treatments at Rosinedalsheden (600 kg/ha total N added). Addition of 35 kg/ha/yr at Norrliden and 20 kg/ha/yr at Rosinedalsheden did not significantly alter soil δ15N. Fungal δ15N and δ13C (adj. r2 = 0.485) correlated positively with %N (reflecting protein content), whereas δ13C correlated negatively with %C (reflecting lipid content), and with day of year (reflecting late season declines in the δ13C of photosynthesis). Genus and species accounted for 61% of variance. At Rosinedalsheden, fungal δ13C increased significantly by 1.4‰ from control to low-N (20 kg N ha-1) to high-N (100 kg N ha-1) treatments, whereas soil δ13C increased by 0.7‰, with similar 13C enrichments in low-N and high-N treatments. Variability in nitrogen acquisition appeared to be under more genetic control than carbon acquisition. Sporocarp %N (adj. r2 = 0.565) was strongly controlled by taxonomy, but treatments contributed 25% of variance, with higher %N correlating with higher nitrogen loadings. Coefficients for δ13C and δ15N for individual taxa were positively correlated, potentially indicating that some taxa assimilate 15N- and 13C-enriched amino acids from the soil.

Henkel, Terry W.(1), Koch, Rachel A.(2), Dentinger, Bryn T.M.(3), Castellano, Michael A.(3), Matheny, P.



Brandon(5), **\*Aime, M. Catherine**(2)



1.Humboldt State University, Department of Biological Sciences, Arcata, CA, 95521, USA;

 

*Contributed Talk C12.4*

**117. Tracking trichomycete traits across scattered states reveals a microscopic milieu in millipedes elevating excitement for Eccrinales endobiont extremes**

**\*Hollar, Sierra**, White, Merlin Boise State University, Department of Biological Sciences, Boise, ID, 83725-1515, USA. sierrahollar@u.boisestate.edu

Trichomycetes is an ecological group of microorganisms, with both fungi and protist members, associated with the guts of arthropods. It was a former class of Fungi that includes four orders, one of which, the Eccrinales, is now recognized as a part of a smaller clade called Mesomycetozoea. Upon dissecting digestive tracts of infested hosts with a stereomicroscope, “eccrinids” appear as unbranched thalli attached to the gut lining by a cement-excreting holdfast. Methodologically, gut linings and any attached thalli are wet mounted on microscope slides, then imaged live and/or stained and preserved as vouchers. Qualitative and quantitative aspects (measurements of informative characters such as thalli, holdfasts, and spores) are the backbone of traditional morphotaxonomy and species identification. Ecologically and in terms of life history, asexual spores, the sporangiospores, are released and either germinate in the same gut or are excreted to the external environment. There they remain until ingested by the same or another individual, with varied infestation rates depending on the population and niche. With a tendency for some degree of host specificity, one common host group of “eccrinids” is Diplopoda. Candidate hosts were collected from sites across the continental USA as part of a preliminary survey, presented herein.

*Poster P1*

**118. Isolation, purification, and identification of compounds from a marine-derived fungus *Arthrinium saccharicola*\*Hong, Joo-Hyun**(1), Ryu, Seung-mok (2), Lee, Dongho (2), Kim, Jae-Jin (1)

1.Korea University, Division of Environmental Science & Ecological Engineering, Seoul, 02841, Republic of Korea; 2.Korea University, Division of Biotechnology, Seoul, 02841, Republic of Korea. jae- jinkim@korea.ac.kr

Marine-derived fungi have been considered as remarkable bioactive compound producers. *Arthrinium saccharicola* KUC21221 isolated from brown algae in Korea showed a strong biological activity. It was cultivated on 5 L of PDA for 7 days and then extracted by using 15 L of methanol. Thus, a 1.245 g of crude extract was obtained. The extract was developed by

using TLC with various compositions of hexane, chloroform, ethyl acetate, and methanol. According to the TLC profiling, *A. saccharicola* extract was isolated and purified by column chromatography and prep- HPLC, which resulted in eleven fractions. Among them, two major compounds and other compounds were identified by LC/MS and proton NMR (500 MHz). As a result, nolichexanthone (C14H10O5) known as isolated from *Arthrinium* sp. was detected in the AS5 fraction. Here, we firstly reported 7- dechlorogriseofulvin (C17H18O6) in the genus *Arthrinium*, which was previously reported in *Penicillium griseofulvum*, *Nibrospora* sp., and *Aspergillus allahabadii*.

*Poster P136*

**119. A new seed-inhabiting species of *Xylaria* from Central Guyana \*Husbands, Dillon R**., Aime, M. Catherine Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA. dhusband@purdue.edu

Greenheart (*Chlorocardium* spp.) is Guyana’s most marketable timber. It is greatly desired for dock and harbor applications due to the incredibly dense wood—one of the densest in the world. It is also regarded as durable because it is nearly immune to decay, resistant to termite damage and can withstand excess moisture for long periods. Greenheart seeds are known to contain volatile secondary compounds that are believed to provide defense against seed predation by other organisms, and have no reported seed pathogens. In 2010 and 2011 an unusual *Xylaria* sp. was documented growing from morbid seeds both of *C. rodiei* and *C. venenosum* in Guyana*.* We conducted extensive surveys in 2016, where the *Xylaria* was observed fruiting from ca. 80% of dispersed seeds in both natural and logged forests in Pibiri Ecological Reserve and Mabura Forest Reserve in the Upper Demerara/Berbice district and Butakari Forest Reserve and Vaitarna Holdings PVT Inc, in the Cuyuni- Mazaruni district. Morphology of the anamorph is consistent with the anamorphic genus *Xylocoremium.* Combined teleomorphic and molecular characteristics indicate that the fungus represents an as yet undescribed species of *Xylaria.* There are only fifteen known seed- and fruit-inhabiting *Xylaria* species from around the world of which most are suspected to be host specific. Herein we present distributional, phylogenetic, and morphological data for this species. *Poster P3*

**120. Characterizing the diversity of plant- associated *Colletotrichum* species in Louisiana** Hutchins, Haley, Veloso, Josiene S., **\*Doyle, Vinson P.**

Louisiana State University AgCenter, Department of Plant Pathology and Crop Physiology, Baton Rouge, LA 70803, USA. vdoyle@agcenter.lsu.edu

*Colletotrichum* can be a plant pathogen or exist asymptomatically as an endophyte. The plants in which it is an endophyte may serve as a source of inoculum for the infection of hosts in which *Colletotrichum* is pathogenic. Understanding the range of hosts that harbor individual *Colletotrichum* species and the diversity of species across North America is fundamental to understanding the biology of this ubiquitous group of fungi. However, there is limited information on the diversity of *Colletotrichum* species in North America. The goal of this research project is to characterize the diversity associated with plants in Louisiana by placing these isolates into a broader phylogenetic context. We isolated fungi characteristic of *Colletotrichum* from healthy and diseased tissue of several host species, extracted genomic DNA, and sequenced loci previously shown to be useful for species delimitation. We found several plant species in Louisiana that host *Colletotrichum*, including ones that are economically important to the state, including *Carya illinoinensis* (pecan)*,* and *Rhododendron spp.* (azalea). Isolated from the samples collected are species of *Colletotrichum* previously unreported from North America. Our results will have implications for fungal systematics, fungal ecology, and plant pathology by providing a more comprehensive understanding of *Colletotrichum* diversity in Louisiana and the role of individual hosts in the movement of these endophytes and plant pathogens.

*Poster P101*

Shrub encroachment is a global phenomenon that causes loss of biodiversity and changes to ecosystem function. Factors proposed to explain encroachment include grazing, disturbance, CO2 enrichment, increased temperature, and variable precipitation. Plant-microbial feedbacks are well known as drivers of plant dynamics, including invasion and abundance. To our knowledge, however, the role of microbes in the encroachment of shrubs into arid grasslands has not been examined. Toward this goal, we surveyed the fungal root endophytes of two Chihuahuan desert plant species, the C3 shrub *Larrea tridentata* (creosote) and the C4 grass *Bouteloua eriopoda* (black grama) at the Sevilleta National Wildlife Refuge, NM, which encompasses several distinct desert biomes, including

an ecotone where creosote shrubland transitions to black-grama grassland along a north-south gradient. In each of two years (2012 and 2015) we sampled roots from 10 creosote plants, 5 black grama plants within the creosote stand, and 5 black grama plants from the grassland. The fungal composition of roots was assessed using both culture-based methods and 454 pyrosequencing of the ribosomal internal transcribed spacer (ITS). ITS sequences showed consistency across years but appreciable differences among the fungal communities of the three sample types (although grama samples were more similar to each other than to creosote). A majority of cultures from creosote roots and a portion of cultures from the transition-zone black grama roots were from the genus *Monosporascus*. No cultures from grassland black- grama roots were represented by *Monosporascus*, although sequences from members of the genus were observed among 454 sequences. While previous studies demonstrated an aridland fungal endophyte community shared across diverse plant species at the Sevilleta, our results demonstrate that endophyte communities are also shaped by host species, supporting the possibility that endophytes influence encroachment.

*Contributed Talk C9.4*

**122. Mycorrhizal specificity can lead to ecophysiological plasticity in plants living off fungi \*Hynson, Nicole A.(1)**, Bidartondo, Martin I.(2), Read, David J.(3)

1.University of Hawaii Manoa,Department of Botany, 3190 Maile Way Room 101, Honolulu, HI 96822 USA; 2.Imperial College London and Royal Botanic Gardens, Department of Biological Sciences, Kew TW9 3DS, UK; 3.University of Sheffield, Department of Animal and Plant Sciences, Sheffield S10 2TN, UK. nhynson@hawaii.edu

Many symbiotic interactions are specific, where hosts and symbionts fine-tune their physiologies to receive the most benefit from their partners. Fully mycoheterotrophic plants that have lost the ability to photosynthesize and rely completely on symbiotic interactions with fungi to meet all of their carbon demands have been touted as prime examples of mycorrhizal specialists. However, the question remains whether this fine-scale fungal partner specificity leads to the fixation of traits that increase plant fitness, or if it is an evolutionary dead end. To address this question we focus on partial mycoheterotrophy (the ability of plants to meet a portion of their carbon demands via symbiotic fungi), and fungal partner specificity as forms of local adaptation. Local adaptation is a concept used to describe how species allocate resources in order to survive in their environments. Using amplicon

**121. Root endophytes associated with creosote and black grama across a shrub to grassland transition**



**zone**



**\*Hutchinson, Miriam**, Natvig, Donald O.



University of New Mexico, Department of Biology,



Albuquerque, NM, 87131, USA. miramira@unm.edu



sequencing and the analysis of carbon and nitrogen stable isotope compositions we examined the fungal partnerships and ecophysiology of a putative partial mycoheterotroph *Moneses uniflora* (Ericaceae). By sampling populations of *M. uniflora* across two continents we reveal that while this species remains highly specific in its mycorrhizal partnerships across a large portion of its natural range, its ability to derive carbon from similar fungi varies among populations. This finding indicates that biogeography and environment are important determinants for mycoheterotrophy, and that partial mycoheterotrophy is a plastic trait within some plant species. We conclude that partial mycoheterotrophy should be considered a local adaptation rather than a fixed functional trait and that fungal partner specificity does not necessarily lead to a decrease in plant fitness. *Contributed Talk C19.3*

**123. Development of new varieties of *Lentinula edodes* through Korean Golden Seed Project \*Jang, Yeongseon**, Ryoo, Rhim, Ka, Kang-Hyeon, Lee, Sung-Suk, Choi, Donha

National Institute of Forest Science, Division of Wood Chemistry & Microbiology, Seoul, 02455, Republic of Korea. idjys@korea.kr

**124. Employing native ectomycorrhizal suilloid fungi for the restoration of whitebark pine on a burn site \*Jenkins, Martha**, Cripps, Cathy L.

Montana State University, Department of Plant Sciences & Plant Pathology, Bozeman, MT, 59717- 3150, USA. martha.l.jenkins@gmail.com

Whitebark pine (*Pinus albicaulis*), a keystone species crucial to high elevation ecosystems in western North America, has been declining throughout the majority of its range over the past few decades due to mountain pine beetle outbreaks, white pine blister rust, climate change, and fire suppression. The recent widespread decline has sparked a movement toward restoration of this pine species mainly through the out- planting of blister rust resistant seedlings in areas of high mortality. However, long term survival of out- planted seedlings has been low and land managers need cost effective methods to optimize seedling resources and to improve upon out-planting success. Ectomycorrhizal fungi are an integral part of natural pine systems, and colonization of seedlings has the potential to increase their long term survival. This study is examining the effects of colonization by native suilloid fungi on whitebark pine seedlings subsequently planted in burn soil with a field study in the Beaverhead-Deerlodge National Forest (MT) and a complementary greenhouse bioassay. Natural burns provide areas cleared of competition and have proven to be successful planting sites for whitebark pine. Results from the greenhouse experiment indicate that native suilloid fungi are capable of colonizing seedlings in burn soil, and show that biomass is higher for colonized seedlings in comparison to uncolonized controls. Preliminary results show that colonized seedlings have a higher foliar nitrogen content as well as lower δ15N likely due to fractionation of N by the ectomycorrhizal fungi during uptake. The ‘in progress’ field study is determining if seedling survival is enhanced by establishment of mutualistic relationships with native ectomycorrhizal fungi prior to planting, and how abiotic site factors affect seedling survival using a GIS spatial analysis. Results for the first monitoring will be presented if available. *Poster P59*

**125. Population divergence and strain hybridization in the amphibian chytrid \*Jenkinson, Thomas S.**(1), Toledo, L. Felipe(2), Longcore, Joyce E.(3), James, Timothy Y.(1) 1.University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, MI, 48109, USA; 2.Universidade Estadual de Campinas, Instituto de Biologia, Departamento de Biologia Animal, Campinas, SP, 13083-862, Brazil; 3.University of

*Lentinula edodes* (Berk.) Pegler, called shiitake, is one of the most popular edible mushrooms in many Asian countries which is produced more than 7.2 million tons worldwide. In Republic of Korea, more than ten species are commercially produced. The amount of shiitake (27,000 tons) production is less

than that of oyster mushroom (*Pleurotus ostreatus*, 66,000 tons), king oyster mushroom (*Pleurotus eryngii*, 44,100 tons), enokitake (*Flammulina velutipes*, 33,400 tons) but the production revenue is the first among them. In 2002, Republic of Korea became the member of UPOV (The International Union for the Protection of New Varieties of Plants) and shiitake has been protected by UPOV convention since 2008. Currently, about 50 Korean shiitake variants are applied and 15 registered in UPOV. The number of Korean variants is small compared to that of China and Japan. The self-sufficiency of seeds is still low. Thus, there’s a need for development of new Korean varieties which would be superior to conventional variants in terms of productivity, quality, disease resistance, and so on. To help reduce the dependence on foreign seeds and increase outcome of farmers, the golden seed project is ongoing since 2013. Through the project, the efforts have been exerted to develop new Korean varieties. Here, we introduce the strategies to develop new Korean varieties and the

achievements of the project.

*Poster P83*

Maine, School of Biology and Ecology, Orono, ME, 04469, USA. tsjenkin@umich.edu

Chytridiomycosis, caused by the chytrid *Batrachochytrium dendrobatidis* (*Bd*), is the emerging infectious disease implicated in recent population declines and extinctions of amphibian species worldwide. In regions where the pathogen has been confirmed as an introduced novel species, only a single hypervirulent clonal genotype (*Bd*-GPL) has been observed to date. In the Atlantic Forest of southeastern Brazil, however, a deeply divergent – and potentially endemic – lineage (*Bd*-Brazil) has been recently described. Population genetic studies suggest that the two lineages have been brought into secondary contact by human activity, with the *Bd*-GPL having recently arrived in the historical range of *Bd*-Brazil. While the long-term consequences of this secondary contact are unknown, our field studies have recovered hybrid strains resulting from outcrossing events between *Bd*-GPL and *Bd*-Brazil in a hybrid zone localized to the Serra da Graciosa mountain range of Paraná State. Here we characterize the population history of these previously allopatric lineages in the Brazilian Atlantic Forest using whole genome resequencing of 51 *Bd* isolates collected from ten field sites in southeastern Brazil. We also assess the patterns of inheritance in hybrid strains to understand genomic regions of hybrid incompatibility between previously separated lineages. Whole genome sequencing reveals a high degree of genomic plasticity among individuals, with variable chromosomal copy number and loss of heterozygosity through mitotic recombination as major drivers of variation. Gradients of intra-lineage population divergence inform historical routes of *Bd*-GPL invasion and suggest a lack of migration between endemic populations. Population differentiation is lowest among pathogen isolates associated with the Brazilian bullfrog trade, providing evidence that bullfrog farming and trade are an important factor in the movement of *Bd* in South America.

*Symposium S8.2*

**126. Investigation of salt tolerance in marine fungi through the use of comparative genomics. \*Johnson, Derek O.**(1), Spatafora, Joseph W.(1), Pangilinan, Jasmyn(2), Tritt, Andrew(2), Ohm, Robin(2), Riley, Robert(2), Lipzen, Anna(2), Grigoriev, Igor V.(2)

1.Oregon State University, Department of Botany and Plant Pathology, 2082 Cordley Hall, Corvallis, OR 97331, USA; 2. DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA. johnsde4@oregonstate.edu

Obligate marine fungi present a novel system in which to study the genomic evolution of salt tolerance

in fungi. While there have been many independent transitions from a terrestrial to a obligate marine lifestyle, the class Sordariomycetes is particularly interesting as there have been at least three major independent transitions to the marine environment. These fungi have undergone significant selective pressure to thrive within the persistent osmotic stresses present in highly saline waters. This includes increased control of the movement of water between the cell and environment, and the exclusion of potentially toxic levels of salt. Given this, transmembrane proteins provide the greatest potential for understanding salt tolerance in marine fungi, as they provide direct contact with both cell and environment. In addition, stress response pathways responsive to hypertonic stress, such as the High Osmolarity Glycerol (HOG) pathway, are also of interest. Here we present a comparative genomic study between the obligate marine fungus, *Corollospora maritima*, a member of the largest family of marine fungi (Halospheriaceae, Microascales), and a phylogenetically closely related relative, the terrestrial fungus *Microascus trigonosorus* (Microascaceae, Microascales). Gene family evolution specific to transmembrane proteins and stress response pathways will be presented including specific gene family expansions and contractions of ENA ATPases, aquaporins, and the HOG pathway. In addition, the results of a differential gene regulation experiment across a salt gradient ranging from trace salt content to twice the salinity of seawater will be presented, and regulatory strategies will be compared between *C. maritima* and *M. trigonosporus*. Results will show which regulatory strategies utilize a threshold response upon reaching a specific salt concentration level, and which utilize a dose response.

*Contributed Talk C14.5*

**127. Amplicon sequencing reveals differences between root microbiomes of a hemiepiphytic orchid, *Vanilla planifolia,* at four Mexican farms \*Johnson, Lynnaun**(1,4), Gónzalez-Chávez, Ma. del Carmen A.(2), Carrillo-González, Rogelio(2), Porras- Alfaro, Andrea(3), Mueller, Gregory M.(4) 1.Northwestern University, Department of Plant Biology and Conservation, Evanston, IL, 60208, USA; 2.Colegio de Postgraduados, Campus Montecillo, Texcoco, México; 3.Western Illinois University, Biological Sciences, Macomb, IL, 61455, USA; 4.Chicago Botanic Garden, Conservation Science, Glencoe, IL, 60022, USA. Lynnaunjohnson2018@u.northwestern.edu

Orchidaceae are one of the most species-rich flowering plant families. This diversity is often attributed to pollinator specificity; however, fungal specificity is also suggested as a cause for some of this



speciation. The majority (73%) of the species richness within Orchidaceae are epiphytes. To investigate differences of fungal communities between epiphytic and terrestrial roots, we investigated the microbiome of the two root types in the hemiepiphytic orchid, *Vanilla planifolia*. It is an economically valuable crop that is native to Mexico. The goal of this study was to use high-throughput (amplicon) sequencing and compare the microbiomes (bacteria and fungi) of epiphytic and terrestrial roots. We collected epiphytic and terrestrial root samples from 20 individuals from four dissimilar Mexican vanilla farms. We tested two hypotheses 1) bacterial and fungal communities (microbiomes) of terrestrial roots were more diverse than microbial communities of epiphytic roots; 2) microbiomes of vanilla roots differed between three agricultural practices (highly managed, traditional, and like-wild natural). Roots were surfaced sterilized, and extracted DNA was amplified for the ITS 2 region for fungi and 16S rRNA gene for bacteria. After sequencing amplicons on an Illumina miSeq we obtained 6 million sequences. Quality filtered reads at 97% similarity resulted in 144 fungal OTUs and 158 bacterial OTUs. Examining similarity with PERMANOV A revealed significant (p = 0.02) differences of fungal communities between farms and root types (p = 0.03). In addition, our results showed a diverse fungal community with ectomycorrhizal fungi (e.g. *Inocybe*), saprotrophs (*Mycena*), and orchid mycorrhizal fungi such as *Ceratobasidium* and *Thanatephorous*. The bacterial community was dominated by Bacteroidetes, Firmicutes and, Proteobacteria.

*Poster P34*

**128. The influence of bark on fungal communities and wood decay in terrestrial and aquatic habitats in a wet tropical forest \*Jones, Jennifer M.**, Brown, Shawn P., Dalling, Jim, Ferrer, Astrid, Heath, Katy D.

1.University of Illinois at Urbana-Champaign, Department of Plant Biology, Urbana, IL, 61801, USA. jmjones9@illinois.edu

Wood characteristics are known to influence decay rate. However, most decomposition studies do not differentiate between bark and wood, even though these tissues differ in structure, nutrient concentrations, and function. I explored whether bark influences decay rate via altering fungal communities, moisture retention, and nutrient availability. To examine how bark influences wood decay rate across habitats, I conducted a decay experiment in which I removed or retained bark from replicate branches of three tree species placed either in freshwater streams or on land. In addition to calculating wood decay rate, I also characterized fungal communities using

environmental sequencing, and I measured moisture and wood and bark nitrogen concentrations. Bark increased decay rate in both terrestrial and freshwater environments. Bark also had higher nitrogen concentrations than wood and increased wood moisture. Fungal communities differed between bark and wood and had higher diversity in bark. Additionally, wood fungal communities differed between bark present and bark removed treatments. This evidence shows that bark increases decay rate and influences fungal community composition. *Contributed Talk C17.6*

**129. Five species of endophytic fungi produce the same antibiotic molecule \*Jreij, Anthony**(1), Connor, Elise(2), Sandy, Moriah(1), Hawkes, Christine V .(2)

1.Freshman Research Initiative, College of Natural Sciences, The University of Texas at Austin; 2.Department of Integrative Biology, The University of Texas at Austin. anthony.jreij1@gmail.com

Endophytic fungi reside in plant tissues and form different symbiotic relationships with plants. In many cases, endophytes have been shown to benefit their plant hosts. For example, some provide a chemical defense against microbial pathogens and herbivores, and others can increase plant tolerance to drought and osmotic stress. Due to their unique relationships with their plant hosts, fungal endophytes are potentially a rich source of bioactive molecules with medicinal and agricultural applications. In this study, metabolite extracts from 19 endophytic fungi isolated from *Panicum virgatum* and previously classified as mutualistic, commensal or antagonistic on plant physiology and growth, were analyzed by LCMS and screened for antibiotic activity. Fungi with common symbiotic relationships with *P . virgatum* produced similar molecules. Additionally, five different species of endophytic fungi identified through BLAST, (*Nigrospora* CHTAR07, *Pestalotiopsis foedans, Cochliobolus kusanoi, Aspergillus niger,* and *Chaetomium bostrychodes*), were found to produce two common metabolites with strong antibiotic activity towards *Staphylococcus aureus* and *Escherichia coli*. Preliminary structure analysis reveals that both of these molecules are structurally related to common coumarin plant metabolites, Aesculin and Aesculetin, which, until now, have not been identified as fungal metabolites.

*Poster P137*

**130. Everything is not everywhere: Designing a synthetic fungal ITS mock community for NGS of environmental samples**

**\*Jusino, Michelle A.**(1), Palmer, Jonathan M.(1), Banik, Mark T.(1), Edgar, Robert C.(2), Lindner, Daniel L.(1) 1.United States Forest Service, Center for Forest Mycology Research, Madison, WI 53726, USA; 2.Independent Investigator, Tiburon, CA 94920, USA. mjusino@fs.fed.us

Next-generation sequencing (NGS) is a powerful tool that is frequently used for examining fungal communities in environmental samples. However, NGS output from environmental samples requires careful interpretation and appropriate and consistent use of positive and negative controls. Thus, it is increasingly common practice to use spiked-in “mock” community samples as positive controls in NGS runs. While mock communities help solve some of the challenges brought on by NGS data, they also bring new challenges to light. We first constructed a spike-in “non-synthetic” mock community control for use in amplicon-based NGS studies of the internal transcribed spacer (ITS) region of fungal rDNA consisting of a taxonomically diverse range of single- copy cloned ITS sequences. Using this positive control, we performed a number of experiments on two NGS platforms, the Ion Torrent Personal Genome Machine (PGM) and the Illumina MiSeq. We show that even on equally mixed communities of plasmid DNA, the initial PCR biases results by preferentially amplifying sequences from certain taxa, regardless of the platform. These results indicate that the number of reads obtained for each taxon is not a reliable proxy for total or relative taxon abundance within a sample. We also discovered an alarming rate of index-bleed or “barcode switching” on both NGS platforms, up to 0.3% on MiSeq, which can further contribute to noisy datasets. Thus, we also developed a synthetic mock community consisting of “pseudo” fungal ITS sequences not found in nature to definitively quantify index or barcode switching. We show how mock community positive controls can be used to effectively fine-tune clustering parameters and mitigate problems associated with PCR bias and index crossover. Mock community controls are necessary to parameterize downstream bioinformatics, especially for diversity and community structure related questions, and we advocate for inclusion of a spike-in mock control in every NGS run. *Contributed Talk C7.4*

**131. Evaluation of three primer pairs for Illmina sequencing of arbuscular mycorrhizal fungi \*Kakouridis, Anne**, Nguyen, Nhu H., Firestone, Mary K.

University of California, Berkeley, Environmental Science, Policy & Management, Berkeley, CA, 94720- 3102, USA. annekakouridis@berkeley.edu

Arbuscular mycorrhizal fungi (AMF) are ubiquitous soil organisms with critical roles in ecosystems, notably as plant root symbionts. The development of molecular methods has made it possible to identify AMF taxa from plant roots and soil instead of relying on morphological characteristics of spores. Illumina sequencing offers new opportunities to investigate the molecular diversity and community ecology of AMF. A number of primers have been used for molecular investigation of AMF with 454 and other previous sequencing methods, but many of these primers cover DNA sequences too long for the Illumina platform. In addition, the primers routinely used may have different specificity and potential to describe the diversity of AMF phylogenetic lineages. To determine if the choice of primers for AMF community analysis affects which taxa appear dominant and the level of diversity detected, we are using mock communities of nine known AMF species representing basal and derived groups of AMF. Seven mock communities, in which the nine AMF species have different relative abundances, were assembled. Three primers pairs spanning regions of increasing variability in the AMF nuclear ribosomal DNA (rDNA) are being tested: WANDA/AML2, which targets a DNA sequence in the small subunit (SSU), Glo454/NDL22, which targets a DNA sequence in the large subunit (LSU), and gITS7/ITS4, which targets a DNA sequence in the internal transcribed spacers (5.8S, ITS2). As different primer pairs may be biased towards certain groups of AMF, we suggest the use of a combination of primer pairs, one spanning a more variable region and one spanning a more conserved region of AMF rDNA. This use of primer pairs with complementary strengths may lead to better resolution and inclusion during molecular analyses, as well as more robust information for understanding AMF community ecology.

*Poster P31*

**132. Cultivating oyster mushrooms on invasive plants: An alternative substrate \*Kaszynski, Kyle**, Volk, Tom 1. University of Wisconsin-La Crosse, Department of Biology, La Crosse, WI, 54601, USA. Kaszynsk.kyle@uwlax.edu

Invasive plant species are taking over forests and other ecosystems everywhere, creating a large reservoir of unused lignocellulolytic biomass. In the upper-Midwest, buckthorn (*Rhamnus cathartica*) and honeysuckle (*Lonicera maackii*) are two prevalent woody invaders of forest ecosystems. The objective of this studied was to determine if these forest waste products could be successfully used as a sustainable alternative substrate for mushroom cultivation. Since *Pleurotus* species produce a wide array of

lignocellulolytic degrading enzymes and can breakdown many different substrates and contaminants, members of this genus were chosen for the study. Two strains of the fungus were chosen for this study, one that is used in commercial cultivation practices and one that was isolated from a fruiting body found growing near the invasive plants used in the study. Days to colonization, days to first harvest, first yield, total yield, and biological efficiency were all measured and then compared to a control treatments of oak and a straw control. Although both strains of *Pleurotus* performed best on the straw substrate, there was no significant difference within a strain of the yield and BE on the buckthorn, honeysuckle, and oak substrates. These results suggest that invasive species can provide an alternative sustainable substrate compared to hardwood woodchips.

*Contributed Talk C6.5*

**133. The distribution and prevalence of the generalist pathogen, *Armillaria mellea*, in eastern North America using ecological niche modeling \*Kerr, Bryce A**., Bergemann, Sarah E.

Middle Tennessee State University, Biology Department, PO Box 60, Murfreesboro, TN 37132, USA. bak3n@mtmail.mtsu.edu

Many natural forests around the world are threatened with increasing frequency by the spread of plant pathogens. *Armillaria mellea* (Physalacriaceae, Basidiomycota) is a generalist pathogen of many woody crops, ornamental plants and forest trees. In eastern North America, *A. mellea* acts an opportunistic pathogen that infects many forest tree species, mostly hardwoods. The aim of this study is to predict the distribution and the risk of invasion of *A. mellea* in eastern North America using environmental niche modeling. Over 300 specimens were selected from available herbaria for analyses. The identity of the pathogen was verified through phylogenetic analyses using two nuclear loci, translation elongation factor subunit 1-alpha and actin subunit. The *A. mellea* locale data and several environmental layers will be input into Maxent modeling software which will use a maximum entropy approach to determine the probability of *A. mellea* occurrence each 200 meter square area in the region. Our preliminary species distribution map reveals a climatic distribution along a latitudinal gradient extending from 33.56° to 48.05° and a longitudinal distribution from -64.41° to - 91.12°. Final Maxent outputs coupled with models of commons hosts should allow for analyses of current *A. mellea* prevalence and predict distributions under future climate projections.

*Poster P64*

*Poster P135*

**135. New species of *Xylaria* from Yasuní National Park, Ecuador \*Kielsmeier-Cook, Joshua**(1), Ordoñez, Maria E.(2), Blanchette, Robert(1)

1.University of Minnesota, Department of Plant Pathology, St. Paul, 55108, USA; 2.Pontificia Universidad Catolica del Ecuador, Quito, 17 01 21 84, Ecuador. joshkc@umn.edu

**134. A reproducible protocol for growing relevant filamentous fungal biofilms and phenotypic phases during biofilm maturation \*Kerrigan, Julia L.**(1), Pettigrew, Charles A.(2), Wright, Kevin I.T.(3)

1.Clemson University, Department of Plant and Environmental Sciences, Clemson, South Carolina, 29634-0310, USA; (2)Procter & Gamble, Global Microbiology, Mason, Ohio, 45040, USA; (3) Procter & Gamble, Global Microbiology, Twickenham, UK. jkerrig@clemson.edu

Filamentous fungal biofilms are ubiquitous in the built environment, their persistence can be problematic due to biodegradation (spoilage, malodor) and potential health impacts (respiratory sensitization, irritation). Standard approaches to their remediation generally involve the combined use of cleaning and applying an antifungal product as an initial preventative intervention step. Antifungals that have been created to reduce or eliminate fungi are often tested against biofilms that, although created with standardized methods, do not reflect those present in the built environment. We have developed a reproducible protocol for establishing biofilms on a standardized glass surface under low shear conditions using a drip flow reactor that better reflect biofilms that occur in real-world situations. Three common species, *Aspergillus niger*, *Aureobasidium pullulans*, and *Cladosporium cladosporioides,* were selected to examine the reproducibility and flexibility of the protocol. The progressive phenotypic changes involved in biofilm development were also recorded. We found that the system could be modified easily to accommodate fungi with variable growth morphologies. A similarity between the development of these three species and models describing the biofilm growth of yeasts and filamentous fungi was observed; however, each species exhibited differences during specific phases. These phases reflect growth in the built environment, this laboratory model could be used to evaluate the dynamic efficacy of antifungal actives. The development of a repeatable filamentous fungus biofilm growth system and understanding the morphological steps involved in biofilm formation allow for future studies on how to prevent and remove them.

Yasuní National Park, Ecuador is one of the most diverse regions on earth, harboring large numbers of species across multiple kingdoms of organisms. Fungi are known to play important roles for carbon and nutrient cycling in all terrestrial environments yet long term research for this kingdom is lacking in this hyper- diverse region. After completing an initial exploratory survey of Ascomyetes in January of 2015 we chose to investigate the diversity and ecology of species in the genus *Xylaria*. A single hectare plot was chosen for intensive sampling. The plot was pre-established for monitoring forest dynamics and divided into a 10 x 10 meter grid. Fruit bodies of *Xylaria* were sampled within a 1.2 m radius of each grid intersection, resulting in 121 individual sample points. Sampling was conducted in June 2015 and February 2016. A total of 363 samples were collected during the two sampling periods. Of these, 277 samples are confirmed (ITS sequence and/or morphology) *Xylaria* species. Of the sequences form which we were able to extract usable ITS sequences these clustered into 65 OTUs at the 97% level. Only 16 OTUs matched known named *Xylaria* sequencs at or above the 97% level. The remainder include 20 OTUs that matched *Xylaria* sequences above 90% w/ the remainder (29 OTUs) only having sequence matches below 90%. Here we describe three novel species. One is consistently found on the rachis of *Tachigali* spp. trees while the other two are found on rachis, petioles, and/or twigs of unknown tree species. We look at the gross morphology, spore morphology, and sequence/taxonomic information. *Contributed Talk C16.4*

**136. Life, sex, and “smut” fungi? Diversification of mating loci and growth forms in Ustilaginomycotina \*Kijpornyongpan, Teeratas**, Aime, M. Catherine Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA. tkijporn@purdue.edu

Smut fungi typically have a complex dimorphic life cycle that includes a haploid saprobic yeast phase (n) and a dikaryotic pathogenic hyphal phase (n+n) which occurs after mating of two sexually compatible yeast cells. Genes from two mating (*MAT*) loci are known to play a critical role in sexual reproductiongenes encoding pheromone peptides and receptors on the *a* locus and genes encoding homeodomain transcription factors (HD) 1 and 2 on the *b* locus. Previous studies on the model smut fungus *Ustilago maydis* and related species in Ustilaginaceae revealed allelic and syntenic conservation of the *MAT a* locus. However, little is known in other lineages of Ustilaginomycotina, which comprises smut fungi and allied lineages such as non-smut phytopathogens,

animal-associated fungi and saprobic yeasts. Herein, we will present comparative analyses on *MAT* loci and growth forms of representative species from each order of Ustilaginomycotina. We show that synteny of the *MAT a* locus is conserved in Ustilaginales, but not across the subphylum. Two genes seem to be tightly linked to the mating genes in examined lineages: a gene encoding N-terminal acetyltransferase linked to the HD2 gene on the *MAT b* locus in Ustilaginomycetes and a gene encoding proteasome regulatory complex subunit RPN10 linked to the *MAT a* locus in most species of Exobasidiomycetes and Malasseziomycetes. *MAT* loci gene arrangements and mating gene copy numbers are most diversified in Exobasidiales. In addition, observed mutations in the mating genes of some studied species may explain their inability to sexually reproduce. Finally, the association between mating system and filamentation in non-model smut fungi will be explored.

*Poster P115*

**137. Comparative analysis on different media usage of *Lentinula edodes* based on genomic and transcriptomic data**Kim, Myungkil, Ryu, Sun-Hwa, Lee, Su-Yeon, Lee, Sung-Suk, Ryoo, Rhim, \***Ka, Kang-Hyeon**, Jang,Yeongseon, Choi, Donha

National Institute of Forest Science, Division of Wood Chemistry & Microbiology, Seoul, 02455, Republic of Korea. mkkim0201@korea.kr

Oak mushroom, *Lentinula edodes,* is a white rot fungus and has an important ecological role in the breakdown of lignocellulosic plants for nutrient mobilization. It is the 1st largest fungal crop in Asian countries and cultivated in different media types such as wood logs and sawdust media. We obtained genomic and transcriptomic data of *L. edodes* by *de novo* whole genome sequencing and systematic large scale RNA sequencing by Pac-bio from two different media-cultured hyphae to understand the genes in various biological processes. The genome size was about 43Mb with 71 scaffolds. A total of 42,382 transcripts were detected of which 20,503 transcripts were from both media types. Based on gene prediction, genes with functions such as catalytic activities, binding, and transporter activities were found, but a large number of genes in the analysis were unknown. *Poster P140*

**138. Climate, not soil resources, constrains most arbuscular mycorrhizal fungal distributions at the global scale \*Kivlin, Stephanie N.**(1), Muscarella, Robert(2), Treseder, Kathleen K.(3) Hawkes, Christine V.(4)

1.University of New Mexico, Department of Biology, Albuquerque, NM, 87131; 2. Aarhus University, Department of Bioscience, 8000 Aarhus, Denmark; 3. University of California, Irvine, Department of Ecology and Evolutionary Biology, Irvine, CA, 92697; 4. University of Texas, Integrative Biology, Austin, TX, 78712. skivlin@unm.edu

Local adaptation of arbuscular mycorrhizal (AM) fungi to soil nutrients and climate suggests that both may control their distribution and fitness across scales. Determining the influence of these drivers on AM fungal distributions is germane as sensitivity to ongoing global change may alter AM fungal distributions in unpredictable ways. We created species distribution models for 128 AM fungal taxa based on data collected from GenBank using BioClim climate variables, soil variables (moisture, phosphorus, carbon, pH, and clay content), and net primary productivity. Individual models were constructed with (1) all variables, (2) climatic variables only (including soil moisture) and (3) resource-related variables only (all other soil parameters and NPP) using the MaxEnt algorithm and evaluated with ENMEval. Because species distribution models do not account for dispersal limitation, we also assessed if spore size was correlated with the geographic range size of AM fungal taxa. Finally, we evaluated if any of the drivers of AM fungal distributions were phylogenetically conserved. The distributions of 53% of AM fungal taxa were affected by both climate and soil resources, whereas 40% were only affected by climate and 7% were only affected by soil resources. Even in models of AM fungi that were affected by both climate and resources, the effects of climatic variables always outweighed those of resources. Soil moisture and isothermality were the main climatic factors and net primary productivity and soil pH were the main resource-related factors influencing AM fungal distributions. AM fungal spore size was not related to the geographic range for any clade. Moreover, closely related AM fungal taxa were not affected by the same environmental drivers. Because the majority of drivers affecting AM fungal distributions were related to climate, future warming and changes in precipitation regimes could have large impacts on AM fungal communities at the global scale. *Symposium S10.2*

**139. Environmental factors driving fungal community composition in a boreal forest \*Kluting, Kerri**(1), Rosling, Anna(1), Clemmensen, Karina(2), Jonaitis, Stanislovas(3), Vasaitis, Rimvya(2), Finlay, Roger(2)

1.Uppsala University, Department of Evolutionary Biology, Evolutionary Biology Center, Uppsala SE-

75263, Sweden; 2.Swedish University of Agricultural Sciences, Department of Forest Mycology and Plant Pathology, Uppsala BioCenter, Uppsala, SE-75007, Sweden; 3.Kretinga Forest Enterprise, Kretinga, LT- 97111, Lithuania. kerri.kluting@ebc.uu.se

In boreal forest soils, root-associated fungal communities are more distinct between vertically stratified soil horizons within a site than when the same soil horizons are analyzed from different sites in the same ecosystem. Nutrient availability is a limiting factor for tree growth in dry, sand dominated soils, and root-associated fungi play a key role in plant uptake of phosphorus and nitrogen, macronutrients that are essential, yet difficult to obtain. We hypothesize that phosphorus availability strongly affects the community composition of root-associated fungi along the Baltic coast, as extensive nitrogen deposition has occurred in this region. To test this hypothesis, we investigated the relationship between variation in soil community structure and variation in inorganic and organic phosphorus availability for soils collected in a coastal pine forest near Palanga, Lithuania. Five soil cores were sampled from each of five transects along a gradient from coastal dune to mature pine forest with stratified soils, and soil was sampled from six different depths in each core for a total of 150 samples. Fungal communities were characterized by sequencing the ITS region using 454 technologies, and levels of bicarbonate and hydroxide extractable phosphorus were quantified for each sample. The presence or absence of roots, soil horizon (mineral or organic), and the depth of each sample were also recorded. These data support our hypothesis that phosphorus availability may be a factor driving community structure in this environment, but ordination methods also reveal a pattern in community structure with relation to the presence or absence of roots and the soil horizon of the sample. These results indicate that nutrient availability and proximity to pine roots are potential drivers of fungal community structuring in this environment.

*Poster P153*

**140. Sticky spores and insatiable Isopterans: Untangling the dispersal strategy of *Guyanagaster necrorhizus*\*Koch, Rachel A.**, Aime, M. Catherine

Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN, 47907, USA. koch17@purdue.edu

With the loss of forcible spore discharge, “gasteromycetes” must evolve a dispersal strategy that engages exogenous forces. The Neotropical gasteromycete, *Guyanagaster necrorhizus*, is remarkable in the sense that it does not possess morphological hallmarks for gasteromycetes adapted

for either mammal or passive mechanical dispersal. During the course of five field seasons, several instances of termites consuming mature *G. necrorhizus* basidiomes were observed. In order to untangle the dispersal strategy of *G. necrorhizus,* we used a suite of approaches, including observational, population genetics analyses and shotgun proteomics. Over an area of five square kilometers, 122 *G. necrorhizus* basidiomes were collected, along with termites in the vicinity. These basidiomes were genotyped at nine polymorphic microsatellite markers developed for this study, while the termites were sequenced at the 28S and COII loci to determine their identity. Population genetic structure analyses found eight distinct populations of *G. necrorhizus* within the study area. Termite identity was correlated with *G. necrorhizus* populations, supporting our hypothesis of termite dispersal. Microscopic analysis of these termites suggests that the likely mode of dispersal is by *G. necrorhizus* spores that adhere to the outside of the termite bodies via a mucilaginous substance. A mucin protein was found to be more abundant in mature *G. necrorhizus* basidiomes compared to immature basidiomes, suggesting the fungus produces this when the spores are mature and ready to be dispersed. To our knowledge, this is the first recorded instance of termites preferentially targeting a specific fungal basidiome and acting as the dispersal vector. *Contributed Talk C20.9*

**141. 50-year-old soils provide an end point for arbuscular mycorrhizal fungi spore longevity \*Koko, Jerry**, Hynson, Nicole A. University of Hawaii at Manoa, Department of Botany, 3910 Maile Way Room 101, Honolulu, HI 96822 USA. jerryk@hawaii.edu

Arbuscular mycorrhizal fungi (AMF) rely on their host plants to receive carbon and survive. Without the host plant, the spores of AMF must hibernate until the roots of a suitable plant are available to colonize. After a major disturbance such as volcanic eruption, land conversion, or stand replacing fire, plant hosts may be unavailable for AMF to colonize. To ensure survival of the underground fungal communities and their respective hosts, successful establishment of compatible host plants within the viability period of spores is necessary. To test the viability of AMF spores, we bioassayed soils that harbored AMF hosts, but had been removed and protected from the environment for over 50 years. The soil cores used in this experiment were collected in 1965 on the island of Hawaii thereafter enclosed in a glass case to display the soil profiles. The cores were taken from three different areas in Hawaii Volcanoes National Park all containing native forest vegetation that form arbuscular mycorrhizal symbioses. Under sterile

conditions, replicate bioassays of soil from each were seeded with corn (*Zea mays*), millet (*Pennisetum glauca*), and onion (*Allium cepa*), and along with negative controls, grown in a sterilized growth chamber for approximately 45 days. The plants were extracted and the roots were stained with acid fucshin. The roots were mounted and observed at 20x magnification to quantify AMF colonization of the roots. In total we examined 1450 sections. We found evidence of AMF colonization in only two out of the 153 bioassays. Using the point-intercept method we found no significant AMF colonization. Apparently, 50 years of hibernation seems to be too long for most AMF spores to survive. Previous to this study, the longest observed viability of AMF spores was 10 years. These results are important in light of restoration projects, it’s important to consider the amount of time that has elapsed since the last disturbance to ensure the viability of AMF spores. *Poster P58*

**142. Spatiotemporal dimensions of the fungal community in chestnut blight cankers on American chestnut (*Castanea dentata*) caused by *Cryphonectria parasitica***

**\*Kolp, Matthew**(1), Double, Mark(2), Jarosz, Andrew(1,3), Fulbright, Dennis(3), MacDonald, William(2) 1.Michigan State University (MSU) Plant Biology and Ecology, Evolutionary Biology and Behavior, East Lansing, MI, 48824 USA; 2.West Virginia University, Division of Plant and Soil Sciences, Morgantown, WV, 26506 USA; 3.MSU Plant Soil and Microbial Sciences, East Lansing, MI, 48824 USA. kolpm@msu.edu

*Cryphonectria parasitica*, the fungal pathogen that causes chestnut blight on American chestnut (*Castanea dentata*), decimated chestnuts throughout its native range. This necrotrophic fungus enters through wounds in the outer bark and rapidly kills host cells. The resulting canker expands and can girdle a stem, killing plant tissues distal to the canker. However, not all cankers expand at the same rate, nor do all cankers completely girdle the tree. We have observed that chestnut blight cankers are complex microbial communities that support a diversity of fungi as well as mycoviruses that infect the pathogen and can reduce its growth and reproduction. We hypothesize that the spatial and temporal dynamics of the canker community influences the survival of infected chestnut trees and by extension host population structure. We sampled chestnut blight cankers annually (2012-2015) at six chestnut populations (five in Michigan and one in Wisconsin USA) to track dynamics of the canker community and tree health. Superficial, non-lethal cankers contained

more mycovirus-infected *C. parasitica* (37.5% of isolates) than lethal cankers (25.1%) that girdle the tree. The fungal community of non-lethal cankers also was more species rich (47 operational taxonomic units [OTUs]) and diverse (Shannon-Weiner Index = 2.18') compared to lethal cankers (39 OTUs; 1.36'). Work is still ongoing to identify non-*C. parasitica* OTUs associated with tree health over time. We rejected one of our hypotheses that if the distribution of fungi within cankers follow a specific pattern of mycovirus- infected *C. parasitica* along the margin of cankers and non-*C. parasitica* OTUs at the center where dead bark accumulates then canker expansion slows and girdling is delayed. Instead, *Penicillium* spp. 4.6% of isolates, *Trichoderma* spp. 2.9%, *Pezicula* spp. 2.2%, *Nectria* spp. 1.8%, *Umbelopsis isabellina* 1% and other fungal groups are distributed as a mosaic in both lethal and non-lethal cankers.

*Poster P65*

**143. Phylogenetic analysis of a morphologically distinct black morel (*Morchella* sp.) from the US Inland Pacific Northwest**Kozhar, Olga, Weber, John M., Carmody, Shannon M., Agarwal, Chiti, Li, Yuxiang, \***Carris, Lori M.**, Peever, Tobin L.

Advanced Fungal Biology Class (PLP 526), Department of Plant Pathology, Washington State University, Pullman, WA 99164-6430, USA. carris@wsu.edu

Our understanding of the taxonomy and ecology of morel mushrooms (*Morchella* spp.) has been advanced by the application of phylogenetic species recognition. Morphologically distinct samples of this popular ascomycete were collected from mixed- conifer habitats at three sites in Latah and Clearwater Counties, Idaho, and

The specimens had narrower caps and stems compared to *Morchella snyderi,* the most common black morel in this region, and the ascospores were striately ornamented. Phylogenetic analyses of sequence data from subunits 1 and 2 of RNA polymerase II, translation elongation factor 1α, and the nuclear large ribosomal subunit were used for comparison with described morel species. A multilocus phylogeny rooted by *Mel-11* including *M. snyderi* (Mel-12), *M. laurentiana* (Mel-36), and *M. eohespera* (Mel-19) demonstrated that the specimens are closely related to, but likely distinct from, the recently described *M. eohespera*. Although morels are considered to be highly endemic, the range of *M. eohespera* includes southwestern Washington, USA, Newfoundland, Canada, China, and Sweden. Additional specimens from western North America are needed in order to determine if the Idaho morels are

*M. eohespera,* or if they represent a distinct sister species. *Poster P94*

**144. Microfungi Collections Consortium specimen data \*Kuhn, Alexander L.**(1), Bates, Scott T.(2), Miller, Andrew N.(1)

1.University of Illinois, Illinois Natural History Survey, Champaign, IL, 61820, USA; 2.Purdue University Northwest, Department of Biological Sciences, Westville, IN 46391, USA. akuhn@illinois.edu

Many institutions across North America with fungaria containing specimens of microfungi have yet to digitize their collections. Because specimen data from these institutional collections is limited, we lack basic understanding of microfungal diversity and distributions. The Microfungi Collections Consortium (MiCC) is working to populate the Mycology Collections Portal (MyCoPortal) online database with digitized microfungal specimens from 63 institutions across the United States and Canada. Specimen labels, as well as ancillary items, are being imaged and transcribed to include information about the collector, collection date, substrate or plant host, and collection locality. To date, there are over 2.5 million specimen records in the MyCoPortal, including over 107,000 type specimens and nearly 300 exsiccate sets. The creation of this large dataset will greatly expand research potential in areas relating to pathogen/host specificity, diversity and distribution patterns over time, as well as historical specimen collection activity over the last two centuries. With data freely accessible online, communication among fungaria and researchers can improve, which will facilitate research, specimen loans, detection and correction of errors, and taxonomic updating. Because public engagement is an integral component of the MiCC, events to foster an interest in the project, such as specimen transcriptions marathons, have been planned. *Poster P16*

**145. Genomics of the cellulosome of anaerobic gut fungi \*Kuo, Alan**(1), Mondo, Stephen(1), Salamov, Asaf(1), LaButti, Kurt(1), Haitjema, Charles(2), Gilmore, Sean(2), Henske, John(2), O'Malley, Michelle(2), Grigoriev, Igor(1)

1.US Dept. Energy Joint Genome Institute, Walnut Creek, CA; 2.UCSB Dept. Chemical Engineering, Santa Barbara, CA. akuo@lbl.gov

As highly proficient degraders of cellulose, the Neocallimastigomycota fungi are key members of the microbiota of large mammalian and reptilian herbivores. Their remarkable cellulolytic capabilities

formed the basis for a class



project in Advanced Fungal Biology at Washington



State University.



have great potential for use in biofuel processing. They differ from other fungi in 1) possessing an extracellular cellulose-degrading complex called a fungal cellulosome, 2) being obligate anaerobes, and 3) developing flagella, a ‘primitive’ characteristic. The genomes of these interesting and important fungi are very AT-rich and highly repetitive, posing challenges to their genomic investigation. We deployed PacBio long-read technology to overcome these challenges and to sequence, assemble, and annotate 3 Neocallimastigomycota genomes. We found modest numbers of genes and gene families, and confirmed low GC-content, high repeat content, absence of many aerobiosis-related genes, and near-basal location in the fungal tree. Next we used the genomes to complement non-genome-based biochemical, proteomic, and transcriptomic methods to compile a comprehensive ‘parts list’ of the cellulosome. We found scaffoldins, very long secreted proteins with multiple cohesin motifs that bind to the dockerin domains (DDs) of dockerin domain proteins (DDPs). The fungal scaffoldins, cohesin motifs, and DDs are not at all homologous to their bacterial cellulosome analogs. Each genome encodes a surprisingly large number of scaffoldins (14-55), which group into several clades. Also, each genome encodes numerous DDPs (200- 500), most but not all of which are cellulolytic or related enzymes. Some of the catalytic domains appear to have originated by horizontal gene transfer from gut bacteria, leading us to hypothesize that the fungal cellulosome is an evolutionarily chimeric structure – an independently evolved fungal organelle that has co- opted useful activities from bacterial neighbors.

*Poster P129*

**146. A global-scale analysis of fungal communities in peatlands \*Lamit, L. Jamie**(1), Basiliko, Nathan(2), Schadt, Christopher W.(3), Waldrop, Mark(4), Tringe, Susannah(5), Lilleskov, Erik(6)

1.School of Forest Resources and Environmental Science, Michigan Technological University, Houghton, MI 49931, USA; 2.Living with Lakes Centre, Laurentian University, Sudbury, Ontario P3E 2C6, Canada; 3.Oak Ridge National Laboratory, Oak Ridge, TN 37831, USA; 4.US Geological Survey, Menlo Park, CA 94025, USA; 5.DOE Joint Genome Institute, Walnut Creek, CA 94598, USA; 6. US Forest Service, Northern Research Station, Houghton, MI 49931, USA. ljlamit@mtu.edu

Peatlands are unique habitats where organic matter accumulates due to water-saturated conditions that depress rates of decomposition relative to primary production. Although they represent less than 5% of the terrestrial land area, peatlands store over 30% of global soil carbon. Peatlands thus represent novel

environments for unique fungal communities, the study of which will inform our understanding of fungal diversity and global carbon cycling. We present preliminary results from the Global Peatland Microbiome Project, a community sequencing effort that aims to characterize fungal and prokaryote communities in the Earth’s peatlands. The analyses presented here focus on understanding biogeographic patterns of peatland fungal communities, and identifying simple predictors of fungal composition and diversity. Our results highlight several points. 1) Communities of temperate and boreal peatlands in North America and Eurasia broadly overlap in operational taxonomic unit (OTU) composition, South American and Australasian peatlands are similar in composition but distinct from northern peatlands, and South East Asian peat swamp forests have the most distinct fungal communities. 2) In contrast to many groups of organisms, fungal OTU richness in peatlands exhibits a curvilinear relationship with latitude, peaking at ~35 degrees. 3) Peatland H 2 O table depth and porewater pH are significant correlates of fungal richness and/or composition at the global scale. These preliminary results suggest a degree of dispersal limitation for peatland fungi at the global scale, and that key environmental characteristics of their habitats (pH and H2O table depth) remain important influences on their communities even at large geographic scales. In contrast to many studies of organisms in upland habitats, peatland fungi as a whole are not most diverse in tropical regions, indicating that peatland fungal diversity is driven by different factors than many organisms in upland habitats.

*Symposium S11.3*

**147. Comparative analysis of the secretome of early lineage fungi \*Lange, Lene**(1), Pilgaard, Bo(1), Busk, Peter K.(1), Gleason, Frank (2), Pedersen, Anders G.(3) 1.Technical University of Denmark, Department of Chemical and Biochemical Engineering, Kgs Lyngby, 2800, Denmark; 2.University of Sydney, New South Wales 2006, Australia; 3.Technical University of Denmark, Department of Systems Biology, Kgs Lyngby, 2800, Denmark. lenl@kt.dtu.dk

This study reports on diversity and composition of the enzyme secretome among early lineage fungi. The results build on a) recent developments in genome sequencing and resolution of the phylogeny of the major fungal groupings Chytridiomycota, Monoblepharidiomycota, Neocallimastigomycota, Blastidiomycota and Cryptomycota; and b) experimental work including cloning, expression and characterization of three types of enzymes from early lineage fungi. The secretome is biologically and

ecologically important as it reflects interaction among organisms and environment; not just what the fungus is but how it grows and competes. Chytridiomycota is considered the earliest diverging fungal lineage of free living fungal species as the physiology of the earlier endoparasitic Cryptomycota has a life form where interaction is not well developed. In the present study genome sequencing of the aerobic lignocellulose degrading chytrid, *Rhizophlyctis rosea,* was made and three of the secreted enzymes were selected for further experimental studies (β 1,4 endoglucanase (GH45), β- xylosidase (GH43) and xylanase (GH11). The study further includes mining of the genomes from all five phyla of early lineage fungi. Significant differences and high level of diversification among enzymes form the five different phyla were observed. The genomes compared are searched using the Peptide Pattern Recognition (PPR) sequence analysis methodology, which allows for alignment-free gene discovery and robust prediction of enzyme function directly from sequence. Further, the study includes analysis of how key substrate decomposing enzymes (cellulases, hemicellulases, amylases, proteases) are phylogenetically related, to shed light on how these enzymes have developed in perspective of similar development of key secretome enzymes of Kingdom Fungi. The resulting phylogenetic trees are used as the basis for discussing the possible roles of mechanisms such as horizontal gene transfer, and gene duplication and loss.

*Contributed Talk C21.4*

**148. Two new *Cytospora* species, *Cytospora vinacea* sp. nov. and *Cytospora viticola* sp. nov., from declining vineyards in eastern North America \*Lawrence, Daniel P.**(1), Travadon, Renaud(1), Pouzoulet, Jérôme(2), Rolshausen, Philippe E.(2), Wilcox, Wayne F.(3), Baumgartner, Kendra(4)

1. University of California, Department of Plant Pathology, Davis, CA 95616, USA.; 2. University of California, Department of Botany and Plant Sciences, Riverside, CA 92521, USA; 3.Department of Plant Pathology and Plant-Microbe Biology, Cornell University, Geneva, NY 14853, USA; 4.United States Department of Agriculture-Agricultural Research Service, Crops Pathology and Genetics Research Unit, Davis, CA 95616, USA. dlawrence@ucdavis.edu

*Cytospora* species are ubiquitous pathogens of woody plants, causing branch dieback and wood cankers in numerous perennial hosts, including agronomic crops (e.g., *Prunus*), timber trees (e.g., *Eucalyptus*), and riparian hosts (e.g., *Salix*). *Cytospora chrysosperma*, *C. cincta*, and *C. leucostoma* have been reported from grapevines showing symptoms of one or more grapevine trunk diseases (Esca, Botryosphaeria dieback, Eutypa dieback, and Phomopsis dieback),

none of which are known to be caused by or associated with *Cytospora* species, but instead by other ascomycetes (*Phaeomoniella chlamydospora* and *Phaeoacremonium minimum*, *Neofusicoccum parvum*, *Eutypa lata*, and *Diaporthe ampelina*, respectively). To understand the role of *Cytospora* in the grapevine trunk-disease complex, 21 *Cytospora* isolates were identified from symptomatic vines of *Vitis vinifera* or *Vitis* hybrids, from vineyards in seven states and two Canadian provinces in eastern North America. Phylogenetic analyses of ITS, translation elongation factor 1-α, and beta-tubulin nuclear regions revealed two new species: *Cytospora vinacea* sp. nov. and *Cytospora viticola* sp. nov. Both species were pathogenic when inoculated to the woody stems of potted *V. vinifera* ‘Thompson Seedless’ in the greenhouse, based on development of wood lesions and fulfillment of Koch’s postulates. *Cytospora viticola* was more virulent, producing the largest lesions (mean lesion length = 17.3 mm at 12 months post-inoculation). Morphological comparisons of these two species revealed that they are clearly distinguishable from each other, based on cultural and conidial dimensions; *C*. *vinacea* producing a distinct vinaceous colony and the shortest conidia (mean conidia length = 5.2 μm). This study represents the first attempt to characterize pathogenic *Cytospora* species associated with grapevine trunk diseases in eastern North America.

*Contributed Talk C16.5*

**149. Phylogenetic systematics of *Syncephalis* (Zoopagales: Zoopagomycota) a genus of ubiquitous mycoparasites \*Lazarus, Katy**(1), Gerald L., Benny(1), Ho, Hsiao- Man(2), Smith E., Matthew(1)

1.University of Florida, Plant Pathology, Gainesville, FL 32611-0680, USA; 2.National Taipei University of Education, Department of Science Education, Taipei, Taiwan. Katylazarus@gmail.com.

Phylogenetic relationships among species of the mycoparasite genus *Syncephalis* were examined using sequences from three nuclear encoded ribsosomal DNA genes and one protein encoded gene. The data consist of 18S, 5.8S and 28S rDNA and RPB1 for 88 *Syncephalis* isolates comprising approximately 38 OTUs and 23 named species. We also revived a culturing technique using beef liver and cellophane to grow several *Syncephalis* isolates without their host fungi to obtain pure parasite DNA. Most isolates, however, were grown in co-cultures with their host fungi and we designed *Syncephalis-*specific primers to obtain sequence data. Individual and combined datasets were analyzed by maximum likelihood (ML) and Bayesian analysis (BA) methods. We recovered 14 well-supported lineages and determined that most

major clades contained isolates from distant localities on multiple continents. Many clades had taxonomic issues, evidently due to high phenotypic plasticity and species dimorphism. We also conducted an analysis of *Syncephalis* ITS sequences using complete ITS sequence data (ITS1-5.8S-ITS2) for 31 isolates comprising 18 named species and determined that *Syncephalis* species, on average, have long ITS sequences relative to other fungi. Commonly employed eukaryotic and fungal primers (ITS1, ITS1- f) appear compatible across phylogentically diverse *Syncephalis* species, but paradoxically *Syncepahlis* sequences are rarely recovered in environmental molecular diversity surveys.

*Contributed Talk C17.3*

**150. Bringing fossils up to date: Character evolution in thyriothecial fungi \*Le Renard, Ludovic**(1), Berbee, Mary. L.(1), Stockey, Ruth. A.

1.University of British Columbia, Department of Botany, Vancouver BC, V6T 1Z4, Canada; 2.Oregon State University, Department of Botany and Plant Pathology, Corvallis, Oregon 97331, USA. ludovic.lerenard@botany.ubc.ca

Critical reinterpretations of morphological features present in fossils of fungi have the potential to improve estimates of the geological timing of fungal radiations. Some of the best fungal fossils are 'thyriothecia': minute flat ascomata with distinctive cellular patterns in their upper walls or ‘scutella’. The fossil record rarely provides diagnostic characters such as asci but the diversity of fossil scutella offers great potential to calibrate ages of extant clades. Our goal is to pinpoint lineage specific combinations of scutellum characters by expanding the sampling of modern fungi. We added 18 new sequences for 11 taxa with thyriothecial morphology. A concatenated dataset of LSU and SSU rDNA comprising members of all the main classes of Ascomycota reveals that this morphology is polyphyletic. All of the 3-5 clades of thyriothecial fungi, except for Micropeltidaceae, cluster with early diverging Dothideomyceta. Lineages of thyriothecial fungi are consistently associated with leaf surfaces, based on our ancestral character state reconstruction of habitat and morphology. A radial pattern of cells in a cohesive scutellum is found in thyriothecial Dothideomyceta. Thyriothecial Asterinales have characteristic lobed appressoria. While superficial mycelia and appressoria were originally described as absent from Microthyriaceae, we report finding both in all taxa sampled from this family. Radial patterns of cells in a cohesive scutellum, superficial mycelia and appressoria are also known from the fossil record. Having established the phylogenetic distribution of these characters among

modern taxa will facilitate use of thyriothecial fossils to date the clades in the phylogeny. *Contributed Talk C15.4*

**151. Truffle-like fungi: Diverse patterns of evolution and diversification worldwide \*Lebel, Teresa**(1), Halling, Roy (2), Sheedy, Elizabeth (3), Orlovich, David (4)

1.Royal Botanic Gardens Victoria, Birdwood Ave, Melbourne, Victoria, 3004 Australia; 2. New York Botanical Garden, Institute of Systematic Botany, Bronx, NY 10458 USA; 3.National Museum of Nature and Science, Department of Botany, Tsukuba, Ibaraki 305-0005, Japan; 4. University of Otago, Department of Botany, Dunedin 9054, New Zealand. teresa.lebel@rbg.vic.gov.au

Truffle-like fungi have evolved from epigeal ancestors in nearly every major lineage of fleshy macrofungi. We examined phylogenies of twenty different lineages, including both ectomycorrhizal and saprophytic fungi, for patterns of evolution and diversification of truffle-like forms. While we have a fair understanding of the higher level relationships of many truffle-like genera, we still have large gaps in our knowledge of closely related epigeal ancestors for many lineages. In the Boletales and Hysterangiales several truffle-like genera are monophyletic (retaining generic status), and once the transition to truffle-like fruit body occurred there followed an explosion of species (eg *Rhizopogon* and *‘Pogiesperma’*) or even genera (eg. *Octaviania*/ *Rossbeevera/ Turmalinea, Hysterangium,* Mesophelliaceae). An exception is *Gymnopaxillus* (Serpulaceae), which has a pattern closer to that of Agaricales (Agaricaceae, Bolbitiaceae, Cortinariceae, Strophariaceae, Hymenogastraceae) and Russulales (eg. *Russula, Lactarius* and *Lactifluus*), of multiple, parallel sequestration events from different mushroom ancestors (not retaining monophyletic generic status). An exception to the Agaricales/Russulales pattern may be *Stephanospora* (Stephanosporaceae), which evolved from a resupinate ancestor then diversified into at least 14 species. From molecular clock analyses of timing of emergence of truffle-like taxa in different lineages, most monospecific genera are recently evolved, or lack resolution as sister taxa may be missing from phylogenies.

Increased integration of truffle-like sequences into analyses of biogeographic patterns and dating of lineages, updated phylogenies, and increased sampling of southern hemisphere epigeal and truffle-like taxa are needed. Whole genome analyses of truffle & mushroom species pairs will provide another set of characters to map, and aid our understanding of genes involved in the transition from mushroom to truffle- like fruit body forms.

*Contributed Talk C10.1*

**152. Uncovering cryptic species in the *Lactifluus clarkeae* complex \*Lebel, Teresa**(1), Tegart, Lachlan(1,2), Cooper, Jerry A.(3) 1.Royal Botanic Gardens Victoria, Melbourne, Victoria, 3004 Australia; 2.University of Melbourne, School of BioSciences, Melbourne Victoria, 3010 Australia; 3.Systematics, Landcare Research Co, Lincoln New Zealand. teresa.lebel@rbg.vic.gov.au

*Lactarius clarkeae* and *Russula flocktoniae* are geographically widespread, easily detected mushrooms with robust, reddish-orange fruit bodies with white or orange flesh. As latex production can be ephemeral under dry conditions, and macro- morphological characters appear variable, mixed collections are to be found in Herbaria; as is incorrectly labelled material. Preliminary analyses of a 3-gene (ITS, nLSU and tef-1α) dataset suggest there may be as many as nine species hiding under these names in New Zealand and Australia, including a truffle-like taxon. Seven cryptic taxa are in one well supported clade, including *L. clarkeae* sensu stricto and *Russula flocktoniae* sensu stricto which is shown to be a *Lactifluus* with variable latex production closely related to *L. panuoides* from Guyana. The remaining five novel taxa show some geographic and host differences: two are from New Zealand in association with *Nothofagus L. aurantioruber* nom prov. and *L. macnabbii* nom. prov. [also found in Tasmania]; ‘*L. clark sp 5’* from NSW (Eucalyptus); ‘*L. clark sp 3’* from Victoria (Eucalyptus); and ‘*L. clark-cream sp. 6’*from Western Australia (Eucalyptus). Three other novel taxa, including one truffle-like, are quite distantly related, appearing in the *L. volemus* clade sister to *L. crocatus* and *L. volemus*. Further sampling over the broader geographic range of the novel taxa is required to be able to map micro- characters to our phylogeny.

*Poster P92*

**153. Genome sequence of *Trichoderma harzianum* KUC1716 \*Lee, Hanbyul**(1), Min, Byoungnam(2), Lee, Young Min(1), Hong, Joo-Hyun(1), Choi, In-Geol(2), Kim, Jae-Jin(1)

1.Korea University, Division of Environmental Science & Ecological Engineering, Seoul, 02841, Republic of Korea; 2. Korea University, Department of Biotechnology, Seoul, 02841, Republic of Korea. jae- jinkim@korea.ac.kr

*Trichoderma harzianum* is well known and widely used for its ability to secrete various cellulolytic enzymes and to hinder the growth of plant pathogens. The genome of *T. harzianum* KUC1716 was sequenced

using PacBio RS II system, generating 5.6 million reads in total. The nuclear genome of *T. harzianum* consists of 12 contigs with a total assembly length 39.7 Mbp, a GC content of 48.31%. We predicted 13,028 genes from the genome, which contain a large number of genes that synthesize secondary metabolites and produce carbohydrate-active enzymes (CAZy). The genome sequence reported here represents lots of useful resources for further research to the biomass- degrading enzymes and biocontrol agents.

*Poster P124*

**154. Report of *Aureobasidium* species in Korea** \***Lee, Young Min**, Lee, Hanbyul, Kim, Jae-Jin Korea University, Division of Environmental Science & Ecological Engineering, Seoul, 02841, Republic of Korea. jae-jinkim@korea.ac.kr

The genus *Aureobasidium* is a member of the family *Aureobasidiaceae* within the class of the *Dothideomycetes*. Members of the genus are ubiquitous and cosmopolitan found in different habitats such as plant materials, water, soil, skin, and air as contaminant or human pathogen. In addition, they are known as wood staining mould and black yeasts due to their melanin production. *Aureobasidium* generally produce dry masses of conidia that are dispersed by air currents. They cause stain either by producing masses of dark spores or pigmented hyphae within the wood cell lumens. *Aureobasidium pullulans*, the type species of the genus, is one of the best-known and most studied species of this genus. However, there are no reports of *Aureobasidium* except *A*. *pullulans* in Korea. The aim of the present study was to explore the diversity of *Aureobasidium* species based on phylogenetic analysis, culture characteristics, and morphology. The analysed isolates showed that four *Aureobasidium* species were present. *Aureobasidium pullulans* was the dominant species, which was followed by *A*. *pullulans* var. *pullulans*, *A*. *leucospermi*, and *A*. *microstictum*. *Aureobasidium leucospermi* and *A*. *microstictum* are unrecorded species in Korea. Therefore, this is the first report of the two species. *Poster P11*

**156. Building a trait-based understanding of the associations between soil microbial communities and grassland plants \*Leff, Jonathan W.**(1), Bardgett, Richard D.(2), Fierer, Noah(1)

1.University of Colorado, Cooperative Institute for Research in Environmental Sciences and Ecology and Evolutionary Biology, Boulder, CO, 80309, USA; 2.University of Manchester, Faculty of Life Sciences, Manchester, M13, UK. jonathan.leff@colorado.edu

Despite their critical role in terrestrial ecosystems, we lack a predictive understanding of how soil

microbial communities vary across landscapes. Grassland ecosystems, which account for a quarter of the Earth’s land surface, contain diverse soil microbial communities whose distributions are potentially predictable based on their direct or indirect interactions with plants. We empirically examined associations between grassland plants and soil bacterial, fungal, protistan, and metazoan communities to evaluate whether plant taxonomy, phylogeny, and traits can facilitate prediction of soil community structure. Using mesocosms established at a grassland in northern England, we grew 20 (n = 4) plant species local to the site in the same soil and found that different plant species promoted differences in soil fungal, protistan, and metazoan communities, but bacterial communities were not affected by plant species identity. In addition, plant traits were correlated with particular soil taxa, perhaps indicating a linkage between their ecological strategies. We then evaluated whether plant community composition (assessed with a combination of conventional and molecular approaches) could facilitate predictions of soil communities using 80 samples from field plots adjacent to the mesocosms where plant species were manipulated to promote high spatial diversity. We found relatively weak relationships between plant and soil bacterial, fungal, and protistan communities. Together, this work demonstrates that interactions between grassland plants and soil organisms can account for some of the variability in the spatial distributions of soil microbial communities but that these plant-microbial interactions are highly context dependent and difficult to predict a priori.

*Symposium S11.2*

**157. Of mustard and morels: The effect of *Alliaria petiolata* (garlic mustard) on two *Morchella* clades *in vitro*\*Leighton, Elizabeth**, Volk, Thomas

University of Wisconsin - La Crosse, La Crosse, WI 54601, USA. leighton.eliz@uwlax.edu

Over the past fifteen years, multiple studies have detailed inhibitory effects of invasive garlic mustard (*Alliaria petiolata*) on arbuscular mycorrhizal and ectomycorrhizal fungi. Aqueous leachates from *A. petiolata* decreased infectivity, sporulation, and abundance of mycorrhizal fungi both in greenhouse and field experiments. However, these studies focused on a handful of fungal species; the response of many other fungi is unknown. Numerous *Morchella* species (morels) are mycorrhizal, and many are prized edibles with significant cultural and economic value. Anecdotal field evidence suggests that morel sporocarp production is reduced in sites invaded by *A. petiolata*. The goal of this study was to examine whether *A. petiolata* leachates affected *Morchella*

mycelia from each of the two major subgeneric clades (Esculentoides and Elata) *in vitro*. Aqueous extracts of roots, shoots, and whole plants were tested, as well as commercial preparations of two of *A. petiolata*’s suspected allelochemicals; allyl and benzyl isothiocyanates. Treatment was applied to five-day-old *Morchella* mycelia *in vitro*. Responses were found to vary within and between *Morchella* isolates, and included changes in mycelial morphology, melanin production, and sclerotial formation. In general, root leachates elicited the strongest responses. Preliminary results suggest that *A. petiolata* root leachates, and potentially exudates, could alter the growth of *Morchella* spp. in the soil.

*Poster P67*

**158. What matter is who you are, not where you are from: The arbuscular mycorrhizal fungal perspective on plant invasions \*Lekberg, Ylva**

MPG Ranch & University of Montana, Missoula MT, 50901, USA. ylekberg@mpgranch.com

Arbuscular mycorrhizal fungi (AMF) may facilitate plant invasion by increasing the competitive ability of exotic plants or by reducing the biotic resistance of native plants. Well-studied systems involving garlic mustard (*Allaria petiolata*) and cheatgrass (*Bromus tectorum*) have prompted suggestions that invasive plants have low mycorrhizal dependencies and disrupt AM associations of native plants. However, we have found that invasions by the exotic forbs knapweed (*Centaurea stoebe*) and leafy spurge (*Euphorbia esula*) can support higher AMF abundance and diversity than cheatgrass invasions and neighboring grass-dominated native communities. Thus, AMF responses to – and potential role in – plant invasions may be highly dependent on plant functional group identity. A meta-analysis of peer-reviewed articles provided further support that plant-AMF interactions are best predicted by plant functional group, not provenance. Whether AM associations differ in the native and exotic range of the invaders, and the underlying mechanisms for potential differences, are little known but will be discussed. *Symposium S7.2*

**159. Forest area and connectivity influence root- associated fungal communities in a fragmented landscape \*Leopold, Devin R.**(1), Vannette, Rachel L.(2), Fukami, Tadashi(1)

1.Stanford University, Department of Biology, Stanford, CA, 94305, USA; 2.University of California, Department of Entomology and Nematology, Davis, CA, 95616, USA. dleopold@stanford.edu

Habitat fragmentation has been identified as a major threat to tropical forests globally, and is well known to affect plant and animal diversity, but its effects on microorganisms are poorly understood. Because root-associated fungi are known to influence the composition and productivity of plants in many ecosystem, a greater understanding of how habitat fragmentation affects fungal communities promises to improve efforts to predict anthropogenic changes to ecosystem structure and function. Using a lava- fragmented landscape on the Island of Hawaii as a model system, we studied the community of fungi associated with the roots of a dominant canopy tree, *Metrosideros polymorpha*. This landscape allowed us to link changes in the community structure of root- associated fungi to the underlying components of habitat fragmentation, namely reduced habitat area and connectivity, while minimizing many of the confounding factors associated with anthropogenically fragmented landscapes. Through Illumina metabarcoding using two regions of the rRNA gene we found that local fungal diversity increased with forest area, but did not vary predictably with forest connectivity. In contrast, fungal species composition was correlated only weakly with area, but strongly with connectivity in a taxon-specific manner. Taken together, our results show that habitat fragmentation can alter microbial diversity and composition via differential response of taxonomic groups to habitat connectivity. *Contributed Talk C13.4*

**160. Fungal community response to water table and plant functional group manipulations in the PEATcosm experiment: Evidence for the Gadgil Effect?**

**\*Lilleskov, Erik A.**(1), Lamit, L. Jamie(2), Lennon, Jay T.(3), Romanowicz, Karl R.(2), Tringe, Susannah G.(4), Kane, Evan S.(1,2), Potvin, Lynette R.(1), Wiedermann, Magdalena M. (5), Chimner, Rodney A.(2), Kolka, Randall K.(6)

1.USDA Forest Service, Northern Research Station, Houghton, MI 49931 USA; 2. Michigan Technological University, School of Forest Resources and Environmental Science, Houghton, MI 49931 USA; 3. Indiana University, Department of Biology, Bloomington, IN 47405 USA; 4.Department of Energy, Joint Genome Institute, Walnut Creek, California, 94598 USA; University of Cincinnati, Department of Biological Sciences, Cincinnati, OH 45221 USA; 5.USDA Forest Service Northern Research Station, Grand Rapids, Minnesota 55744, USA.

elilleskov@fs.fed.us. Peatlands store over 30% of global soil organic

carbon (C), which is protected in part by high water

tables that are subject to climate change. Plant communities might also regulate decomposition, modulating the impacts of climate change on C reserves. Divergent root traits could have opposing impacts on decomposers. Ericaceae have ericoid mycorrhizal (ErM) symbionts that do not possess the full complement of white rot oxidative enzymes and could competitively suppress free-living saprotrophs, slowing decomposition (the Gadgil Effect). In contrast, peatland sedges are non-mycorrhizal, aerenchymous (air-filled tubes that transport oxygen) and deeply rooted, thus potentially priming free-living saprotrophs via exudates and oxidation. In the PEATcosm experiment we factorially manipulated water tables (high, low) and plant functional groups (PFGs; sedge, Ericaceae, unmanipulated controls). We found that fungi were abundant in the more oxic surface peat (10-20 cm), and dropped rapidly in abundance with depth (30-40 cm and below), where prokaryotes dominated. Surface peat was dominated by ErM fungi, followed by root endophytes and saprotrophs. After 3 years there was a strong divergence in the fungal communities in response to both water table and PFG treatments. The sedge only treatments in the surface peat diverged from the other PFG treatments, driven primarily by the loss of ErM fungi. When only saprotrophic basidiomycetes were analyzed, we found a significant change in the community, including an increase in the white rot basidiomycete *Galerina sphagnicola* under sedges. These community changes were paralleled by accelerated cellulose decomposition and reduced *Sphagnum* decomposition in the surface peat when Ericaceae were present. These results support the hypothesis that Ericaceae alter decomposer communities, suppress decomposition of some complex substrates, and thus potentially alter the trajectory of response to climate-mediated changes in water tables.

*Contributed Talk C5.1*

**161. Resolving fungal phylogenies with low- coverage whole-genome next-generation sequencing: Faster, cheaper, better? \*Lindner, Daniel L.**, Palmer, Jonathan M., Banik, Mark T., Jusino, Michelle A.

US Forest Service, Center for Forest Mycology Research, Northern Research Station, Madison, WI 53726, USA; dlindner@fs.fed.us

Next-generation sequencing (NGS) has revolutionized comparative genomics and environmental sampling of fungi. Although rarely used to date, NGS has the capacity to revolutionize fungal phylogenetics, with the potential to provide fast and cheap resolution of phylogenies with unparalleled statistical support. In order to study the utility of low-

coverage whole-genome NGS for fungal phylogenetics, we examined the genus *Laetiporus*, where species have been defined previously using mating compatibility, various rDNA loci, morphology and ecological data. Sixteen *Laetiporus* isolates and an outgroup, *Wolfiporia dilatohypha*, were selected for low-coverage whole-genome sequencing based on previous phylogenic relationships and morphologies. Using the *L. sulphereus* reference genome, we extracted consensus sequence for 75 loci (the AFTOL1 + AFTOL2 loci) from the NGS reads for each isolate. The concatenated data from 75 loci (~227,000 bps) were analyzed using maximum likelihood and the results were compared to analyses using the AFTOL1 loci (~13,000 bps) and a single locus phylogeny based on ITS (~570 bps). The AFTOL2 dataset produced a fully resolved phylogeny with complete statistical support for all nodes, while the AFTOL1 and ITS datasets produced phylogenies with many poorly supported nodes. In addition to determining relationships among all species, the AFTOL2 analysis demonstrated that the adaptation to grow exclusively on conifers arose once, while the evolution of different pore colors (white vs. yellow) arose multiple times. In addition, two enigmatic isolates that have never before been definitively placed in previous phylogenies were shown to represent an independent lineage, suggesting they represent a novel species. Comparison of the NGS methods used in this study to previous methods targeting 3-5 loci indicates that low-coverage genomic data are capable of producing fully resolved fungal phylogenies far faster and more cost effectively than traditional methods. *Contributed Talk C7.2*

**162. Tracking a ghost of mycorrhizal past? Host associations for the curious ectomycorrhizal fungus *Suillus subaureus*\*Lofgren, Lotus**(1), Nguyen, Nhu H(2). Kennedy, Peter G.(1,3)

1.University of Minnesota, Department of Plant Biology, St. Paul MN, 55108 USA. 2.University of California Berkeley, Department of Environmental Science, Policy, and Management, Berkeley CA, 94720 USA. 3.University of Minnesota, Department of Ecology, Evolution, and Behavior, St. Paul MN, 55108 USA. LLofgren@umn.edu

Although the vast majority of ectomycorrhizal fungi associate with hosts from multiple tree genera, fungi in the genus *Suillus* are known to have high specificity for the family Pineaceae. A single species, *S. subaureus,* has long been rumored to associate with angiosperm hosts. To examine the validity of this claim, we sequenced plant cDNA from ectomycorrhizal root tips colonized by *S. subaureus* at a field site in Minnesota. We then conducted a series

of bioassays in which angiosperm and gymnosperms seedlings were planted in different neighborhoods (conspecific vs. heterospecific) and inoculated with *S. subaureus* spores. We found that *S. subaureus* successfully formed ectomycorrhizal root tips with *Quercus rubra* at our field site. The bioassay results further validated that *S. subaureus* do associate *Quercus* hosts, but that the presence of a *Pinus* host is required for spore germination. Collectively, our results indicate that *Pinus* is the primary host of *S. subaureus*, but unlike all other S*uilloid* fungi, this species can also colonize angiosperm hosts. *Contributed Talk C15.5*

**\*Looney, Brian P.**(1), Adamčík, Slavomír(2), Matheny, P . Brandon(1) 1.University of Tennessee, Department of Ecology and Evolutionary Biology, Knoxville, TN, 37996, USA; 2.Slovak Academy of Sciences, Institute of Botany, Bratislava, 84523, Slovakia. blooney@vols.utk.edu

Numerous clades of mushroom-forming fungi have been subject to hyper-diversification events throughout their evolutionary history. However, inferring phylogenetic relationships and recognizing species with confidence within these clades can be difficult and requires the proper selection of informative loci to resolve relationships at different scales. Here we combine morphological, phylogenetic, and evolutionary evidence to develop an optimized protocol for systematic revisions of diverse clades as a model for good practices in species delimitation and description. This study will use a multi-locus approach for species delimitation in the hyper-diverse genus *Russula* in order to compare the efficacy of proposed genetic markers for resolving interspecific relationships. The targeted group is composed of species morphologically placed in *Russula* subsection *Roseinae*, comprised of seven morphological species described from North America and two from Europe. Species hypotheses based on morphological differentiation and phylogenetic analyses will be used to evaluate different coalescent model approaches. *Contributed Talk C10.4*

**164. Identification of Tongan fungi using morphology and DNA sequencing \*Louis, Leo V.**, Thomas, Michael B., Hynson, Nicole. University of Hawaii at Mānoa, Department of Botany, Honolulu, HI, 96822, USA. leolouis@hawaii.edu

In 1991 it was estimated that there were 1.5 million fungal species worldwide, at the time only 70,000 had been described. High-throughput sequencing methods have increased the estimated

**163. Coalescent approaches to species delimitation in *Russula* subsection *Roseinae***



number of fungal species to 5.1 million. While the number of documented species remains quite small. The low number of documented fungi largely results from a lack of alpha taxonomists, and an abundance of understudied regions. This study seeks to address these issues, through a preliminary survey of the fungal diversity on the island of ‘Eua in the kingdom of Tonga. Few studies have investigated the fungal diversity on ‘Eua, believed to be one of the oldest islands in the Pacific. These historical studies yielded 200 individual specimens. The few collections from ‘Eua were made by 49 people, most of whom gathered less than 10 specimens. Here we describe a sub sample of the 67 fungal specimens we collected from July 4th to August 4th 2014, the second largest collection from ‘Eua. Based on tentative determinations using morphological features, we believe that 27 of the collected fungi are new island records. Future work will include making robust species determinations utilizing Sanger sequencing of the nuclear ribosomal ITS region. This study will contribute to scientific knowledge of fungal diversity in an understudied region. Additionally, because of the old age of ‘Eua this study may provide novel insight into fungal dispersal throughout the pacific.

*Poster P23*

**165. Hi-C assembly of *Rhizopogon vesiculosus* reveals the genome wide organization and architecture of an ectomycorrhizal truffle in *Boletales***

**\*Lu, Dabao**(1), Liachko, Ivan(2), Sullivan, Shawn T.(3), Mujic, Alija B.(4), Dunham, Maitreya(2), Spatafora, Joseph W.(1) 1.Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97330, USA; 2.University of Washington, Department of Genome Science, Seattle, W A, 98195-5065, USA; 3.Phase Genomics, Seattle, WA, 98195, USA; 4.University of Florida, Department of Plant Pathology, Gainesville, FL, 32611, USA. luda@science.oregonstate.edu

Genome sequencing of fungi through the 1000 Fungal Genome Project has resulted in the sequencing and annotation of multiple *Rhizopogon* species, generating data that are advancing studies in the evolutionary biology of the Boletales. All current genomes of *Rhizopogon* have been sequenced using short read sequencing technologies alone, however, and the assemblies comprise thousands of contigs. While these assemblies are sufficient for capturing gene space, they are limited in their resolution of complex repetitive regions and analysis of genome organization. The chromatin conformation capture assay (Hi-C) was developed to capture 3D genome architecture through genome-wide proximity contact

maps, but the long-range contiguity information in these datasets has proven useful for other applications such as scaffolding in reference-guided and *de novo* genome assemblies, haplotype phasing, and the identification of fungal centromeres. In order to advance the assembly of *Rhizopogon* genomes, Hi-C was performed on *R. vesiculosus*, and resultant Hi-C reads were mapped to the Illumina reference assembly of the same strain prior to scaffolding. Clustering analysis supported scaffolding the *R. vesiculosus* reference assembly into 10 chromosome-scale scaffolds containing 97.1% of the original assembly’s sequence length. Blast results on single copy genes provided evidence that the individual haplotypes of the parent dikaryon were co-assembled. Based on these results, we predict that *R. vesiculosus* has 10 chromosomes, spanning lengths from 2.8 to 10.1 Mbp. This Hi-C-based assembly was annotated with RNA and protein data, resulting in the first Boletales genome with a chromosome level annotation, revealing the large-scale genome organization in this group. Here, we will highlight the nature of transposable and centromeres, and the use of this Hi- C-based genome assembly in comparative analyses of *Rhizopogon* and Boletales.

*Contributed Talk C3.6*

**166. E-monograph of Magnaporthales \*Luo, Jing**(1), Zhang, Ning(1, 2) 1. Rutgers University, Department of Plant Biology & Pathology, New Brunswick, NJ, 08901, USA; 2.Rutgers University, Department of Biochemistry & Microbiology, New Brunswick, NJ, 08901, USA. Luojing999@hotmail.com

Magnaporthales (Sordariomycetes, Ascomycota) includes important cereal and grass pathogens, such as the rice blast fungus *Pyricularia oryzae* and the take- all pathogen *Gaeumannomyces graminis*, as well as endophytes and saprotrophs. The studies on Magnaporthales can date back to the late 19th century and the rice blast fungus has been used as a popular model system for understanding host-pathogen interactions. However, the taxonomy of Magnaporthales remains obscure because of limited studies on the non-model species. The objectives of this project are 1) to reconstruct a robust phylogenomic tree of Magnaporthales to understand the evolution of pathogenicity and morphological and ecological characters; 2) to discover and describe new taxa in Magnaporthales by using both culture-based and metagenomic sequencing methods; and 3) to produce a global e-monograph of Magnaporthales. With the help of recent multi-gene and genomic data, a well-supported phylogeny of Magnaporthales was generated and taxonomic revisions were made accordingly. To date over 200 species names are

accepted in this order, three families and 28 genera are suggested. Meanwhile the metagenomic primers were designed and will be used to detect Magnaporthales taxa directly from plant samples on the Illumina sequencing platform. A total of 70 specimens were loaned from the Herbarium Patavinum of the University of Padova (PAD), the New York Botanical Garden (NYBG) and U.S. National Fungus Collections (BPI). Additionally, 20 culture isolates from Centraalbureau voor Schimmelcultures (CBS) and other labs were used to induce sporulation for observation. Culture specimens successfully producing reproductive structures were deposited in the Rutgers Mycological Herbarium (RUTPP). Photograph, measurement, description and geographical data of all specimens were collected and deposited in the Magnaporthales database. All other available specimens worldwide will be examined and recorded. Based on the obtained data, a BRAHMS online database will be initiated. It will include images, descriptions, host and distribution, identification keys and DNA barcodes. Genomic sequences for the representative taxa also will be linked to the cyber- enabled monograph.

*Contributed Talk C4.7*

**167. Removing trees for healthy forests: Impacts on the American matsutake mushroom resource \*Luoma, Daniel L.**, Eberhart, Joyce L. Oregon State University, Department of Forest Ecosystems and Society, Corvallis, OR, USA. luomad@fsl.orst.edu

This study assessed impacts of active forest management on the persistence of *Tricholoma magnivelare* (American matsutake) shiros in the soil. The study was motivated by concerns raised by mushroom harvesters regarding forest managers’ abilities to sustain matsutake mushroom harvests over the long-term. Goals included bringing appropriate forest stands into a condition where re-introduction of fire operates as a natural fuels reduction agent while maintaining the forests in a sustainable condition to continue long-term harvesting of matsutake. Four sampling areas in each of 3 forest cover-types (*Pinus contorta, Pinus ponderosa*, and mixed conifer) were established, yielding 12 experimental units*.* Thirty matsutake shiros were sampled in each unit pre- treatment with an additional 20 shiros sampled in control areas for each forest type. Four soil samples were taken within each of the shiros. Treatment consisted of thinning by logging when a minimum 60 cm snow depth cover was present. Logging methods were the same for each forest type. Soil samples were frozen until DNA could be extracted. Due to volcanic glass in these soils, it was not possible to amplify DNA using extraction techniques that require bead

beating or vortexing. We developed a modification of a simple chemical plant extraction method by Xin *et al*. using 0.5 grams of soil from each sample. PCR was preformed using *Tricholoma magnivelare* specific primers developed by Dr. Becky Bravi. In the pre- treatment phase, 74% of the 1676 samples tested positive for *Tricholoma magnivelare* DNA. After logging, a total of 1,390 post-treatment soil samples were tested and 60% were positive for *Tricholoma magnivelare*. In a dilution series we found that we could easily detect the fungus at levels of 1:100,000 that of the pure mushroom extract. Overall, samples from the initial post-treatment sample period showed a 19% reduction in detectable matsutake DNA. *Contributed Talk C6.4*

**168. Neonatal gut microbiota predicts childhood multi-sensitized atopy and is influenced by microbes in the built environment \*Lynch, Susan V.**

University of California, Division of Gastroenterology, Department of Medicine, San Francisco, CA 94143, USA. susan.lynch@ucsf.edu

Gut microbiome composition and metabolic activity have been implicated in childhood atopy and asthma. Bacterial profiling of 298 early-life fecal samples from a US birth cohort identified three neonatal (median age 35 days) gut microbial-states (NGM1-3) incurring significantly different relative- risk for multi-sensitized atopy at age-two years and doctor-diagnosed asthma at age-four years. The highest risk group, NGM3, exhibited specific bacterial depletions (*Bifidobacterium* and *Faecalibacterium)*, fungal expansions (*Candida* and *Rhodotorula*) and a distinct fecal metabolic microenvironment. *Ex vivo*, sterile NGM3-derived fecal water increased the proportion of CD4+ T-helper 2 cells, IL4 expression and suppressed T-regulatory populations. Network analysis identified a metabolic module containing the asthma-associated oxylipin, 12,13 DiHOME which discriminated NGM3 from lower risk NGMs. *Ex vivo*, 12,13 DiHOME exposure recapitulated the CD4+ T- regulatory cell suppression phenotype observed with fecal water. Parallel bacterial and fungal profiling of paired house dust from the homes of these participants identified factors that shape built environment bacterial and fungal communities, which include the age of the building and human and furred pet residents. Preliminary data also indicates that a subset of organisms in the neonatal gut are sourced from their built environment. Hence microbial exposures in the built environment are related to neonatal gut microbiome composition, dysbiosis of which is associated with a luminal metabolic microenvironment that drives T-cell dysfunction associated with childhood atopy.

*Symposium S4.2*

**169. New diversity of *Cladosporium* from China, with a psychrophilic xylan-main-chain degrading system revealed by genomic analyses**Ma, Rui(1, 2), **\*Chen, Qian**(3), Fan, Yunliu(2), Cai, Lei(3), Yao, Bin(1)

1.Feed Research Institute, Chinese Academy of Agricultural Sciences, Key Laboratory of Feed Biotechnology of the Ministry of Agriculture, Beijing, 100081, China; 2.Biotechnology Institute, Chinese Academy of Agricultural Sciences, Beijing, 100081, China; 3.Institute of Microbiology, Chinese Academy of Sciences, State Key Laboratory of Mycology, Beijing, 100101, China. binyao@caas.cn

*Cladosporium* species distribute in all types of environments, and are characterized by determinate, non-proliferating conidiophores, branched chains of small conidia with a coronate scar. *Cladosporium* currently contains 170 species, mostly belonging to three major complexes, i.e. *C. herbarum*, *C. sphaerospermum* and *C. cladosporioides*. A recent preliminary investigation of *Cladosporium* diversity from soil in China revealed 8 novel species in *C. cladosporioides* complex. The new species were introduced and described based on morphological and multi-locus phylogenetic characterizations. Strain SL- 16 of *Cladosporium xinjiangensis* sp. nov., was isolated from alpine tundra soil and showed optimal growth and high xylanolytic activity at 15°C. The whole genome of SL-16 was sequenced, and 2916 genes were identified with the average length of 922 bp. Ninety-two glycoside hydrolase encoding genes were predicted, including a xylan-main-chain degrading system of seven components, in which xylanases *Ca*Xyn10A and *Ca*Xyn11A, and a xylosidase *Ca*Xyl43A showed high expression levels under xylan induction. These enzymes were successfully expressed in *Escherichia coli* for further functional characterization. All purified recombinant enzymes showed similar neutral, cold-active and thermolabile properties, but varied in low-temperature kinetics and substrate specificity. This is the first report of cold-adaptive xylanolytic system with high xylan conversion efficiency, which is valuable for the production of xylooligosaccharides and fermentable xylose in a more economical approach.

*Poster P12*

**170.Comparative microbiome analysis among crop rotations and field management strategies \*MacCready, Kristi Gdanetz**, Trail, Frances 1.Michigan State University, Department of Plant Biology, East Lansing, 48824, USA. gdanetzk@msu.edu

Microbiomes of plants are essential determinants of plant health outcomes, as are microbiomes of humans. To manipulate a crop’s microbial community to assure positive outcomes necessitates some knowledge of the microbial community and what environmental and genetic factors effect changes in the community. Michigan State University’s Kellogg Biological Station Long Term Ecological Research site harbors a set of plots in a wheat/corn/soybean rotation, providing an ideal site to conduct long-term characterization of these economically important row crops. The site has been farmed since 1989 with six replicate hectare plots for each of four treatments: conventional management, no-till, reduced inputs, and organic. We compared the diversity of the microbial communities across the four treatments and three different plant tissues, during one cycle of the crop rotation. The fungal ITS2 and bacterial 16S regions were PCR-amplified and sequenced from plots grown under each of these treatments and in successive years. We assessed how below-ground and above-ground microbial communities differed, as well as the differences between the four treatments. *Contributed Talk C8.1*

**171. Identifying fungi present in bigleaf maple canopy and forest floor soils in a coastal old-growth temperate rainforest in western Washington \*Mafune, Korena**(1), Vogt, Daniel(1), Vogt, Kristiina(1), Godfrey, Bruce(2)

1.University of Washington, School of Environmental and Forest Sciences, Seattle, WA 98195-2100, USA; 2. University of Washington, Department of Biology, Seattle, WA 98195-2100, USA. kmafune@uw.edu

The temperate rainforests of Western Washington are known for their old-growth forests and unique ecosystem processes. In these stands of old-growth, it is common for trees to be over 300 years old. Over time, epiphytic mats form on the branches. The bottom layer of these mats decomposes, forming a layer of organic matter known as *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. Adventitious roots have the capability to form fungal relations, but science has not pursued the extent and role of these relationships. The specific aims of this research were to attempt to 1) taxonomically identify fungal species, specifically mycorrhizas, in adventitious canopy and forest floor roots, and 2) compare the identified species between the canopy and forest floor root-tips. Twenty-four root-tips were sampled from the canopy and forest floor soils of four big leaf maples (*Acer macrophyllum* Pursh) located in the Olympic National Rainforest in the Queets River Watershed, Washington. Root-tip DNA was extracted for PCR, cloning, and DNA

sequencing. The resulting sequences were identified and aligned using the NCBI BLAST Database and the EMBI Clustal program, respectively. PHYLIP was used to observe phylogenetic differences among roots collected from the canopy and the forest floor. Mycorrhizas, saprobes, and dark septate endophytes were successfully identified from both the canopy and forest floor roots. Current results suggest we are working with a diversity of fungal species that may be unknown, that form mushroom fruiting bodies, and that have never been reported in association with the host tree.

*Contributed Talk C19.7*

**172. Puerto Rican strains of *Beauveria bassiana* with potential for biocontrol of the coffee berry borer *Hypothenemus hampei***Mariño-Cárdenas, Yobana(1), García, Noelia M.(1), Rehner, Stephen A.(2), **\*Bayman, Paul**(1) 1.University of Puerto Rico - Río Piedras, San Juan, PR 00931; 2.USDA-ARS; Systematic Mycology and Microbiology Laboratory, Beltsville, MD 20705. bayman.upr@gmail.com

The coffee berry borer *Hypothenemus hampei* (or CBB) is the most damaging insect pest of coffee worldwide. Management of CBB is difficult and new strategies are needed. Several biological control agents are used in CBB management; one of the most important is the entomopathogenic fungus *Beauveria bassiana* (Bb). In Puerto Rico it is applied as Mycotrol®. Native Bb strains are common on coffee farms and are presumably adapted to local conditions. The obectives of this study were to compare virulence and number of conidia produced per CBB among native strains and the strain used in Mycotrol®. To measure virulence, groups of 10 female CBB were exposed to 4 x 106 conidia on filter paper; each fungus was replicated 15x. CBB deaths were noted each day for 8 days. Dead CBB were plated on potato dextrose agar to verify infection with Bb. Sporulation on dead CBBs was estimated. Differences among strains were significant for virulence and for number of conidia produced per CBB. Two local strains caused mortality at levels similar to the Mycotrol® strain: 80% and 72% vs. 85%; they were also similar in sporulation. These results suggest that these strains are potentially useful for programs of integrated pest management of the CBB in Puerto Rico. *Poster P76*

*Poster P147*

**174. Population genomics of *Rhizopus stolonifer* \*Masonjones, Sawyer R.**, Stajich, Jason E. University of California - Riverside, Genetics, Genomics, and Bioinformatics, Riverside, CA 92507, USA. sawyer.masonjones@email.ucr.edu

Worldwide, about one third of food goes uneaten due to postharvest losses and waste. One culprit of this loss is *Rhizopus stolonifer*, a Mucoromycota fungus that causes soft rot in many fruits and vegetables globally. The recommended control strategy is quick harvesting, packing, etc at cool temperatures combined

|  |
| --- |
| University of Puerto Rico Medical Sciences Campus, |
| Microbiology and Medical Zoology Department, San Juan, Puerto Rico, 00936. benjamin.bolanos@upr.edu  In the United States of America, allergies affect 20% of all individuals, being the most common immunity disorder. It has been proved that the exposition to indoor and/or outdoor fungi is a risk factor that leads to the development of asthma. The prevalence of asthma in children in Puerto Rico (14%) is more than twice the prevalence of asthma in children in the USA (6%). It is likely that tropical environmental factors such as very high levels of basidiospores and ascospores in the outdoor air may be responsible of this high asthma prevalence. The bracket fungus *Ganoderma applanatum* is a basidiomycete abundant in Puerto Rico. Puerto Rican patients with asthma responded to mites and*G. applanatum* spore crude cytoplasmic extract to the same extend (44%) at the skin prick test, suggesting that basidiomycetes are important allergen sources. Even though the allergenicity of *G. applanatum* has been described, none of the mycelial proteins or allergens has been characterized and there is no commercial diagnostic method for detection of basidiomycete sensitization. *G. applanatum’ s* cap piece was recovered from the nature in San Juan, P.R. and then cultivated in Malt Extract Agar for 7 days at 25oC. Then it was sub cultivated in Malt Extract Broth and incubated for 12 days at 25oC in a shaker at 200rpm. The resultant fungi is processed with ammonium bicarbonate buffer with protease inhibitors in a beat beater with glass beads, ultracentrifuged and lyophilized to obtain the crude cytoplasmic extract. The *G. applanatum’s* extract has approximately fifteen proteins. Western Blot technique was used to identify allergenic proteins. Human serums from Puerto Rican atopic and non-atopic patients were tested against *G. applanatum* mycelium crude cytoplasmic extract. Results show serological reactivity to cytoplasmic components of *G. applanatum* mycelium. We can conclude that Puerto Rican atopic population recognizes some allergenic cytoplasmic components of *Ganoderma applanatum* mycelium. |
| **173. Detection of allergenic proteins from the crude** |
| **cytoplasmic extract *applanatum* mycelium cultures \*Martínez Zapata, Isabelita**, Bolaños-Rosero, Benjamín  **of *Ganoderma*** |

with treatment of fungicides. However, not all are approved for human contact limiting their use in strawberry. In addition, fungicide resistance is expected to evolve in populations with frequent application. The organic farming sector’s limited use of fungicides with mixed efficacy, could impact or establish population structures of *R. stolonifer*. We present preliminary work in phenotyping in 30 geographically and substrate diverse strains and genomic diversity from 8 geographically diverse *R. stolonifer* samples. Strains are being cultured from strawberries grown in organic and conventional farms found in California and from culture stocks at the NRRL. Fungicide resistance is being assayed in a collection of strains from global distribution and isolates from California and Florida strawberry fields. Initial growth rate experiments of 30 samples vary from 0.5 cm/day to 3.4 cm/day with a mean of 1.98 and a standard deviation of .54, and ANOVA demonstrates wide variation between samples (p<<0.05) for the current collection. Further growth experiments will measure growth rate under various abiotic stressors. Genomic resequencing of 8 strains obtained from NRRL were analyzed for patterns of variation in the genomes to establish if there is a strong signal of population structure and demography. The identified variants were further analyzed to scan for gene loci with high accumulation of differences and evidence for transposable element activity. Future work with expanded collections of strains will scan for selection and variation.

*Poster P106*

**175. Endophyte communities in prairie grass are dynamic through space and time \*May, Georgiana**(1), Condon, Bradford(1), Lumibao, Candice(1), Seabloom, Eric(1), Borer, Elizabeth(1), Kinkel, Linda(2)

1. University of Minnesota, Department of Ecology, Evolution and Behavior, St. Paul, MN 55108, USA; 2. University of Minnesota, Department of Plant Pathology, St. Paul, MN 55108, USA. gmay@umn.edu

Despite the widespread recognition of a vast microbial diversity lodged within most eukaryotic hosts, our understanding the ecological forces that shape the assembly of these microbial communities and the evolution of their functions remains limited. In this study, we used an experimental ecological approach to determine factors affecting the structure of fungal endophytic communities in the iconic prairie grass, *Andropogon gerardii* over plant developmental and seasonal time Young and mature leaves were sampled from the same individual plants over the summer season and across experimental treatments that manipulated soil mineral nutrients and herbivore

pressure. Using metagenomic amplicon sequencing approaches, results showed that leaf maturity and seasonal date had the strongest effects on the richness, evenness, and diversity of endophytic communities whereas surprisingly, nutrient treatment and herbivore exclusion did not strongly effect endophyte communities. Endophyte communities in young and mature leaves were similar early in the season, but became increasingly different later in the season. Site- wide and within plots, taxa (as Operational Taxonomic Units; OTUs) that were abundant early in the season persisted throughout the rest of the summer, although their representation measured by read counts often decreased. Together, results suggest that both deterministic and stochastic factors structure temporally dynamic endophyte communities. In a system with high dispersal across a hetergenous landscape, the biology of individual taxa may be the most important factor affecting the assembly of microbial communities.

*Contributed Talk C9.3*

**176. Two geographic clades of the ancient ambrosia beetle genus *Scolytoplatypus* have mycangial symbionts in two early-diverging lineages in the *Ceratocystidaceae***

**\*Mayers, Chase G.**(1), Harrington, Thomas C.(1), Jordal, Bjarte H.(2), Masuya, Hayato(3) 1.Iowa State University, Department of Plant Pathology and Microbiology, Ames, IA, 50011, USA; 2.University of Bergen, University Museum of Bergen, Bergen, NO-5020, Norway. 3.Tohoku Research Center of Forestry & Forest Products Research Institute, Morioka, Iwate, 020-0123, Japan. cgmayers@iastate.edu

The ambrosia beetle symbiosis is the oldest and most species-rich of the insect-fungus symbioses. Ambrosia fungi are carried by their beetle symbionts in specialized sacs called mycangia and are introduced into sapwood as the beetles excavate galleries. The fungi produce specialized conidia and conidiophores that serve as the primary food for the larval progeny. Most genera of ambrosia beetles carry species of *Raffaelea* (Ophiostomatales) in their mycangia, but beetle genera with the most elaborate mycangia within the tribes Xyleborini, Corthylini and Xyloterini carry species of *Ambrosiella, Meredithiella,* and *Phialophoropsis* (Microascales, *Ceratocystidaceae*), respectively. We investigated the mycangial fungi of ambrosia beetles in the ancient genus *Scolytoplatypus* (tribe Scolytoplatypodini)*,* which have large, elaborate, pronotal mycangia and were assumed to harbor *Ambrosiella* spp. Phylogenetic analyses (18S rDNA and *TEF-1a*) of the symbionts of two geographic lineages of *Scolytoplatypus* suggest that the fungi belong in two monophyletic groups within

the *Ceratocystidaceae*: a group sister to *Phialophoropsis* that lacks aleurioconidia and is associated with African and Madagascan *Scolytoplatypus* spp., and a second group closer to *Ambrosiella* that forms aleurioconidia and is associated with Asian *Scolytoplatypus* spp. Comparison of the phylogeny of ambrosia fungi in the *Ceratocystidaceae* to the estimated divergence times of their beetle hosts suggests that the *Scolytoplatypus* lineages and their fungal associates represent an ancient divide in the history of the symbioses. The *Ceratocystidaceae* symbionts that lack aleurioconidia (including *Phialophoropsis*) may have arisen through co-adaptation with the African species of *Scolytoplatypus*, and the aleurioconidia-producing symbionts (including *Ambrosiella* and *Meredithiella*) may have arisen through co-adaptation with the Asian *Scolytoplatypus*.

*Contributed Talk C4.5*

**177. Corralling the collar and reeling in the appendage: An SEM study of the ultrastructure of *Zancudomyces culisetae*\*McCormick, Michael**, Bourland, Bill, White, Merlin Boise State University, Department of Biological Sciences, 1910 University Drive, Boise, Idaho, 83725- 1515, USA. mikemccormick@u.boisestate.edu

Trichomycetes are obligate gut fungi found in many different non-predaceous arthropod hosts, including immature aquatic stages of mosquitoes. During the Fall of 2015 mosquito larvae collected from the streamside puddles of the mountainous regions of Idaho were dissected. *Zancudomyces culisetae* was removed from the hindgut and an axenic culture was established, from which thalli and spores were processed for Scanning Electron Microscopy (SEM). SEM sheds light (or electrons) on the ultrastructure of fungal features including the thallus, generative cells, spores, collar, and appendage but has been underutilized in trichomycetology. For example, at the light microscopy level, the collar and appendage of *Z. culisetae* are notably variable in form and often difficult to distinguish. With SEM of this isolate, details of the trichospore development as well as the collar and its containment and release of the single spore appendage are presented. Trichospores are the dominant dispersal spore recovered by routine dissecting, particularly with mosquito larvae. Whether hosts occur in such lentic systems (or lotic ones) the spores are consumed by larvae when feeding on algae, bacteria, detritus, and other particulates often found in an aquatic environment. A finer picture of features of the spore and appendage allude to dispersal mechanisms and ways of possibly increasing likelihood of being ingested by the same or other mosquitoes.

*Poster P132*

**178. Untangling the webs: The fungi that form aerial litter traps in the Neotropics**McCoy, Austin G., **\*Helfers, Seth J.**, Koch, Rachel A., Aime, M. Catherine.

Purdue University, Department of Botany & Plant Pathology, West Lafayette, IN 47907

Aerial litter-trapping (ALT) webs formed by fungi are common in the Neotropics and play a pivotal role in ecosystems by creating high turnover rates of organic matter. Given that these webs are created by vegetative structures, the identity of the fungi responsible for forming them remains largely unknown. In this study, we opportunistically collected ALT webs formed at different heights and in various forest types in the Pakaraima Mountains of western Guyana. Sampling was performed in the upper Potaro River Basin and each sample was photographed *in situ*, preserved, and examined for the formation of fruiting bodies. Fruiting bodies, when present, were described before preserving separately. Samples of individual webs and fruiting bodies were then sequenced at the internal transcribed spacer (ITS) rDNA region. Sequences were compared by Blast analysis to the NCBI BLAST database and also to an unpublished database containing ITS sequences for most morphospecies of fungi previously collected in the same region of Guyana. Our results indicate that at least four distinct species, belonging to three genera within the Agaricales and Russulales, are responsible for forming these webs in the Pakaraima Mountains. Of these, only a single species of *Gymnopus* was ever observed to produce fruiting bodies directly from the vegetative webs. We expanded the number of sequenced loci to conduct phylogenetic analyses to further resolve the evolutionary relationships of these web-forming fungi. *Poster P20*

**178.1 Fungal conservation in the NatureServe Network: Cultivating partnerships for conservation data in the U.S., Canada, and beyond. \*McIntyre, Patrick**(1), Kagan, Jimmy(2), Francis, Anne(3), Klein, Mary(3)

1.California Natural Diversity Database, 1416 9th Street, Suite 1266 Sacramento, CA 95814; 2.Oregon Biodiversity Information Center, Portland State University, PO Box 751, Portland, OR 97207-0751; 3.NatureServe, 4600 N. Fairfax Dr., 7th Floor, Arlington, V A 22203 Patrick.McIntyre@wildlife.ca.gov

NatureServe is a non-profit organization that provides high-quality scientific expertise for species focused conservation, with network members in all U.S. states, Canadian provinces, and over 10 countries

in Latin America. In this talk we present 1) an overview of current fungal conservation efforts in the broader context of the NatureServe network, 2) a case story of recent success in fungal conservation from the Oregon Natural Heritage Program, 3) a discussion of data gaps, and 4) areas of potential synergy between NatureServe and members of the Mycological Society of America in improving and promoting fungal conservation in North America and beyond. At present, approximately 5,300 fungi (4,200 lichens and 1,100 non-lichenized fungi) are listed the NatureServe database from the US and Canada. Reflecting broader challenges in fungal conservation, over 65% of even this small fraction of fungal biodiversity lack basic information such as a Global Conservation Status Rank. While NatureServe is working globally with the IUCN RedList to promote conservation assessments for fungi, the strength of the NatureServe conservation network lies in helping form local and regional partnerships to provide data and information for conservation decision-making. For example, the Oregon Natural Heritage Program, over the past decade, has worked with members of the mycological community from universities, government agencies and beyond to conduct status assessments of fungi in the Pacific Northwest to identify the fungi of the greatest conservation concern. The 2016 update of “Rare, Threatened and Endangered Species of Oregon” will now include approximately 205 taxa of fungi and 70 species of lichen from Oregon alone, all with up-to-date ranking and distribution information, and many with all known occurrences tracked. Efforts such as these can help cultivate sustainable conservation initiatives for fungal conservation that help bring them to forefront of conservation efforts. *Symposium S9.3*

**179. The skin mycobiome of temperate and tropical amphibians in relation to *Batrachochytrium* infection status**Medina, Daniel(1), Franklin, Josh(2), Hughey, Myra(1), Walke, Jenifer(1), Becker, Matthew(1), Sun, Shan(2), Badgley, Brian(2), **\*Belden, Lisa K.**(1) 1.Virginia Tech, Department of Biological Sciences, Blacksburg, VA, 24061, USA; 2.Virginia Tech, Department of Crop and Soil Environmental Sciences, Blacksburg, VA, 24061, USA. belden@vt.edu

Animals harbor diverse communities of symbiotic microbes that contribute various functions to their hosts, including, often, a role in disease resistance. Amphibian population declines caused by the pathogenic fungus, *Batrachochytrium dendrobatidis* (Bd), have prompted studies on the bacterial symbiont community that resides on amphibian skin, as researchers try to identify antifungal bacteria that could serve as probiotics. However, studies addressing

the fungal portion of these symbiont communities have lagged behind. We characterized the fungal skin communities of four temperate and four tropical amphibian species (total N=93) using ITS gene amplicon sequencing. For each species, we sampled both Bd-positive and Bd-negative individuals (based on Bd qPCR results), so that we could determine potential interactions between the fungal skin community and Bd infection status. Fungal community richness and evenness did not vary significantly among species. Fungal community structure did differ among species, but was not strongly linked to Bd infection status. Our results suggest that the fungal portion of the amphibian skin microbiome might be diverse and variable across species and regions.

*Symposium S2.1*

**180. The oldest fossil mushroom \*Miller, Andrew N.**(1), Heads, Sam W.(1), Crane, J. Leland(1), Thomas, M. Jared(1), Ruffatto, Danielle M.(1), Methven, Andrew S.(2), Raudabaugh, Daniel B.(1,3) 1.University of Illinois, Illinois Natural History Survey, Champaign, IL, 61820, USA; 2.Savannah State University, Department of Biology, Savannah, GA, 31404, USA; 3.University of Illinois, Department of Plant Biology, Champaign, IL, 61801, USA. amiller7@illinois.edu

Exceptionally preserved fossils can shed important and unprecedented light on the history of life. Particularly remarkable deposits, known as Lagerstätten, yield fossils characterized by preservation of soft, labile tissues that decay rapidly and which are not normally preserved. Mushrooms (in the strict sense) produce gilled fruiting bodies and, while certainly ancient, have an extremely depauperate fossil record with only five species known from Miocene to Cretaceous amber dating from ~15-100 mya. Here we report the first mushroom compression fossil from the Lower Cretaceous which represents the oldest fossil mushroom from ~120 mya. The specimen comes from the laminated limestones of the Crato Formation, which outcrop on the northern flanks of the Chapada do Araripe in Ceará, Brazil. While precise locality details are unknown, the lithology of the matrix is consistent with the specimen having been collected in one of the extensive quarry complexes near the town of Nova Olinda. The specimen comprises a single, nearly complete mushroom preserved as a primarily goethitic replacement on a small slab of buff-coloured, millimetrically laminated limestone from the Nova Olinda Member, the lowermost unit of the Crato Formation. This specimen represents the oldest reported fossilized mushroom, the first report of a mushroom fossil from South

America, and the only fossilized mushroom known from a compression. *Poster P39*

**181. The phenology of fungal wood decay shows coordination between fruiting and enzyme production \*Milo, Amy M.**(1), Zanne, Amy E.(1), McCormick, Melissa(2), McMahon, Sean(2)

1.The George Washington University, Department of Biological Sciences, Washington, DC, 20052, USA; 2.Smithsonian Environmental Research Center, Edgewater, MD, 21037, USA. ammilo@gwu.edu

Wood decay fungi obtain resources by secreting enzymes to break down complex carbohydrates such as lignin, cellulose, and chitin, and absorb the resulting products to fuel fungal growth and reproduction. Over the past 30 years, fungal fruiting phenology has demonstrated shifts corresponding to earlier springs and warmer falls due to changing climate. Whether shifts in fungal fruiting phenology might indicate similar changes in the timing of fungal resource acquisition is unclear. We set out to determine how closely fungal fruiting phenology is linked to the cryptic phenology of fungal decay enzyme activity. We performed monthly surveys of fungal fruiting bodies at the Smithsonian Environmental Research Center in Edgewater, MD, and paired these with sampling of wood substrates for extracellular enzyme activity. We targeted 3 cellulose degrading enzymes and 1 chitin degrading enzyme in our assays. The distribution of fruiting abundances was compared with the distribution of enzyme activity potentials to look for coordination in the timing of reproductive and resource acquisition activities in fungal communities. Between June 2013 and December 2015, fruiting fungal communities showed distinct seasonal turnover, and peak fruiting abundances occurred in the fall each year. Enzyme activity potentials were assayed monthly during 2014 and 2015. All three cellulose degrading enzymes showed peak activity in late spring, whereas chitinase activity peaked in mid to late summer. The offset between the peak activity of these enzymes might indicate a shift in fungal foraging for resources from woody carbohydrates to fungal biomass recycling in the later summer, corresponding with a turnover in fungal fruiting communities. Overall our findings suggest that maximum decay potential precedes maximum fruiting. *Contributed Talk C6.3*

**182. Pathogenicity and taxonomy of a new monotypic genus of Gnomoniaceae on *Styrax obassia* in Japan.**Minoshima, Ayaka(1), Kim, Sangwon(1), Horie, Hiromichi(1), Takemoto, Shuhei(2), Hosoya,

Tsuyoshi(3), **\*Walker, Allison K.**(4), Walker, Donald M.(5), Hirooka, Y uuri (1) 1.Department of Clinical Plant Science, University of Hosei, Koganei, Tokyo, 184-8584, Japan; 2.Graduate School of Agricultural and Life Sciences, The University of Tokyo, Nishi-Tokyo, Tokyo, 188-0002, Japan; 3.Department of Botany, National Museum of Nature and Science, Tsukuba, Ibaraki, 305-0005, Japan; 4.Department of Biology, Acadia University, Wolfville, Nova Scotia, B4P 2R6, Canada; 5.Department of Biology, Tennessee Technological University, Cookeville, TN, 38505, USA. minoopy9245@yahoo.co.jp

Members of the Gnomoniaceae (Diaporthales) are commonly isolated as endophytes, saprobes, and plant pathogens from a broad diversity of herbaceous, shade tree, and agriculturally significant plants. In Japan, an unknown fungus in the Gnomoniaceae has been found on overwintered leaves and petioles of *Styrax obassia* (Styracaceae) since 2011. The objectives of this study were to characterize this fungus using morphological examination, phylogenetic analysis of three molecular markers, and to determine the pathogenicity of this species. This fungus is characterized by dark brown to glossy black immersed or partially erumpent ascomata with long necks. Its fusiform, oval to obovoid asci with acute or long tapering stipe bear eight fusiform to filiform, 10.7-20.6 × 1.1-3.0 μm ascospores. Its growth rate in pure culture is relatively slow to moderate (15mm/week). This is the first documented record of a species of Gnomoniaceae on a host in the Styracaceae. Phylogenetic analyses of the markers LSU, *rpb2,* and *tef-1α* indicated that this is a new monotypic genus in the Gnomoniaceae. We carried out Koch’s postulates to confirm this species as the causative agent of leaf blotch on *Styrax obassia.* The pathogenicity of this fungus was investigated by inoculation of healthy leaves and branches. One week after inoculation, this fungus produced small necrotic spots on the leaves and petioles and confirmed that this fungus has weak pathogenicity on *Styrax obassia*. We have observed and speculate that the weak pathogenicity may promote early defoliation of *Styrax obassia* during the fall.

*Poster P10*

**6 183. N -methyladenine marks**

**active gene**

**expression in early diverged fungi \*Mondo, Stephen**(1), Dannebaum, Richard(1), Kuo, Rita(1), Labutti, Kurt(1), Haridas, Sajeet(1), Kuo, Alan(1), Salamov, Asaf(1), Ahrendt, Steven 2), Lipzen, Anna(1), Sullivan, William(1), Andreopoulos, William(1), Clum, Alicia(1), Lindquist, Erika(1), Daum, Christopher(1), Ramamoorthy, Govindarajan(1), Gryganskyi, Andrii(3), Culley, David(4), Magnuson, Jon(4), James,

Timothy(5), O’Malley, Michelle(6), Stajich, Jason(7), Spatafora, Joseph(8), Visel, Axel(1,9), Grigoriev, Igor(1) 1.US Department of Energy Joint Genome Institute, Walnut Creek, CA, USA; 2.University of California, Department of Plant and Microbial Biology, Berkeley, CA, USA; 3.L.F. Lambert Spawn Co, Coatesville, PA, USA; 4.Pacific Northwest National Laboratory, Richland, WA, USA; 5.University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, MI, USA; 6.University of California, Department of Chemical Engineering, Santa Barbara, CA, USA; 7.University of California, Department of Plant Pathology and Microbiology, Riverside, California, USA; 8.Oregon State University, Department of Botany and Plant Pathology, Corvallis, Oregon, USA; 9.University of California, School of Natural Sciences, Merced, CA, USA.

N6-methyldeoxyadenine (6mA) canonical eukaryotic DNA base modification present at low levels in plant and animal genomes. Here we report abundant 6mA associated with transcriptionally active fungal genes. Using single-molecule long-read sequencing, we assembled genomes and characterized methylomes of 15 species from diverse lineages across the fungal kingdom. We found heavy utilization of 6mA in early-diverging fungi where up to 2.8% of all adenines were methylated, vastly exceeding the levels observed in other eukaryotes and more derived fungi. 6mA occurred symmetrically at ApT dinucleotides, implying a methylation imprint transmissible across nuclear division. Gene promoters were particularly enriched in 6mA and ≈95% of methylated genes were expressed. 6mA congregated in dense ‘islands’ that were positioned nearby promoter thymine-blocks, suggesting a role for 6mA in nucleosome organization. Our results reinforce the importance of 6mA as an epigenomic mark in eukaryotes and suggest differential utilization of 6mA in gene regulation across kingdoms. *Poster P111*

**184. Interpopulation mating to associate the phenotype of growth at low temperature with specific genes in *Neurospora crassa* populations. \*Montoya, Liliam A.**(1), Catcheside, David(2), Ellison, Chris (3), Freitag, Michael(4), Gladieux, Pierre (5), Daskalov, Asen (1), Glass, N. Lousie(1), Taylor, John W.(1) 1. University of California, Berkeley, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA. 2. Flinders University, School of Biological Sciences, GPO Box 2100, Adelaide 5001, South Australia. 3. University of California, Berkeley, Integrative Biology, Berkeley, CA, 94720-3102, USA. 4. Oregon State University, Department of Biochemistry and Biophysics, Corvallis, OR 97331-

7305. 5. Campus International de Baillarguet, UMR BGPI, INRA, 34398 Montpellier, France. liliam.amontoya@berkeley.edu

The search for genes that have been selected to promote adaptation using a “reverse ecology” approach detects regions of high differentiation referred to as “islands” of differentiation that arise by hybridization and introgression due to the presence of adaptive genes. Ellison et al. (2011, PNAS) used this approach to make and test hypotheses about genes that promote adaptation to low temperature in populations of *Neurospora crassa* from subtropical Louisiana, where the average yearly minimum temperature is 9°C cooler than the Caribbean basin. However, the reverse ecology approach cannot be used to identify genes with more subtle signatures of selection. To find additional genes involved in adaptation to growth at low temperature, we mated strains from Louisiana and the Caribbean, selected 250 progeny, evaluated their growth at 10oC and 25oC, and sequenced the parental and progeny genomes. We now plan to associate SNPs scored in the progeny genomes with the phenotype of the ratio of growth rates at 10oC and 25oC to detect genes responsible for thermal adaptation. We then will test our hypotheses using the *Neurospora crassa* gene deletion collection. Islands of differentiation that arise by hybridization and introgression due to the presence of adaptive genes can be detected using a “reverse ecology” approach. Ellison et al. used this approach to make and test hypotheses about genes that promote adaptation to low temperature in populations of *Neurospora crassa* from subtropical Louisiana, where the average yearly minimum temperature is 9°C cooler than the Caribbean basin. Regions of high differentiation present in the two *N. crassa* populations are associated with the temperature difference between the two geographic regions. However, the reverse ecology approach cannot be used to identify genes with more subtle signatures of selection. To find additional genes involved in adaptation to growth at low temperature, we mated strains from Louisiana and the Caribbean and selected 250 progeny. We sequenced the parental and progeny genomes and evaluated their growth at 10oC and 25oC. We now plan to associate SNPs scored in the progeny genomes with the phenotype of the ratio of growth rates at 10oC and 25oC to detect genes responsible for thermal adaptation. We then will test our hypotheses using the *Neurospora crassa* gene deletion collection. *Poster P107*

**185. Genomic investigation of the *Aspergillus bombycis* type strain \*Moore, Geromy G.**, Mack, Brian M., Beltz, Shannon B.

is a non -

Southern Regional Research Center, Agricultural Research Service, USDA, New Orleans, LA, 70124, USA. geromy.moore@ars.usda.gov

*Aspergillus bombycis* is an aflatoxigenic species in Section *Flavi* that is oft misidentified because its macro-morphological characteristics and chemotype profile are very similar to other closely-related species. Only through micro-morphological examination, chemotype profiling and molecular investigations can *A. bombycis* be accurately delimited. We sequenced the genome of the Type strain (NRRL 26010) and found it to have a genome size of 37 Mb which is comparable to other sequenced Aspergilli. Venn analysis revealed the presence of 829 genes unique to *A. bombycis*. Phylogenomic analysis inferred *A. bombycis* as sharing a most recent common ancestor with *A. nomius*. An investigation of the mating-type locus revealed NRRL 26010 to be heterothallic and possessing a single *MAT1-2* idiomorph. This organism is considered an insect pathogen; in particular, of silkworms. It has not been reported as a plant or human pathogen, but its potential for misidentification may mean that *A. bombycis* is of greater pathogenic importance than previously thought. *Poster P119*

**186. Illumina sequencing reveals high levels of diversity and host specificity in communities of arbuscular mycorrhizal fungi in a threatened tropical seasonally dry forest**

\***Morgan, Benjamin**(1,2), Egerton-Warburton, Louise(1,2) 1.Chicago Botanic Garden, Plant Science, Glencoe, IL, 60022, USA; 2.Northwestern University, Plant Biology and Conservation, Evanston, IL, 60208, USA. benmorgan@u.northwestern.edu

Tropical seasonally dry forests are the most abundant tropical forests on earth, and are globally threatened by anthropogenic climate change and rapid urbanization. Arbuscular mycorrhizal fungi (AMF) are the dominant fungal symbionts of plants in these systems, and are essential drivers of plant individual fitness, community diversity, and ecosystem resilience. Despite this, the diversity, host specificity, and functional roles of AMF remain poorly resolved. In this study, we address this challenge in a Mexican tropical seasonally dry forest system by sampling AMF communities from the roots and rhizosphere soil of five ecologically important tree species (*Brosimum alicastrum*, *Bursera simaruba*, *Ceiba pentandra*, *Metopium brownei, Vachellia cornigera*) from two minimally managed sites in the Yucatan Peninsula. We adapted proven AMF-specific ribosomal small subunit primers for use with Illumina sequencing platforms, and identified 142 molecular taxa; this is one of the highest levels of AMF diversity recorded to

date. All but three were identified to genus or species level with at least 80% confidence. We also identified host-species-specific AMF communities. The majority of AMF taxa were assigned to the genus *Glomus*. However, the different tree species and sites hosted distinct AMF communities that could be distinguished by the presence and abundance of *Diversispora* species. Our results indicate that AMF communities are highly diverse and variable across this ecosystem, suggesting that AMF diversity should be accounted for in conservation and restoration efforts. Further, the methods established in this study provide an avenue for investigating major knowledge gaps in AMF host- and system-specificity, community response to anthropogenic change, and AMF phylogenetic diversity and cryptic species complexes. *Contributed Talk C17.5*

**187. Effects of temperature on carbon use efficiency of saprotrophic fungi \*Morrison, Eric W.**, Frey, Serita D. University of New Hampshire, Natural Resources and the Environment, Durham, NH, 03824, USA. eric.morrison@unh.edu

Increased temperatures are generally expected to decrease microbial carbon use efficiency (CUE), but empirical observations and theory suggest that microbial CUE will acclimate to warming over long time periods. One mechanism underlying potential acclimation is a shift in microbial community composition, wherein increased temperatures favor microbes with a lower Q10 of CUE. Acclimation of CUE through this mechanism may also result in a shift in community functioning if functional guilds of decomposers have different CUEs. Fungi are the primary decomposers of leaf litter, and different species specialize on different types of litter compounds, but potential differences in CUE of these functional guilds are largely unknown. In order to address these hypotheses, fungi were isolated from decomposing litter at the Harvard Forest LTER, Massachusetts, USA. Isolates were compared to fungal meta-barcoding data to identify species that were abundant or widespread in litter. Maximum specific growth rate and specific respiration rate were measured in order to estimate CUE. *Panellus stipticus*, *Trichoderma koningii*, and an unidentified *Ceuthospora* isolate all had decreased CUE in response to a 10°C increase in temperature, while CUE of an unidentified *Cylindrium* isolate had no response. *P. stipticus* had the lowest CUE and the lowest growth rates of all the isolates, but also had the lowest change in CUE with increased temperature where the Q10 of CUE was 0.95. The Q10 of CUE was 0.92 and 0.94 for the *Ceuthospora* isolate and *T. koningii* respectively. The basidiomycete *P. stipticus*

has the greatest potential for lignin decomposition of these species, suggesting that warming may favor species with higher ligninolytic potential. *Contributed Talk C13.7*

**188. Red-listing North American fungal species and the data we need from you!**Mueller, Gregory M.(1), Dahlberg, Anders(2), \*V**ellinga, Else C.**(3), et al.

1.Chicago Botanical Garden, 1000 Lake Cook Road, Glencoe, IL 60022, USA; 2.Swedish University of

Agricultural Sciences,

3.University Herbarium, University of California at Berkeley, CA 94320, USA.

ecvellinga@comcast.net A critical way to help politicians and citizens be

more aware of the importance of fungi and the need to conserve them, is to have fungal species included in the IUCN (International Union for Conservation of Nature) Global Red List. This list is a compilation of rigorous assessments of the extinction risk for individual species made using strict universal criteria and categories (www.iucnredlist.org). Fungi face the same threats as animals and plants: habitat loss, pollution, and climate change. However, until recently fungi were nearly absent from the IUCN red list and there are only 2 lichen-forming species on the USA Endangered Species Act, Even the protection many species in the Pacific Northwest receive under the Survey and Manage Standards and Guidelines of the Northwest Forest Plan is uncertain. Recently more than 50 species of North American mushrooms were evaluated for inclusion in the IUCN Global Red List (see http://iucn.ekoo.se/iucn/species\_list/). Many more are likely threatened, but lack critical data to be assessed. We identified a preliminary "watch list" of species that we need you to look out for. In the northeast *Boletus billieae, B. peckii*, and *B. rhodosanguineus*, *Camarophyllopsis peckiana, Caulorhiza hygrophoroides, Inocybe comatella, Naiadolina flavomerulina*, and *Stereopsis lentofragilis*; in the mid-west *Psathyrella cystidiosa,* and *Ps. rhodospora*; in the Rocky Mountains *Cercopemyces crocodilinus*, and *Laccaria pseudomontana*; in the Smoky Mountains *Cercopemyces ponderosus*, in the northwest (Alaska and British Columbia) *Lactarius cordovaensis*; and in the western states and provinces, look for *Biscogniauxia bartholomaei, Hydnellum cyanopodium, Lepiota luteophylla* and *L. rhodophylla*, pink Leptonias, and *Tubaria punicea*. This is a collaborative effort of Jean Berubé, Brenda Callan, Michael Castellano, Anders Dahlberg, Annabelle Langlois, Patrick Leacock, David Lewis, Todd Osmundson, Christian Schwarz, Noah Siegel, Rick Van de Poll, and Else Vellinga.

*Poster P13*

**189. Out of western North America: Systematics and phylogeography of *Rhizopogon* subgenus *Villosuli* based on genome-scale sequence typing \*Mujic, Alija Bajro**(1), Huang, Bo(2), Chen, Ming- Jun(2), Wang, Pi-Han(3), Gernandt, David (4), Hosaka, Kentaro (5), Spatafora, Joseph W (6). 1.University of Florida, Department of Plant Pathology, Gainesville, FL, 32611, USA; 2.Anhui Agricultural University, Hefei, Anhui, 230026, China; 3.Tunghai University, Department of Biology, Taichung City, Xitun District, 407, Taiwan; 4.National Autonomous University of Mexico, Institute of Biology, Mexico City, 04510, Mexico; 5.National Museum of Nature and Science, Department of Botany, Tsukuba, 305-0005, Japan; 6.Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, United States of America

The shared life history traits and shared distributions of ectomycorrhizal (EM) fungi and their hosts suggest that comigration and cospeciation have had an influential role in the evolution of the EM symbiosis. However, the generalist nature of many EM fungi and regional host effects upon EM community structure pose difficulties in the study of these phenomena and they have currently been documented from only a limited number of systems. In order to test the hypotheses of comigration and cospeciation between EM symbionts we have conducted a genome-scale phylogeographic analysis of host specific EM fungi in genus *Rhizopogon* that associate with trees in genus *Pseudotsuga.* Four years of multinational, intercontinental sampling efforts throughout the northern Pacific Rim have produced *Rhizopogon* samples from throughout the natural range of all *Pseudotsuga* species. We have used sthroughout our sampling range. The results of phylogenetic analysis strongly support a single evolutionary origin of the EM symbiosis between *Rhizopogon* and *Pseudotsuga* in western North America and phylogeographic trends in the distribution of *Rhizopogon* species show concordance with the population structure and species divergence events of their *Pseudotsuga* hosts. Our results support the hypothesis that the *Rhizopogon-Pseudotsuga* EM symbiosis predates species radiation in *Pseudotsuga* and that these genera have undergone processes of comigration and cospeciation. We detail the process of genome-scale sequence typing (GSST), which can be adapted for any set of taxa for which a large number of orthologous gene clusters can be identified. *Contributed Talk C3.7*

P .O. Box 7026, 750



07 UPPSALA, Sweden;



**190. Ectomycorrhizal community dynamics of Pinaceae invasions in Patagonian *Nothofagus* forests \*Mujic, Alija Bajro**(1), Policelli, Nahuel(2), Nuñez, Martin A.(2), Smith, Matthew E.(1)

1 University of Florida, Department of Plant Pathology, Gainesville, FL, 32611, United States; 2 Grupo de Ecología de Invasiones - Instituto de Investigaciones en Biodiversidad y Medio Ambiente- CONICET- Universidad Nacional del Comahue, San Carlos de Bariloche, 8400, Argentina

*Nothofagus* species are the only widespread ectomycorrhizal (ECM) host trees native to Southern South America (SSA). Invasion of ECM Pinaceae, 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 characterized the community of ECM fungi colonizing the roots of invasive Pinaceae trees in SSA and demonstrated that Pinaceae invasions in this region 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 many unpredictable effects upon the structure and composition of native *Nothofagus* ECM fungal communities. To address this concern, we have employed a metagenomic approach to characterize the fungal communities associated with *Nothofagus* rhizosphere soil in sites with Pinaceae invasions. Pinaceae invasions of *Nothofagus antarctica* and *Nothofagus dombeyi* forests were studied in the region of San Carlos de Bariloche, Argentina. *Nothofagus antarctica* is typically present in xeric sites where invasions of *Pinus contorta* are common. *Nothofagus dombe*yi is associated with mesic sites that are commonly invaded by *Pseudotsuga menziesi*i. The ITS1 region was sequenced from all fungi in the rhizosphere of *Nothofagus* species within invaded sites and along a spatial gradient into adjacent, uninvaded, *Nothofagus* stands without Pinaceae. This study characterizes the community compositional response of *Nothofagus* ECM fungi to Pinaceae invasions and helps to inform conservation efforts in SSA. This is the first data available detailing the response of native *Nothofagus* ECM fungal communities in SSA to co- invasion of Pinaceae trees and their fungal symbionts. *Poster P70*

**191. The phylogeny and trophic mode of**

***Trappeindia himalayensis***

Mujic, Alija Bajro(1), Zheng, Nan(1), Kim, Kristy(1), Castellano, Michael(2), **\*Smith, Matthew E.**(1) 1.University of Florida, Department of Plant Pathology, Gainesville FL 32611, USA; 2.United States Department of Agriculture, Forest Service,

Northern Research Station, 3200 Jefferson Way, Corvallis, OR 97331, USA. trufflesmith@ufl.edu

In the northwestern Himalayan Mountains of India, local villagers harvest a truffle-like fungus called *Trappeindia himalayensis* that fruits in coniferous forests with *Cedrus deodara.* This truffle goes by the names “Bankae” or “Janda” and is regularly consumed as food. *Trappeindia himalayensis* has unique basidiospores that are ornamented with a raised, irregular reticulation. Although *Trappeindia* is regularly collected in *Cedrus* forests, both the trophic mode and phylogenetic affinity of this fungus are currently unresolved. According to the original description, the gleba color and texture suggest a taxonomic affinity with *Scleroderma* (Boletales) whereas the spores are more similar to those of *Leucogaster* (Russulales) or *Strobilomyces* (Boletales). We generated the first molecular data for this unusual, *Cedrus-*associated truffle in order to clarify its phylogenetic affinities and ecology. Our analyses based on multiple DNA loci suggest that that *Trappeindia* is nested within the *Suillus*-*Rhizopogon* lineage of the Boletales and is an ectomycorrhizal symbiont of *Cedrus*. *Poster P8*

**192. Comparative genomics and the evolution of virulence in dimorphic human pathogenic fungi from the Ajellomycetaceae**Muñoz, José F.(1,2), Young, Sarah(3), **\*McEwen, Juan G.**(1,4), Clay, Oliver K.(1,5), Cuomo, Christina A.(3)

1.Corporación para Investigaciones Biológicas, Cellular and Molecular Biology Unit, Medellín, Colombia. 2.Universidad de Antioquia, Institute of Biology, Medellín, Colombia. 3.Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA. 4.Universidad de Antioquia, School of Medicine, Medellín, Colombia. 5.Universidad del Rosario, School of Medicine and Health Sciences, Bogotá, Colombia. mcewen@une.net.co

The Ajellomycetaceae family includes several of the dimorphic human pathogenic fungi such as *Paracoccidioides*, *Blastomyces* and *Histoplasma*. Related genera less commonly observed or studied within or at the fringes of the same family are *Emmonsia*, *Polytolypa* and *Spiromastix.* Although these fungi are from the same family they are categorized as very rarely causing disease in humans or even non-pathogenic. Considering the evolutionary proximity of these fungi we sequenced the genomes of *Emmonsia*, *Polytolypa* and *Spiromastix*, and then performed comparative genomic analyses in order to find relevant functional differences at the genome level that could explain the pathogenicity and virulence of the dimorphic pathogens. We sequenced,

assembled, and annotated for the first time the genomes of three *Emmonsia* species, *P. hystricis* and *S. grisea*. The inclusion of these species allowed us to perform more precise comparative analyses of the Ajellomycetaceae family, i.e., of these typically non- pathogenic fungi together with the genomes of the well-known dimorphic human pathogenic fungi. Here we present results of our NGS sequencing, *de novo* assembly, annotation and genomic analyses of *Emmonsia*, *Polytolypa* and *Spiromastix*. Comparative analyses of these fungi with the dimorphic human pathogens identified patterns of gene conservation, protein family evolution and genomic features correlated with virulence. Our comparative study provided insight into the pathogenesis and life cycles of the dimorphic human pathogenic fungi.

*Poster P112*

**193. Mycoviruses in early-diverging fungi Myers, Jillian\***, James, Timothy University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, Michigan, 48109- 1048, USA. jimyers@umich.edu

Mycoviruses are hypothesized to be of ancient origin and to have coevolved with their hosts by vertical transmission. Infected fungi usually lack disease symptoms, which supports this hypothesis since vertical transmission should select for avirulence. However, further insights are limited by the lack of sampling of mycoviruses infecting fungal lineages diverging prior to the Dikarya. To address this, we are conducting mass screenings of fungi in early-diverging lineages and will sequence the genomes of novel mycoviruses discovered. Thus far we have found persistent dsRNA viruses in fungi in *Chytridiomycota* and *Blastocladiomycota*. Future work aims to further describe the coevolutionary relationship between mycoviruses and fungi, and assess mycoviral impacts on hosts. *Poster P66*

**194. Thermophilic fungi in 2016: The Emerson legacy \*Natvig, Donald O.**(1), Hutchinson, Miriam I.(1), Powell, Amy J.(2), Porras-Alfaro, Andrea(3) 1.University of New Mexico, Department of Biology, Albuquerque, NM, 87131, USA; 2.Sandia National Laboratories, Albuquerque, NM, USA, 87123; 3.Western Illinois University, Department of Biological Sciences, Macomb, IL, 61455, USA. dnatvig@gmail.com

Although thermophilic fungi were described by Lindt and Miehe in the late 19th and early 20th centuries, fungal thermophily was largely ignored prior to WWII. In the mid 1940s this situation changed when Ralph Emerson was recruited to

support microbial studies associated with the USDA Guayule Rubber Extraction Research Unit in Salinas, CA. The effort to develop the aridland shrub guayule (*Parthenium argentatum*) for rubber production arose when the United States lost access to *Hevea* rubber supply chains from Asian plantations. One process for extracting rubber from guayule began with a partial microbial deconstruction step (retting) that was accompanied by substantial thermogenensis (up to 60 ̊C). The characterization of the organisms involved in retting led to Emerson’s rediscovery of fungal thermophiles, and it ultimately resulted in the description of new species and the detailed characterization of thermophile growth and physiology (see *Thermophilic Fungi*, D.G. Cooney and R. Emerson, Freeman and Company, 1964). Thermophilic fungi now receive substantial attention in academic and industrial realms. Several patents exist for processes related to carbohydrate active enzymes, and at least two species have central roles in commercial processes. In the past decade our laboratories have engaged in studies designed to explore the distribution of thermophilic fungi in natural and agricultural environments, develop genetic models for research, characterize genomes of diverse species, and solve taxonomic problems within certain groups. This talk will highlight our recent efforts and discuss our results in the context of Ralph Emerson’s pioneering work.

*Contributed Talk C21.3*

**195. Seasonal variation of dark septate fungi in an arid grassland and their potential roles on plant growth \*Ndinga Muniania, Cedric**(1), Sandona Katrina(1), Belnap Jayne(3), Reed Sasha(3), Muller Rebecca(3), Kuske Cheryl R.(2), Porras-Alfaro Andrea(1) 1.Western Illinois University, Biological Science, Macomb, IL, 61455, USA; 2. Los Alamos National Lab, Environmental Microbiology, Los Alamos, NM, 87545, USA; 3. US Geological Survey, Climate Variability & Change, Moab, UT, 84532, USA. C- NdingaMuniania@wiu.edu

The high temperatures and long extended drought periods in arid ecosystems promote the colonization of diverse microenvironments by dominant communities of dark septate fungi (DSF). Due to their abundance, DSF are likely to contribute to soil nutrient cycling, soil stabilization, and plant survival under these stressful conditions, but the role of DSF and their diversity are still poorly understood. We collected soil and isolated fungi from different microenvironments in an arid grassland near Moab, UT. The biocrust fungi were isolated from and below lichen-, moss-, and cyanobacteria-dominated biocrusts, and rhizosphere soils were collected from two plants: the

exotic invasive *Bromus tectorum* and the native *Pleuraphis jamesii.* Fungi were isolated using a serial dilution technique and identified using ITS rRNA sequencing. Seasonal variation of DSF was evaluated using culture-based approaches and compared with fungal community profiles from Illumina sequencing. Our imaging pigment analysis revealed that DSF were more abundant in biocrusts compared to the plant rhizosphere and showed differences in colonization rates by season, with an increase in the rhizosphere and below biocrust samples during the summer months. Trends seen in culture data were confirmed with the analysis of Illumina data, which showed an increase in abundance of dark septate fungi (e.g., *Alternaria* and *Phoma)* in the rhizosphere and below biocrust soil during the summer months. From the 813 fungi isolated, Pleosporales was the dominant order in both biocrust and rhizosphere soil. The most dominant DSF genera included *Alternaria, Preussia, Cladosporium, Phoma,* and unknown Pleosporales*.* Seed germination experiments using dominant taxa were conducted in corn and soybean to determine their potential roles on plant growth. *Cladosporium* and *Alternaria* in particular, showed growth promoting ability, stimulating root production and stem elongation. This variation in abundance and colonization of DSF could reflect an adaptation to summer environmental conditions, as well as potential plant demand when heat and drought conditions are high.

*Contributed Talk C12.7*

**196. Investigation of the distribution and composition of nectar-dwelling yeast and bacteria communities in flowering plants in Northeastern Wisconsin**

**\*Nellis, Samantha E.**, Grubisha, Lisa C., Moyer, Joshua R., Wolf, Amy T. University of Wisconsin-Green Bay, Natural and Applied Sciences, Green Bay, WI, 54311, USA. nellse09@uwgb.edu

Many studies have examined the relationship between plants and pollinators, yet little is known about the third party species that take advantage of this mutualism. Nectar-dwelling yeast and bacteria have been shown to be pervasive and at times abundant in several plant species. This study aims to gain a better understanding of the role of microorganisms in the nectar of five flowering species growing in Northeast Wisconsin. A common theory is that visiting pollinators transport microorganisms to the initially sterile nectar. To test this hypothesis, selected flowers were bagged prior to opening with a fine mesh bag to exclude pollinator species but allow rain, wind and sunlight exposure. Nectar samples from the “bagged” flowers were acquired as well as nectar from nearby

open (not bagged) flowers. To assess the composition of these communities, DNA was isolated from the nectar, amplified via PCR (ITS1 and the V4 16S region for yeast and bacteria, respectively) and sequenced using the Illumina MISeq platform. Bacteria and yeast will be identified to the genus or species level using BLAST searches of the GenBank sequencing database. Additionally, the flower density of individual field plots was measured and sub-meter GPS coordinates were taken for each sample to assess spatial limitations of dispersal. Nectar samples were collected throughout the flowering season of each species, which may allow us to uncover temporal trends within the nectar community. Finally, the sugar composition (proportion of sucrose, fructose and glucose) of each sample will be determined using high-performance liquid chromatography to assess changes to the pollinator reward caused by the bacteria and yeast species. Results will contribute new knowledge to the current understanding of nectar- dwelling microbial communities, their distribution, diversity, dispersal limitations and effect on the plant- pollinator mutualism.

*Poster P37*

**197. Fungal endophytes of the liverwort**

***Marchantia polymorpha***

**\*Nelson, Jessica**

Duke University, Department of Biology, Durham, NC, 27707, USA. jmn31@duke.edu

Plant-fungal symbioses are ancient and are thought to have facilitated the initial colonization of land by plant ancestors. In modern ecosystems, plants harbor diverse communities of microbial endophytes, including fungi, inside their healthy tissues. Fungal endophyte communities have been found to be hyperdiverse and include members from the Ascomycota, Basidiomycota, Glomeromycota, and Mucoromycotina. From studies of angiosperm fungal endophytes, we know they can affect plant success by improving plant growth, competitiveness, disease resistance, or tolerance of abiotic stress conditions. Studying bryophyte (moss, liverwort, and hornwort) endophyte communities provides an evolutionarily significant comparison to Tracheophyte models. The liverwort *Marchantia polymorpha* provides an useful model for studying the impacts of such fungal associations not only because of its early-branching position in land plant evolution and hypothesized similarity of structure to early land plants, but also because of its production of asexual propagules that can be axenically cultivated. Using *M. polymorpha*, I have developed a system for testing the effects of culturable endophytic fungi in liverworts. I have isolated fungal cultures from surface-sterilized tissues of *M. polymorpha* collected from the eastern and

northwestern United States and established axenic cultures of the liverwort. I have tested the effects of each of 100 isolated Ascomycete fungi on growth of axenic clones of *M. polymorpha* under controlled laboratory conditions. I have observed positive, negative, and neutral effects, ranging from lethal fungi to ones that strongly enhance plant growth. Mapping these effects onto a fungal phylogeny has begun to reveal that, at least under laboratory conditions, some fungi known as pathogens in angiosperms may be commensal or even beneficial partners to *M. polymorpha* and that closely related fungi can have very different effects on their liverwort host. *Contributed Talk C9.5*

**199. Improving support for molecular identification of the built mycobiome \*Nilsson, R. Henrik**(1), Abarenkov, Kessy (2), Kõljalg, Urmas (2), Taylor, Andy (3)

1.University of Gothenburg, Sweden; 2. University of Tartu, Estonia; 3. University of Aberdeen, Scotland. *henrik.nilsson@bioenv.gu.se*

There are many reasons why the built mycobiome, much like fungi at large, is not easy to characterize using molecular methods. There is no reference DNA sequence for the majority of the described fungal species, and the vast majority of extant fungal species are not described to begin with. Public sequences from the built environment are not always annotated in a way that invites further scrutiny and promotes dissemination of results and findings. In the context of an Alfred P. Sloan Foundation grant to the UNITE database to improve the support for molecular identification of fungi from the built environment, this presentation will go through the main goals of the project: 1) sequence and release the ITS and LSU regions from type material relevant to the built environment; 2) organize two workshops to improve taxonomic and metadata annotations of sequences from the built environment; and 3) improve support for the built environment in the UNITE database, for example by integrating the new MIxS- BE standard and by highlighting fungal lineages in particular need of taxonomic scrutiny. All data and results from the project will be shared with the mycological community in an open and timely way. The presentation will also include preliminary results from the sequence metadata annotation workshop held in May 2016 at the University of Gothenburg. *Symposium S4.3*

**200. Assessment of the diversity of endophytic fungi in green and red senescent needles of whitebark pine (*Pinus albicaulis*) in Montana** \***Noffsinger, Chance R.(**1), Cripps, Cathy L.(1)

1.Montana State University, Plant Sciences and Plant Pathology, Bozeman, MT, 59717, USA. chancenoff@gmail.com

Endophytic fungi can be defined as living within a plant for at least part of their life cycle without causing apparent disease, and some are considered mutualistic. A few have been shown to induce resistance to pathogens in the host. More specifically, it has been postulated that fungal endophytes might induce resistance to white pine blister rust (*Cronartium ribicola*), a pathogen partially responsible for the massive destruction of whitebark pine (*Pinus albicaulis*) in western North America. This species is endangered in Canada and awaits this status in the U.S.; however, little is known about the endophytes in whitebark pine. This project compared the diversity of endophytes in green and red needles to 1) determine if endophytes are present and 2) if the fungal community changes on needle senescence. Red and green needles were sampled from twenty mature whitebark pine trees across four high elevation treeline sites in southwestern Montana. To determine the most effective method of fungal isolation, needles were surface sterilized using either a ‘flame’ or ‘soak’ method and plated onto PDA agar media. Only the ‘soak’ method was analyzed quantitatively as a significantly higher number of endophytes were isolated. In this study 18 morphologically distinct cultures (OTUs) were identified. On average there were 0.8 and 1.8 isolates per needle in green and red respectively. Three of the OTU’s were observed in both red and green needles; there appeared to be little overlap in OTUs among sites. One exception is OTU 7, which appeared in red needles at every site. This Isolate also appeared to be a common transitional fungus, and could play an important role in eliminating dead or parasitic needles. The ITS region will be sequenced for all OTUs. This research provides insight into the diversity of endophytes in whitebark pine and results could lead towards application of endophytes to nursery seedlings as a possible defense against rust or the mountain pine beetle. *Poster P27*

**201. Cryptic milkcap species in Europe unmasked \*Nuytinck, Jorinde**(1), Bafort, Quinten(2), Verbeken, Annemieke (2), Eberhardt, Ursula(3) 1.Naturalis Biodiversity Center, Understanding Evolution, Leiden, 2300 RA, The Netherlands; 2.Ghent University, Department of Biology, Ghent, 9000, Belgium; 3.Staatliches Museum f. Naturkunde, Abt. Botanik, Stuttgart, 70191, Germany. jorinde.nuytinck@naturalis.nl

The genus *Lactarius* (the milkcaps p.p.) has a large economic and ecological importance due to its

culinary value and widespread and dominant ectomycorrhizal associations. This study tries to gain insight in species delimitation and the recovery of those species by barcode based species delimitation methods. Although *Lactarius* species are easily recognized as a milkcap in the field, identification at species level is often much harder due to overlap in macro-morphology and the subtle nature of some morphological differences. The first objective of this study is to identify and describe cryptic *Lactarius* species in the Western Palearctic. Starting from a comprehensive dataset containing ITS sequences of all known European species, additional *rpb1* and *rpb2* sequences and the prevailing morphological and ecological species concepts, discordant patterns between morphological and phylogenetic species are identified. Three types of discordant patterns and an additional problematic species category are distinguished. Morphologically cryptic species are subsequently studied in an integrative taxonomical framework combining traditional characters and molecular evidence obtained from genealogical concordance between three molecular markers and Bayesian species delimitation. A new method to analyze the DNA sequence chromatograms is used that allows to resolve ambiguity due to intragenomic ITS polymorphisms and to obtain different haplotypes within the same individual (phasing). This increases the resolution of the ITS region for species delimitation purposes. Secondly, the results of this integrative taxonomical study were used to test the performance of commonly used barcode based species delimitation or OTU picking methods. Although these methods have the potential to delimit a large proportion of the species correctly, their success is highly dependent the dataset used, the quality of the input tree, and the largely arbitrary choice of the setting.

*Contributed Talk C18.5*

**202. Three dimensional wood decay community interactions**O’Leary, Jade(1), Müller, Carsten(1), Eastwood, Dan(2), **\*Boddy, Lynne(1)**

1.Cardiff University, School of Biosciences, Cardiff CF10 3AX, UK; 2.Swansea University, Biosciences. BoddyL@cf.ac.uk

Wood decay is brought about by a community of fungi which interact antagonistically with each other, causing the community composition to change. In the past, these interactions have usually been studied by pairing fungi in different combinations, but this is unrepresentative of the real world, where many fungi interact simultaneously. This project, therefore, has simulated multiple interactions in 3 dimensions, by constructing 3x3x3 “Rubik’s cube” configured

systems from 2x2x2 cm3 wood (*Fagus sylvatica*) blocks pre-colonised with individual fungi, as well as pair-wise interactions, 2-dimensional linear three-way interactions and more complex 9-block interactions for comparison. By carrying out destructive sampling of interactions to determine which fungi were replaced by others, the orientation of xylem vessels and the spatial distribution of fungi within systems were found to be major determinants of the defensive abilities of fungi. Additionally, systems were sampled over 3 time points to assess the implications of combative interactions to the community over time. Despite hierarchal orders to the combative success of individual fungi within the competing community, individual combative abilities changed over time. The use of 3-dimenional decay systems in this study highlights the difficulties of effective study of these organisms in the 2-dimensional systems commonly used in the past, due to the dynamic nature and complexity of multiple species interactions within ecologically relevant multi-dimensional systems. *Poster P50*

**203. Distinct microbial community in root and soil associated with the fairy ring of *Tricholoma matsutake* (pine mushroom) \*Oh, Seung-Yoon**, Lim, Young Woon

Seoul National University, School of Biological Sciences, Seoul, 08826, Republic of Korea. syoh@snu.ac.kr

*Tricholoma matsutake* is expensive mushroom because of pine-like aroma and unculturable state. Ecologically, *T. matsutake* forms ectomycorrhizal relationships primarily with trees in the genus *Pinus*. From ectomycorrhiza of *T. matsutake*, extraradical mycelia extend and form soil-hyphal aggregating structure called fairy ring (shiro). Previous studies showed that microbial community in the soil of fairy ring of *T. matsutake* was different compared to it of adjacent soil. However, microbial community in the root of *Pinus densiflora* colonized with *T. matsutake* is largely unknown. Using Illumina Miseq platform, we investigated microbial community in the root and soil around the fairy ring of *T. matsutake*. Microbial community in the root showed different structure compared to it in soil. Similar to previous study about soil microbial community in fairy ring, root microbial community in the fairy ring was different from it in non-fairy ring. In addition, some fungi (*e.g. Umbelopsis*) and bacteria (*e.g. Burkholderia*) showed significant enrichment in the fairy ring*.* Overall, the root and soil in the fairy ring of *T. matsutake* have distinct microbial community, and it may indicate close relationship between *T. matsutake* and the specific microbial organisms. *Contributed Talk C17.7*

**204. Experimental drought and soil depth interactively influence fungal community composition in piñon-juniper woodland**Olivas, E, Pockman, William T., Pangle, Robert E., **\*Taylor, D. Lee**

University of New Mexico, Department of Biology, Albuquerque, NM 87131, USA. fflt@unm.edu

Changes in the structure of mycorrhizal communities due to disturbances such as fire or drought likely influence post-disturbance vegetation dynamics. However, such microbial legacies are understudied empirically and have yet to be incorporated into vegetation models. Climate change models predict increasing intensity and duration of drought events in aridlands globally. Disturbance intensity is mediated by soil depth, but fungal responses to drought across depths have not been studied. We tested the potential for mycorrhizal legacies following drought by sampling soils from a long-term moisture manipulation experiment in piñon- juniper woodlands within the Sevilleta LTER site in New Mexico. Fungal community composition at two soil depths was compared in irrigated, control and drought plots using Illumina ITS amplicon sequencing. Bioinformatics utilized a mock community, QIIME and FUNGUILD. We found that surface soils had higher fungal diversity but much lower abundances of ectomycorrhizal taxa than did deep soils (20 cm depth). The drought treatment caused 18-36% declines in fungal species richness in surface and deep soils, respectively. Moreover, the drought treatment caused a significant shift in community composition (perMANOV A, surface: *p*=0.0001, *F*=5.734; deep: *p*=0.001, *F*=11.832) and a decline in relative abundance of ectomycorrhizal taxa relative to paired control plots (Wilcoxon rank test *p*=0.04934, *W*=30). SIMPER analyses revealed that the most responsive species were primarily ectomycorrhizal taxa, with an array of basidiomycete taxa essentially disappearing under drought. Because these shifts were most pronounced in the plots with highest tree mortality, we speculate that death of host piñon pines had a larger impact on the fungal community than did direct effects of soil moisture deficit. Our results suggest that piñon regeneration following drought may be delayed due to loss of ectomycorrhizal fungi in a depth and habitat- dependent fashion.

*Contributed Talk C5.3*

**205. Community diversity and structure of foliar fungal endophytes across landscapes and within individual leaves \*Oono, Ryoko**(1), Rasmussen, Anna(1), Lefèvre, Emilie(2)

1. University of California, Department of Ecology, Evolution, and Marine Biology, Santa Barbara, CA, 93106 USA; 2. Duke University, Department of Civil and Environmental Engineering, Durham, NC, 27708 USA. ryoko.oono@lifesci.ucsb.edu

Fungal endophytes living inside tissues of woody plants are incredibly species rich and phylogenetically diverse even within a single leaf. The community assembly and structure of foliar fungal endophytes have been shown to depend on host taxa and climate, but there is relatively little known how they change at different spatial scales. Understanding the factors driving fungal endophyte beta-diversity yields insights into mechanisms underlying their high species diversity. This study presents data on foliar fungal endophytes associated with the globally-distributed plant genus*, Pinus.* In particular, we have used the widespread loblolly pine, *Pinus taeda*, as a model to explore how beta-diversity of fungal endophytes varies over different spatial scales, across landscapes and within individual leaves. We find a relationship with geographic distance (across landscapes without major climatic changes) and community similarity, but this relationship depends on scale as well as continuity of the landscape. Furthermore, communities of abundant and rare endophyte species behave differently at different spatial scales. The results highlight the importance of considering multiple spatial scales, taxon abundance data, and sufficient sample size for understanding microbial biogeography. *Contributed Talk C9.1*

**206. Species pools and dark diversity of arbuscular mycorrhizal fungi \*Öpik, Maarja**University of Tartu, 40 Lai Street, 51005 Tartu, Estonia. Maarja.opik@ut.ee

Understanding about the global biodiversity of Glomeromycota (arbuscular mycorrhizal fungi, AMF) and its patterns has considerably improved in recent years. Evidence on low global scale endemism of AMF and environmental and spatial factors shaping the diversity patterns at local scale raise further questions on the roles of factors that may influence AMF communities at different spatial scales: rate of speciation, dispersal properties, abiotic and biotic filtering. Namely, do AMF have species pools – sets of species adapted to specific conditions? If they do, what determines the species pool size? What is the relationship of observed diversity and potential available diversity (species pool) and what determines the size of dark (potential, but missing) diversity? In my presentation I intend to shed light on the recently gained understanding regarding these questions and illustrate how consideration of species pools and dark



diversity is informative when studying communities of AMF. *Symposium S10.3*



**207. Host and geographical distance effects on leaf- associated fungal community structure: Implications for biodiversity estimation in a tropical Pacific island ecosystem**

**\*Osmundson, Todd W.**(1), Bergemann, Sarah E.(2); Garbelotto, Matteo(3) 1.University of Wisconsin–La Crosse, Department of Biology, La Crosse, WI, 54601, USA.; 2.Middle Tennessee State University, Department of Biology, Murfreesboro, Tennessee, 37132, USA.; 3.University of California, Department of Environmental Science, Policy and Management, Berkeley, CA, 94720, USA. tosmundson@uwlax.edu

Estimating biodiversity for highly diverse and/or poorly known organismal groups such as fungi requires extrapolation from local estimates of species richness. The degree and scale of heterogeneity of species assemblages strongly affect the accuracy of these extrapolated values. As part of an effort to characterize fungal diversity on the French Polynesian island of Moorea, we conducted three studies examining the relationship between host diversity and/or geographical distance and community richness of leaf-associated (endophytic and phyllosphere- inhabiting) fungi, using culture-independent methods. In the first study – a comparison of three dominant canopy tree species – a mean of 69.3% of operational taxonomic units were found to be unique to each host; no overlapping fungal OTUs were observed between leaf and wood samples. The second study examined leaf-associated fungi on the invasive plant *Miconia calvescens* along an elevational gradient. Significant differences in fungal community structure correlated to differences in elevation; furthermore, these differences correlated to different degrees of *in vitro* antagonism of isolated endophytic fungi to a biocontrol fungus introduced to counteract *M. calvescens* invasion. A third study examined both host and geographical effects on fungal community diversity by surveying entire plant communities within lowland forest plots situated at various points throughout the island, using high-throughput DNA sequencing; data analysis is currently in progress. Results of these studies thus far suggest a strong host effect on leaf-associated fungal community structure; geographical effects appear to be less important within a similar habitat or climate (within the limited area of the island), but are significant across elevational and/or environmental gradients. *Contributed Talk C20.6*

**208. Shining light on white-nose syndrome: Comparative genomics of *Pseudogymnoascus destructans* reveals an evolutionary history of pathogenesis and sensitivity to ultra-violet light \*Palmer, Jonathan M.**(1), Drees, Kevin P.(2), Linder, Daniel L.(1), and Foster, Jeffrey T.(2)

1. US Forest Service, Northern Research Station, Center for Forest Mycology Research, Madison, WI, 53726 USA; 2. University of New Hampshire, Department of Molecular, Cellular, and Biomedical Sciences, Durham, New Hampshire, USA. jmpalmer@fs.fed.us

Little is known about the biology or ecology of *Pseudogymnoascus destructans,* the fungus causing white-nose syndrome (WNS) of bats. Here we sequenced, assembled, and annotated the genomes of *P. destructans,* as well as six closely-related *Pseudogymnoascus* species not known to be pathogenic. Our analyses identified 3,827 single-copy orthologous genes found in seven of the *Pseudogymnoascus* species, indicating that a large number of protein-coding genes are shared among these members of the Pseudeurotiaceae. *Pseudogymnoascus destructans* contains 1,760 unique proteins absent from the non-pathogenic species, and, conversely, there are 978 proteins absent in *P. destructans* that are conserved in the other six species. The genome of *P. destructans* contains less than 50% of the carbohydrate utilizing enzymes (CAZYmes) present in the non-pathogenic *Pseudogymnoascus* species and this reduction in CAZYmes correlated with reduced saprobic growth when tested on 190 different carbon sources. Additionally, the *P . destructans* genome contains nearly 50% reduction in secreted proteins, a characteristic shared with other mammalian fungal pathogens. Targeted re-sequencing of isolates of *P. destructans* from the two mating types (*MAT1-1* and *MAT1-2*) uncovered a 50 kb inversion surrounding the mating type locus that results in substantial variation in the genes associated with the mating type locus. Further investigation into the functional consequences associated with divergence between the two mating types led to the serendipitous discovery that *P. destructans* is missing a key DNA endonuclease involved in repair of UV-induced DNA damage, which renders the fungus extremely sensitive to UV light. Sensitivity to UV light is a potential “Achilles Heel” that could be exploited for management of WNS. Taken together, these data suggest a long evolutionary history of pathogenicity of *P. destructans* on bats and provides a framework for understanding the genetics of pathogenicity of WNS. *Symposium S8.4*

**209. Diversity and community distribution pattern of marine-derived *Penicillium* in the intertidal zone of Korea**Park, Myung Soo(1), **\*Oh, Seung-Yoon**(1), Lee, Seobihn(1), Lim, Young Woon(1)

1. Seoul National University, School of Biological Sciences, Seoul, 08826, Republic of Korea. syoh@snu.ac.kr

*Penicillium* is important fungal genus because it secretes numerous bioactive compounds (*e.g.* Penicillin). *Penicillium* species lives diverse environment such as soil, plant, indoor, and marine. Recently, marine-derived *Penicillium* has been received great attention because novel bioactive compounds are largely found from marine-derived *Penicillium.* Although *Penicillium* is one of the commonly isolated genus in the intertidal zone in Korea, little of the diversity and community distribution of *Penicillium* in the intertidal zone are known. Using Illumina Miseq platform, we investigated diversity and community distribution pattern of marine-derived *Penicillium* from tidal flat and sea sand during winter and summer seasons. For increasing sequencing depth and precise identification, *Penicillium* specific primers for beta tubulin were used for PCR amplification. A total of 73 *Penicillium* species were detected from tidal flat and sea sand. The most frequently observed species was *P. antarcticum*, followed by *P. koreense*, *P. crustosum*, and *P. brevicompactum*. Diversity of *Penicillium* was high in winter and in western sea compared to it in summer and in southern sea, respectively. Community structure was significantly different by season and sea side. Therefore, diverse *Penicillium* species live in intertidal zone of Korea, and may play important ecological roles such as decomposers in marine environments. *Poster P88*

**210. A new species of *Bannoa* from the Island of Guam \*Parra, Pedro Pablo,** Aime, M. Catherine Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN 47907, USA. pparragi@purdue.edu

The Cystobasidiomycetes is mostly comprised of pink colored yeast-like fungi with mycoparasitic characteristics in three orders: Cystobasidiales, Erythrobasidiales and Naohideales. The genus *Bannoa* in the Erythrobasidiales consists of four described species: *B. hahajimensis, B, bischofiae, B. syzygii* and *B. ogasawarensis*. In this study we present molecular and morphological data for a new species of *Bannoa* collected on the south pacific island of Guam. Eight isolates were obtained from the phylloplane of plants in the Poaceae and Asteraceae across the island. Single

cell cultures were obtained and cultured on Yeast Malt (YM) broth and YM agar for morphological characterization. Assimilation of carbon and nitrogen compounds as well as fermentation ability was assessed. For phylogenetic analysis, rDNA ITS and LSU regions were amplified with primers ITS1F/ITS4 and LROR/LR5, respectively, and sequences were analyzed with RAxML. Additionally, mating experiments were performed by pairing strains in all possible combinations (28) on yeast carbon base and corn meal agar under different temperature and light growth regimes. After 7 days in YM broth uninucleate cells are ellipsoidal to narrowly ellipsoidal (6.31–8.32 X 2.8–4.23 μm). On YM agar colonies are smooth and glistering, butyrous in texture and light red in color after 7 days. Monopolar and bipolar budding was observed. Assimilation of galactitol, galactose, soluble starch, melibiose and D-glucose is variable, L-lysine is positive and D-tryptophan assimilation is variable. Fermentation is absent. Clamp connections and basidia were observed in one cross 42 days after pairing in darkness. Mating was not evidenced in experiments incubated under other culture conditions. Phylogenetic reconstruction places *B. hahajimensis* as sister species of the new species of *Bannoa*.

*Poster P9*

**211. Dispersal influences fungal biodiversity at multiple spatial and genetic scales \*Peay, Kabir G.**(1), Talbot, Jennifer M.(2), Branco, Sara(3), Glassman, Sydney I.(4), Taylor, John W.(4), Vilgalys, Rytas(5), Bruns, Thomas D.(4)

1.Stanford University, Department of Biology, Stanford, CA, 94305, USA; 2. Boston University, Department of Biology, Boston, MA, 02215, USA; 3. University of Paris, Sud, Departement Genetique et Ecologie Evolutives, Orsay, 91405, France; 4. University of California, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA; 5.Duke University, Department of Biology, Durham, NC, 27708, USA. kpeay@stanford.edu

Early biologists thought that distributions of fungi were not constrained by dispersal. As a result, fungi were thought to exhibit no interesting biogeographic patterns, and spatial patterns in diversity were thought to reflect primarily features of the local environment. However, improvements in DNA sequencing have enabled much more accurate quantification of fungal biodiversity, and recent studies based on these techniques have revealed much spatial variability in fungal biodiversity and community structure than previously expected. These results have also raised new questions about the ecological and evolutionary mechanisms generating and maintaining such high levels of diversity. In this talk we will review evidence that dispersal is one of the critical ecological and

evolutionary processes impacting fungal biodiversity. We will show that dispersal influences fungal biodiversity at a range of spatial scales, from single roots systems, to landscapes, to the North American continent. We will examine these results from the perspective of multiple dimensions of biodiversity, including species numbers (richness or alpha- diversity), changes in community composition (beta- diversity), and how these dimensions of taxonomic diversity are linked to the functional and phylogenetic composition of fungal communities. While fungi are prolific dispersers, the accumulation of evidence from molecular studies of fungal biodiversity suggests that the unlimited dispersal paradigm is incorrect, and that only by taking dispersal into account can we adequately explain patterns of fungal biodiversity at multiple spatial and genetic scales.

*Symposium S1.2*

**212. Large-scale insect outbreak homogenizes the spatial structure of soil fungal communities \*Pec, Gregory J.**, Cahill, Jr., James F. University of Alberta, Department of Biological Sciences, B717a, Biological Sciences Building, Edmonton, Alberta, T6G 2E9, Canada. gpec@ualberta.ca

The recent mountain pine beetle (*Dendroctonus ponderosae*) outbreak has disturbed pine-dominated landscapes across western North America with dramatic implications for soil communities. The underlying mechanisms that drive the spatial patterning of these soil communities, particularly for ectomycorrhizal and saprotrophic fungi in pine forests, are complex and often intertwined. Critical to enhancing understanding will be disentangling the degree to which spatial structure varies between these two groups of soil fungal communities and how these patterns may be driven by the relative importance of host tree mortality from changes in soil conditions following tree death. Here, we use a gradient of mountain pine beetle induced tree mortality across eleven stands in lodgepole pine (*Pinus contorta*) forests of western Canada to investigate what environmental factors determine the spatial structure of soil fungal communities and how these spatial patterns may vary following a large-scale biotic disturbance. We found that the spatial structuring of both groups of soil fungal communities was influenced by tree mortality, variation in aboveground understory productivity, and soil moisture. Communities of ectomycorrhizal and saprotrophic fungi became more similar with increased tree death as rare fungal OTUs disappeared in severely beetle-killed stands. Productivity of aboveground understory vegetation and soil moisture availability, which increased along the same gradient of tree mortality, also had a strong

impact on both groups of soil fungal communities. Together, our results demonstrate that although ectomycorrhizal and saprotrophic fungi vary based on their trophic lifestyle, large-scale biotic disturbance essentially homogenizes the spatial patterning for both groups of soil communities by similar underlying environmental factors.

*Contributed Talk C13.2*

**213. Genetic diversity of *Talaromyces* species isolated from maize in North America. \*Peterson, Stephen**USDA-Agricultural Research Service, Mycotoxin Prevention and Applied Microbiology Research Unit, 1815 North University Street, Peoria, IL 61604 USA. Stephen.Peterson@ars.usda.gov

*Talaromyces* species isolated from maize in the US, primarily between 1970 and 2014 were grown up from lyophilized storage to identify potential seed endophytes. These isolates had been predominantly identified as *Penicillium funiculosum* following the taxonomic system of Raper & Thom (1949), although a large number were also identified as *P. wortmannii, P . variabile, P . diversum, P . pinophilum, P . vermiculatum, T. flavus* and *T. purpurogenus*. Sequence analysis of the maize isolates revealed significant undescribed genetic and taxonomic diversity. The ability of some *Talaromyces* isolates to inhibit the growth of other, sometimes pathogenic, fungi have been described. We are interested in the potential inhibition of the toxin producing *Fusarium verticillioides* growing in maize. Laboratory interaction assays revealed that some *Talaromyces* species inhibit the growth of *Fusarium graminearum* and *F. verticillioides* in vivo. Field tests showed reduction of fumonisin contamination of maize in test plots inoculated with certain *Talaromyces* isolates. The nature of the *Talaromyces* and *Fusarium* interaction is being further studied to reveal how the inhibition functions, trying to find ways to implement this phenomenon in field settings and reduce the fumonisin burden in maize. *Poster P123*

**214. New species of sequestrate fungi from the Transmexican Volcanic Belt \*Piña Páez, Carolina**(1), Castellano, Michael A.(2), Garibay-Orijel, Roberto(1)

1. Universidad Nacional Autónoma de México, Instituto de Biología, México; 2.U.S. Department of Agriculture, Forest Service, Northern Research Station, Forestry Sciences Laboratory, Corvallis, Oregon, 97331. carolina.ppaez@gmail.com

This taxonomic study was conducted with the purpose of contributing to the knowledge of the diversity and distribution of sequestrate fungi within

the Trans-Mexican Volcanic Belt (TMVB) in pine, fir and oak forests. Historically, research on Mexican sequestrate fungi has been limited and little is known about their diversity, ecology or mycophagy partners. To date there are 23 reports that include records of sequestrate fungi from Mexico; unfortunately the majority of these were opportunistic collections where the original objective focused on other groups of fungi. The general objective of this project was to describe the diversity of species of sequestrate fungi along the TMVB. Collections were found in seven sites, including a Biosphere Reserve (Los Volcanes), 5 National Parks (Cumbres del Ajusco, La Malinche, Nevado de Colima, Nevado de Toluca and Pico de Orizaba) and a Biological Corridor (Chichinautzin). Specimens were described macro- and microscopically in detail, and microphotographs using an optical microscope and SEM are provided. DNA sequences were algorithmically compared using *BLAST* with the *GenBank* database to facilitate their taxonomic placement and comparison with close species. Seven new species in five genera are presented: *Gautieria, Gymnomyces, Leucogaster, Melanogaster and Russula* (Basidiomycota).

*Poster P22*

**215. A short history of *Penicillium* taxonomy \*Pitt, John I.**CSIRO Food and Nutrition, North Ryde, NSW 2113, Australia. John.Pitt@csiro.au

Link described *Penicillium* in 1809 with three species but, as fruiting structures disintegrate in age, species became recognisable only 100 years later, with the advent of pure culture techniques. Thom in 1910 recognised the importance of cultural conditions and designated *P. expansum*, the common apple rot species, as type. Biourge in 1923, Thom in 1930 and Raper and Thom in 1949 produced monographs, each of increasing complexity and utility. Due to confusion over Fries’ interpretation of *Penicillium*, the genus was conserved by Hawksworth *et al*. in 1976. I started work on *Penicillium* in 1968 as a Postdoctoral Fellow at USDA NRRL, where Raper had worked, and continued after my return to Sydney in 1969. I developed the use of controlled cultural conditions and semi-defined media and published a monograph in 1980. During the 1980s, Frisvad demonstrated that secondary metabolites provided a more accurate means of delimiting species – the correlation with morphological taxonomy was remarkably close. Frisvad also showed that, unlike most thinking at that time, *Penicillium* species are often quite habitat specific. After a period of relative taxonomic stability, culminating in a definitive “List of Names in Current Use” in 1992, molecular techniques began to reshape thinking. Molecular taxonomy has in some cases

improved species concepts, but in others it may have resulted in excessive splitting. Current molecular taxonomy lacks agreement with morphology and ecology in some sections of the genus. Finally, “one name, one species” has resulted in splitting the genus. One teleomorph genus, *Eupenicillium,* has sensibly been synonymised with *Penicillium*, now taking a narrower circumscription, while subgenus *Biverticillium* has been synonymised with the other major teleomorph genus, *Talaromyces.* Will a new period of stability now ensue?

*Contributed Talk C16.3*

**216. The importance of maintaining the generic name *Eurotium* for a major genus of spoilage fungi** Pitt, John I.(1),**\*Taylor, John W.**(2) 1.CSIRO Food and Nutrition, North Ryde, NSW, 2113, Australia; 2.University of California, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA. John.Pitt@csiro.au

For the past 40 years, *Eurotium* has been the name applied to a very important genus of fungi, that cause spoilage to all kinds of biological materials with a water activity just above safe levels, including textiles, paper and leather goods, paintings, museum artefacts and microscope or camera lenses. *Eurotium* is of particular importance to food mycologists, as species from this genus consistently cause large economic losses to a very wide variety of dried, concentrated and processed foods. As classically circumscribed, *Eurotium* species are very distinctive, as on suitable media the characteristic ascomycete stage is almost always formed in culture. Variations in the gross and microscopic morphology of the sexual stage are used to differentiate species. All *Eurotium* species produce a characteristic *Aspergillus* asexual state, and the transition to one name, one fungus has led to the question as to whether *Eurotium* or *Aspergillus* should be the single generic name by which the species are known in the future. This paper will put forward morphological, physiological, ecological, taxonomic and phylogenetic reasons why the name *Eurotium* should be retained for these fungi. *Poster P120*

**217. Biological soil crusts microbiome diversity at Joshua Tree National Park, Granite Mountain, and Kelso Dunes \*Pombubpa, Nuttapon**(1), De Ley, Paul(2), Pietrasiak, Nicole(3), Stajich, Jason E(1)

1.Department of Plant Pathology and Microbiology and Institute of Integrative Genome Biology, University of California, Riverside, Riverside, California 92521 USA; 2.Department of Nematology, University of California, Riverside, Riverside, California 92521 USA 3.Plant and Environmental

Sciences Department, New Mexico State University, Las Cruces, NM 88003. npomb001@ucr.edu

Biological soil crusts contain diverse variety of microbial communities that are essential to desert environments. Mosses, lichens, eukaryotic algae, cyanobacteria, bacteria, and fungi can combine to form different types of biological soil crusts. Previous studies have mostly characterized biological soil crusts based on their external morphology, which may underestimate the function and diversity of microbial communities that cannot be observed visually. As a result, this project aims to explore the composition of microbial communities and capture the Biological Soil Crusts Microbiome (BSCM). The functions and diversity of the microorganisms living in the crusts, especially fungi, in arid environment are still poorly understood. Understanding how microbes interact to form crust layers requires detailed accounting of their microbial diversity, community structure, and measurable functions. Moreover, loss of biological soil crusts can contribute to increased soil erosion and reduced biodiversity in desert environments. Our study will explore biological soil crusts microbiome, and test the hypothesis that crust microbial diversity is different between sites and by crust type, at both the morphological and molecular level. We have used amplicon sequencing of environmental DNA to assess the composition of bacteria and fungal communities. Biological soil crusts were sampled from Joshua Tree National Park, Granite Mountain, and Kelso Dunes in California. Our preliminary sequencing and analysis of 16S from three sites shows that the bacterial contribution to BSCM is dominated by Cyanobacteria, Proteobacteria, and Actinobacteria phyla. Results from ITS fungal sequencing on BSCM show significant variation between crust types that are dominated by Dothideomycetes and Eurotiomycetes. Our BSCM will indicate the most abundant taxa in desert systems which can be used to prioritize culturing efforts and to begin exploring functional diversity of the dominant microbes.

*Poster P33*

**218. A genetic screen for bioluminescence genes in the fungus *Armillaria mellea,* through the use of *Agrobacterium tumefaciens-*mediated random insertional mutagenesis**

**\*Poole, Virginia**(1), Robertson, J. Brian(1), Baumgartner, Kendra(2), Bergemann, Sarah(1) 1.Middle Tennessee State University, Biology, Murfreesboro, Tennessee 37130, USA; 2.University of California, United States Department of Agriculture- Agricultural Research Service, Davis, California 95616, USA. vap2k@mtmail.mtsu.edu

Bioluminescence is reported from 71 saprobic species of fungi from four, distant lineages in the order

Agaricales. Analyses of the fungal luminescent chemistry shows that all four lineages share a functionally conserved substrate and luciferase, indicating that the bioluminescent pathway is likely conserved throughout Basidiomycota; however, the genes encoding for bioluminescence are unknown. *Armillaria mellea* is an ideal candidate for bioluminescence research because it luminesces at a high, consistent magnitude, fruits *in vitro*, and mycelia and basidiospores can be easily transformed with foreign DNA. Transformations are achieved using *Agrobacterium-*mediated insertional mutagenesis to randomly transfer an engineered Ti plasmid (T-DNA) with a hygromycin resistance selective marker into the genome of haploid *A. mellea* basidiospores. Isolates are cultured on 1% MEA+hygromycin and screened for luminescence to identify *A. mellea* transformants that lack the luminescent phenotype. To date, approximately one hundred fifty *A. mellea* transformants have been screened for luminescence and a single haploid isolate lacking the luminescent phenotype was identified. The goal of the study is to characterize the genes involved in fungal bioluminescence, and to understand the origin and evolution of this physiological mechanism in the Agaricales.

*Poster P138*

**219. Prior and post white-nose syndrome: Study of microbial diversity and its potential applications \*Porras-Alfaro, Andrea**(1), Edwards, Herbert(1), Lueschow, Shiloh(1), Hamm, Paris(1), Northup, Diana E.(2)

1.Western Illinois University, Department of Biological Sciences, Macomb, IL, USA; 2.University of New Mexico, Department of Biology, Albuquerque, NM, USA. a-porras-alfaro@wiu.edu

*Pseudogymnoascus destructans*, the fungus responsible for white-nose syndrome, has spread across many states in the U.S. and Canada, devastating bat populations. With the appearance of this invasive fungal disease, fungal ecology in caves has become especially relevant, and new research in this area has shown significant gaps in our understanding of cave microbiology. We are studying the diversity of microbial communities and the impact of *P. destructans*’s arrival on bats and caves. Our data from Illinois and New Mexico revealed that bat wings contain diverse microbial communities with low specificity among bats and caves. Actinobacteria are abundant and novel, showing significant antifungal activity against *P. destructans.* Significant changes on bat microbial communities were observed after *P. destructans*’s arrival using 454 sequencing. Early stages of infection in bats show significant wing damage in the stratum corneum and pre-corneous



layers of the epidermis with clear degradation of the bat wing keratin components. The fast deterioration of bat wings in early stages of infection and the microbial shifts observed on bats are key components that require more attention to develop adequate strategies for the control of this disease.

*Contributed Talk C1.1*

The biogeography of fungi is poorly understood. By using both historical records and molecular data, we have established the fungus *Amanita phalloides* as an introduction currently expanding its range on the West Coast of North America. The fungus is native to Europe. Although is has also been introduced to the East Coast of North America, it is not spreading here. By collecting mapped populations of fungi from California, Europe, and the Northeast U.S., and using genetic fingerprints created with AFLP protocols to map genetic individuals, we show that most mushrooms in a habitat are unique genetic individuals. Data suggest that genets of *A. phalloides* are typically less than 1 m in diameter. The pattern holds across California, Europe, and the Northeast, and is the same for sites where populations are assumed to be young, and sites where *A. phalloides* has been collected for over 30 years. There appears to be no correlation between body size and geographic origin or age of a population. In contrast, although the mushrooms of *A. phalloides* appear at specific times of year in Europe and on the East Coast, in California mushrooms can form at any time of year. Moreover, mushrooms are twice as large in California, as compared to mushrooms on the East Coast or in Europe. *Symposium S7.3*

**222. Soil microbial community responses to long- term multifactorial global change in a California annual grassland ecosystem \*Qin, Kenneth**, Dirzo, Rodolfo, Peay, Kabir G. Stanford University, Department of Biology, Stanford, California, 94305-5008, USA. kennethqin15@gmail.com.

While field-based, manipulative global change experiments have helped to build a nuanced understanding of plant community responses to multiple interacting anthropogenic changes in a variety of ecosystems, relatively little research has investigated the response of soil microbial communities (SMCs) to similar conditions. We used next-generation DNA sequencing (Illumina MiSeq) to assess the soil fungal and bacterial communities in the bulk soil (0–7cm depth) of the Jasper Ridge Global Change Experiment, a full-factorial global change experiment that has tested two levels of nitrogen deposition, CO2 concentration, temperature, and precipitation in a California annual grassland since 1998. Of the four global change treatments, nitrogen deposition had the strongest effect on the composition of SMCs, and also explained the most variation in fungal richness. Although all individual treatments had significant effects on SMC composition and diversity, treatment interactions in this experiment were infrequent and could only be identified at finer taxonomic scales in the bacterial community.

**220. Whole genome DNA-methylation (methylome) profiling in the Agaricomycotina \*Powers, Rob**, James, Tim Y. University of Michigan, Ecology and Evolutionary Biology, 830 N. University, Ann Arbor, MI 48109, USA. robpower@umich.edu

DNA methylation, a type 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 Basidiomycota. In particular, while it has been shown that DNA methylation in CpG contexts is important for the silencing of repetitive DNA elements, no clear evidence has been shown to support its role in state-specific gene regulation in the Agaricomycotina. Here, we investigate the role and changes of DNA methylation patterning across five Agaricomycotina taxa: *Coprinopsis cinerea, Heterobasidion irregulare, Phanerochaete chrysosporium, Coprinellus disseminatus* and *Cyathus stercoreus.* Using whole-genome bisulfite sequencing (WGBS) we are generating genome-wide methylation profiles (methylomes) of two mating compatible monokaryotic isolates of each of our five target species. Additionally, we are sequencing methylomes of each species after complete dikaryotization and mating have occurred. This will provide insight into the changes in methylomes patterning both within different life stages of the same species, and between different taxa in the Agaricomycotina.

*Poster P139*

**221. Biogeographic patterns in the body size and phenology of an introduced symbiont: *Amanita phalloides*\*Pringle, A.**(1), Cross, H.B.(2), Wolfe, B.(3), Richard, F.(4)

1.University of Wisconsin-Madison, Botany & Bacteriology, Madison WI, USA; 2.Norsk Institutt for Biookonomi, Ås, NORWAY; 3.Tufts University, Biology, Medford MA, USA; 4 Université Montpellier, Montpellier, FRANCE. anne.pringle@wisc.edu

Furthermore, SMC composition and diversity were usually best explained by non-manipulated variables, rather than the global change treatments themselves. In particular, fungal and bacterial community composition were the best covariates for each other, suggesting that despite differential effects of global change on fungal and bacterial communities, their relationship is fairly resilient to global change. Finally, we found a consistent decrease in the relative abundance of arbuscular mycorrhizal fungi under elevated CO 2 , which contradicts the results of studies that use traditional, non-molecular methods to assess arbuscular mycorrhizal fungal abundance. Our results support the hypothesis that increased nutrient inputs can cause strong shifts in SMCs in grasslands, and demonstrate the necessity for a trait-based understanding of SMCs in a changing world.

*Poster P41*

**223. New genome sequence from amoebae parasite links Cryptomycota and Microsporidia in genome reduction and energy theft \*Quandt, C. Alisha**(1), Beaudet, Denis(2), Corsaro, Daniele(3), Michel, Rolf(4), Corradi, Nicolas(2), James, Timothy Y.(1)

1.University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, MI, USA; (2)University of Ottawa, Canadian Institute for Advanced Research, Department of Biology, ON, Canada; (3)CHLAREAS Chlamydia Research Association, Nancy, France; (4)Central Institute of the Federal Armed Forces Medical Services, Laboratory of Medical Parasitology, Koblenz, Germany. alishaq@umich.edu

The phylogenetic relationship between *Rozella allomycis*, an intracellular mycoparasite of *Allomyces*, and Microsporidia, intracellular parasites of animals, has been solidified by the use of phylogenomics, yet the ecological and genetic similarities between these distant relatives remains unclear. The nuclear and mitochondrial genomes of *Rozella allomycis* lack many of the basic genes for primary metabolism but have not undergone genome compaction to the extent seen in the multiple Microsporidia genomes sequenced, or the closely related *Mitosporidium daphniae*, a parasite of *Daphnia*. More recently, the discovery of diverse and seemingly ubiquitous cryptic fungi closely related to *R. allomycis*, has led to proposal of a single clade of early diverging fungi, called by various names (*e.g.* Cryptomycota, Rozellomycota, Opisthosporidia). Here, we present a comparative genomic analysis of the previously sequenced Cryptomycota and Microsporidia along with the genome of an intranuclear parasite of amoebae, *Paramicrosporidium saccamoebae*, which we generated from a metagenomic sample. We discuss

the general evolutionary relationships within this super phylum, and the general pattern of decreasing genome size and gene number, including the reduction (in *R. allomycis* and *M. daphniae*) and eventual loss of a true mitochondrion in all the other sequenced species including *P. saccamoebae*. We also analyzed the genes involved in nucleotide metabolism in these genomes, as those in *R. allomycis* and Microsporidia have been shown to be the product of horizontal transfer from bacteria or viruses. Because these genes are hypothesized to be involved in energy and nucleotide theft, we hypothesize they may have facilitated the evolution of parasitism within Cryptomycota.

*Contributed Talk C11.2*

**224. Fungi who love eggs: Sequencing the soybean cyst nematode microenvironment in search of sustainable biocontrol strategies \*Rajendran, Deepak**(1), Hu, Weiming(1), Xhu, Yingbo(2) Bushley, E, Kathryn(3), Chen, Senyu(1, 2) 1.University of Minnesota, Plant Pathology, 1991 Upper Buford Circle, St. Paul, MN 55108, USA; 2.University of Minnesotath Southern Research and Outreach Center, 35838 120 St., Waseca, MN 56093; 3.University of Minnesota, Plant Biology, 1479 Gortner Avenue, St. Paul, MN 55108, USA. rajen023@umn.edu

Understanding the microenvironments and niches of fungi in agricultural ecosystems is critical to ensure successful establishment of biocontrol agents in the environment. In *Glycine max* (soybean)-*Heterodera glycines* (Soybean Cyst Nematode – SCN) pathosystem, several fungal species have been reported worldwide to be effective biocontrol agents, mostly parasites of SCN second-stage juveniles (J2) or eggs. In this study, cyst-colonizing fungi collected from plots subjected to different crop rotation sequences were identified over two crop seasons in 2014 and 2015 using their ITS1 sequences. Relative abundances of community members were also studied. The major players in the field were *Fusarium* spp.*, Dactylonectria/Ilyonectria* spp*.,* and *Cylindrocarpon* spp*.* Their relative percent colonization of the cysts when compared to the other species remained high across the two years (2014 and 2015). *Lachnum* spp*, Exophiala* spp. and *Mariannea* spp. were less abundant, but consistently found in the field. Several unknown fungi (<97% query cover and/or <97% sequence identity to database listings) were also observed. This is an on-going research project, and the diversity of fungi will be analyzed across different crop sequences and seasons. *Poster P77*

**225. Fungal diversity of Illinois caves**

Raudabaugh, Daniel B.(1,2), Taylor, Steven J.(1), Yannarell, Anthony C.(3), Heske, Edward J.(1),Merritt, Joseph F.(1), Mateus-Pinilla, Nohra(1**),** Bach, Elizabeth(4), **\*Kuhn, Alex L.**(1), Miller, Andrew N.(1)

1.University of Illinois, Illinois Natural History Survey, Champaign, IL, 61820, USA; 2.University of Illinois, Department of Plant Biology, Urbana, IL, 61801, USA; 3.University of Illinois, Department of Natural Resources and Environmental Science, Urbana, IL, 61801, USA; 4.Colorado State University, Department of Biology, Fort Collins, CO, 80523, USA. akuhn@illinois.edu

Interest in cave/mine inhabiting microorganisms has increased due to the introduction of bat white-nose syndrome to North America in 2006. The aim of this research was to inventory Illinois cave/mine fungi through culture-dependent and culture-independent methods by sampling multiple substrates (soil, wall, ceiling, guano, and bats) from 8–10 Illinois caves/mines from 2012 to 2014. Pure cultures were obtained by lawn plating a 400 μl aliquot of soil/substrate dilution (10-1, 10-2, 10-3) onto PDA and SDA petri plates containing streptomycin sulfate and penicillin G (0.015 g/L) or swab streaking onto agar plates. For environmental sampling, DNA was extracted using both the MP FastDNA® Spin Kit for soil and MOBIO PowerSoil® DNA isolation kit, amplified using the Fluidigm® platform and sequenced using Illumina® MiSeq. In total, 2849 fungal cultures were successfully obtained of which 1505 isolates were identified through ITS sequencing resulting in ~250 species. Environmental sequencing results indicated an additional 254 OTUs resulting in 504 total species within 337 genera. These results suggest that caves harbor a diverse mycobiome and continued research is needed to understand the true extent of this diversity. *Poster P17*

**226. Going to extremes: Contrasting population genetic structures among cryptic species of the entomopathogen *Beauveria bassiana*\*Rehner, Stephen A.**(1), Kepler, Ryan M.(1), Doyle, Vinson P.(2), Bushley, Kathryn E.(3)

1.USDA-ARS, Systematic Mycology and Microbiology Laboratory, Beltsville, MD, USA; 2. Louisiana State University, Department of Plant Pathology and Crop Physiology, Baton Rouge, LA, 70803, USA; 3. University of Minnesota, Department of Plant Biology, Saint Paul, MN 55108, USA. stephen.rehner@ars.usda.gov

*Beauveria bassiana* (Ascomycota:Hypocreales) is a ubiquitous, soil-borne generalist entomopathogen with mixed but predominantly clonal reproduction, widely used for biological control of pest insects. To

illustrate its hierarchical genetic structure, a comprehensive multilocus phylogeny of the *B. bassiana* complex and population genetic analyses of selected cryptic species is presented. Multilocus phylogenetics reveals extensive lineage diversity and surveys conducted at local to global scales show that *B. bassiana* cryptic lineages consistently occur in mixed assemblages across most terrestrial habitats. Many species have intercontinental distributions, demonstrating their capacity to disperse across significant geographic barriers. In the western U.S., co-occurring cryptic species differ greatly in abundance and regionally abundant species display dramatic differences in population genetic diversity. At one extreme, a commonly occurring species (A) exhibits high levels of polymorphism at microsatellite loci and both mating types are present in this population sample. Further, the significant minority of allelic diversity in this species that is restricted to individual genotypes suggests that some clones of species A are evolutionarily persistent given this accumulation of within-clone genetic divergence. At the opposite extreme, genetic diversity in a second, broadly sympatric species (B) is exclusively limited to a frequently encountered clone. The extreme differences in population genetic variability between species A and B are consistent with predictions of the central-marginal hypothesis of within-population genetic diversity, under which effective

*Contributed Talk C3.4*

**227. New *Microperella* species from the Brazilian Cerrado**Reis, Luciane N.A., Pereira-Carvalho, Rita C., Souza, Erica S.C., Pinho, Danilo B., **\*Dianese, José C.** Universidade de Brasília, Departamento de Fitopatologia, Brasília, 70910-900, Brazil. jcarmine@gmail.com

*Microperella* (type species: *Microperella quercus* Höhn.) is a monotypical Pezizomycotina (Ascomycota) assexual morph, known since 1902 exclusively from Japan, infecting leaves of *Quercus glaca* (Fagaceae). The type material was reviewed and illustrated by Sutton in his 1980 coelomycete book. A new species was now found on a herbaceous host (*Baccharis* sp. – Asteracae), native in the Brazilian Cerrado, collected at 15o 34 ́ 34.5 ́ ́S × 47o 36 ́26 ́ ́W within the Estação Ecológica de Águas Emendadas, Brasília, Distrito Federal. The herbarium voucher was registered as UB-Mycological Collection 23304, while

size, genetic diversity, and genetic connectivity are predicted to be greatest at the population center and lowest at the margins of the species range, respectively. Interestingly, in genetically variable population samples, clone-correction typically

population

 

indicates relatively few (15-30) genetic individuals.



genomic DNA was extracted from fresh material for the appropriate rDNA sequencing. However, the morphological analysis leaves no doubt about the taxonomic novelty here reported. The new species, besides the phylogenetic distance of both hosts and distinctive geographical distribution, showed larger conidia and conidiomata, multiseptate spores instead of 1-2-celled ones, and stromata showing mostly *textura prismatica*. The new species shows: *M*

encodes the transformation of tryptophan to psilocybin and its transport. To test this functional hypothesis, we heterologously expressed a decarboxylase and a phosphotransferase from the cluster and assayed chemical transformations *in vitro*. Using ultra performance liquid chromatography and tandem mass spectrometry, we inferred they have specific activity on tryptophan and its derivatives. Additional gene sequences from other psilocybin-containing species obtained by degenerate PCR were used in the phylogenetic reconstruction of the cluster’s origin and distribution. These analyses suggest a psilocybin cluster origin in Agaricales by horizontal transfer of multiple genes from Atheliales, and a horizontal cluster transfer from dung-inhabiting *Psilocybe* to *Panaeolus*. The patterns of dispersal of this cluster may reflect at least one role for psilocybin as a defense against mycophagous invertebrates.

*Contributed Talk C14.2*

**229. A preliminary molecular view of the mycoparasite genus *Piptocephalis* (Zoopaginomycotina) \*Reynolds, Nicole**(1), Benny, G.L.(1), Ho, H.M.(2), Smith, Matthew E.(1)

1.University of Florida, Department of Plant Pathology, Gainesville, FL 32611 USA; 2.National Taipei University of Education, Department of Science Education, Taipei, 106 Taiwan. nicolereynolds1@ufl.edu

Although zygomycetes include the earliest diverging lineages of filamentous, non-flagellated fungi, many of the taxa remain understudied and incompletely characterized. Among the least studied of all zygomycete fungi are the members of the subphylum Zoopaginomycotina, which includes diverse species of mycoparasites and microscopic parasites of small animals (e.g. nematodes, rotifers, and amoebae). One common and diverse group of Zoopaginomycotina is the mycoparasitic, haustoria- forming genus *Piptocephalis*. Most *Piptocephalis* species parasitize widespread saprobic zygomycetes in the Mucoromycotina and Mortierellamycotina, 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 a ubiquitous and 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 primer mismatching or other

*ycelium*

immersed, branched, septate, pale brown that penetrates and occupies host epidermal cells*. Conidiomata* 352 (262) 1249 μm x 231 (768) 468 μm, eustromatic often confluent, typically pulvinate, brown to black, multilocular; *locules* simple, globose to irregular situated on top of a basal stromatic layer, ostiolate; *osltiole* depressed; *locules* 61 (143) 286 x 48 (114) 322 μm. *Conidiogenous cells* holoblastic, determinate, discrete, hyaline, lageniform, smooth, lining the internal wall of the locules. *Conidia* 30 (36)

41 μm x 5 (6) 8 μm hyaline, fusiform and 2-3 septate.

The new species will be published following the requirements of the International code for the Melbourne Code, after conclusion of the molecular analysis.

*Poster P6*

**228. Horizontal transfer of a psilocybin gene cluster among divergent lineages of Agaricales** Reynolds, Hannah(1), Vijayakumar, Vinod(1), Korotkin, Hailee(2), Matheny, Brandon(2), **\*Slot, Jason**(1)

1.The Ohio State University, Department of Plant Pathology, Columbus, OH, 43210, USA; 2.The University of Tennessee, Ecology and Evolutionary Biology, Knoxville, TN, 37996, USA. slot.1@osu.edu

Psilocybin occurs in several unrelated lineages of Agaricales (*Pluteus*, *Conocybe*, *Inocybe*, *Gymnopilus*, *Panaeolus*, *Psilocybe*) in hallucinogenic (“magic”) mushrooms with ecological roles varying from wood- and dung- decomposition to ectomycorrhizae. Despite recent advances in the therapeutic potential of psilocybin-containing mushrooms, an understanding of their biology and evolution has lagged behind. A pathway for psilocybin (O-phosphoryl-4-hydroxy-N,N dimethyl tryptamine) biosynthesis was inferred in the 1960s, but no genetic mechanism for its production has since been identified. To understand the genetic and evolutionary underpinnings of psilocybin synthesis among divergent mushroom clades, we sequenced the genomes of three distantly related psilocybin-containing species, *Psilocybe cyanescens*, *Panaeolus cyanescens*, and *Gymnopilus luteofolius*. Parallel searches for physical clusters of genes that are restricted to psilocybin producing taxa, and clusters of genes with psilocybin-related metabolic functions converged upon a five-gene cluster that putatively

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) design *Piptocephalis*-specific primers to preferentially amplify ITS and 28s rDNA of *Piptocephalis* from mixed templates (e.g. co-cultures of *Piptocephalis* and their host fungi), and 2) use molecular data to determine the major lineages and estimate the molecular diversity of *Piptocephalis*. Here we document the lineage-specific primer sets we have developed and discuss our preliminary molecular phylogenetic results.

*Poster P97*

**230. Comparative genomics of biotechnologically important yeasts \*Riley, Robert**(1), Haridas, Sajeet(1), Wolfe, Kenneth H.(2), Lopes, Mariana R. (3,4), Hittinger, Chris Todd (3,5), Göker, Markus(6), Salamov, Asaf (1), Wisecaver, Jen (7), Long, Tanya M.(8), Aerts, Andrea L.(1), Barry, Kerrie(1), Choi, Cindy(1), Clum, Alicia(1), Coughlan, Aisling Y . (2), Deshpande, Shweta(1), Douglass, Alexander P. (2), Hanson, Sara J. (2), Klenk, Hans-Peter (6,9), LaButti, Kurt(1), Lapidus, Alla (1), Lindquist, Erika(1), Lipzen, Anna(1), Meier-Kolthoff , Jan P.(6), Ohm, Robin A.(1), Otillar, Robert P.(1), Pangilinan, Jasmyn (1), Peng, Yi(1), Rokas, Antonis (7), Rosa, Carlos A.(4), Scheuner, Carmen(6), Sibirny , Andriy A.(10), Slot, Jason C.(11), Stielow , J. Benjamin (6,12), Sun, Hui(1), Kurtzman, Cletus P .(13), Blackwell, Meredith(14,15), Grigoriev, Igor V.(1), Jeffries, Thomas W.(8).

1.Department of Energy Joint Genome Institute, Walnut Creek, CA 94598; 2. University College Dublin, UCD Conway Institute, School of Medicine, Dublin 4, Ireland; 3. University of Wisconsin- Madison, Laboratory of Genetics, Genome Center of Wisconsin, Wisconsin Energy Institute, J. F. Crow Institute for the Study of Evolution, Madison, WI; 4. Universidade Federal de Minas Gerais, Departamento de Microbiologia, ICB, C.P. 486, Belo Horizonte, MG, 31270-901, Brazil; 5. Department of Energy Great Lakes Bioenergy Research Center, University of Wisconsin-Madison, Madison, WI; 6.Leibniz Institute DSMZ – German Collection of Microorganisms and Cell Cultures, Inhoffenstraße 7B, 38124 Braunschweig, Germany; 7. Vanderbilt University, Department of Biological Sciences, Nashville, TN 37235, USA; 8.University of Wisconsin-Madison, Department of Bacteriology and USDA Forest Products Laboratory, Madison, WI, USA; 9.Newcastle University, School of Biology, Ridley Building, Newcastle upon Tyne, UK; 10. NAS of Ukraine, Department of Molecular Genetics and Biotechnology,

Institute of Cell Biology, Lviv 79005 Ukraine and Department of Biotechnology and Microbiology, University of Rzeszow, 35-601 Poland; 11. Ohio State University, Department of Plant Pathology, Columbus, OH 43210; 12.CBS-KNAW Fungal Biodiversity Centre, Utrecht, the Netherlands; 13.US Department of Agriculture ARS NCAUR, Peoria IL 61604; 14. Louisiana State University, Department of Biological Sciences, Baton Rouge, LA 70803 USA; 15. University of South Carolina, Department of Biological Sciences, Columbia, SC, 29208 USA. ivgrigoriev@lbl.gov.

Ascomycete yeasts are metabolically diverse with great potential for biotechnology. Here we report the comparative genome analysis of 29 taxonomically and biotechnologically important yeasts, including 16 newly sequenced. We identify a genetic code change, CUG-Ala, in *Pachysolen tannophilus* which is sister to the known CUG-Ser clade. Our well-resolved yeast phylogeny shows that some traits such as methylotrophy are restricted to single clades, whereas others such as L-rhamnose utilization have patchy phylogenetic distributions. Many pathways of interest are encoded by gene clusters, with variable organization and distribution. Genomics can predict some biochemical traits precisely, but the genomic basis of others such as xylose utilization remains unresolved. Our data also provide insight into early evolution of ascomycetes. We document the loss of H3K9me2/3 heterochromatin, the origin of ascomycete mating-type switching, and pan- ascomycete synteny at the *MAT* locus. These data and analyses provide strategies for engineering efficient biosynthetic and degradative pathways, and gateways for genomic manipulation. *Poster P127*

**231. The mitochondrial genome of the rugulosin (anti-insectan) producing spruce needle endophyte, *Phialocephala scopiformis* DAOMC 229536 \*Robicheau, Brent M.**, Young, Alex P., Walker, Allison K.

Acadia University, Biology Department, Wolfville, Nova Scotia, B4P 2R6, Canada. allison.walker@acadiau.ca

Despite the recent surge in mitochondrial (mt) genome sequencing, published mtDNA sequences for fungi remain underrepresented in GenBank. We describe the 43,742 bp mt genome of the spruce needle endophyte, *Phialocephala scopiformis* (Helotiales Ascomycota) strain DAOMC 229535, which produces the potent anti-insectan compound rugulosin. Mitochondrial sequence was obtained from whole genome shotgun sequencing of *P. scopiformis* strain DAOMC 229535. Evolutionary comparison to the only other published complete *Phialocephala* mt

genome, *P. subalpina*, indicates that the suite of common mt genes – CO1-3 & B, NAD1-6 & 4L, ATP6 & 9, rrnL & rrnS – has retained an identical gene order. In addition, NAD4L remains one of the most conserved genes within the genus. Further analysis of partial mt sequences for other *Phialocephala* spp. also resolved two gene duplication events which help explain evolutionary branches within the *Phialocephala fortinii* s.l. – *Acephala appalanata* species complex (PAC). The objectives for completing this work included: (1) developing strain- specific biomarkers, (2) using large scale genetic patterns, such as gene order, to infer evolutionary relationships within the PAC fungal species complex, and (3) to document mitochondrial diversity within the diverse fungal order Helotiales, which comprises >3,800 species.

*Poster P99*

**232. Evolution and ecology of *Monosporascus* isolates in aridlands \*Robinson, Aaron J.**(1), Natvig, Donald O.(1), Porras-Alfaro, Andrea(2)

1.University of New Mexico, Department of Biology, Albuquerque, NM, 87131, USA; 2.Western Illinois University, Department of Biological Sciences, Macomb, IL, 61455, USA. aaronjonrobinson@gmail.com

Fungal endophytes represent a unique group of fungi with a broad distribution and numerous, often unresolved, ecological roles. Known and hypothesized roles range from plant protection to facultative pathogenicity. Surveys of arid grasslands and shrublands at the Sevilleta National Wildlife Refuge (SNWR) and other locations in central New Mexico have demonstrated that species of *Monosporascus* are ubiquitously associated with the roots of the dominant grass *Bouteloua gracilis* and all or nearly all other plant species examined. Of the three described species of *Monosporascus*, the most studied is *M. cannonballus*, which along with *M. eutypoides* is a devastating pathogen of cantaloupe and other cucurbits. A third species, *M. ibericus*, has been described as an endophyte of several plant species found in sand flats and salt marshes in Spain. A comparison of the ribosomal internal transcribed spacer (ITS) DNA region indicates substantial diversity among isolates of *Monosporascus* from New Mexico. The New Mexico isolates include close relatives of the three described species in addition to strains that appear to represent previously unrecognized lineages. There currently is no evidence for pathogenicity among any of the New Mexico lineages. To better resolve the relationships within the genus and the placement of the genus within the Ascomycota, we are performing phylogenomic

analyses that include sequencing and assembling the genomes of *M. cannonballus*, *M. ibericus* and several isolates obtained at the SNWR. Laboratory experiments suggest important life-cycle differences between described species and isolates from New Mexico. In contrast with *M. cannonballus* (homothallic), sexual reproduction has not been observed among the New Mexico isolates. Finally, we are performing growth chamber experiments to determine whether isolates from New Mexico can be pathogenic on agricultural cucurbit lines.

*Poster 104*

**233. Genet size and annual persistence of the ectomhicorryzal species *Lactarius deceptivus*, associated to oak forests in Colombia \*Rodríguez Cruz, María Camila**, Vargas, Natalia, Restrepo, Silvia

1.Universidad de los Andes, Department of Biological Sciences, Bogotá, 111711, Colombia. mc.rodriguez2802@uniandes.edu.co

ECtoMycorrhizal (ECM) fungi are mutual associations between plant roots and fungal mycelia belonging mostly to the class Agaricomycetes (Phylum Basidiomycota). These fungi provide their hosts with water and nutrients, benefiting a growth niche and resistance against abiotic and biotic factors. Knowledge about the population structure of ECM fungi is important to understand their diversity, distribution, and mode of dispersion within the ecosystems. The aim of this study was to determine the genet size (or genetic clone), distribution of the diversity, and annual persistence of the ectomycorrhizal fungus Lactarius deceptivus in 3 oak (Quercus humboldtii) forests in the departments of Boyacá and Santander, Colombia. The sporocarps were collected, and the species (L. deceptivus) was confirmed using morphological markers and nuclear gene sequences (ITS, nLSU, EF-1). Individual sporocarps were assigned to a genet according to their microsatellite profile. Estimated genet sizes ranged from 1.5 to 15.28 m, suggesting that the genets of L. deceptivus are small, contrary to previous findings that suggest larger genet sizes in other species belonging to the genus Lactarius, which show a tendency for late stage successions. These results suggest that L. deceptivus, in oak forests in Colombia, is an early colonizer probably using spore propagation for dispersal. Additional microsatellite markers are being analyzed to further support these findings.

*Poster 144*

**234. Oomycete community diversity: The soybean root rot complex \*Rojas, Alejandro**(1,2), Jacobs, Janette(1), Napieralski, Stephanie(1), Karaj, Behirda(1), Bradley,

Carl(3,4), Chase, Tom(5), Esker, Paul(6,7), Giesler, Loren(8), Jardine, Doug(9), Malvick, Dean(10), Markell, Sam(11), Nelson, Berlin(11), Robertson, Alison(12), Rupe, John(13), Smith, Damon(6), Sweets, Laura(14), Tenuta, Albert(15), Wise, Kiersten(16), Chilvers, Martin (1,2). rojasfle@msu.edu

1. Michigan State University, Department of Plant, Soil and Microbial Sciences, East Lansing, MI 48824, USA; 2.Michigan State University, Program in Ecology, Evolutionary Biology and Behavior, East Lansing, MI 48824, USA; 3.University of Illinois, Department of Crop Sciences, Urbana, IL 61801, USA; 4.University of Kentucky, Department of Plant Pathology, Princeton KY 42445, USA; 5.South Dakota State University, Department of Plant Science, Brookings, SD 57007, USA; 6.University of Wisconsin-Madison, Department of Plant Pathology, Madison, WI 53706, USA; 7.University of Costa Rica, School of Agronomy, San Jose, CR; 8.University of Nebraska-Lincoln, Department of Plant Pathology, Lincoln, NE 68583, USA; 9.Kansas State University, Department of Plant Pathology, Manhattan, KS 66506, USA; 10.University of Minnesota, Department of Plant Pathology, St. Paul, MN 55108, USA; 11. North Dakota State University, Department of Plant Pathology, Fargo, ND 58105, USA; 12.Iowa State University Department of Plant Pathology and Microbiology, Ames, IA 50011, USA; 13.University of Arkansas, Department of Plant Pathology, , Fayetteville, AR 72701, USA; 14.University of Missouri, Division of Plant Sciences, Columbia, MO 65211; 15.Ontario Ministry of Agriculture, Food & Rural Affairs, Ridgetown, ON N0P2C0, Canada; 16.Purdue University, Department of Botany and Plant Pathology, West Lafayette, IN 47907

The root and surrounding rhizosphere ecosystem is a dynamic and complex environment subject to the interaction of different microbial communities, which affect the outcome of the plant-phytobiome. In the root ecosystem, oomycetes are part of the microbial community and are some of the most aggressive and important plant pathogens. In the United States, soybeans are produced across 76 million acres of highly productive land, but can be severely impacted by diseases caused by oomycetes. We initially utilized a two-year culture based survey to study oomycetes associated with soybean seedlings from across 11 states in the Midwest, characterizing the communities and profiling phenotypic traits such as pathogenicity and aggressiveness. With this approach a total of 83 different oomycete species were identified and characterized. The survey served as a basis to develop markers and phenotypic data that could be used to further investigate and characterize oomycete communities associated with agricultural systems. We

are currently utilizing this phenotype information and amplicon-based community analysis to evaluate the role of climatic, edaphic and biotic factors on the oomycete community structure. Improved understanding of the phytobiome, especially in the root system, and the factors that influence it will enable improved disease management and enhance plant health.

*Contributed Talk C8.2*

**235. The making of biodiversity across the yeast subphylum \*Rokas, Antonis**(1), Hittinger, Chris Todd(2), Kurtzman, Cletus P .(3), Shen, Xing-Xing(1), Zhou, Xiaofan(1), Kominek, Jacek(2), Opulente, Dana A.(2), Peris, David(2), DeVirgilio, Jeremy(3), Hulfachor, Amanda B.(2)

1.Department of Biological Sciences, Vanderbilt University, Nashville, TN, 37235, USA; 2.Laboratory of Genetics, Genome Center of Wisconsin, DOE Great Lakes Bioenergy Research Center, Wisconsin Energy Institute, J. F. Crow Institute for the Study of Evolution, University of Wisconsin-Madison, Madison, WI, 53706, USA; 3.Mycotoxin Prevention and Applied Microbiology Research Unit, National Center for Agricultural Utilization Research, Peoria, IL, 61604, USA. antonis.rokas@vanderbilt.edu

Yeasts are unicellular fungi that do not form fruiting bodies. Although the yeast lifestyle has evolved multiple times, most known species belong to the subphylum Saccharomycotina (syn. Hemiascomycota, hereafter yeasts). This diverse group includes the premier eukaryotic model system, *Saccharomyces cerevisiae*; the common human commensal and opportunistic pathogen, *Candida albicans*; and over 1000 other known species (with more continuing to be discovered). Yeasts are found in every biome and continent and are more genetically diverse than angiosperms or chordates. Ease of culture, simple life cycles, and small genomes (10– 20 Mbp) have made yeasts exceptional models for molecular genetics, biotechnology, and evolutionary genomics. Since only a tiny fraction of yeast biodiversity and metabolic capabilities has been tapped by industry and science, expanding the taxonomic breadth of deep genomic investigations will further illuminate how genome function evolves to encode their diverse metabolisms and ecologies. As part of NSF’s Dimensions of Biodiversity program, we have undertaken a large-scale comparative genomic study to uncover the genetic basis of metabolic diversity in the entire Saccharomycotina subphylum. So far, we have surveyed nearly 100 published yeast genomes and another 300 genomes obtained in-house. In my talk, I will discuss the team’s efforts to develop efficient workflows for genomic,

evolutionary, and phylogenomic analyses and examples of novel evolutionary events involved in the making of yeast metabolic diversity. *Symposium S1.3*

**236. A species-based analysis of fungal communities in Jasper Ridge Biological Preserve \*Romano, Nicholas Herrington**Stanford University, Biology Department, Stanford, CA 94305, USA. nromano2@stanford.edu

group of fungi. Molecular research strongly suggests that this group is polyphyletic, consisting of six distinct clades. These filamentous fungi mark the transition from the aquatic, zoosporic life style observed in early diverging lineages such as the Chytridiomycota and Blastocladiomycota, to the non- flagellated, terrestrial life style of the Basidiomycota and Ascomycota. As part of an NSF-funded collaborative research effort to resolve the evolutionary relationships of the zygomycetes (i.e., ZygoLife), which includes genome sequencing and analyses, discovery and description of zygomycete fossils, we have begun to elucidate the subcellular characteristics of selected zygomycetous fungi using both light and electron microscopic techniques. Here we present data on hyphal growth, apical vesicle organization, spindle pole body features, septal pore organization (when applicable), and other subcellular organelles and inclusions in three zygomycetous fungi: *Cunninghamella echinulata* (Mucorales), *Conidiobolus coronatus* (Entomophthorales), and L*inderina pennispora* (Kickxellales).

*Poster P142*

**238. Exploring *Neurospora discreta*’s ability to decompose organic carbon under global warming \*Romero-Olivares, Adriana L.**(1), Taylor, John(2), Treseder, Kathleen K.(1)

1.University of California Irvine, Department of Ecology and Evolutionary Biology, Irvine, CA 92697; 2.

alromer1@uci.edu

Fungal ecology has benefitted greatly from the discovery of ectomycorrhizal fungi which associate mutually with plants around the globe. More recently have we gained interest in the endophytic fungi, living between plant cells and present in all tissue types of many plants. Endophytic fungi confer many boons to their plant hosts, including disease resistance, pest protection, and water stress mitigation. Since endophytes can transition from a mutualist to a parasite over a plant’s lifetime, the ecological role of endophytes is still under question. This study aims to unravel the ecological role of endophytic fungi, as well as tease apart the relationship between ectomycorrhizal fungi and endophytic fungi. Our study site is the Jasper Ridge Biological Preserve near Stanford’s main campus, and we examine four trees— *Quercus agrifolia, Pseudotsuga menziesii, Arbutus menziesii,* and *Populus trichocarpa.* These trees are of significant ecological importance in California’s forests, and *Populus trichocarpa,* the black cottonwood, is gaining more attention from researchers as a model tree for many types of research. Next generation sequencing methods will be used to ascertain the identity and abundance of all fungal species present in and around the roots of each tree species. These results will be used in conjunction with soil data to determine what the major influence on fungal species composition is— tree species or soil conditions. Culturing of fungal endophytes will be done in the lab to confirm sequencing results, as well as to gain greater knowledge of the growth of endophytes and their ability to be inoculated onto trees. This project serves as a preliminary study of fungal communities in Jasper Ridge and will allow for more in-depth work to be done on the possible use of endophytes as biological agents for disease and pest

control.

University of California, Plant and Microbial



Biology, Berkeley, CA, 94720-3102, USA.



*Neurospora discreta* is a decomposer fungus distributed worldwide. It has been widely used as a model organism to address questions in evolution, cell biology, and population genetics. In our work, we are using *N. discreta* as a model organism to understand the effects of global warming on the decomposer community. If global warming increases decomposition rates of long-lived soil carbon (i.e., recalcitrant C), atmospheric CO2 inputs may rise, providing a positive feedback to global warming. We used a collection of cold- and warm-adapted isolates of *N. discreta* to explore the capacity of this fungus to decompose labile (i.e., short-lived C) and recalcitrant carbon at different temperatures. We hypothesized that warm-adapted *N. discreta* would be more successful at decomposing recalcitrant carbon at warmer temperatures, compared to cold-adapted *N. discreta*. At warmer temperatures, warm-adapted strains would benefit from the availability of recalcitrant C compared to cold-adapted strains. We performed 28- day long C use x temperature assays combined with counts of decomposing gene copies from whole genomes of *N. discreta* individuals. We found that

*Poster 26*

**237. Subcellular characters of three zygomycetous fungi**Romberger, Isobel, Koessel, Karissa, Valecourt, Archer, Fisher, Karen, **\*Roberson, Robert W.** Arizona State University, School of Life Sciences, Tempe, AZ, 85287, USA. robby2@asu.edu

The zygomycetous fungi represent a diverse

there was a small but significant correlation between the mean annual temperature of the site of isolation of *N. discreta* and the use of recalcitrant C. Our findings suggest that warmer temperatures may elicit decomposition of recalcitrant C and this may provide a



positive feedback to global warming.



*Poster P42*

**239. Effects of fire on prairie macrofungi in the Pacific Northwest \*Roy, Bitty A.**(1), Hamman, Sarah(2), Thomas, Daniel C.(1), Nelson, Aaron(1), Messinger, Wes(3) 1.University of Oregon, Institute of Ecology and Evolution, Eugene, Oregon 97403, USA; 2.Center for Natural Lands Management, Olympia, Washington 98501, USA; 3.U.S. Army Corps of Engineers, Fern Ridge Project Office, Junction City, Oregon 97448, USA.

Prairies were once much more extensive in the Pacific Northwest (PNW) west of the Cascades, but have largely been lost due to Euro-American settlement, agriculture, and changes in fire regime. It has long been appreciated that remnant prairies contain a large number of now rare plant species, but it is not known if there is also a prairie-associated mushroom flora with species of conservation interest. We used a combination of transects along a burn chronosequence (unburned, burned in 2012, 2014, or 2015) and walking surveys of prairies to begin to determine which macrofungi are associated with PNW prairies and how management affects them. The results strongly depended on the region where the prairies were located (OR versus WA). Over the course of a single year we found 43 macrofungal species in OR prairies; of these, at least two are known to be rare or uncommon (*Amanita pruitii* and *Tetrapyrgos subdendrophora*). We found fewer prairie-associated species in WA, around 20. The species present in the fire chronosequences also differed by region; most of the fungi we found in the OR chronosequence were the strongly grass-associated *Mycena citrinomarginata* (97% of 4896) versus a majority of brown-spored fungi such as *Galerina* (91% of 1343) in WA. Fire influenced fruiting in complex ways. Repeated measures analysis of the OR data, which had more years with fires, revealed significant differences in numbers of fruiting *M. citrinomarginata* depending on the time since fire (most in 2015 burns and unburned), whether the prairie was an upland or wetland (more in uplands), and when during the year the census took place. While fruiting of *M. citrinomarginata* was high immediately postfire, there was then a reduction in fruiting for at least three years postfire. We conclude that a diversity of macrofungi inhabit PNW prairies, including rare ones, and that management practices influence

fruiting. For these reasons fungi should be considered in management decisions. *Contributed Talk 12.2*

**240. Are molecular operational taxonomic units good approximations of species? \*Ryberg, Martin**Uppsala University, Department of Organismal Biology, Systematic Biology Program, Uppsala, 75236, Sweden. martin.ryberg@ebc.uu.se

The use of molecular methods to study fungi has lead to many new insights. The internal transcribed spacer (ITS) region of nuclear ribosomal DNA has been the main marker for taxonomic identification of fungi from environmental samples. Partially because it is easy to amplify using PCR, and partially because it offers species level resolution in many taxa. Sequences from environmental sample can be identified by comparing them to a reference database. However, no reference database is complete regarding neither taxonomy or sequence variation within taxa. Most studies based on environmental samples therefore rely on some clustering algorithm to group sequences into taxonomic units. The units are often referred to as molecular operational taxonomic units (MOTUs), but are often treated as species when interpreting the results of the study. How well MOTUs approximate species will depend on the clustering algorithm, the within species variation, and the between species variation. All *de novo* clustering algorithms (that only depend on the information in the data to be clustered) have problems delimiting species when the sequence distance within species is large compared to the distance between species. Together with the rate of molecular evolution, within species variation is largely determined by population size, while between species variation is largely determined by speciation rate. Estimates of speciation rates indicate that the probability of lumping species is large with commonly used clustering algorithms and cut-offs. At the same time these cut-offs are also likely to split species assuming a standard coalescence process, reasonable generation times, and population sizes (e.g. population size 50 000, generation time 3 yrs, and 3 substitutions per base and billion years). That there often is an overlap in within and between species sequence distances, is confirmed by many studies delimiting species by testing sexual compatibility. *Contributed Talk C7.6*

**241. Population genetic structure in two species of *Lophodermium* inhabiting five-needle pines of the US Pacific Slope revealed by ddRAD-seq \*Salas-Lizana, Rodolfo**(1,2) Oono, Ryoko(1) (1)University of California, Department of Ecology, Evolution and Marine Biology, Santa Barbara,

California 93106, USA; (2)Universidad Nacional Autónoma de México, Facultad de Ciencias, Mexico City 04510, Mexico. rsalas@ciencias.unam.mx

Fungal endophyte communities of pine needles are dominated by species of *Lophodermium*, which have high genetic diversity possibly due to cryptic species without morphological diversification. In order to uncover cryptic species and investigate the processes underlying genetic diversification, we combined morphological and genomic data from Lophodermium inhabiting natural populations of *Pinus monticola* and *P. lambertiana* in 16 localities of western US. We cultured more than 250 strains from both apothecia and healthy green needles and sequenced ITS nrDNA from 154 of them for an initial species delimitation. We then sequenced double- digested Restriction Associated DNA sequence (ddRAD-seq) libraries using Illumina MiSeq platform. We also made microscopic observations of apothecia to determine if morphological variation correlated with DNA variation. ITS sequences alone revealed two well-differentiated lineages, which correspond morphologically to L. nitens and a potential new species. Using the pyRAD v.3.066 pipeline, ddRad- seq revealed 40 and 20 thousand loci on average per individual for L. nitens and L. sp. nov., respectively. The mean number of shared loci among a set of 20 individuals of the same species was 500 for *L. nitens* and 179 for *L. sp. nov.* We found no spatial structure for *L. nitens* using Structure v.2.3.4, but identified two clear distinct populations for *L. sp. nov.* that were not evident with ITS alone. Haplotype networks of a group of ddRad loci confirmed these results. The lack of a clear pattern for *L. nitens* may be due to a combination of incomplete lineage sorting and gene flow, which has previously been observed for Mexican populations. In contrast, the two populations of *L. sp. nov.* may represent cryptic sister species with identical morphology and the result of allopatric speciation. A complete genome of *L. nitens* in progress will allow us to explore the mechanisms of speciation for these species in depth. *Contributed Talk C3.3*

**242. *Guyanagarika*, a new ectomycorrhizal genus of Agaricales from the Neotropics \*Sánchez-García, Marisol**(1), Henkel, Terry(2), Aime, Catherine(3), Smith, Matthew(4), Matheny, Brandon(1)

1.Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA; 2.Department of Biological Sciences, Humboldt State University, Arcata, CA 95521, USA; 3.Department of Botany & Plant Pathology, Purdue University, West Lafayette, IN 47907, USA; 4.Department of Plant

Pathology, University of Florida, Gainesville, FL 32611, USA. msanche8@vols.utk.edu

A new genus and three new species of Agaricales are described from the Pakaraima Mountains of Guyana in the central Guiana Shield. These taxa have been found to form ectomycorrhizal (ECM) associations with *Dicymbe* spp. Multi-locus molecular phylogenetic analyses place *Guyanagarika* gen. nov. within the *Catathelasma* clade, a lineage in the suborder Tricholomatineae of the Agaricales. We formally recognize this “*Catathelasma* clade” as an expanded family Catathelasmataceae that includes the genera *Callistosporium, Catathelasma, Guyanagarika, Macrocybe*, *Pleurocollybia,* and *Pseudolaccaria*. Within the Catathalasmataceae, *Catathelasma* and *Guyanagarika* represent independent origins of the ectomycorrhizal habit. *Guyanagarika* is the first documented case of an ECM Agaricales genus known only from the Neotropics. *Poster P4*

**243. Tranzscheliellaceae fam. nov. (Ustilaginales, Ustilaginomycotina) and the phylogeny of *Tranzscheliella*\*Savchenko, Kyryll G.**, Carris, Lori M.

Department of Plant Pathology, Washington State University, Pullman, WA 99164, USA. kyryll.savchenko@wsu.edu

*Tranzscheliella* is a genus of grass-parasitic smut fungi with seventeen species found in tropical and temperate regions of both hemispheres. Previous multigene phylogenetic study on Ustilaginomycotina placed *Tranzscheliella* within Ustilaginales (Begerow 2006), however its relation to any of the described families was unclear. The present study is a first attempt to clarify the phylogenetic position of the genus within Ustilaginales and the species diversity of *Tranzscheliella* analyzing both morphological and molecular data. Our analysis was focused on the three most widespread species, *T. hypodytes, T. minima,* and *T. williamsii,* with two additional species included in the analysis. More than 100 geographically diverse specimens from all known genera of host plants were examined and analyzed. DNA extracted from teliospores from 51 specimens from different hosts from Europe, Australasia, North and South America was used to amplify ITS, LSU and TEF regions used in phylogenetic analyses. The results of Bayesian analysis demonstrated that *Tranzscheliella* is monophyletic and a sister lineage to Ustilaginaceae, hence a new family will be proposed, *Tranzschelielaceae* fam. nov. The analysis also provided evidence that the genus originated on Stipeoid hosts, and that *T. hypodytes, T. minima,* and *T. williamsii* are polyphyletic. Hierarchical clustering analyses of morphological characters assessed with

light and scanning electron microscopy (spore size and ornamentation) showed high support for the differentiation of several clades as distinct from *T. hypodytes, T. minima,* and *T. williamsii* (Fig. 1). Further studies will likely reveal additional lineages of these complex smut fungi.

*Poster P95*

**244. A most intimate symbiosis: Seed-endophyte growth and transcriptome changes associated with vertical transmission \*Schardl, Christopher L.**(1), Nagabhyru, Padmaja(1), Liu, JinGe(1), Dinkins, Randy D.(2) 1.University of Kentucky, Plant Pathology, Lexington, KY 40546-0312, USA; 2. United States Department of Agriculture Agricultural Research Service, Forage and Animal Production Research Unity, Lexington, KY 40546-0312, USA. schardl@uky.edu

Recent discoveries have demonstrated that seed transmission of symbiotic ascomycetes involves greater diversity of fungi and host plants than previously appreciated. Such intimate symbioses have long been associated with the fungal family Clavicipitaceae (order Hypocreales) in grass plants (order Poales), but have been documented recently for Pleosporales in Fabales, Hypocreales in Solanales, and Chaetothyreales in Solanales. For over a century, symbioses of *Epichloe* species with *Lolium* species of grasses have been a model for studying systemic, seed-transmitted symbiosis. Tracking *Epichloe festucae* through the life cycle of its host, *Lolium perenne* (perennial ryegrass), we observed colonization of inflorescence primordia, ovaries, ovules, embryos and seedlings. Our results suggest a pause-and-resume model of growth whereby, while host reproductive primordia differentiate the fungus pauses, after which the fungus resumes rapid growth to invade and ramify the newly differentiated tissues. Transcriptome analysis of *Epichloe coenophiala* in *Lolium arundinaceum* (tall fescue) indicated that, in host reproductive primordia such as pre-anthesis ovaries, the fungus dramatic increases expression of genes for heat-shock proteins (HSP) and responses to reactive oxygen species (ROS), including ROS scavenging. In contrast, analysis of the plant transcriptome gives no indication of any response to heat-shock or ROS in the corresponding host tissues. Several published reports indicate that fungus-derived ROS autoregulates *E. festucae* in differentiated and expanding vegetative tissues of the plant, suppressing invasive growth and maintaining intercalary growth of the fungus. We suggest that in differentiating tissues ROS signals the fungus to pause, and then ROS scavenging signals the fungus to resume rapid proliferation. We suggest, further, that invasive growth requires rapid protein synthesis, in turn requiring

increased expression of chaperones and chaperonins; i.e., HSPs. *Contributed Talk C1.6*

**245. Who got there first? Effects of yeast/bacterial colonization patterns on biofilm structure in kombucha, a food product and potential model for studies in multispecies biofilm formation**

**\*Schilz, Benjamin,** Osmundson, Todd W. University of Wisconsin – La Crosse, Department of Biology, La Crosse, WI, 54601, USA. benjaminschilz15@gmail.com

Bacterial-fungal biofilms are important in medicine, food production and safety, and natural and agricultural environments; however, much remains to be learned about the factors that influence the formation, maintenance, and dynamics of these multispecies communities. In this experiment, we examined biofilm formation in kombucha, a fermented beverage and potential model system for multispecies bacterial-fungal biofilm formation. Kombucha is comprised of a variety of yeasts and bacteria that inhabit a gelatinous mass of bacterial cellulose that acts as a scaffold. Previous research in yeast community assembly suggests an important role of priority effects – i.e., that the order of species’ arrival affects the structure of the community. We examined the process and structure of biofilm formation of kombucha as it relates to the colonization order of bacteria and yeast species. Priority effects on physical structure, community structure, and patterns of spatial distribution of species, as well as evidence for changes in these variables over time, will be discussed.

*Poster P79*

**246. Making GenBank data beneficial to the publick and preventing it from being a burthen to the curators and taxonomists \*Schoch, Conrad L.,** Strope, Pooja, Robbertse, Barbara

National Institutes of Health, National Library of Medicine, National Center for Biotechnology Information, 45 Center Drive, MSC 6510, Bethesda, Maryland, 20892, USA. schoch2@ncbi.nlm.nih.gov

As part of the International Nucleotide Sequence Database Collaboration (INSDC) GenBank fulfils a dual role, acting as archive as well as database. RefSeq is a companion database where data is curated. We will present the latest ways to enhance and improve fungal identification, using both databases. This will involve elucidating recent efforts to improve the database representations by focusing on sets of well defined, high profile genera. As part of this process continued efforts to annotate sequences obtained from type and reference material at NCBI Taxonomy will be discussed. The potential for fast verification and

semi-automated taxonomic changes in full genomes will be discussed, focused on an original proposal by Scott Federhen at NCBI. *Contributed Talk C15.2*

**247. The roles of flippases in morphology and secretion of *Aspergillus nidulans*\*Schultzhaus, Zachary**, Shaw, Brian Texas A&M University, Department of Plant Pathology and Microbiology, College Station, Texas, 77845, USA. schultzz@tamu.edu

Despite the being excellent systems for the study of cell biology, the fundamental molecular mechanisms controlling growth and development of filamentous fungi are still unclear. One incontestable process that functions in fungal growth, however, is membrane trafficking. Hyphal extension is driven by targeted vesicle fusion that reshapes and builds upon the plasma membrane at the cell tip, while during the development of other cell types (e.g. conidiophores), the machinery involved in hyphal growth is reorganized in order to direct membrane fusion appropriately. Many proteins and lipids are involved in maintaining and reorganizing growth. One conserved family, the type 4 P-type ATPases, also known as flippases, has been shown to include porteins involved in secretion, drug resistance, conidiation, pathogenicity, and growth in fungi, but a thorough, directed investigation of their functions in these processes has not been completed. Here, we present data suggesting that *A. nidulans* flippases DnfA and DnfB regulate vesicle turnover in the hyphal tip, as well as the stability of the zone of secretion. Additionally, another flippases, DnfD, plays a surprising role in asexual development but has no discernible role in hyphal growth. These results demonstrate that different flippases in fungi may play distinct roles in reproduction and somatic growth through modulation of the secretory pathway. *Contributed Talk C20.8*

**248. The Santa Cruz Mycoflora Project: Fostering local initiatives; the need for Nexus Folks, and other strategies for Actually Doing It. \*Schwarz, Christian**, Ryszka, Adam, Lay, Chris Norris Center for Natural History, University of California, Environmental Studies Department, Santa Cruz, CA, 95060, USA. cfs.myko@gmail.com

Many researchers in ecology and evolution, land managers, taxonomists, and biodiversity enthusiasts have long expressed a desire for basic mycofloristic knowledge in North America. However, to this day, fundamental data about the biodiversity of macrofungi in our area continues to be frustratingly thin, fragmented, and/or inaccessible. Accumulation of such data is hampered in part by little taxonomic expertise

at academic institutions, and in part by inefficient and often uncoordinated efforts to compile the data that does exist. The North American Mycoflora Project was conceived as an initiative to help address this unmet desire, but has failed to gain traction for a number of reasons. A model for fostering local mycoflora initiatives has been put into action in Santa Cruz County (CA): By lowering barriers to contributon, defining the role of Nexus Folks, building functional relationships with academics, and by using narrative techniques to stimulate, harness, and focus the enthusiasm of amateur mycologists, we have made significant progress in compiling a mycoflora for our county. For each species, we aim to represent basic biodiversity data comprising six components: 1. photography, 2. microscopic morphology data, 3. DNA sequence(s) 4. fruiting phenology data, 5. known geographic distribution, and 6. ecological information at www.scmycoflora.org. We recommend that this model be replicated on small scales around the country. Linking the data generated by such regional projects is the most effective strategy for making forward progress on a North American Mycoflora. *Poster P14*

**249. Taxonomy of fungi producing emerging mycotoxins \*Seifert, Keith A.**Ottawa Research & Development Centre, Agriculture & Agri-Food Canada, Ottawa, K1A 0C6, Ontario, Canada. keith.seifert@agr.gc.ca

The European Food Safety Association (EFSA) published a list of mycotoxins being newly considered for regulation in human food and animal feed, which alongside reductions already implemented for limits to previously regulated mycotoxins, changes the landscape for export commodities in North America. The list of major toxins produced by *Aspergillus, Fusarium* and *Penicillium* species could be emended to include additional toxins, while mycotoxins produced by *Alternaria* and *Claviceps* may be added. Sloppy taxonomy combined with inadequate chemical analysis has caused huge confusion about what species produce what toxins; we must learn from these past mistakes. Among the toxins being re-evaluated are citrinin, patulin and sterigmatocystin (all widely distributed in *Eurotiales*), penitrem A, PR-toxin, roquefortine C (*P . roquefortii*), ergot alkaloids (*Claviceps* spp.), beavericins, enniatins, T2-toxin and deoxynivalenol glucosides (*Fusarium* spp.), AAL- toxin and various derivatives of alternariol (*Alternaria alternata* complex). Existing controversies about the generic concepts of *Alternaria, Aspergillus* and *Fusarium* do not help the situation, but except for *Aspergillus*, would not affect the names of mycotoxigenic species. Phylogenetic species concepts

are well defined, probably stable, and supported by carefully curated sequence databases in *Aspergillus, Fusarium* and *Penicillium*, but almost unexplored in *Claviceps,* and controversial in *Alternaria.* Full genome sequencing is now beginning to affect the taxonomy of mycotoxigenic fungi, especially in *Alternaria, Aspergillus,* and *Fusarium.* We can envisage a time within 5-10 years when simultaneous identification of both species and mycotoxigenic capacity will be possible and routine.

*Contributed Talk C16.2*

**250. Endohyphal bacterium (*Chitinophaga* sp.) influences broad-spectrum substrate use by its host fungus (*Fusarium keratoplasticum*) \*Shaffer, Justin P.**(1), Baltrus, David A.(1), Arnold, A. Elizabeth(1,2)

1.University of Arizona, School of Plant Sciences, Tucson, 85721, USA; 2.University of Arizona, Department of Ecology and Evolutionary Biology, Tucson, 85721, USA. justinshaffer@email.arizona.edu

Plant-associated fungi are major drivers of tropical tree demography, population structure, and community dynamics, and are one of the most critical but least-studied aspects of tropical forest ecology. Diverse Ascomycota associate with seeds in the soil, influencing seed survival, germination, and ultimately forest structure and regeneration. Often the outcomes of seed-fungus interactions are context-dependent, and can be influenced by additional microbes that alter fungal phenotypes. Recently, we detected diverse bacterial endosymbionts (endohyphal bacteria) in seed-associated fungi from lowland tropical forests. Many endohyphal bacteria in these fungi can be removed using antibiotic treatment, providing a basis for experimentally assessing the effects of bacteria on the functional traits of their fungal hosts. Here we examined the effects of a focal endohyphal bacterium (*Chitinophaga* sp.*,* Bacteroidetes) on substrate use by its host, a seed-associated fungus (*Fusarium keratoplasticum* strain PS0362a). We compared growth between naturally infected and cured fungal clones across 95 carbon- and nitrogen sources. Across the majority of substrates (64.2%), clones harboring the bacterium significantly outperformed cured clones as measured by respiration and hyphal growth. These substrates include many particularly important for plant- and seed-fungus interactions. We highlight the potential influence of endohyphal bacteria on the breadth and efficiency of substrate use by *F. keratoplasticum,* and complement these trials with assessments of seed germination following inoculation with naturally infected and cured clones. We found seed germination to be significantly greater when seeds were treated with infected vs. cured fungal clones. Here we propose a model in which additive or

synergistic substrate use by the fungus-bacterium pair enhances fungal growth, resulting in subsequent degradation of seed coat integrity, and a hastening of imbibition and germination by the seed.

*Contributed Talk C13.6*

**251. Interspecific and intraspecific hybrid *Epichloë* species hosted by *Poa alsodes*: Distributions, phylogenies, morphologies, and alkaloids \*Shymanovich, Tatsiana**(1), Charlton, Nikki(2), Cech, Nadja(3), Young, Carolyn(2), Faeth, Stanley(1) 1.University of North Carolina at Greensboro, Biology Department, Greensboro, NC, 27412, USA; 2.The Samuel Roberts Noble Foundation, Forage Improvement Division, Ardmore, OK, 73401, USA. 3.University of North Carolina at Greensboro, Biochemistry Department, Greensboro, NC, 27412, USA. t\_shyman@uncg.edu

Latitudinal sampling of the woodland grass, *Poa alsodes*, from 23 populations located from North Carolina to New York showed 92% infection with endophytic *Epichloë* species. Two distinct endophyte genotypes, PalTG-1 and PalTG-2, that represented different *Epichloë* species, were identified. The endophyte genotype PalTG-1 was present in 22 populations mostly at high infection frequencies of 96- 100%. Only five populations harbored PalTG-2, which were limited to Pennsylvania, and four of these also harbored PalTG-1. Phylogenetic analyses of PalTG-1 revealed an undescribed interspecific hybrid (proposed name *E. alsodes*) with ancestral progenitors of *Epichloë amarillans* and *Epichloë typhina* subsp. *poae*. PalTG-1 contains both mating types, whereby the *MTA* and *MTB* idiomorphs are from *E. typhina* subsp. *poae* and *E. amarillans*, respectively. Genetic markers associated with peramine (*perA* gene), loline (*lolC*, *lolA* and *lolO* genes) and ergot alkaloid (*dmaW* and *easC* genes) production were identified, but only *N*-acetylnorloline (0.37 mg/g to 4.36 mg/g) was detected in PalTG-1 infected plant material. Point mutations identified in *perA* (encoding peramine synthestase) and *dmaW* (encoding the first step in ergot alkaloid biosynthesis) would render these genes non-functional. In culture, three PalTG-1 morphotypes were observed with growth rates from 7.7 to 11.4 mm/week. Single conidiophores produce obovate to reniform, oblong, or allantiod conidia. PalTG-2 is phylogenetically similar to *E. schardlii*, an intraspecific hybrid of two *E. typhina* subsp. *poae* strains. Only the *perA* gene is present, but peramine was not detected in PalTG-2 infected plant material. The lack of peramine may indicate that *perA* is not functional, although no mutations have been identified. PalTG-2 produces both single and sympodial conidiophores and has faster colony growth than *E. schardlii*. Additional analyses will be required

to determine if *E. schardlii* and PalTG-2 are the same species. *Contributed Talk C2.1*

**252. Immobilization of laccase onto chitosan beads to enhance its capability to degrade synthetic dyes \*Si, Jing**, Cui, Bao-Kai, Zheng, Fei, Dai, Yu-Cheng Beijing Forestry University, Institute of Microbiology, Beijing, 100083, P.R. China. Jingsi1788@126.com

Loss in activity and denaturation remain key challenges to the potential use of laccase in industrial applications. One of the most important aims of enzyme technology is to enhance the stability and reusability of enzymes through immobilization processes. Here, a purified laccase (Tplac) from the white rot fungus *Trametes pubescens* was entrapped onto chitosan beads with the crosslinker glutaraldehyde, in order to improve the stability and recovery rate of Tplac, and was applied in decolorization of various synthetic dyes. The optimal conditions for Tplac immobilized onto chitosan beads were 0.8% (v/v) glutaraldehyde concentration, 3 h crosslinking time, 2 mL enzyme solution (approximately 43.672 U/mL), and 4 h immobilization time. The pH adaptability and resistance to thermal denaturation of immobilized Tplac were considerably enhanced compared with free Tplac, and both the operational stability and durability during multiple reuses were superior to those of free Tplac; after six cycles of continuous use, the activity of immobilized enzyme remained above 60%. Also, immobilized Tplac was able to degrade various synthetic dyes, especially metal-complex dye Acid Black 172. Results of this study demonstrated that, alongside the better stability and reusability of immobilized Tplac, the immobilized enzyme could be used in many applications.

*Poster P152*

**253. New *Raffaelea* species (Ophiostomatales) from the United States and Taiwan associated with ambrosia beetles and plant hosts. \*Simmons, D. Rabern**(1), De Beer, Z. Wilhelm(2), Huang, Yin-Tse(1), Bateman, Craig C.(1), Campbell, Alina S.(3), Dreaden, Tyler J.(4), Li, You(1), Ploetz, Randy C.(3), Wingfield, Michael J.(2), Hulcr, Jiri(1) 1.University of Florida, School of Forest Resources and Conservation, Gainesville, FL, 32611, USA; 2.University of Pretoria, Forestry and Agricultural Biotechnology Institute (FABI), Pretoria 0002, Gauteng Province, South Africa; 3.University of Florida, Tropical Research and Education Center, Homestead, FL, 33031, USA; 4.USDA-Forst Service, Southern Research Station, Lexington, KY, 40517, USA. hulcr@ufl.edu

*Raffaelea* (Ophiostomatales) is a genus of more than 20 fungi commonly in symbioses with wood- boring ambrosia beetles. We examined ambrosia beetles and plant hosts in the United States and Taiwan for the presence of these mycosymbionts and found 22 isolates representing known and undescribed lineages of *Raffaelea*. From 28S rDNA and βT sequences, we generated a molecular phylogeny of the Ophiostomatales, observed morphological features of seven cultures representing undescribed lineages in *Raffaelea s. str*., and describe five new *Raffaelea* species. Our analyses also identified two plant- pathogenic species of *Raffaelea* associated with previously undocumented beetle hosts: (1) *R. quercivora*, the causative agent of Japanese oak wilt, from *Cyclorhipidion ohnoi* and *Crossotarsus emancipatus* in Taiwan, and (2) *R. lauricola*, the pathogen of laurel wilt, from *Ambrosiodmus lecontei* in Florida. The results of this study show that *Raffaelea* and associated ophiostomatoid fungi have been poorly sampled and that future investigations on ambrosia beetle mycosymbionts should reveal a substantially increased diversity. *Poster P89*

**254. Where are the *Phytophthora ramorum* infected bay laurels in California coastal oak forests during drought? \*Sims, Laura**, Garbelotto, Matteo

University of California, Environmental Science, Policy, and Management Department, Berkeley, CA, 94720, USA. simslaura@berkeley.edu

*Phytophthora ramorum,* causal agent of sudden oak death (SOD), is less active during drought, but where does it remain? In addition, what is the distribution of infected bay laurels (*Umbellularia californica*) during a drought? Bay laurels are the most important carrier of *P. ramorum,* and only bay laurel, tanoak (*Notholithocarpus densiflorus*), and possibly redwood (*Sequoia sempervirens*) are epidemiologically important for the spread of SOD in California. During a severe multi-year drought, we sampled 25 randomly selected bay laurels in each of thirty plots to improve our understanding of the drought ecology of SOD and inform management options. In addition, we tallied all bay laurel, redwoods, and tanoaks per plot. We evaluated the spatial distribution patterns of infected/uninfected bay laurels. We found that 119 bay laurels were infected and their distribution was thin (average 6 per plot, range 1-11), and widespread (25 of the 30 plots). In most cases, infected bay laurels appeared aggregated in small groupings within a plot, and there may be a relationship between aggregation, bay laurel density and/or carrier density. Further evaluation is necessary to determine if infested bay laurel removal in lower

density plots would help to lower local inoculum levels once the conducive periods return. *Poster P63*

*Contributed Talk C7.1*

**256. Broken covenant: Experimental symbiont switching in the ambrosia beetle symbiosis \*Skelton, James**, Nolen, Zachary, Bateman, Craig, Johnson, Andrew, Hulcr, Jiri

University of Florida, School of Forest Resources and Conservation, Gainesville FL, 32603 USA. skelto3@gmail.com

Mutualisms between insects and fungi provide many of the most fascinating and well-known examples of co-evolution. Mutual dependence and partner fidelity are thought to catapult symbiotic lineages down trajectories of co-speciation and co- extinction. However, the ties that bind mutualists together are not always clear and sometimes looser than they appear. Several related genera of wood- boring ambrosia beetles cultivate gardens of *Ambrosiella* fungi (Microascales: Ceratocystidacea). The beetles feed extensively on fungal gardens and have large glandular organs called mycangia, used for transporting live fungal inoculum to new galleries. Observational studies indicate high partner fidelity between ambrosia beetles and their fungal symbionts across often global distributions, suggesting that these associations may be strictly species-specific. In this study, we experimentally examined fungal symbiont specificity in the black twig borer (*Xylosandrus compactus*). We reared beetle eggs and pupae in sterilized wooden galleries inoculated with a variety of fungi from multiple ambrosial clades. Adult beetles were successfully reared on multiple fungal species. Moreover, culture and DNA sequencing confirmed that the mycangia of some emergent beetles contained thousands of viable spores from alternative fungal taxa. Our results show that ambrosia symbioses are not necessarily species-specific because the beetles can feed on multiple fungal species, and multiple fungal species may proliferate within the beetle’s mycangium. Thus we suggest that the apparent specificity observed in ambrosia beetle symbioses may be a result of divergence in isolation, deterministic outcomes of competitive interactions between fungi, or under sampling. *Contributed Talk C9.6*

**257. Tall fescue-*Epichloë coenophiala* associations affect belowground fungi and host, symbiont response to climate change**Slaughter, Lindsey(1), Nelson, Jim(1), Carlisle, A. Elizabeth(1), Bourguignon, Marie(2), Dinkins, Randy(3), Phillips, Tim(1), **\*McCulley, Rebecca L.**(1)



**255. Influence of barcode choice on automated clustering of OTUs and implications for**

**metagenomic studies: A case study**

**\*Skaltsas, Demetra** (1), Castlebury, Lisa(2), Gazis,

Romina(3), Chaverri, Priscila(1,4

1. University of Maryland, Department of Plant Science and Landscape Architecture, 2102 Plant

Sciences Building, College Park, Maryland 20742

U.S. Department of Agriculture, Agricultural Research Service, Systematic Mycology and Microbiology Laboratory, 10300 Baltimore Avenue, Building 010A,

Beltsville, Maryland 20705

;

3. University of

Tennessee, Department of Entomology and Plant Pathology, 2505 E. J. Chapman Drive, 370 Plant

Biotechnology Building, Knoxville, TN 37996

Escuela de Biología, Universidad de Costa Rica,

ADDRESS San Pedro, San José, Costa Rica.

demetraskaltsas@gmail.com

)

; 2.

; 4.

choice when amplification of several markers is not

feasible.

  

The internal transcribed spacer region (ITS), the recommended fungal DNA barcode, is commonly used for clustering sequences into Operational Taxonomic Units (OTU) which are used in diversity estimates or to select representative isolates for further sequencing efforts. Automated clustering methods (ie. MOTHUR) are a popular choice for the large datasets produced by next generation sequencing. Due to sequence amplification length limitations, metagenomic projects usually target ITS1, or more commonly ITS2. In an effort to evaluate the performance of traditional fungal markers for automated clustering in MOTHUR, results obtained using only ITS2 were compared against ITS (entire), TEF-1, TUB, and HIS. Gene and multigene phylogenetic trees were then built. The number and composition of the OTUs detected by MOTHUR were compared to those inferred through phylogenetic reconstruction. As a case study, the highly diverse and ubiquitous fungal genus *Diaporthe* was selected. 970 sequences obtained from two tropical tree genera (*Hevea* and *Micrandra*) and sequences gathered from NCBI that represented ex-type cultures were used. TEF1 was the most efficient locus for initial clustering of sequences into OTUs, while ITS2 performed the poorest. TEF1 clustering was concordant to the phylogenetic species inferred through multilocus analysis. Clustering based solely on ITS2 gave disparate results; some individuals of the same species were split into different OTUs while different species were clustered into the same OTU. These results show that choice of barcode have major implications on diversity estimates and that perhaps TEF1 is a better

1.University of Kentucky, Department of Plant & Soil Sciences, Lexington, KY 40546-0091 USA; 2.Iowa State University, Department of Agronomy, Ames, IA 50011 USA; 3.USDA-ARS Forage Animal Production Research Unit, Lexington, KY 40546-0091 USA. rebecca.mcculley@uky.edu

Plants interact with myriad microorganisms, which influence ecosystem processes and can regulate ecosystem response to global change. One important symbiosis occurs between the grass, tall fescue (*Schedonorus arundinaceus*), and the asexual fungal endophyte *Epichloë coenophiala*. Because the common toxic endophyte (CTE) strain harms grazing livestock, non-livestock toxic endophyte (NTE) strains are increasingly deployed in pastures. Little is known about how these symbioses impact other plant- microbe-soil interactions in grasslands or how these relationships will respond to climate change. Utilizing a climate change study, where grassland plots were subjected to factorial combinations of increased heat (+3°C, year-round) and precipitation (+30% of long- term annual mean precipitation), we planted cloned pairs of two tall fescue genotypes and subjected them to two years of climate manipulation. Within a clone pair, one individual was endophyte-infected (either CTE+ or NTE+) and the other was endophyte-free (CTE- or NTE-). We investigated how belowground fungal symbioses were altered by tall fescue-*E. coenophiala* genetics and climate change treatments by measuring root arbuscular mycorrhizal fungi (AMF) and fungal dark septate endophyte (DSE) colonization and estimated length of extraradical AMF hyphae (ERH) in soils via microscopy. We hypothesized that 1) unique combinations of host and endophyte genotypes differentially affect belowground fungal colonization, and 2) these associations would be impacted by warming and added precipitation. AMF arbuscules and vesicles and ERH were significantly affected by tall fescue genotype, endophyte status, and climate change treatments. Root DSE were reduced by endophyte presence but stimulated by warming. Genetically distinct *E. coenophiala*-tall fescue associations may have divergent long-term impacts on other host-symbiont interactions and belowground communities under future climate change conditions. *Symposium S6.1*

**258. A survey of root-colonizing basidiomycete saprotrophs reveals formation of mantle and Hartig net-like structures \*Smith, Gabriel R.**(1), Finlay, Roger(2), Stenlid, Jan(2), Vasaitis, Rimvydas(2), Menkis, Audrius(2) 1.Stanford University, Department of Biology, Stanford, CA, 94305, USA; 2.Swedish University of Agricultural Sciences, Department of Forest Mycology

& Plant Pathology, Uppsala, 756 51, Sweden. gabrielsmith1@gmail.com

The ectomycorrhizal (ECM) symbiosis has evolved a minimum of 78 times independently from saprotrophic lineages; some phylogenies have even posited reversals in which ECM groups return to saprotrophy. These multiple instances of convergent evolution have resulted in functional overlap between ectomycorrhizal and saprotrophic fungi, which affects global biogeochemical cycles. While ECM fungi exhibit certain capacity to participate in decomposition or to act as facultative saprotrophs, there is increasing evidence that saprotrophic fungi may also exhibit the ability to enter into facultative relationships with plant roots without causing symptoms of disease. However, the latter phenomenon is not well studied and it is not known how widespread this capacity may be, nor which systems would be most promising for further research. In order to address this, we investigated the morphology of living conifer seedling roots colonized *in vitro* by an array of over 200 basidiomycete fungi, revealing formation of mantle and Hartig net-like structures. These features suggest the possibility of an active functional symbiosis between fungus and plant, demonstrating notable potential for genomic and transcriptomic work in these systems, which would provide a new vantage-point from which to study the

evolution of the ECM symbiosis.

*Poster P57*

**259. The Humungous Fungus of northern Michigan three decades on**Smith, Myron L.(1), Rodrigue, Nicolas(1), Bruhn, Johann N.(2), **\*Anderson, James B.**(3)

1.Department of Biology, Carleton University, Ottawa, ON Canada K1S 5B6; 2.Division of Plant Sciences, University of Missouri, Columbia, MO 65211; 3.University of Toronto, Department of Biology, Mississauga, ON, Canada L5L 1C6. jb.anderson@utoronto.ca

Nearly three decades ago, in 1988, we began collecting and genotyping samples of the basidiomycete fungus *Armillaria gallic*a from a 150 X 50 m clear cut site and surrounding mixed-hardwood forest on the Upper Peninsula of Michigan. We quickly learned that many of the collections over several hectares in and around the clear cut had identical genotypes and hence belonged to the same large genetic individual, which subsequently became widely known as “The Humungous Fungus.” Since each genetic individual arises in a unique mating event and then grows vegetatively over a territory, we came to realize that such fungal individuals could reveal the spatial and temporal record of spontaneous mutation, which is not accessible in most populations of organisms. To test this idea, we returned to the

Michigan site in 2015 to make 152 viable collections of *A. gallica*, each spatially mapped by GPS. Of these, 102 collections matched the genotype of the original large individual, which still resides on the site. Fifteen of the 102 collections that were spatially well distributed over the large individual were subjected to whole-genome, Illumina sequencing. There was no variability in the ca. 100 kb mtDNA in the fifteen collections and in a viable culture of the large individual from 1988, but numerous SNPs and indels distinguished the mtDNAs of four additional *A. gallica* individuals, two co-existing on the Michigan site in proximity to the large individual, and two from Ontario. The search for variation in the ca. 90 mb nuclear genome of the large individual is now in progress.

*Contributed Talk C3.5*

**261. Sink drains to sea turtle eggs: Unraveling the ecology and epidemiology of infectious fusaria in humans and animals \*Smyth, Christopher**(1), Sarmiento-Ramírez, J. M. (3), D. Short(2), Diéguez-Uribeondo, J. (3), Geiser, D.(2)

1.Department of Plant Pathology and Environmental Microbiology, Penn State University, University Park, PA 16802; 2.Department of Plant Pathology, West Virginia University, Morgantown, WV; 3.Spanish National Research Council, Real Jardin Botanico de Madrid, Madrid, Spain. cws187@psu.edu

Emerging fungal diseases of wildlife are increasingly common, with devastating consequences for biodiversity and ecosystem health. White-nose syndrome, snake fungal disease and chytridiomycosis of amphibians are all examples of fungal diseases that have taken, and continue to take, a major toll on populations of bats, snakes, and frogs, respectively. *Fusarium keratoplasticum* (Fk) and *Fusarium falciforme* (Ff) have been implicated in mass mortalities in the nests of endangered sea turtles. These are common, cosmopolitan species of filamentous fungi that are known opportunistic pathogens of immunosuppressed, and sometimes healthy, humans. Ff is an ubiquitous soil-associated species, while Fk occurs more frequently in areas under high anthropogenic influence, particularly in sink drains and in human infections. 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. 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.

*Contributed Talk C1.3*

**262. A comparison of clustering methods across diverse fungal communities using next-generation sequencing**Song, Zewei(1), Cline, Lauren C.(2), Al-Ghalith, Gabriel A.(3), Knights, Dan(3,4), **\*Kennedy, Peter G.**(2,5)

1.University of Minnesota, Department of Plant Pathology, St. Paul, MN, 55108 USA; 2.University of Minnesota, Department of Plant Biology, St. Paul, MN, 55108 USA; 3.Biomedical Informatics and Computational Biology, University of Minnesota, Minneapolis, Minnesota, USA; 4.Department of Computer Science and Engineering, University of Minnesota, Minneapolis, Minnesota, USA; 5.University of Minnesota, Department of Ecology, Evolution, and Behavior, St. Paul, MN, 55108 USA. kennedyp@umn.edu

Given the rapid proliferation of bioinformatics tools available for processing fungal next-generation sequencing data, there is a clear need to identify strengths and weaknesses among methods. Here we compared MiSeq-based ITS amplicon data from four habitats (soil, dead wood, living wood and living leaves) using two closed reference (NINJA-OPS and Blast) and four de novo (USEARCH, VSEARCH, CD-HIT, and SWARM) clustering methods. All of the clustering methods except USEARCH performed equally well in terms of capturing the richness and composition of a known mock community, particularly when rare OTUs (<10 reads) were excluded. In terms of community characterization, the closed reference and de novo methods provided taxonomically similar results for the soil, wood, and leaf endophyte communities, but only the de novo methods sufficiently characterized the wood endophyte communities, which contained many poorly known fungi. The four denovo methods consistently captured higher OTU richness than the closed reference methods, although leaf endophyte richness was inflated with both the SWARM and CD-HIT algorithms. Despite clear differences in absolute OTU richness between clustering methods, richness comparisons across habitats were equivalent between closed reference and de novo methods. Furthermore, measures of fungal community composition were remarkably similar when using both incidence- and abundance-based distance metrics. Collectively, these results suggest that de novo clustering methods remain the most robust approach for fungal community analyses, but that closed reference methods can

accurately capture the same general ecological patterns for communities containing relatively well-studied fungi. *Contributed Talk C7.5*

**263. A phylum-level phylogenetic classification of zygomycete fungi based on genome-scale data \*Spatafora, Joseph W.**(1), Stajich, Jason E.(2), ZyGoLife Research Consortium.(3)

1.Dept. of Botany and Plant Pathology, Oregon State University, Corvallis, OR 97331 USA; 2.Dept. of Plant Pathology and Microbiology, University of California, Riverside, Riverside, CA 92521 USA; 3.http://zygolife.org/home/.

Zygomycete fungi were classified as a single phylum, Zygomycota, based on sexual reproduction by zygospores, frequent asexual reproduction by sporangia, absence of multicellular fruiting bodies, and production of coenocytic hyphae; all with some exceptions. Molecular phylogenies based on one or a few genes did not support the monophyly of the phylum, however, and the phylum was subsequently abandoned. Here we present phylogenetic analyses of a genome-scale data set for 46 taxa, including 25 zygomycetes and 192 proteins, and we demonstrate that zygomycetes comprise two clades that form a paraphyletic grade. A formal phylogenetic classification is proposed and includes two phyla, six subphyla, four classes and sixteen orders. On the basis of these results, the phyla Mucoromycota and Zoopagomycota are circumscribed. Zoopagomycota comprises Entomophtoromycotina, Kickxellomycotina and Zoopagomycotina; it constitutes the earliest diverging lineage of zygomycetes and contains species that are primarily parasites and pathogens of small animals (e.g., amoeba, insects, etc.) and other fungi, i.e., mycoparasites. Mucoromycota comprises Glomeromycotina, Mortierellomycotina and Mucoromycotina and is sister to Dikarya. It is the more derived clade of zygomycetes and mainly consists of mycorrhizal fungi, root endophytes, and decomposers of plant material. Evolution of trophic modes, morphology and analysis of genome-scale data will be discussed. *Contributed Talk C17.1*

**264. Cortical basidiomycetous yeasts in the largest radiation of macrolichens \*Spribille, Toby**(1,2), Tuovinen, Veera(3), McCutcheon, John(1)

1.University of Montana, Division of Biological Sciences, Missoula, MT 59812, USA; 2.University of Graz, Institute of Plant Sciences, Holteigasse 6, A- 8010 Graz, Austria; 3.Evolutionary Biology Centre, Uppsala University, Norbyvägen 18D, Uppsala 752 36, Sweden. toby.spribille@mso.umt.edu

For over 140 years, lichens have been regarded as a symbiosis between a fungus, usually an ascomycete, and one or more photosynthesizing partners. Together these symbionts form a body plan (thallus) with no known precedent in the ancestry of either symbiont. Secondary fungi present in lichen thalli have until now always been considered extrinsic to the symbiosis. In fact, the one lichen-one fungus paradigm has gone unchallenged for so long that it has been codified into lichen nomenclature. In a recent metagenomics study we uncovered evidence of a stably associated accessory fungus in healthy thalli of the family Parmeliaceae, the largest group of macrolichens worldwide. The secondary fungus derives from a new, major lineage of basidiomycetes that has rarely been sequenced. Fluorescent microscopy revealed that this fungus occurs as yeasts embedded in the lichen cortex, which plays a major role is thallus physiology. Our results suggest basidiomycete yeasts are ubiquitous in parmelioid macrolichens and in many cases highly species-specific. *Contributed Talk 19.4*

**265. New results on the phylogeography and functional biodiversity of the Xylariaceae (Sordariomycetes) \*Stadler, Marc**

Helmholtz Centre for Infection Research, Department Microbial Drugs, Inhoffenstrasse 7, 38124 Braunschweig, Germany. marc.stadler@helmholtz- hzi.de

The Xylariaceae are a large, hyperdiverse family of the Ascomycota. Several of these fungi have been known for a long time because they may produce conspicuous stromata on wood or dung. However, it has meanwhile been well-established that they also belong to the predominant endophytic mycobiota of seed plants, and may even dwell in marine algae, liverworts, lichens, or fruitbodies of basidiomycetes. Some species have even been recovered from insects, or from anatomic samples derived from hospitals. On the other hand, xylariaceous fungi are under investigation as producers of bioactive metabolites with selective activities against human, animal and plant pathogens, as well as industrial enzymes, or as biocontrol agents. However, little is currently known about their taxonomy, phylogeny, biogeography, and ecology. Our recent work involves taxonomic and chorological studies on the tropical members of the family, as well as the establishment of a multi-gene genealogy to provide a basis for concise identification of the genus *Hypoxylon* and allied taxa. In addition, we have studied the stromata and cultures of these fungi for the occurrence of biologically active secondary metabolites. While some of these compounds constitute valuable chemotaxonomic

marker molecules that helped to resolve species complexes, others show strong and selective activities in biological systems and may serve as lead compounds for development of anticancer agents, antibiotics or agrochemical fungicides. The results of our taxonomic work, with particular emphasis of a study of *Annulohypoxylon* and *Hypoxylon* in Argentina will be presented. Furthermore, some of our recent work on the discovery of novel secondary metabolites will be highlighted.

*Contributed Talk C4.1*

**266. Fungal population genomics of emerging diseases in plants, frogs, and people**\***Stajich, Jason E**.(1), Demers, Elora(2), Olarte, Rod(1,3), Masonjones, Sawyer(1), Carrillo, Joseph(1), Eskalen, Akif(1), O'Donnell, Kerry(4), Hogan, Deborah(2)

1.Dept of Plant Pathology & Microbiology, University of California, Riverside 92521, USA; 2.Geisel School of Medicine, Dartmouth University, Hanover, NH 03755, USA; 3.Dept of Ecology, Evolution, and Behavior, Plant Biology, University of Minnesota, MN, Saint Paul, MN 55108, USA; 4.USDA ARS NCAUR, Peoria, IL 61604 jason.stajich@ucr.edu

Whole genome sequencing of individuals from populations provides new approaches to study the diversification, adaptation, and demography of fungal populations. In our approaches we have studied the emerging infectious disease (EID) of amphibians *Batrachochytrium dendrobatidis* to understand its origin, spread, and mechanisms of diversification. We used these methods to better understand the types of diversity, changes in ploidy or CNVs, and to associate geographic locations with genetic diversity hotspots to suggest origins of the EID. We also undertook approaches to study the population biology of the recently emerging disease of avocado caused by *Fusarium euwallacea* in Southern California. This work has provided insight into the diversification, spread, and origins of this recently introduced pathogen. Evidence based on RADseq and whole genome sequencing suggests separate origins of introductions into the California agricultural and riparian ecosystems. Finally, studies of populations of *Candida lusitaniae* isolated from patient lungs reveals unexpected differences within a single individual patient and differences between individuals that indicate local adaptation or specialization. Together these observations provide some perspective on the approaches to studying emerging diseases and utility of population genomics to understand recent evolution of host-associated fungi and the interplay of adaptation and pathogenesis.

*Symposium S8.1*

**267. Copy Number Variation contributes to cryptic genetic variation in lineages of *Cryptococcus gattii* \*Steenwyk, Jacob L.**(1), Soghigian, John S.(1), Perfect, John R.(2), Gibbons, John G.(1)

1.Clark University, Department of Biology and Department of Biochemistry and Molecular Biology, Worcester, Massachusetts, 01610, USA; 2.Duke University School of Medicine, Department of Medicine, Durham, North Carolina, 27708, USA. jgibbons@clarku.edu

Copy number variation (CNV) can take the form of deletions, duplications and complex multi-loci variants. Recent advances in bioinformatics methodologies and sequencing technologies have enabled the high-resolution quantification of genome- wide CNV patterns. CNVs in pathogenic fungi have been shown to alter gene expression, influence host specificity, and drive fungicide resistance. Using publicly available sequencing data, we analyzed CNV profiles across 213 *Cryptococcus gattii* genomes, with a focus on isolates belonging to the VGII subgroups responsible for the recent deadly outbreaks in the North American Pacific Northwest. Population structure was determined using a panel of 1,223 SNPs with STRUCTURE and Discriminant Analysis of Principal Components revealing the presence of 8 subpopulations. CNV calling was performed using the read depth approach as implemented in Control-FREEC. We identified a total sum of 81,901 copy number variable regions (CNVRs) ranging from 100 bp to >700 kb across all samples. Analysis of CNV genes present in all VGII subgroups revealed enrichment of gene ontology terms associated with metabolism, biosynthetic pathways, membrane, and transport. Assessment of divergent CNV loci in subgroups belonging to the VGII lineage revealed 67 highly divergent CNV regions (CNVRs) harboring 58 genes. Analysis of PFAM domains located within divergent CNVRs revealed enrichment of protein domains associated with catabolism, metabolism, transport, external encapsulating structure and cell wall composition and organization. CNVRs identified in this study may contribute to virulence, gene expression, fungicide resistance, host specificity and a recent niche habitat expansion of *C. gattii*. The functional relevance and importance of the identified CNVRs requires further experimentation to provide insight to their contributions to difference in phenotype and pathogenicity. *Contributed Talk C11.4*

**268. Richness and biomass of truffle-producing fungi in the northeastern US from field surveys and eastern chipmunk (*Tamias striatus*) scat \*Stephens, Ryan S.**(1), Remick, Tyler J.(1,2), Ducey, Mark J.(1), Rowe, Rebecca J.(1)



1.University of New Hampshire, Natural Resources and the Environment, Durham NH 03824, USA; 2.Missouri State University, College of Natural and Applied Sciences, Springfield, MO, 65897 USA. ryan.stephens@unh.edu



In forested ecosystems, many mycorrhizal and small mammal species are mutualists. Mycorrhizal fungi produce sequestrate fruiting bodies (truffles) which provide a food source for small mammals. In exchange, mammals disperse fungal spores to new areas. Despite this important interaction, little is known about the diversity and biomass of truffle producing fungi in the northeastern US. We surveyed for truffles across hardwood (*n* = 256), mixed (*n* = 256), and softwood (*n* = 256) forest types at Bartlett Experimental Forest in the White Mountains of New Hampshire from June to October 2014. Additionally, we collected scat samples (*n* = 171) from eastern chipmunks (*Tamias striatus*) at the same sites and during the same period as truffle surveys. Our objectives were to quantify variation in the types and biomass of truffles among forest types and across the summer season and 2) whether eastern chipmunks consumed truffles relative to their availability. In total, field surveys yielded 14 species of truffles comprising 5 genera. Truffle biomass was highest in softwood (28.3 kg/ha) and mixed forest (24.7 kg/ha) and lowest in hardwood forest sites (3.29 kg/ha). Overall 85% of total biomass was contributed by one species, *Elaphomyces verruculosus*. Analysis of eastern chipmunk scat yielded 21 truffle taxa comprising 13 genera. Eastern chipmunks consumed *E. verruculosus* relative to availability, but selected for other taxa. Based on surveys and scat analysis, richness was higher in softwood and mixed forest than in hardwood forest. However, richness from surveys was constant over the season whereas taxa in scat increased linearly. Our study demonstrates that truffle production is quite high in northeastern forests and provides a key food source for eastern chipmunks. Based on the diversity 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. *Contributed Talk C10.2*

**269. Fungal communities of soybean cyst nematode-infested soils under monoculture and crop rotations \*Strom, Noah B.**, Bushley, Kathryn E.

University of Minnesota, Plant Biology, Saint Paul, MN 55108-1095, USA. stro0070@umn.edu

Soils that enable plants to resist infection, termed "suppressive soils," rely on the activity of resident microbes, including fungi, to keep plant pathogens in check. Development of fungal communities involved

in suppression of the soybean cyst nematode may follow a trajectory over continuous years of soybean monoculture. ITS amplicon sequencing was used to analyze fungal communities in bulk soils, rhizosphere soils, and roots in soybeans under annual and 5-year rotations with corn and under continuous monoculture in experimental plots at the University of Minnesota Southern Research and Outreach Center. The plots showed varying degrees of suppression to the soybean cyst nematode. Sequencing was performed on the Illumina MiSeq platform, and sequence data were filtered and trimmed using the bioinformatics package, mothur. OTU clustering and initial analyses were performed in QIIME, using the UNITE database as a reference to assign taxonomy to OTUs. Comparisons were made between community compositions determined using ITS1 or ITS2 amplicon sequencing. ITS1 sequencing resulted in fewer unassigned OTUs than ITS2 sequencing. Preliminary results show taxonomic differences in root, rhizosphere, and bulk soil communities and in fungal communities of soybean or corn under different crop rotation schedules. These data will help elucidate the effects of crop rotation and monoculture on soil fungal communities and the role of plant hosts in shaping their root and rhizosphere microbiomes in response to pathogen attack.

*Poster P75*

**270. Mycobiome in the gut of giant panda**

Su, Yuanying(1), Qi, Dunwu(2), James, Timothy Y.(3), Chen, Wen(4), Wang, Xuewei(1), Gao, Cheng(1), Yang, Wei(1), Chen, Liang(1), Liang, Junmin(1), **\*Cai, Lei(1)**

1.Institute of Microbiology, Chinese Academy of Sciences, State Key Laboratory of Mycology, Beijing, 100101, China; 2.Chengdu Research Base of Giant Panda Breeding of Sichuan, Sichuan, 610081, China; 3.University of Michigan, Department of Ecology and Evolutionary Biology, Ann Arbor, Michigan, 48109, USA; 4.Agriculture and Agri-Food Canada, Eastern Cereal and Oilseed Research Centre, 960 Carling Ave., Ottawa, ON, K2W 1C7, Canada. cail@im.ac.cn

The giant panda, *Ailuropoda melanoleuca*, is an endangered animal species that completely depends on bamboo for nutrition yet has evolved from ancestors with a carnivorous digestive system. The genome sequence of the panda lacks evidence of coding genes for enzymes capable of digesting cellulose, suggesting that the survival of panda requires exogenous metabolizing resources, possibly the gut microbiome. To describe the diversity of the panda gut mycoflora and to identify putative cellulose-degrading fungal taxa in the panda’s intestinal microbiome, we used both culture-based techniques and 454 pyrosequencing on fecal samples from captive giant pandas. A total of

1293 strains belonging to 19 fungal species were isolated by culturing, most of which are thermophilic or thermotolerant with high cellulose degradation abilities. Sequencing of ITS region using 454 pyrosequencing revealed 880 aerobic and 38 anaerobic fungal OTUs. Most of the anaerobic OTUs were clustered with previously unknown lineages in the zoosporic phylum Neocallimastigomycota. The diversity uncovered by NGS greatly exceeds that of the culture-dependent methods. Comparison of fungal community profiles between bamboo leaves and panda feces suggested that the endophytic fungal communities in bamboo differ primarily in abundance rather than composition from the mycoflora structure in panda feces as 95% of OTUs were shared between bamboo and panda feces. In conclusion, the presence of fungal taxa found commonly in the panda’s gastrointestinal tract with known cellulolytic potential, suggests that the intestinal mycoflora plays an important role in the fiber digestion processes, a necessity for panda to survive only on bamboo.

*Poster P18*

**271. Molecular phylogeny of the *Trichophyton mentagrophytes* complex based on multigene sequence analysis, and application of MALDI-TOF mass spectrometry for rapid identification of the dermatophytes**

**\*Suh, Sung-Oui**, Grosso, Kendra M., Carrion, Miguel E. American Type Culture Collection (ATCC), 10801 University Blvd., Manassas, Virginia 20110, USA. ssuh@atcc.org

Dermatophytes are fungi that cause superficial skin infections by invading keratinized tissue, such as hair, nails, and feathers; further penetration into deeper tissue can occur in immunocompromised hosts. Quick and accurate identification of these fungi is clinically relevant to provide proper treatments to patients. Fungi of the *Trichophyton mentagrophytes* complex are common dermatophytes worldwide, but its taxonomy has not been well established due to the gap between the traditional species concept based on clinical, morphological, or physiological characteristics versus phylogenetic species concept from DNA sequences. In this study, more than 70 selected dermatophyte strains were analyzed via nucleotide sequencing of rRNA repeats and β-tubulin gene to clarify phylogenetic relationships in the *T. mentagrophytes* complex. The results show that strains of the species complex can be divided into 3 major groups corresponding to the teleomorphic species, *Arthroderma benhamiae* (Aben), *A. simii* (Asim), and *A. vanbreuseghemii* (Avan), and their related *Trichophyton* spp. These major groups could be further divided into 19 subclades based on their phylogenetic distance and the

current taxonomy, which were considered as ‘phylospecies’ of the complex. The phylogeny also indicates that some subclades of Aben and Avan may represent potential novel species. For rapid identification of those phylospecies, each subclade was tested by MALDI-TOF mass spectrometry (MS) using the bioMérieux VITEK® MS system. We developed customized standard spectra for each subclade and were able to identify most of the phylospecies with 88-100% accuracy. Strains in the Avan group showed a lower rate of correct identification. Although a further study is needed to improve the identification accuracy for some groups, the results prove that MALDI-TOF MS could be a rapid and efficient tool for identifying these closely related dermatophytes by their protein fingerprints. *Poster P91*

**272. Biochemical analysis of a moss host with the symbiont *Daldinia loculata*\*Swanson, Lidia**(1), U’Ren, Jana M.(2), Lutzoni, François(3), Carbone, Ignazio(4), Arnold, A. Elizabeth(1), Jones, Jason(1), May, Georgiana(1). 1.Dept. Ecology, Evolution and Behavior, University of Minnesota, St. Paul, MN, 55108. USA; 2.University of Arizona, Agricultural and Biosystems Engineering, Tucson, AZ, 85721, USA; 3.Duke University, Department of Biology, Durham, NC, 27708, USA; 4.North Carolina State University, Department of Plant Pathology, Raleigh, NC, 27607, USA; 5.University of Arizona, School of Plant Sciences, Tucson, AZ, 85721, USA. Swan2030@umn.edu

Fungal endophytes, fungi living within plants without causing apparent disease, may play important roles in their symbiotic relationship with plants. While various endophytes can coexist within a single host, here we focus on *Daldinia loculata* isolated from boreal forest plants and lichens. The effect of the fungal endophyte on its plant host, a moss, was studied using a unified biochemical assay to assess changes in the biochemical composition of a plant host. The interactions between the moss protonema and the fungal hyphae were analyzed microscopically to understand the symbiotic relationship. A co-culture experiment using 12 strains *D. loculata*, isolated from three host in Alaska, one moss host *Polytrichum sp.,* explored the effects of the fungus on the host’ pigments, carbohydrates, proteins and lipids. Results show that while some strains enhanced the growth and pigments production of the moss host, other strains showed inhibitory effects. By studying variation in a fungal endophyte’s effect on the moss host, we can provide a basic understanding on the biology of these ubiquitous fungal symbionts. *Poster P114*

**273. Foliar endophytic fungi of native Hawaiian Scaevola \*Swift, Sean O.I.**, Perry, Brian A. California State University, East Bay, Biological Sciences, Hayward, CA, 94541, USA. sswift@horizon.csueastbay.edu

Foliar endophytic fungi (FEF) have been found living asymptomatically within the leaf tissues of all plants sampled thus far. Despite their ubiquity, little is known about the diversity and evolution of these cryptic fungal symbionts. The isolation of the Hawaiian archipelago provides a strong barrier to colonization by both host plants and their associated endophytes, making it a unique landscape for examining endophyte diversity and evolution. In Hawaiʻi, the native plant genus *Scaevola* (Goodeniaceae) is the result three separate colonization events. *Scaevola* species have adapted to a variety of habitats, including coastal strand, rain forest, and exposed lava flow. This project focused on quantitatively assessing FEF diversity and community structure in *Scaevola* using a combination of culture based methods and Illumina sequencing of fungal DNA extracted from leaf tissue. Leaf samples were collected from 28 individuals of *Scaevola* representing 8 species from 3 islands. Cultured endophytes were grouped into OTUs based on 97% similarity of the nuclear ribosomal internal transcribed spacer region (ITS). Sequence data from the nuclear large ribosomal subunit (LSU) were obtained from isolates representing each OTU. Phylogenies were constructed using a combined data set of ITS and LSU sequence data. FEF community composition and evolutionary relationships were compared across host species, colonization events, habitats, islands, and sample sites. *Poster P100*

**274. Impact of water damage on fungal communities in residential buildings \*Sylvain, Iman**(1), Taylor, John W.(1), Spilak, Michal(2), Waring, Michael(2),Adams, Rachel (1) 1.University of California Berkeley, Department of Plant and Microbial Biology, USA; 2. Drexel University, Department of Civil, Architectural and Environmental Engineering, USA. isylvain@berkeley.edu

Housing is well established as an important social determinant of health. Living in substandard or inadequate housing exposes residents to a number of environmental diseases and injuries, pests, lead paint hazards, fires, and mold. Damp and moldy homes are associated with asthma and a number of other chronic respiratory symptoms. Public housing residents have the worst health of any population in the United States, largely attributable to building structural and maintenance deficiencies. In 2012 Superstorm Sandy

caused flooding, elevator malfunction, cockroach and rodent infestation, and mold contamination in New York City Housing Authority public housing projects. The damage from the hurricane has yet to be sufficiently remediated. We worked with two local non-profit organizations to determine the impact of water damage on microbial communities in residential building. The use of high-throughput sequencing technologies (HTS) has been used to characterize the microbiota of healthy buildings, but to date, the use of HTS has not been widely used to assess fungal communities in water damaged residences with paired monitoring of physical building characteristics and replication.

We collected house dust from 60 residential units in public and privately owned apartments in two neighborhoods in NYC across two seasons (winter and summer). During three-week periods, continuous measurements of indoor air parameters were performed, and different collection strategies (plastic dust collectors, vacuums, and swabs) were employed for tracking the microbial community. PCR was used to amplify the ITS1 universal barcode sequences for fungi in house dust. Quantitative PCR was used to assess abundance within samples, and amplicon libraries were prepared for Illumina MiSeq to discern taxonomy. Analysis is on-going, but preliminary results suggest that fungal biomass is influenced by temperature, relative humidity, CO2 levels, adult occupancy, and the presence of cats indoors. While it is expected that measurable fungal biomass would increase with greater water availability in homes, this was not observed in our study. Also, principal components analysis of community distance suggests that vacuums, swabs, and dust collectors detect distinct fungal communities. By comparing fungal composition in paired indoor and outdoor dust collector samples, we found putative indoor origins for a number of taxa.

*Symposium S3.3*

**275. Effects of climate change across seasons on northern soil fungal communities \*Talbot, Jennifer M.**(1), Garcia, Maria O.(1), Sorensen, Patrick(1), Finzi, Adrien(1), Groffman, Peter M.(2), Campbell, John(3), Sanders-Demott, Rebecca(1), Templer, Pamela H.(1)

1.Boston University, Biology Department, Boston, MA, USA; 2.Cary Institute of Ecosystem Studies, Millbrook, NY, USA; 3.U.S. Forest Service, Northern Research Station, Durham, NH, USA. jmtalbot@bu.edu

Climate warming over the next century is expected to have cascading effects on northern ecosystems, including warmer soils in the growing season and increases in the frequency of winter soil

freeze/thaw events. These events can change soil nutrient cycling processes, yet it is unclear which microbial taxa might be responsible. The objective of this study was to test the hypothesis that soil warming and freeze-thaw cycles affect soil fungal community composition by selecting for groups with different ecological activity. To test this hypothesis, soil samples were collected from the Climate Change Across Seasons Experiment (CCASE) at Hubbard Brook Experimental Forest in 2014 at five time points: post-snowmelt, budburst, leaf-out, peak biomass, and senescence. Field plots received one of three different climate change treatments: warming (+5°C above ambient), warming + freeze-thaw cycles (+5°C above ambient + 4 freeze-thaw cycles during winter), and control. DNA was extracted from soil samples and the ITS2 rDNA was amplified and sequenced on an Illumina Miseq by the Joint Genome Institute. Sequences were quality checked, trimmed, and clustered at 97% similarity and assigned to functional guilds. Fungal community composition in soil was significantly different among treatments (*P*< 0.0001). The relative abundance of ectomycorrhizal species in soil was lower in the warmed and warmed + freeze- thaw plots relative to reference plots (*P*= 0.02). However, winter soil freeze-thaw increased the relative abundance of free-living saprotrophs (P = 0.023) and animal parasites (P = 0.009). Warming also significantly increased the abundance of animal parasites during peak leaf-out. These results indicate that the relative abundance of fungal functional groups track shifts in host phenology under climate change, with potential consequences for forest trophic structure.

*Contributed Talk C5.2*

**276. Antisense RNA technology as a tool to evaluate oxidative stress response in *Paracoccidioides brasiliensis***Tamayo, Diana(1,2), Almeida, Agostinho J.(1,3), Restrepo, Angela(1), Hernández, Orville(1,4), **\*McEwen, Juan G.**(1,5)

1. Corporación para Investigaciones Biológicas, Cellular and Molecular Biology Unit, Medellín, Colombia; 2. Universidad de Antioquia, Institute of Biology, Medellín, Colombia; 3.Universidad EAFIT, Department of Biological Sciences, School of Sciences, Medellín, Colombia; 4. Universidad de Antioquia, MICROBA Research Group. School of Microbiology, Medellín, Colombia. 5. Universidad de Antioquia, School of Medicine, Medellín, Colombia. mcewen@une.net.co

Antisense RNA technology (asRNA) has been widely used to specifically target gene expression. asRNA are small, diffusible, highly structured RNA molecules that act via sequence complementarity on

target mRNA. Both, mRNA and asRNA form a duplex promoting degradation and interfering with the translation of the target gene. In the case of the human dimorphic pathogenic fungus *P. brasiliensis*, asRNA has been particularly useful to gain experimental insights into its biology, owing to the fact that knockout strains are not yet available in this fungus. In order to obtain asRNA knockdown strains, we employed *Agrobacterium tumefaciens* cells previously transformed with a binary vector containing asRNA encoded within the Transfer-DNA (T-DNA). Additionally, these cells are equipped with virulence genes that assist the integration of the T-DNA into the fungus’ genome. Previous studies in our laboratory addressed *Paracoccidioides* genes involved in the antioxidant defense during host-pathogen interactions. Furtherly, asRNA technology allowed us to obtain *P. brasiliensis* knockdown strains for these genes, *SOD1* (60%), *SOD3* (65%) and *CATP* (60%). We found that *PbSOD3*-aRNA strain was more susceptible to the action of human PMNs and in a mouse model of infection than *PbSOD1*-aRNA and the control strains. Decreased expression of *PbCATP* had no deleterious consequences during the interaction with human PMNs, however it had detrimental consequences during fungal survival *in vivo*. Thus, although *PbSOD1* seems to play an important role in defending the fungus against phagocytes, *PbSOD3* and *PbCATP* appear to be relevant during the establishment and development of the disease. Based on our results, we postulate that *P. brasiliensis* might counteract the immune cells’ oxidative burst by inducing the expression of antioxidant genes such as the ones studied herein.

*Poster P113*

**277. Sequencing the hell out of fungi \*Tedersoo, Leho**Natural History Museum, University of Tartu, 14a Ravila 50411, Tartu, Estonia

High-throughput sequencing (HTS) has become a standard technique for genomics, metagenomics and taxonomy, but these analyses typically require large amounts of high-quality DNA that is difficult to obtain from uncultivable organisms including fungi with no living culture or fruit-body representatives. By using 1 ng DNA and low coverage Illumina HiSeq HTS, we evaluated the usefulness of genomics and metagenomics tools to recover fungal barcoding genes from old and problematic specimens of fruit-bodies and ectomycorrhizal (EcM) root tips. Ribosomal DNA and single-copy genes were successfully recovered from both fruit-body and EcM specimens typically <10 years old (maximum, 17 years). Samples with maximum obtained DNA concentration <0.2 ng μl-1 were sequenced poorly. Fungal rDNA molecules

assembled from complex mock community and soil revealed a large proportion of chimeras and artefactual consensus sequences of closely related taxa. Genomics and metagenomics tools enable recovery of fungal genomes from very low initial amounts of DNA from fruit-bodies and ectomycorrhizas, but these genomes include a large proportion of prokaryote and other eukaryote DNA. Nonetheless, the recovered scaffolds provide an important source for phylogenetic and phylogenomic analyses and mining of functional genes. Check it out, man: Tedersoo, L. et al. (2016) MycoKeys 13: 1–20 (doi: 10.3897/mycokeys.13.8140)

*Poster P103*

**278. Global distribution of known and previously undrecognized fungal lineages \*Tedersoo, Leho**Natural History Museum, University of Tartu, 14a Ravila 50411, Tartu, Estonia

Fungi inhabit all terrestrial and aquatic ecosystems on earth as decomposers, parasites and symbionts. Little is known about the biogeographic patterns of individual fungal groups, especially those that lack scientific name. From global soil samples, we sequenced both the SSU, ITS and LSU regions using a combination of specific and universal primers as well as Sanger and 454 sequencing methods. Besides known taxonomic groups, our analysis recovered >30 at least class-level taxonomic groups that were previously unrecognized. Here I present the phylogenetic position, main ecological predictors and biogeographic patterns of these fungal lineages and discuss these finding in context with previous global studies of fungi and other organisms.

*Symposium S10.1*

**279. Evolutionary metabolomics in *Tolypocladium* to guide natural products discovery \*Tehan, Richard**(1), Arvidson, Rheannon(2), Chaverri, Priscila(3), Gazis, Romina(4), Spatafora, Joseph(2), McPhail, Kerry(1)

1.Oregon State University, College of Pharmacy, Corvallis, OR, 97331, USA; 2.Oregon State University, Department of Botany and Plant Pathology, Corvallis, OR, 97331, USA; 3.University of Maryland, Department of Plant Science and Landscape Architecture, College Park, MD, 20742, USA; 4.University of Tennessee, Department of Entomology and Plant Pathology, Knoxville, TN, 37996, USA. tehanr@oregonstate.edu

The fungal genus *Tolypocladium* (Hypocreales, Ophiocordycipitaceae) contains several species known to produce biologically active secondary metabolites (SMs), some of which are of medicinal interest. These include the clinically important immunosuppressant,

cyclosporin A, originally isolated from *T. inflatum*. Ongoing genomic analyses of *Tolypocladium* indicate this genus as a potentially rich source of new SMs of various classes including peptides, polyketides, and alkaloids. Fourteen isolates of eleven *Tolypocladium* species were grown in twelve different media conditions to elicit differential production of SMs, as evaluated by LC-MS/MS, for comparison with RNA-Seq data to identify SM biosynthetic gene clusters, particularly for peptides produced by non- ribosomal peptide synthetases (NRPSs). LC/MS-based metabolomics tools were used to survey the secondary metabolome of *Tolypocladium*, guide the discovery of new peptide SMs, and to trace the evolution of secondary metabolism in hypocrealean fungi. In the process of LC-MS metabolic profiling, new peptaibiotics were detected in several *Tolypocladium* species. Known peptides not previously reported from *Tolypocladium,* as well as new structural analogues thereof, were also detected. These peptides will be targeted for isolation, structure elucidation, pairing with biosynthetic gene clusters, and biological characterization.

*Contributed Talk C2.4*

**280. Macrofungi Collections Consortium \*Thiers, Barbara**, Halling, Roy E. 1.New York Botanical Garden, Bronx, Herbarium and Institute of Systematic Botany, Bronx, NY 10458 USA. bthiers@nybg.org; rhalling@nybg.org

730,600 specimen labels and 417,300 supplemental images (e.g., specimen photographs, drawings, field notes). The Mycoportal now contains approximately 1.5 million specimen occurrence records for macrofungi, combining records that were created for the project, as well as previously created records and those donated

by non-funded institutions.

The Macrofungi Collections Consortium (MaCC) project was funded by The National Science Foundation in 2012 to digitize herbarium specimens of fungi from 34 U.S. institutions, and to share these through the Mycoportal (http://mycoportal.org). To date, approximately 1,150,000 items have been



digitized for this project, including



The data generated through

this project will allow researchers to address the questions: To what extent do the diversity and distribution of macrofungi determine the diversity and distribution of the organisms with which they form commensal or symbiotic relationships, and by extension, how will changes in macrofungal diversity and distribution affect those organisms and ultimately human affairs? Most of the participating institutions have now completed their work on the project, although some will continue through June 2016. Many of the MaCC participants are now part of a parallel project, the Microfungi Collection Consortium

(MiCC) that began in July 2015, is now contributing equivalent information about microfungi. Through these digitization grants, essentially all of the approximately four million fungal collections in the U.S. will be digitized by 2020, creating a resource to support fungal research worldwide and hopefully stimulating similar national initiatives in other



countries.



*Contributed Talk C15.3*

**281. Fungi are Complex! Using a Individual-based models to explore the Foraging Ascomycete Hypothesis \*Thomas, Daniel**; Vandegrift, Roo; Carroll, George C.; Roy, Bitty A.

University of Oregon, Institute of Ecology and Evolution, Eugene, OR 97403. dthomas@uoregon.edu Mycological ecology presents unique challenges

to ecological modeling, as fungi play by very different rules than other organisms that have been studied with classical models. They exhibit highly variable scales of dispersal, highly variable host and habitat requirements, ambiguous definitions of individuals and species, bewildering diversity, mysterious life- history transitions, and physical properties of both macro- and micro-organisms. These traits can cause difficulties when constructing traditional statistical models of abundances of species as functions of linear combinations of environmental variables, or models of rates of population growth as differential equations (e.g. Lotka-Volterra equations). These two most common methods of ecological modeling remain invaluable but could under-emphasize spatial effects and possible emergent properties resulting from complex interactions typical of fungi. Here we propose that another class of models, Individual-based models, that can be a useful additional tool for understanding complex ecological systems. Such models can be built in simple programming environments, and results can be displayed in an intuitive manner. As a case study, we have constructed an individual-based model of fungal dispersal following the predictions of the Foraging Ascomycete Hypothesis. This hypothesis proposes that some endophytic fungi alternate leaf endophyte and forest-floor decomposer life stages in order to bridge scarcity of suitable substrate in time and space. We parameterized our model using real ecological data from a study conducted in Ecuador of 2012. Even with this very simple model, we are able to reproduce several patterns of fungal endophyte distribution that we observe in nature. We suggest that construction of Individual-Based Models may become an important part of ecological research efforts, alongside statistical models.

*Contributed Talk C1.5*

**282. Fungal colonization of wood in ground contact**

**\*Torres Andrade, Paola**(1), Cappellazzi, Jed(1), Morrell, Jeff J.(1) 1.Oregon State University, College of Forestry, Department of Wood Science, Corvallis, OR, 97331, USA. patoan5@gmail.com

Fungal colonization patterns in wood vary with wood species, uses and exposure conditions. These patterns are fundamental to understanding the microbial ecology of the decay process. There is limited knowledge about fungal community composition changes over the course of wood decay in ground contact. In this study, patterns of fungal colonization of western red cedar, Douglas-fir and alder were assessed using a culture-dependent molecular approach in a ground-contact field test. Field stakes were installed near Corvallis-Oregon, US and retrieved for fungi colonization evaluation at 3- months intervals over 24 months of exposure. Multivariate analyses of data from fungal cultures recovered and sequenced from individual wood samples were conducted using PC-ORD 7.29. Questions of interest included: 1) Do fungal communities differ between wood species and among periods of outdoor exposure? 2) What species differentiate wood types and periods of exposure? The wood types supported a diverse fungal community. *Ascomycota* were far more abundant than *Basidiomycetes.* Decay fungi incluede *Trametes versicolor, Postia placenta* and *Phanerochaetae sp*. Fungal community composition fluctuated seasonally over time and among the wood types according to Multi-Response Permutation Procedures (MRPP) analysis. Composition of fungal communities was associated with changes in precipitation and temperature at each exposure period. Fungal frequency was much higher in less durable wood species (sapwood of Douglas -fir or alder). Molds and sapstain fungi such as *Phialophora mustea*, which are commonly found in soil were the predominant species. Further analysis is undergoing. *Poster P51*

**283. Discovery of a novel taxon within Mucoromycotina \*Torres-Cruz, Terry J.**(1), Billingsley Tobias, Terri(1), Almatruk, Maryam(1), Hesse, Cedar(2), Desirò, Alessandro(3), Benucci, Gian Maria Niccolò(3), Bonito, Gregory (3), Stajich, Jason (4), Dunlap, Christopher(5), Kuske, Cheryl(2), Porras- Alfaro, Andrea(1)

1.Western Illinois University, Department of Biological Sciences, Macomb, IL, 61455, USA; 2.Los Alamos National Laboratory, Bioscience Division, Los Alamos, NM, 87545, USA; 3.Michigan State University, Department of Plants, Soil and Microbial

Sciences, East Lansing, MI, 48824, USA; 4.University of California, Department of Plant Pathology & Microbiology, Riverside, CA, 92521, USA; 5.U.S. Department of Agriculture, National Center for Agricultural Utilization Research, Agricultural Research Service, Peoria, IL, 61604, USA. tj- torrescruz@wiu.edu

In this study we report on the discovery and characterization a novel fungal species within Mucoromycotina, and its associated bacteria. Fungal isolates were obtained from the Duke Forest Free Air Carbon Enrichment Site using particle filtration and soil dilutions on PYG+ media at 25oC. Morphological characteristics were described and a phylogenetic analysis was conducted using multiple genetic regions and a draft genome. Bacterial symbionts associated with the fungal mycelium were also analyzed by 454 sequencing and culturing. Metagenome data from the field site indicates the novel taxon is more abundant in lower soil horizons and responds favorably to long- term N fertilization. The most similar ITS sequences for the isolates belong to uncultured soil fungal sequences obtained from metagenomic analyses and an isolate from endophytic fungi in mosses. Light and electron microscopy showed dimorphism with abundant coenocytic hyphae in MEA media and the presence of yeast cells. Potential chlamydospores were also observed. Bacteria were observed on the hyphal surface using electron microscopy. *Bacillus licheniformis* were cultured from this fungus. Additionally, 454 sequencing detected *Methylobacterium* species in all isolates. Analysis of SSU and phylogenomic analysis using low coverage genome data indicates this new fungal species represents a novel lineage within Mucoromycotina closely related to *Endogone*. This discovery is important to understanding the evolution and ecology of early diverging terrestrial fungi.

*Contributed Talk C16.1*

**284. Botryosphaeriaceae species associated with canker disease of California bay laurel in Northern California with the description of a new *Dothiorella* species**

Trouillas, Florent P., **\*Lawrence, Daniel P.**, Peduto Hand, Francesca, Gubler, W. Douglas Department of Plant Pathology, University of California, One Shields Avenue,

Davis, CA 95616, USA. flotrouillas@ucanr.edu Species in the Botryosphaeriaceae are cosmopolitan and may act as saprobes, endophytes, or destructive plant pathogens in many natural and man- made environments. Botryosphaeriaceous fungi were collected from cankers in declining California bay laurel trees (*Umbellularia californica*) in Northern California and identified via morphological and

phylogenetic analyses. Three species (*Botryosphaeria dothidea*, *Neofusicoccum nonquaesitum*, and *Dothiorella californica* sp. nov.) were revealed based on phylogenetic analyses of three loci (ITS, beta- tubulin, and translation elongation factor 1-alpha). This study represents the first report of *B*. *dothidea* and any *Dothiorella* species from California bay laurel. Pathogenicity testing performed on 2 to 4-year- old twigs of *U. californica* revealed that *B. dothidea* and *N. nonquaesitum* caused significantly longer lesions as compared to the mock-inoculated control. *Neofusicoccum nonquaesitum* produced the largest lesions averaging 8 cm at 12 months post-inoculation, and 22 cm at 24 months. The newly described species, *Dothiorella californica*, did not cause lesions significantly larger than the control in *U. californica*. To our knowledge, this is the first study that examines the diversity and role of botryosphaeriaceous taxa associated with canker disease of California bay laurel in natural ecosystems.

*Poster P61*

**285. Ectomycorrhizal fungal communities and soil enzymes across elevation gradients in *Nothofagus pumilio* forest \*Truong, Camille**(1), Gabbarini, Luciano A.(2), Moretto, Alicia(3), Mujic, Alija B.(1), Escobar, Julio M.(3), Smith, Matthew E.(1)

1.University of Florida, Department of Plant Pathology, Gainesville FL, USA. 2.Universidad Nacional de Quilmes, Laboratorio de Bioquímica, Microbiología e Interacciones Biológicas en el Suelo, Bernal, Buenos Aires, Argentina. 3.Centro Austral de Investigaciones Científicas CADIC–CONICET, Laboratorio de Ecología Terrestre, Ushuaia, Tierra del Fuego, Argentina.

Ectomycorrhizal (ECM) fungi promote tree growth and survival in nutrient-poor soils by facilitating the degradation of organic matter and mobilizing essential nutrients to the plant. The response of ECM communities to temperature will therefore strongly influence forest dynamics in the context of climate change. Because temperature decreases with elevation, mountain ecosystems offer the opportunity to study the effects of climate over relatively short distances. However, because vegetation usually varies with elevation, it is difficult to differentiate between abiotic (i.e. edaphic) and biotic (host plant) factors that affect ECM communities along elevation gradients. In Southern temperate forests of Tierra del Fuego the ECM tree *Nothofagus pumilio* forms continuous monospecific forests along mountain slopes (ca. 150–750 m elevation). This represents a unique opportunity to study how elevation (a proxy for temperature) impacts ECM communities without interference from other

ECM tree species. We collected 180 soil samples in *N. pumilio* forests along six altitudinal transects and identified fungal communities by ITS1 Illumina sequencing. We recorded soil properties and measured the activity of eight fungal enzymes involved in carbohydrate degradation (CAZymes) and nutrient mobilization (acid phosphatases). ECM fungi dominated the soil community and were most diverse at middle altitude (ca. 400 m) following a mid-domain effect. Shifts in fungal community composition occurred along altitudinal gradients, associated with variation of pH, soil moisture and organic content. In contrast, fungal enzyme activity mostly varied according to local nutrient conditions and was minimally influenced by elevation. The high turnover of ECM fungal communities across elevation gradients coupled with low variation in enzyme activity suggests that *N. pumilio* maintains high fitness across environments and may be resilient to impending climatic changes.

*Contributed Talk C12.6*

**286. A new sequestrate *Amanita* species from *Nothofagus* forests in Patagonia**Truong, Camille(1), Kuhar, Francisco(2), Kaplan, Zach(1), **\*Smith, Matthew E.**(1)

1. University of Florida, Department of Plant Pathology, Gainesville FL 32611, USA; 2. Centro de Investigacion y Extension Forestal Andino Patagonico, Esquel, Argentina. trufflesmith@ufl.edu

*Amanita* is a diverse and cosmopolitan genus of ectomycorrhizal fungi. Although most *Amanita* species are mushrooms that fruit aboveground, several sequestrate (secotioid or “truffle-like”) species have been documented from Australia and Spain. During our investigation of ectomycorrhizal communities in *Nothofagus* forests of Patagonia (South America), we encountered a new sequestrate species of *Amanita* associated with *Nothofagus antarctica*. This species constitutes the first report of a sequestrate *Amanita* from the Americas. We investigate the phylogenetic affinities of this new “truffle-like” *Amanita* species, provide a preliminary description, and discuss the biogeographic implications of this new species.

*Poster P7*

**287. Multigene phylogeny and ITS2 secondary structures reveal novel evolutionary lineages of diaporthalean fungi associated with *Fragaria* and *Rubus***

**\*Udayanga, Dhanushka**, Castlebury, Lisa A Systematic Mycology and Microbiology Laboratory, United States Department of Agriculture- Agricultural Research Service, Beltsville, MD 20705, USA. Lisa.Castlebury@ars.usda.gov

Diaporthales contains numerous species causing diseases of economically important crops worldwide. Although at least 13 families and 50 genera are known to date and several phylogenies have been published, confusion exists concerning some family and generic boundaries and the placement of several significant phytopathogenic species. Diaporthalean taxa associated with *Fragaria* spp. (strawberry) and *Rubus* spp. (blackberry, raspberry) were studied based on fresh collections of isolates from USA and isolates available in culture collections. A combined analysis of five nuclear loci, including the large (28S) and small (18S) subunits of nuclear ribosomal DNA, ribosomal internal transcribed spacer (ITS) regions, second largest subunit of RNA polymerase II (RPB2) and translation elongation factor 1-α (TEF), was used to reconstruct the phylogeny. RNA secondary structure assisted alignments were used to improve the phylogenetic analysis of ribosomal gene regions. Base pairs with non-conserved, co-evolving nucleotides that maintain base pairing in the 2D structure of ITS2 were mapped on predicted structure models to strengthen the phylogenetic inferences. Results confirm that the leaf blight pathogen of strawberry currently known as “*Phomopsis*” *obscurans* does not belong in the genus *Diaporthe* (syn. *Phomopsis*) or in family Diaporthaceae*.* The root rot and petiole blight pathogen “*Gnomonia*” *fragariae* and a species occurring on *Rubus* currently known as “*Gnomonia” rostellata* (syn. “*G. rubi*”) are not congeneric and actually represent two distinct evolutionary lineages within the Sydowiellaceae. The leaf blotch pathogen, *Gnomoniopsis fructicola* (Gnomoniaceae), a well- known diaporthalean fungus associated with strawberry is also distinguished although identification based on morphology is difficult. A consolidated approach to define robust clades within Diaporthales based on morphological characters, structural analysis and multigene phylogeny is presented. *Poster P90*

**288. Visualizing fungal bacterial interactions; applications of microfluidics & time-lapse videography \*Uehling, Jessie**(1), Millet, Larry(2,3), Aufrecht, Jayde(2,3), Labbé, Jessy(2), Doktycz, Mitchel(2,3), Retterer, Scott(2,3), Vilgalys, Rytas(1)

1.Duke University, Bioogy Department, Durham 27708, USA; 2.Oak Ridge National Laboratory, Biosciences Division, Oak Ridge, 37831 USA; 3.Oak Ridge National Laboratory, Center for Nanophase Materials Sciences, Oak Ridge, 37831 USA. Jessie.Uehling@Duke.edu

Rhizosphere fungi are known to interact with their soil bacterial communities to enhance plant growth and soil functioning. One group of bacteria, the

‘Mycorrhizal Helper Bacteria’ (MHB), have been shown to increase fungal growth and plant colonization during mycorrhizal symbiosis. Several mechanisms for these inter-kingdom relationships have been proposed, including trophic resource sharing and chemical communication, but research is ongoing and definitive empirical evidence for different hypotheses is lacking. Previous MHB mechanistic studies have shown these interactions likely involve competition for resources and diffusible signaling (*e.g.* Galet et al. 2015 & Riedlinger et al. 2006). While plate assays have been useful for demonstrating growth responses by fungal and bacterial colonies comprised of many cells, they do not detect more subtle responses that involve direct interaction between individual hyphae and bacteria. To investigate the MHB mechanism on a cellular level, we performed high-resolution, time-lapse imaging of single hyphae and bacteria within microfluidic sample environments. We used a microfluidic platform to visualize and quantify the interactions between the following *Populus* rhizosphere isolates; fungus *Mortierella elongata* strain AG77 (Mortierellomycotina) and MHB *Burkholderia* strain BT03 (Proteobacteria, Burkholderiaceae). We present and discuss the design and application of a custom microfluidic sample environment to dissect experimental hypotheses about MHB interaction mechanisms.

*Contributed Talk C13.5*

**289. Preliminary results on the diversity of fungi associated with romaine lettuce**Urbina, Hector, **\*Newerth, Shannon**, Aime, M. Catherine.

Purdue University, Department of Botany and Plant Pathology, West Lafayette IN 47907 USA. snewerth@purdue.edu

Many outbreaks of human pathogens have been associated with romaine lettuce, hence an increased need to understand the dynamics of microbial communities inhabiting popular leafy greens. In order to illustrate the fungal species found in both conventionally and organically farmed romaine lettuce, we examined 39 lettuce heads acquired from several grocery establishments in West Lafayette and Lafayette, Indiana, and Chicago and Champaign, Illinois. From each lettuce head a sample of 25 g of leaves was blended in 225 mL of 100 mM phosphate buffer and an aliquot of 100 μL was plated on yeast- malt-extract agar, potato-dextrose agar and rose- Bengal-dextrose agar amended with antibiotics and acidified with 800 μL/L of concentrated HCl. After a period of 4–5 days of incubation at room temperature, fungal colonies were subcultured multiple times until axenic. Although work is ongoing, thus far we have isolated more than 250 fungal strains from romaine

lettuce. We have observed that the preponderance of colony forming units (CFU) are of ascomycete and basidiomycete yeasts. In particular, red anamorphic yeasts of the Sporidiobolaceae are common constituents of the romaine lettuce mycobiota. Other common constituents include soil-inhabiting fungi such as *Aspergillus* spp., *Penicillium* spp. and *Mucor/Rhizopus* spp. As was expected, the microbial biomass was significantly higher in organic lettuce (20,720 ± 4461 CFU g/mL) than conventionally farmed lettuce (9,440 ± 3,741 CFU g/mL) since the application of synthetic antimicrobial compounds are restricted in organic farming. Expanding our knowledge of the native mycobiota associated with romaine lettuce may help to identify possible fungal pathogens and provide data for preventing future outbreaks.

*Poster P29*

**290. Host and environmental control in arbuscular mycorrhizal fungal communities and the impact on phylogenetic clustering \*Vályi, Kriszta**, Rillig, Matthias C, Bergmann, Joana, Hempel, Stefan

Plant, Fungal and Soil Ecology Lab, Institute of Biology, Freie Universität Berlin, Berlin-Brandenburg Institute of Advanced Biodiversity Research, Berlin, D-14195, Germany. valyi@zedat.fu-berlin.de

The arbuscular mycorrhiza (AM) is a particular multispecies symbiosis between plant roots and Glomeromycota, because even though AM fungi are obligate endosymbionts and completely rely on the plant partner for carbon, they also must forage in the soil for other nutrients. Therefore, they are a compelling target for symbiont community ecology. We used a community phylogeny framework to explore how root traits, host ecological preferences, host phylogeny and land use influence the structure of intraradical AM fungal communities in 150 grassland plots using pyrosequencing. AM fungal communities in the root, as opposed to previous results from soil, were consistently phylogenetically clustered, a possible sign of more “filtering” in the root niche than competition among co-colonizers. The ability of plants to control their symbionts (including the ability to discriminate between different AM fungi) varies not only with plant identity, but with environmental conditions as well. This is a possible explanation why, for example, plants of shade without extensive root systems had less clustered AM fungal communities. It was previously shown that shade decreased the ability of plants to selectively reward beneficial AM fungi due to decreased nutrient allocation to roots. Less host control and the resulting increased competition can explain the observed decrease in phylogenetic clustering. In soils, fertilizer treatments resulted in

decreased clustering as well. Increasing soil fertility was shown to result in less nutrient allocation to roots and thus to AM fungi. Taking these results together a hierarchically structured system of control on AM fungal communities emerges. Environmental conditions, in relation to host plant preferences, define nutrient allocation to roots and host control (“filtering”) of AM fungi. This interplay between competition and host control then determines AM fungal community structure.

*Contributed Talk C20.1*

**291. Beyond rDNA: Using next-generation sequencing technologies to resolve the *Mortierellales* phylogeny \*Vande Pol, Natalie**(1), Desiró, Alessandro(2), Stajich, Jason(3), O’Donnell, Kerry(4), Bonito, Gregory(2)

1.Michigan State University, Microbiology and Molecular Genetics, East Lansing, MI 48824, USA; 2.Michigan State University, Plant Soil and Microbial Sciences, East Lansing, MI 48824, USA; 3.University of California, Plant Pathology and Microbiology and Institute for Integrative Genome Biology, Riverside, CA 92521, USA; 4.NCAUR-ARS-USDA, Mycotoxin Prevention & Applied Microbiology Research Unit, Peoria, IL 61614. vandepo7@msu.edu

The *Mortierellales* comprise a polyphyletic lineage of early diverging, globally distributed, soil fungi. Several *Mortierella* species are known to interact with roots and promote plant growth, even though they do not make traditional mycorrhizal structures. *Mortierella* also harbor bacterial endosymbionts and have unique oleaginous biology that makes these fungi industrially important. Inter- and intra-species diversity in the *Mortierellales* has been most thoroughly sampled in continental Europe and North America and characterized using the ITS and LSU rDNA regions. In order to better understand the biogeography and global diversity of the *Mortierellales*, we are making efforts to isolate and identify these fungi from geographically distinct and undersampled environments including North American caves, Australia, Fiji, and Africa by baiting from soils using chitin as a substrate. Preliminary results indicate the presence of novel *Mortierella* species from our sampled regions, but also that some species, such as *M. elongata,* are globally distributed. Most phylogenetic analyses of *Mortierellales* are performed using rDNA. However, strong sequence divergence limits the possible resolution of the overall structure of this polyphyletic order. To address this limitation we are pursuing two non-rDNA approaches to improve phylogenetic resolution: multi-locus sequence typing and low-coverage genome sequencing. We will compare these phylogenetic

approaches in their ability to resolve the phylogeny and to distinguish species based on genealogical concordance. Finally, we plan to use this phylogeny as a framework within which to place previously unidentified ITS sequences from GenBank having affinity to *Mortierella*.

*Contributed Talk C10.6*

**292. Spatial ecology in the Xylariaceae: Combining traditional collection and next-generation sequence-based microbial survey techniques. \*Vandegrift, Roo**(1), Thomas, Daniel C.(1), Ju, Yu- Ming(2), Soukup, Hannah(1), Carroll, George C.(1), Roy, Bitty A.(1)

1.University of Oregon, Institute of Ecology and Evolution, Eugene, OR 97403-5289; 2.Academia Sinica, Institute of Plant and Microbial Biology, Nankang, Taipei 115, Taiwan. awv@uoregon.edu

We examine one potential ecological explanation for cases of endophytism. The Foraging Ascomycete (FA) hypothesis proposes that some decomposer fungi may utilize endophytism as a way to bridge spatial and temporal gaps in preferred substrate. The FA framework leads to several testable hypotheses: (1) host generalism for the endophytic phase; (2) spatial linkage between the saprotrophic and endophytic phase; (3) reduced dispersal limitation in the endophytic phase as compared to the general endophyte community; (4) reduced environmental sensitivity in the endophytic phase; and (5) phylogenetic conservatism of the FA ecological strategy. Here we focus on the Ascomycete family Xylariaceae, which are common endophytes and include members proposed to utilize a FA strategy. We used a novel technique to examine spatial ecology of the Xylariaceae, pairing traditional collection with the preparation of a next-generation sequencing metabarcode library of endophytes. Sequences generated from our collections were used to query the metabarcode library, such that we could spatially pair decomposers with deep sampling of endophytes. We found (1) evidence of host generalism; (2) some spatial linkage between the saprotrophic and endophytic phase; (3) no clear evidence of dispersal limitation in the endophytic phase on the scale of our sampling, and some evidence for dispersal limitation in the decomposer phase; (4) endophytic phase fungi to be less sensitive to environment than saprotrophic phase fungi; and (5) some evidence for taxonomic signal of the FA lifestyle at the sub-family level. We find evidence for diverse spatial ecologies in the Xylariaceae, including evidence in support of a FA strategy in some taxa, particularly in the subfamily Xylarioideae. The pairing of traditional mycological collection with NGS metabarcode libraries is a novel approach with much potential for elucidating the

spatial patterns of fungi with diverse ecologies and mixed lifestyles. *Contributed Talk C4.2*

**293. Microfungal oasis in an oligotrophic desert: Community structure in freshwater systems of Cuatro Ciénegas, Mexico \*Velez, Patricia**(1), Gasca-Pineda, Jaime(1), Rosique- Gil, Edmundo(2), Eguiarte, Luis E.(1), Espinosa- Asuar, Laura(1), Souza, Valeria(1)

1.National Autonomous University of Mexico, Ecology Institute, Department of Evolutive Ecology, Mexico City, C.P. 04510, Mexico; 2.Juarez Autonomous University of Tabasco, Academic Division of Biological Sciences, Villahermosa, 86039, México. pvelezaguilar@gmail.com

The Cuatro Ciénegas Basin (CCB) comprises several oligotrophic aquatic ecosystems limited by phosphorus, which are dominated by a highly competitive prokaryotic diversity. Although fungi constitute a diverse and important component of microbial diversity, the microfungal diversity in the CCB remains unknown. Therefore, the aim of this work was to explore microfungal diversity and ecological patterns in this area. We analyzed cultivable taxa from sediment and water, as well as lignocellulolytic taxa obtained from submerged plant debris, and wood panels in three contrasting freshwater systems in the CCB. We evaluated sequence data from the nuclear ribosomal internal transcribed spacer including the 5.8 rDNA region for 126 isolates, clustering into 37 OTUs. The assigned OTUs affiliated to several genera in the fungal phyla: Zygomycota, Basidiomycota, and Ascomycota. Remarkably, we recorded OTUs with saline affinity, agreeing with previous findings on the prokaryotic communities with ancestral marine resemblances. Our results suggest that the CCB has a moderate taxonomical diversity compared to other arid environments, probably as a result of high selective pressures. All the studied systems showed moderate diversity levels. Moreover, our results indicated that lignocellulolytic microfungal communities preferably occurred on resident plant debris and are dominated by transient fungal taxa, as resident species were not recorded perhaps as a result of the long-term strong competition with the highly adapted prokaryotic community. Decisively, the assessment of microfungal diversity freshwater systems is important, since this ecological group of microorganisms represents an important indicator of trophic complexity and biotic interactions among microbial communities, having important implications for understanding eukaryotic survival at the oligotrophic limit for life. *Poster P38*

**294. New trichome-inhabiting hyphomycete on *Banisteriopsis gardneriana* from the Brazilian Cerrado**Vélez-Zambrano, Sergio M., \***Dianese, José C.** Universidade de Brasília, Departamento de Fitopatologia, Brasília, 70910-900, Brazil. jcarmine@gmail.com

In 2009 eight new genera of trichomatous hyphomycetes from the Cerrado were described (Mycological Research 113: 261-274), and incorporated by Seifert et al. in “The Genera of Hyphomycetes” in 2011, where over 1500 genera were described and neatly illustrated. A specimen now studied could not be fitted in any of those genera, and similar fungus was not shown in the presently published literature. Thus, it is considered as belonging in a new genus. The still monotypical *Trichomatosphaera* also from the Cerrado, found on trichomes of *Eugenia lutescens* (Myrtaceae) in 2004, and included among the eight genera mentioned above, is the closest genus to the specimen studied. However, *Trichomatosphaera cerradensis* produces a conglomerate of microsclerotia on top of the trichomes that germinate to form hyaline conidiophores, conidiogenous cells, and 1-septate conidia. On the other hand, the new fungus merely forms chains of brown thick walled chlamydospores that germinate originating brown septate conidiophores bearing polyblastic conidiogenous cells, and light brown aseptate conidia. Another genus, *Scleroconidioma*, is slightly similar to the new fungus, however it is not trichomatous, and shows phialidic conidiogenous cells. The fungus was not isolated, and will be described and published based on its morphological characteristics observing the rules of the Melbourne Code.

*Poster P5*

**294.1 Data and infrastructure for fungal conservation in North America \*Vellinga, Else C.**University Herbarium, University of California at Berkeley, CA 94320, USA. ecvellinga@comcast.net

Fungi face the same threats as animals and plants for their survival: habitat loss, pollution, climate change are the biggest factors. And yet, fungi are hardly ever mentioned in environmental impact reports, and only two lichenized fungi are included in the USA’s Endangered Species Act. Several factors play a role: the lack of data on fungi, and a lack of infrastructure to make good use of the data that are available. The first step in data acquisition is to have good taxonomic data on the species; mushroom societies across the USA are now involved in documenting, vouchering and sequencing projects to achieve this. Mycoportal is the database for mycology collections throughout North

America, providing a wealth of easily accessible, historical data. Two current individual mushroom observation websites, MushroomObserver.org and iNaturalist.org, are excellent, but how to bring more structure to recording and vouchering specimens is a challenge. Education of the general public including politicians, is where all mycologists, amateur or professional, can play an important role, and have a significant impact. The importance of fungi for ecosystem functioning has to be stressed so that fungi can take their rightful position beside plants and animals in broader biodiversity discussions.

*Symposium S9.2*

**295. Revising the *Mycosphaerellaceae*: Chaos or clarity?**Videira, Sandra I.R.(1), Groenewald, Johannes Z.(1), Nakashima, Chiharu(2), **\*Crous, Pedro W.**(1) 1.CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 *Contributed Talk* , Utrecht, the Netherlands; 2.Graduate School of Bioresources, Mie University, 1577 Kurima-machiya, Tsu, Mie 514- 8507, Japan. p.crous@cbs.knaw.nl

Members of *Mycosphaerellaceae* are able to colonise diverse ecological niches and vary in lifestyle from pathogens to endophytes, saprobes, epiphytes and fungicolous species. As initially circumscribed, the *Mycosphaerellaceae* was in fact polyphyletic, and split into several families, namely the *Cladosporiaceae*, *Dissoconiaceae*, *Extremaceae, Schizothyriaceae* and *Teratosphaeriaceae.* Approximately 78 genera have thus far been recognised in *Mycosphaerellaceae*. The mycosphaerella-like sexual morphs are usually morphologically conserved, and hence these genera are chiefly distinguished based on the morphology of their asexual morphs. In order to improve the generic delimitation in *Mycosphaerellaceae*, a polyphasic approach based on multilocus DNA sequences, morphological and cultural data was used in this study. Results of this study found that several genera that were formally considered as well circumscribed, e.g. *Passalora*, *Ramularia*, *Zasmidium*, etc., were polyphyletic. Consequently several novel sexual and asexual genera are introduced to accommodate isolates that are not congeneric with the type species of the genera in which they were originally classified based on morphology. In conclusion, the *Mycosphaerellaceae* is shown to contain more than 100 genera. In future it would be very difficult if not impossible to allocate fresh isolates to generic level without the benefit of DNA data. *Contributed Talk C4.6*

**296. Bridging the gap between cultured and uncultured fungi in the built environment**

**\*Visagie, Cobus M.**(1,2), Seifert, Keith A.(1,2) 1.University of Ottawa, Dept of Biology, Ottawa, ON, K1N6N5, Canada; 2.Agriculture & Agri-Food Canada, Ottawa Research & Development Centre, Ottawa, ON, K1A0C6, Canada. cobusvisagie9@gmail.com

Humans spend ~90% of their lives indoors. We are constantly exposed to spores, cell fragments and metabolites of indoor fungi, making the built environment one of the most intense human-microbe interfaces. Fungi affect us as pathogens, allergens, food spoilers and cause structural damage to building materials. Ecological studies surveying indoor microbial communities, recently most often with next- generation sequencing (NGS), frequently detect a significant number of unidentified OTU’s, reflecting a gap in reliable reference data (ITS barcode sequences) for fungal species. Our project aims to close this gap using classical, culture and morphology based taxonomy. First, we sampled fungal diversity from the built environment by doing isolations from house dust, then we identified strains using morphological and multi-gene sequencing, ultimately producing reference ITS barcodes. In our early studies, we isolated ~7000 fungal strains using dilution to extinction methods, yielding 3200 ITS barcodes. So far, we have described 30 new species, with many more descriptions underway. Although new species discovery is central to our project, we have also generated DNA barcodes for previously unsequenced species and captured infraspecies variation in ITS barcodes from the species sampled. Recent work focused on xerophilic fungi (i.e. growing at aw < 0.85), which are common in the indoor environment but require special media to isolate. Consequently, reference sequences are often lacking for xerophiles. About 1000 xerophilic strains were isolated from samples obtained from across Canada and parts of the US. Many of the identified species are well known, but we have found 20-30 new xerophilic species. The sequences produced for these fungi will provide valuable reference data to ensure that future sequence-based identifications will be more reliable and help bridge the gap between culture- dependent and -independent detection techniques such as those using NGS. *Symposium S3.1*

**297. What lies beneath? Fungal diversity at the bottom of the Great Lakes**Wahl, Hannah E.(1,2), **\*Miller, Andrew N.**(1), Bach, Elizabeth M.(3), Raudabaugh, Daniel B.(1,2), Luttenton, Mark R.(4), Cichewicz, Robert H.(5). 1.University of Illinois, Department of Plant Biology, Champaign, IL, 61801, USA; 2.University of Illinois, Illinois Natural History Survey, Champaign, IL, 61820, USA; 3.Colorado State University, Department

of Biology, Fort Collins, CO, 80523, USA; 4.Grand Valley State University, Department of Biology, Allendale, MI, 49401, USA; 5.University of Oklahoma, Department of Chemistry and Biochemistry, Norman, OK, 73019, USA. amiller7@illinois.edu

Fungi are diverse organisms found in nearly every global environment as key drivers of nutrient cycling and decomposition. To date, most fungal diversity has been documented from terrestrial habitats leaving aquatic habitats rarely explored. Even less is known about fungi inhabiting freshwater lakes, particularly the benthic zone that may serve as an untapped resource for fungal biodiversity. We employed both culture-dependent and culture-independent methods for studying the diversity of Great Lakes fungi found in the benthic zone. Initial analyses of the culture- dependent data indicates ~150 genera representing ~270 unique species. Similarly, the culture- independent analysis resulted in ~240 operational taxonomic units. However, only a fraction (~30 or 11%) of these unique isolates overlap between the two methods. This study will greatly add to our understanding of the ecology, diversity, and biogeography of deep water fungi in the Great Lakes. *Poster P40*

**298. Foliar endophytic diversity of the endangered Eastern Mountain Avens, *Geum peckii* Pursh (Rosaceae), along a habitat disturbance gradient in Digby County, Nova Scotia, Canada**

**\*Walker, Allison K.**(1), Adams, Sarah J.(2), Robicheau, Brent M.(1), LaRue, Diane(3), Browne, Robin(4). 1.Acadia University, Department of Biology, Wolfville, NS, Canada, 2.Acadia University, Department of Environmental Science, Wolfville, NS, Canada, 3.Mersey Tobeatic Research Institute, Kempt, NS, Canada, 4.K.C. Irving Environmental Science Center, Wolfville, NS, Canada. allison.walker@acadiau.ca

The Eastern Mountain Avens, *Geum peckii* Pursh (Rosaceae), is a globally rare and endangered plant found only in coastal bogs in Digby County, Nova Scotia, Canada and high elevation alpine sites in New Hampshire, United States. The Nova Scotian population is in decline due to habitat degradation. The foliar endophytic fungal community was investigated for application in the recovery of this species. Endophytes are fungi that colonize living plant tissue without showing symptoms of disease. Some endophytes produce beneficial compounds aiding in plant protection from herbivory and disease. We investigated the diversity of fungal species culturable from living leaves of wild *G. peckii* collected from 5 sites along a habitat disturbance

gradient (pristine to degraded habitats), as well as *G. peckii* plants propagated indoors from seed. In the laboratory, leaf samples were surface-sterilized and plated onto two types of nutrient agar (2% MEA and a modified Murashige and Skoog medium commonly used in native plant tissue culture propagation). Endophytes grown from leaf samples were isolated into pure culture, photographed and cryopreserved. Species-level identifications were made by ITS rDNA barcoding and phylogenetic placement as possible. Differences in diversity and foliar endophytic community composition were observed along the habitat disturbance gradient sampled, with a predominance of the fungal family Gnomoniaceae (Sordariomycetes, Ascomycota). Recovering sites showed lower endophytic diversity (15 to 17 species) than the highly degraded site (23 species) and the reference pristine site (30 species). Only one species, *Gnomoniopsis* sp. 1, was found at all five sites sampled. We recovered entirely different foliar endophytic communities from *G. peckii* plants propagated from seed. Several of the fungal species isolated in our study may represent novel species and will be characterized further. Roles of endophytes within the plant and within the habitat are being evaluated for potential applications in plant propagation and habitat restoration, to aid in the recovery of this endangered plant species in Nova Scotia.

*Contributed Talk C5.5*

**299. Expansion and diversification of the MSDIN family of cyclic peptide genes in *Amanita phalloides* and *A. bisporigera*\*Walton, Jonathan D.**(1,2), Pulman, Jane A.(1,3), Childs, Kevin L.(1,3)

1. Michigan State University, Department of Plant Biology, East Lansing, MI 48824 USA; 2.Michigan State University, Department of Energy Plant Research Laboratory, East Lansing, MI 48824 USA; 3. Michigan State University, Center for Genomics- Enabled Plant Science, East Lansing, MI 48824 USA. walton@msu.edu

The characteristic toxins of poisonous *Amanita* mushrooms, including α-amanitin and phalloidin, are ribosomally synthesized cyclic peptides encoded by the “MSDIN” gene family. Within the genus *Amanita*, this gene family has been found only in section *Phalloideae*. Ten members of the MSDIN family were previously identified in *Amanita bisporigera*. However, the full complement in any one species, and hence the genetic capacity for these fungi to make cyclic peptides, is still unknown. Genome sequences of two toxin-producing mushrooms, the “death cap” *A. phalloides* and the “destroying angel” *A. bisporigera*, were obtained. Each species has ~30 MSDIN genes,

most of which are predicted to encode unknown cyclic peptides. Only three genes (encoding α-amanitin, phallacidin, and an unknown) are common to both species, giving a total of 56 unique predicted cyclic peptide toxins between them. In *A. bisporigera*, 21 of its 31 MSDIN family members are expressed at the RNA level. In addition to the genes for the major amatoxins and phallotoxins, a gene encoding cycloamanide B, a chemically characterized immunosuppressive homodetic cyclic heptapeptide, was also present in the genome of *A. phalloides*, but genes were not present for several other cyclic peptides known to be made by *A. phalloides*, including cycloamanides A, C, and D, and antamanide. Ten MSDIN family members reported earlier from another specimen of *A. bisporigera* were not found in the current genome assembly. These discrepancies probably represent natural variation among the members of the poorly defined species complex known as *A. bisporigera*. The MSDIN gene family has expanded and diverged rapidly since it first appeared in *Amanita* section *Phalloideae*. *A. bisporigera* and *A. phalloides* are predicted to have the capacity to make many unknown cyclic peptides of 6 to 10 amino acids. *Contributed Talk C14.4*

**300. Genome-wide survey of gut fungi (Harpellales) reveals the first horizontally transferred ubiquitin gene from a mosquito host \*Wang, Yan**(1,2), White, Merlin M.(3), Kvist, Sebastian(1,2), Moncalvo, Jean-Marc(1,2) 1.University of Toronto, Department of Ecology and Evolutionary Biology, Toronto, M5S 3B2, Canada; 2.Royal Ontario Museum, Department of Natural History, Toronto, M5S 2C6, Canada; 3.Boise State University, Department of Biological Sciences, Boise, 83725-1515, USA. Yanxw.wang@mail.utoronto.ca

Ubiquitin and ubiquitin-like proteins are universally involved in protein degradation and regulation of immune response in eukaryotic organisms. Harpellales, an early-diverging fungal lineage, is associated with the digestive tracts of its aquatic arthropod hosts. Concurrent with the production and annotation of the first four Harpellales genomes, we discovered that *Zancudomyces culisetae*, one of the most widely distributed Harpellales species, encodes an insect-like polyubiquitin chain. Phylogenetic analyses inferred that this polyubiquitin variant has a mosquito origin and this horizontal gene transfer event was further supported by comparison of amino acid composition, the fungal nature of adjacent upstream and downstream genes, and the animal-like secondary structure of the *Z. culisetae* protein. The single-copy polyubiquitin gene from *Z. culisetae* has lower GC ratio compared to homologs of insect species, which implies homogenization of the gene

since its putatively ancient transfer. The acquired polyubiquitin gene may have served to improve important functions within *Z. culisetae*, by perhaps exploiting the insect hosts’ ubiquitin-proteasome systems in the gut environment. Preliminary comparisons among the first four Harpellales genomes highlight the reduced genome size of *Z. culisetae*, which corroborates its distinguishable symbiotic lifestyle. This is the first record of a horizontally transferred ubiquitin gene from disease-bearing insects to their gut-dwelling fungal endobiont and should invite further exploration in an evolutionary context. *Contributed Talk C14.3*

**301. Evolution of virulence of a fungal pathogen in a multihost system \*Watson, Monica**University of Minnesota, Department of Ecology, Evolution, and Behavior, Minneapolis, 55455, United States. Watso541@umn.edu

Fundamental models interactions have most often focused on the dynamics of one host and one pathogen. While such deterministic methods of inquiry have led to significant advances in medicine and epidemiology, more complex combinations of host-parasite interactions are commonly found in natural systems and thus merit our attention. Despite the growing realization that many disease dynamics involve complex multiparasite and multihost interactions the impact of symbionts interactions with multiple hosts on disease transmission and the evolution of virulence is little explored. This project addresses the dynamics of multihost systems in which the fungal symbiont presents different symbiotic traits in two phylogenetically disparate host species. The system I am using is fungal pathogen, *Fusarium verticillioides*, which infects both an insect species, *Spodoptera frugiperda* and a plant species, *Zea mays*. I intend to characterize the variability of virulence of fungal isolates, experimentally evolve the fungal pathogen using a serial passaging technique in both host species, and quantify the changes in virulence over the course of the experiment. I hypothesize that a tradeoff between virulence in one host species limits the ability of the symbiont to induce disease in both hosts. If so, successive steps in the passaging experiment will increase virulence in one host while decreasing virulence in the alternate host species. *Poster P109*

**302. Effect of manganese limitation on decay capacity of saprotrophic fungi \*Whalen, Emily D.,** Frey, Serita D.

of host-pathogen

University of New Hampshire, Department of Natural Resources and the Environment, Durham, NH, 03824, USA. edw1002@wildcats.unh.edu

Long-term atmospheric nitrogen deposition has been shown to reduce leaf litter and lignin decomposition in northern forest soils. A concomitant loss of soil and litter manganese following nitrogen deposition may explain this trend. However, the manganese loss mechanism has not been explored in depth. Manganese is a cofactor of critical lignin-decay enzymes produced by saprotrophic fungi, and its availability may influence the rate at which fungi decompose litter. This study evaluated the interacting influence of manganese and nitrogen availability on fungal leaf litter decay. Oak litter, inoculated with one of three basidiomycete fungi, was incubated in the lab on culture media amended with manganese. Litter mass loss and ligninolytic enzyme activities were quantified after 7 and 14 weeks of litter decay. Preliminary results suggest that fungal responses to manganese are species and decay stage specific. Manganese amendments (mimicking soil Mn concentrations) enhanced decomposition at 14 weeks in *Panellus stipticus (P*=0.03), but had no effect on decay by *Irpex lacteus* or *Rhodocollybia butyracea*. Leaf litter chemistry, rather than soil-level manganese amendments, influenced decomposition in *I. lacteus* and phenol oxidase activity in all species. In *I. lacteus,* decomposition was suppressed under N enrichment (*P*=0.02), and there was a trend for enhanced decomposition under higher total Mn concentrations (*P*=0.08). Phenol oxidase activity was suppressed in N-amended litter for *I. lacteus, R. butyracea* and *P. stipticus*, corresponding with lower manganese concentrations in N-amended litter. Lower Mn availability in N-amended litter may partially explain reduced decomposition and phenol oxidase activity in N-enriched environments. *Poster P44*

**303. Arbuscular mycorrhizal fungal diversity associated with coast redwood along a strong precipitation gradient \*Willing, Claire**(1), Bruns, Thomas D(1,2), Coleman- Derr, Devin(2, 3), Dawson, Todd E(1, 4) 1.Department of Environmental Science, Policy, and Management, University of California, Berkeley, Berkeley, CA 94720, USA; 2.Department of Plant and Microbial Biology, University of California, Berkeley, Berkeley, CA 94720, USA; 3.Plant Gene Expression Center, USDA-ARS, Albany, CA 94710; 4.Department of Integrative Biology, University of California, Berkeley, Berkeley, CA 94720, USA. cwilling@berkeley.edu

The California coast redwood (*Sequoia sempervirens*) is an iconic species that boasts the

second highest standing biomass on earth and fixes and sequesters 3-5 times more carbon per unit area than the Amazon rainforest. Early work showed that coast redwood form symbiotic associations with arbuscular-mycorrhizal fungi (AMF), yet we know little about the identity of these symbionts or the role they play in coast redwood physiology. Furthermore, with coastal climates changing rapidly, enhancing our understanding of AMF in redwood functional ecology will be essential in determining the role these fungi play in physiological response to drought and the ability of these forests to sequester carbon. In this project I have (1) adapted molecular techniques to sequence the AMF via Illumina Miseq, (2) analyzed AMF community composition of coast redwood in both the soil and roots of coast redwood along a precipitation gradient, and (3) compared AMF colonization of roots both seasonally and between years. These findings provide insight as to how AMF communities function in an evergreen-dominate forest using next-generation sequencing techniques.

*Poster P30*

**304. Ecology and evolution of fungi in fermented foods \*Wolfe, Benjamin\***Tufts University, Department of Biology, Medford, MA, 02155 USA. benjamin.wolfe@tufts.edu

Fermented foods, such as cheese, sauerkraut, and kombucha, provide simplified and reproducible human- constructed microbial ecosystems to identify the ecological and evolutionary processes that generate microbiome diversity. Ongoing work in my lab is identifying the key roles that fungi play in driving diversity of fermented foods. For example, in the production of surface-ripened cheeses, fungi from cheese making environments (*Candida* spp., *Debaryomyces* spp.), industrial starter cultures (*Galactomyces geotrichum*, *Penicillium camemberti*, *Fusarium domesticum*), and the built environment (*Aspergillus* spp., *Penicillium* spp., *Scopulariopsis* spp., *Chrysosporium* spp., *Sporendonema* spp.) colonize cheese and interact with neighboring bacterial

species.

From an increasing number of high-throughput sequencing surveys, broad patterns of eukaryotic and prokaryotic microbial community diversity are beginning to emerge. However, our understanding of processes driving these patterns of diversity is still limited due to the complexities of experimentally



manipulating most microbial communities.



Bacteria are more responsive to the presence



of fungi than fungi are to bacteria, suggesting that biotic interactions with fungi can be major drivers of community assembly. Using a combination of *in vitro* community reconstructions, RNA-seq, and comparative genomics, we are identifying the



molecular mechanisms by which fungi structure cheese rind bacterial communities. Compositional overlap with other microbial communities and conserved molecular mechanisms driving species interactions will allow us to translate our findings from cheese rinds to less tractable microbial



communities.

*Symposium S4.1*

**305. Studies on the fungal biodiversity from the indoor environment \*Woudenberg, Joyce H.C.**, Samson, Robert A. CBS-KNAW Fungal Biodiversity Centre, Applied and Industrial Mycology, Utrecht, 3584 CT, The Netherlands. j.woudenberg@cbs.knaw.nl

In the indoor environment many anamorphic Ascomycetes can be found. *Alternaria* is one genus that is often detected in the indoor (and outdoor) environment. A population genetic study on indoor *Alternaria* isolates from the USA showed that *A. alternata* is the most prevalent species found indoor. However, no specific indoor population could be detected in the *A. alternata* isolates. Population assignment analyses suggested that indoor *A. alternata* isolates, although extremely diverse, have a continental distribution and high levels of gene flow over the continent. The genus *Ulocladium,* recently synonymized under *Alternaria*, is also often found in the indoor environment. The typical *Ulocladium* morphology is found in three sections in the genus *Alternaria*. A phylogenetic study on indoor *Ulocladium* isolates shows that isolates are evenly distributed in section *Ulocladium* and section *Ulocladioides*. However, the molecular identification of species in section *Ulocladium* is hampered, since individual gene trees from isolates in this section are incongruent. Isolates from section *Pseudoulocladium* do not frequently occur, but there seems to be a geographical preference, which acquires more study. A third genus often found indoors is *Scopulariopsis*. Recent phylogenetic studies in this genus, and its related sexual genus *Microascus,* made it possible to molecularly identify the isolates from the indoor environment. In *Scopulariopsis* two species are commonly found indoors, *S. brevicaulis* and *S. candida*. In *Microascus* seven indoor species were identified, of which *M. paisii* (former *S. brumptii*) is most common, and one will be newly described. A phylogenetic study on the genus *Cephalotrichum*, identified six indoor species in this anamorphic genus. Two of these will be newly described. The most commonly found indoor species in this genus is *C. heliciforme. Contributed Talk C14.1*

**306. *Neurospora crassa* mRNA reveals secrets of plant cell wall deconstruction by filamentous fungi \*Wu, Vincent W.**(1), Kowbel, David(1), Xiong, Yi(1,2), Lipzen, Anna(2), Singan, Vasanth(2), Gregoriev, Igor(1,2), Glass, N. Louise(1,2)

Conversion of lignocellulosic plant biomass to biofuels holds great potential for alleviating humanity’s reliance on fossil fuels. A major goal in this area of research is to engineer strains of fungi that can produce high quantities of hydrolytic enzymes for deconstruction of plant biomass. To better engineer fungi, an understanding of how filamentous fungi respond to and degrade this compositionally diverse material is required. Using Neurospora crassa as a model, our lab has begun to characterize the transcriptional response of *Neurospora crassa* to different carbon, nitrogen, phosphate and sulfur sources. This project focuses on collecting mRNA transcripts from N. crassa grown on a wide variety of specific plant cell wall components from mono and disaccharides to complex polysaccharide components, such as cellulose, hemicellulose and pectin. By comparative analyses between transcriptomes, we have identified several new transcription factors responsible for the positive regulation of unique subsets of plant cell wall degrading enzymes. Additionally we have discovered a number of sugar transporters we think are crucial to *N. crassa*’s ability to detect and deploy proteins for plant cell wall deconstruction. We hope to further mine this data for additional information for insight into how these fungi break down the plant cell wall. *Contributed Talk C20.4*

**307. Diversity and persistence of genomic variants of the yeast *Saccharomyces paradoxus* in a natural woodland population \*Xia, Wenjing**, Kohn, Linda M., Anderson, James B. Unversity of Toronto Mississauga, Department of Cell and Systems Biology, Mississauga, L5L 1C6, Ontario, Canada. w.xia@mail.utoronto.ca

Genetic diversity in experimental, domesticated and wild populations of the closely related yeasts, *Saccharomyces cerevisiae* and *S. paradoxus* has been well described at the global scale. Little is known, however, about (a) population structure in the field at the local scale and (b) how such structure may change over time. We investigated the population genomics and phenotypes of a local population to address two main questions. First, is there genomic variation in a *S. paradoxus* population at a spatial scale spanning centimeters (microsites) to

1.University of California, Plant and Microbial Biology, Berkeley, CA, 94720-3102, USA; 2.Joint Genome Institute, Walnut Creek, CA, 94598.

 

vwu104@berkeley.edu



tens of meters? Second, does the distribution of genomic variants persist over time? We recovered 4 additional fermentative yeast species but no *S. cerevisiae*. Our sample consisted of 42 *S. paradoxus* strains from 2014 and 43 strains from 2015 collected from the same 72 microsites around four host trees (*Quercus rubra* and *Q. alba*) within 1km2 in a mixed hardwood forest in southern Ontario. The six additional *S. paradoxus* strains recovered from 36 sites around 2 adjacent maple and 2 beech trees in 2015 are also included in the sample. Whole-genome Illumina sequencing and genomic SNP analysis differentiated five groups within the sampled area. The signal of genotype persistence in microsites from 2014 to 2015 was highly significant. Isolates from the same tree were more related than strains from different trees, with limited evidence of dispersal between trees. In growth assays, measurement of lag phase and maximal growth rate revealed little variation among the *S. paradoxus* strains. One genotype, however, had a significantly longer lag phase than the other strains. Our results indicate that genomically differentiated groups co-exist at fine spatial scale and that population structure persists in soil over time in these wild yeasts. *Contributed Talk C14.7*

**308. *Penicillium* species occurring in bat hibernacula from New Brunswick, Canada \*Yilmaz, Neriman**(1), Visagie, Cobus M.(1,2), Vanderwolf, Karen J.(3, 4), Malloch, David(3), McAlpine, Donald F.(3), Seifert, Keith A.(1,2) 1.Biodiversity (Mycology), Ottawa Research and Development Centre, Agriculture & Agri-Food Canada, 960 Carling Ave., Ottawa, Ontario, K1A 0C6, Canada; 2.University of Ottawa, Dept of Biology, Ottawa, ON, K1N6N5, Canada; 3.New Brunswick Museum, 277 Douglas Ave, Saint John E2K 1E5, NB, Canada; 4.Canadian Wildlife Federation, 350 Promenade Michael Cowpland Drive, Kanata K2M 2G4, ON, Canada. nerimanyilmaz82@gmail.com

The study of fungi associated with bats and their habitats has become important after the spread of White-nose syndrome (WNS) caused by *Pseudogymnoascus destructans* (*Pd*), resulted in an ongoing rapid decline of bat populations in North America.. Much effort has focused on populations of *Pd* from positive caves. Characterization of fungal populations and identification of other fungal species may reveal possible antagonists to *Pd*. Surveys from caves and mines commonly find *Penicillium* as one of the most abundant genera. In this survey, various samples were collected from six *Pd*-positive bat hibernacula in New Brunswick, Canada and one *Pd*- negative bat hibernaculum in Quebec, Canada. Fungal strains were isolated from arthropods, bats, rodents (i.e. *Peromyscus maniculatus*) and their dung, and

cavewalls. Hundreds of fungal species were obtained, of which *Penicillium* represented a major component. These strains were grouped by colony characters on MEA. From each morphogroup, the β-tubulin gene was sequenced for representatives and used for identifications. Thirteen *Penicillium* species were identified, one of them undescribed. The new species is described using macro- and micromorphological characters, and multigene phylogenies, including ITS, β-tubulin, calmodulin and *RPB2.* The new species belong to *Penicillium* subgenus *Penicillium* section *Fasciculata*, a group that is psychrotolerant and grows well at low water activities. The new species resembles *P. discolor* most closely. However, *P. discolor* has globose to subglobose, rough walled conidia in contrast to the ellipsoidal, smooth walled conidia of the new species*.*

*Poster P98*

**309. A defined enzyme cocktail from the anaerobic fungus *Orpinomyces* sp. strain C1A effectively releases sugars from pretreated corn stover and switchgrass**

**\*Youssef, Noha H.**, Morrison, Jessica M., Elshahed, Mostafa S. Department of Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK, 74078 USA. Noha@okstate.edu

The anaerobic fungus *Orpinomyces* strain C1A is capable of growth on various types of lignocellulosic substrates, and harbors an impressive reservoir of carbohydrate active enzymes (CAZymes). Using a minimum enzyme cocktail strategy, we constituted a four-component lignocellulolytic cocktail derived from highly transcribed C1A, and evaluated its efficacy against pretreated corn stover and switchgrass. Hydrolysis yields ranged between 65- 77.4%, depending on the lignocellulosic substrate and pretreatment applied. Addition of a highly expressed anaerobic fungal swollenin improved hydrolysis yields by up to 7%. Compared to the commercial cocktail CTec2, these anaerobic fungal cocktails provided comparable or slightly lower hydrolysis yields. Further, the differences in efficacy between commercial and anaerobic cocktails were often only realized after extended (168 hr) incubations. Under certain conditions, the hydrolysis yields of the anaerobic fungal cocktail was slightly superior to that realized by CTec2. We attribute the observed high hydrolysis yields to the high specific activity and affinity of the individual enzymes of the cocktail, as well as the high level of synergy and multi- functionality observed in multiple components. Collectively, this effort provides a novel platform for constructing highly effective enzymes for biofuel production and represents the first lignocellulolytic

enzyme cocktail created from anaerobic fungal enzymes. *Poster P126*

**310. Anaerobic fungi as a novel platform for sugar extraction and biofuel production from lignocellulosic biomass \*Youssef, N. H.**(1), Ranganathan, A.(1), Smith, O. P.(1), Struchtemeyer, C. G.(2), Atiyeh, H. K.(2), Elshahed, Mostafa(1)

1.Department of Microbiology and Molecular Genetics; 2.Department of Biosystems and Agricultural Engineering, Oklahoma State University, Stillwater, OK 74078, USA. noha@okstate.edu

Lignocellulosic biomass is a vast and underutilized resource for the production of sugars and biofuels. However, the structural complexity of lignocellulosic biomass and the need for multiple pretreatment and enzymatic steps for sugar release renders this process economically challenging. Here, we report a novel approach for direct, single container, exogenous enzyme-free conversion of lignocellulolytic biomass to sugars and biofuels using the anaerobic fungal isolate *Orpinomyces* sp. strain C1A. This approach utilizes simple physiological manipulations for timely inhibition and uncoupling of saccharolytic and fermentative capabilities of strain C1A, leading to the accumulation of sugar monomers (glucose and xylose) in the culture medium. The produced sugars, in addition to fungal hyphal lysate, are subsequently converted by *Escherichia Coli* strain KO11 to ethanol. Using this approach, we successfully recovered 17.0% (w/w) of alkali-pretreated corn stover (20.0% of its glucan and xylan content) as sugar monomers in the culture media. More importantly, 14.1% of pretreated corn stover (17.1% of glucan and xylan content) was recovered as ethanol after the addition of the ethanologenic strain KO11. The high ethanol yield obtained is due to its accumulation as a minor fermentation end product by strain C1A during its initial growth phase, the complete conversion of sugars to ethanol by strain KO11, and the possible conversion of unspecified substrates in the hyphal lysate of strain C1A to ethanol by strain KO11. The potential cost savings, input and output versatility, and operational consolidation render this anaerobic fungal- based platform a promising alternative for low cost biofuel production from lignocellulosic biomass. *Poster P125*

**311. Endophytes and pathogens in endangered Hawaiian endemics: Plant conservation from a microbial perspective \*Zahn, Geoffrey**, Amend, Anthony

University of Hawaii at Manoa, Botany Departmen, Honolulu, HI, 96822, USA. zahn.geoff@gmail.com

Hawaiian ecosystems are highly susceptible to invading organisms, including microbes. Two critically endangered plants endemic to O'ahu, *Phyllostegia kaalaensis* and *P. mollis*, are currently being devastated by the powdery mildew pathogen, Neoerysiphe galeopsidis. Despite the fact that fungal endophytes form an integral component of plant fitness, recent conservation efforts have focused on regular high-dose applications of a mixture of fungicides, which prevent mortality in a greenhouse setting but are unsustainable for re-introduction efforts. Greenhouse-raised individuals show limited to no survivorship when out-planted, and we hypothesize that this is, in part, due to the lack of diverse endophytic communities in the plants when they are moved into wild habitats. We are working with conservation agencies to develop low-tech methods for inoculating plants with beneficial fungal endophyte communities to increase survivorship in outplanted individuals. Preliminary results from two separate trials both show significant reductions in pathogen loads in plants inoculated with a simple slurry from healthy wild relatives, but which taxa may be responsible for this effect has yet to be determined. DNA extractions from before, during, and after fungal inoculations will be used to track transplantation successA wide variety of conservation goals may benefit from a microbial perspective.

*Contributed Talk C6.1*

**312. Artificial N-glycosylation motif engineering for heterologous protein production in *Aspergillus niger*\*Zhang, Jinxiang**(1,3), Paša-Tolić, Ljiljana(5), Zink, Erika(5), Jacobs, Jon(5), Simmons, Blake(1,4), Baker, Scott(1,5), Gladden John(1,3), Magnuson, Jon(1,2) 1.Joint BioEnergy Institute, Emeryville, CA; 2.Pacific Northwest National Laboratory, Richland, W A; 3.Sandia National Laboratory, Livermore, CA; 4.Lawrence Berkeley National Laboratory, Berkeley, CA; 5.Environmental Molecular Sciences Laboratory, Pacific Northwest National Laboratory, Richland, WA. Jon.Magnuson@pnnl.gov

*Aspergillus niger* is a genetically tractable model organism for scientific discovery and a platform organism used in industry for the production of enzymes. Expression of secreted native enzymes at tens of grams per liter have been discussed by those in industry, but expression of heterologous genes in fungi is still challenging and poorly understood, and hence it is an interesting area of fundamental scientific research. Important aspects of this research are the effects of glycosylation on trafficking through organelles, secretion of the enzymes, and enzymatic activity and stability. Hence, we are focusing on the effects of glycosylation modification on heterologous

expression. A thermostable non-glycosylated enzyme is being engineered by adding a series of potential single glycosylation motifs. Based on the 3D structure of heterologous protein, we generated seven individual artificial N-glycosylation motifs on the surface of the heterologous protein Genes with single glycosylation site variations have been expressed in *A. niger*. The results indicated that only one out of seven was glycosylated. Also, we categorized the glycosylation patterns with respect to our measurements of enzyme activity and stability, and total expression level. Comparative transcriptomic analysis was used to understand the cellular responses to expression of the heterologous protein with glycosylation variations. *Poster P121*

**\*Zhang, Rui**(1, 2), Shi, Xiaofei(2), Liu, Peigui(2), Mueller, Gregory M.(3) 1. Northwestern University, Program in Plant Biology and Conservation, Evanston, Illinois 60201 and Chicago Botanic Garden, Glencoe, Illinois 60022, USA; 2. Chinese Academy of Sciences, Key Laboratory of Biodiversity and Biogeography, Kunming Institute of Botany, Heilong Tan, Kunming 650201, Yunnan province, China; 3. Chicago Botanic Garden, Plant Conservation Science, Glencoe, Illinois 60022, USA. xiaorui0203@gmail.com

Evolutionary history of Ectomycorrhizal (EM) fungi in genus level is largely unknown due to lack of fossil records. The only known EM fungal fossil is from Eocene *Pinus* root tips identified as *Suillus* or *Rhizopogon*. Previous studies assigned this EM fossil as the common ancestor of *Suillus* and *Rhizopogon*. But another scenario exists that basal *Suillus* species associate with *Larix* then switch host to *Pinus*. The fossil could represent a recently evolved lineage in *Suillus*. We aim to identify ancestral hosts of *Suillus* in the contexts of the two calibration scenarios and compare with the evolutionary history of Pinaceae. We built the first multigene (28S, TEF1, RPB1, RPB2) phylogeny of *Suillus* including 63 species, of which 23 were new from East Asia. Taxonomic and geographic coverage was checked in a comprehensive ITS phylogenetic tree. Host identifications were supported by environmental samples and mycological references. The ancestor of *Suillus* species was reconstructed to be in association with *Larix* originating from early Eocene. During Oligocene, one *Suillus* lineage switched to *Pseudotsuga* and another one switched to *Pinus* subgenus *Strobus*, more specifically, to section *Quinquefoliae*. Another scenario of *Suillus–Pinus* fossil was less possible as the origin of *Suillus* and *Pinus* association was pushed back to early Eocene. At

which time the two sections of *Pinus* sub. *Strobus* were not divided. Our findings provide a checkpoint of fossil calibration for other fungal evolutionary studies. *Contributed Talk C15.6*

**314. Metagenomic and traditional approaches revealed high diversity of Mycobiota from two caves in China**Zhang, Zhifeng(1, 2), Liu, Fang(1), Zhou, Xin(1, 2), Liu, Xingzhong(1), Liu, Shuangjiang(3), **\*Cai, Lei**(1) 1.Institute of Microbiology, Chinese Academy of Sciences, State Key Laboratory of Mycology, Beijing, 100101, China; 2.University of Chinese Academy of Sciences, Beijing, 100049, China; 3.Institute of Microbiology, Chinese Academy of Sciences, State Key Laboratory of Microbial Resources, Beijing, 100101, China. cail@im.ac.cn

Karst caves are distinctly characterized by darkness, constantly low temperature and high humidity, and scarcity of organic matters. During the years of 2014–2015, we carried out an exploration of fungal diversity in two unnamed karst caves in Guizhou province, China. We obtained 564 fungal strains by dilution plate method, which belonged to 247 taxa in 114 genera. Among these taxa, 85.4% (211 taxa) belonged to Ascomycota; 7.3% (18 taxa) belonged to Basidiomycota; 6.9% (17 taxa) belonged to Zygomycota and 0.4% (1 taxon) belonged to Oomycota. The majority of these taxa have been previously known from other environments, mostly from plants or animals as pathogens, endophytes or mycorrhizas. While 59.3% of these taxa were discovered for the first time from karst caves, including 20 new species. Metagenomic sequencing (Illumina MiSeq) of ITS1 region was employed to infer the distribution of fungal communities. The studied caves were found to harbor high levels of fungal diversity, with 4971 fungal OTUs that span 24 classes and 6 phyla (Ascomycota 49%; Basidiomycota 22%; Chytridiomycota 3%; Glomeromycota, 1%, Zygomycota 1%, Rozellomycota 1%, and undetermined 23%). Among the 4 types of collected samples (air, rock, soil, water), water appeared to harbor most abundant OTUs, followed by soil, rock and air samples, and most of the OTUs discovered in the later 3 type of samples (94.2%, 78%, 70%) also presented in the water samples. We conclude that the karst caves encompass a high fungal diversity, including a number of previously unknown species. We hypothesize that the fungal communities in the studied caves were primarily determined by the water flow entered into the caves through leakage or other routes.

*Poster P19*